College	Student Name	Registration No.	Торіс	
Roll No.				
502	Sekhar Kundu	A01-1152-115-001-2019	Designing IgG Antibodies for Therapeutic Use – a Review	
503	Arghya Acharyya	A01-1112-115-002-2019	Is nucleotide diversity in mitochondrial gene as an early diagnostic of their	
			conservation status ?	
504	Sukriti Maity	A01-1112-115-003-2019	Evolution of Snake Venom Metalloproteinase (SVMP) in the context of Atrajin from	
			Naja atra	
509	Utsab Halder	A01-1122-115-005-2019	Observation of pollinators vitis Vitis triflorum:	
510	Shaibal Mondal	A01-1122-115-006-2019	Flower visitors observation on Hibiscus rosa-sinensis	
513	Manas Saha	A01-1152-115-008-2019	Pollinator observation on Hibiscus	
514	Sanmitra Biswas	A01-1112-115-009-2019	An observation report on the pollinators of ixora coccinea	
515	Arka Prava Mukhopadhyay	A01-1112-115-010-2019	Review on the advance floral morphology and pollination syndrome in various	
			plants	
518	Sayonil Sen	A01-1112-115-011-2019	Pollination in Holy basil (ocimum tenuiflorum	
519	Safikul Alam	A01-1141-115-012-2019	Flower visiting on Tulsi (Ocimum tenuiflorum)	
522	Priyanshu Saha	A01-1112-115-014-2019	Antigen presentation of MHC class II	
524	Mrinmoy Ghosh	A01-1112-115-016-2019	Parental Care and swimming behaviour of black Swan.	
526	Dhruba Datta	A01-1112-115-018-2019	Phylogenetic study of different snake species with respect to their geographic	
			variation by using mitochondrial gene cyt-b and finding the anomalous origin by	
			using multiple sequence alignment.	
527	Arnab Mandal	A01-1122-115-019-2019	A Brief Review on Exposing Rate of IHS (Anaphylaxis) after Vaccination at Male and	
			Female.	
528	Swapnaneel Chakraborty	A01-1112-115-020-2019	Pollinator observation on Hibiscus	
529	Titas Koley	A01-1112-115-021-2019	Annotations and Analysis of Whole Mitochondrial Genome of Snake Species of India	
530	Pratin Gayen	A01-1112-115-022-2019	Review on the advance floral morphology and pollination syndrome in various	
			plants	
531	Rishav Naha	A01-1112-115-023-2019	Experimental observation on some local dragon flies in the area of river and canal of	
			Nawab Ganj Ganga Ghat ,24PGS North.	
532	Anomitra Neogy	A01-1112-115-024-2019	A Study to find the Evolutionary Trend of Snake species present in Indian	
			subcontinent in respect of Mitochondrial Genes, Cytochrome B and COX1	
536	Shashwata Roy	A01-1112-115-026-2019	Comparison between the Cox1 and Cytb Gene Data of the Common Snake Species	
			Found in India.	

537	Subhankar Mahapatra	A01-1112-115-027-2019	nterleukin-17 role in immunity and inflammation			
540	Santu Pramanik	A01-1112-115-028-2019	Cytokine Storm in COVED-19			
541	Pijush Basak	A01-1152-115-029-2019	Flower visitors observation on Ocimum tenuiflorum			
542	Sayan Banik	A01-1112-115-030-2019	Pollination Strategy of Lantana camara			
543	Manash Mukherjee	A01-1112-115-031-2019	Review work on insect visitors and pollinators of Tabernaemontana divaricata			
			(Togor)			
545	Avijit Ghosh	A01-1112-115-033-2019	Pollinator observation on Hibiscus			
546	Ronit Das	A01-1112-115-034-2019	019 Observation of flower visiting insect on Lantana camara			
549	Debpratim Paramanik	A01-1152-115-036-2019	19 Immediate Hypersensitivity to Wheat Consumption: A Brief Review			
550	Indrajit Mondal	A01-1152-115-037-2019	Observation of a Flower Visiting Insect on Ixora coccinea			
555	Pritam Lahiri	A01-1112-115-041-2019	Flower visitors observation on Hibiscus rosa-sinensis			
557	Soumik Ray	A01-1112-115-043-2019	Study of geotaxix behaviour in earthworm			
558	Sibajit Sarkar	A01-1112-115-044-2019	Behavioural observation of animals			
559	Ashikesh Mondal	A01-1112-115-045-2019	Aggnesive behaviour inTephritidae fruit fly			
1566	Manojit Nandi	A01-1112-115-021-2018	Pollination Observation on Moringa oleifera			

Designing IgG Antibodies for Therapeutic Use – a Review

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Introduction :- Monoclonal antibodies are became the important therapeutic action for many diseases and expected to play a greater role in the treatment of diseases , so many efforts have been made in devoloping monoclonal immunoglobulin IgG antibodies for use in clinical practice. Recent researchers suggests that fc region of igG could also represent an exciting approach toward naive therapeutic strategies. The high specificity of monoclonal antibodies in association with their multi-functional properties, high effectivity, long half-life permitting low dosing and prolonged pharamcological effects, and general lack of off-target toxicity makes them ideal therapeutics 28 recombinant monoclonal antibodies are currently approved by the FDA.

A wide variety of monoclonal therapeutic antibodies currently licenced with hundreds more in pre clinical and clinical development .These therapeutic antibodies can be administered for a wide array of diseases ; although majority of them are used for cancer , autoimmune disorder, transplantation.

Pharmacological differentiation of therapeutic antibodies can be potentially achieved by optimizing several areas: the epitope which the antibody binds to, the affinity to the target, the pharmacokinetics, the effector function of the constant region (Fc region) and the safety profile of the antibody, such as immunogenicity. This review covers the fundamental methods that are required to modify IgG in developing therapeutic antibodies.

OBJECTIVE :-i.IgG antibodies can be engineered to have improved binding properties , effector functions and pharmacological properties.

ii. The objective of using monoclonal IgG antibodies is to stimulate the patient's immune system to fight against unwanted pathogens like virus , bacteria and other cells , for example Use monoclonal IgG antibodies involves indirect transfer of antibodies for pre/post exposure prophylaxis or for treatment.

III. one of most important objective is to modify the physical or chemical properties for potent effect. These are -

Modifying the fc part of IgG monoclonal antibodies involves various kinds of processes like fc glycosylation , modifying residues of one subclass with another. fc region is the most important part in developing the therapeutic antibodies with specific targeting activities therefore reducing both potential harmful side effects and dosage.

Modifying the binding property of therapeutic IgG this involves several processes including Random mutagenesis, Targeted mutagenesis, etc.

Altering the specificity involves_ several immunological techniques such as to reduce the cross reactivity to other antigens, binding two different anbodies by a single binding site etc.

Improving the pharmaceutical properties of monoclonal antibodies_____ this involves optimizing the hydrophobic core of antibodies, modifying VL/VH domain residues, avoiding deamidation and isomerization and that helps to retain biological activity during storage.

DISCUSSION:- monoclonal antibodies plays a very important role in finding other alternatives to regular drugs .These are produced by B cells for targeting specific antigens . Discovery of Hybridoma technology by Kohler and Milstein has made it possible to produce a large number of pure IgG antibodies artificially. Monoclonal IgG antibodies are developed to complement the use of drugs, vaccines. These antibodies have a specific structure that provides them a specific kind of function. So to develop a therapeutic antibody the desired function must be considered and also merge that into the design and examine that for maximum potency and safety. Currently around the globe the monoclonal therapeutic antibodies have sufficient supply chain with a current market price of \$115.2 billion in 2018 and it is still increasing . irrespective of that massive growth rate new companies shows only a small interest to buy the shares .extensive researches suggests that IgA or anti-FcaRI can represent an exciting path toward new therapeutic strategies. Fcy receptor family include six variants(FcyRI, FcyRIIA, FcyRIIB, FcyRIIC, FcyRIIIA, FcyRIIIB) which differ in their cellular distribution, binding affinity to Fc, and the resulting biological function. Therefore, during developing any tumor specific therapeutic antibodies, including single-targeted antibodies, bi-specific antibodies (BsAbs), and antibody-drug conjugates (ADCs), many things, such as drug target specificity, cellular distribution of the targets, the internal environments of tumor types, as well as the particular mechanism of function, must be taken into consideration. The quality of igG antibody should be maintain during storage and administration. Moreover recent studies also shows that aggregation of igG monoclonal antibodies is one of most dangerous risk factor that compromises safety and efficacy. During the process of igG manufacturing, 0.22-µm membrane filters are mainly used to remove the aggregates. The recent researchers shows that removal technique with non native igG antibody adsorbent that helps in long storage process. It also facilitate the quality of immunogenicity igG preparations. Also there is a huge prospect of these therapeutic monoclonal antibody use. It is well known that high amount of igG antibodies isolated from human plasma imparts anti inflammatory effect in a variety of immunological prospects. Increasing number of immunoefficient monoclonal antibodies and IgG Fc fusion proteins are either useable or in early-to-late phase clinical trials for the cure of chronic inflammatory conditions, like autoimmune diseases and organ transplant rejection. The optimized specificity of monoclonal antibodies, in association with their multifunctional properties, high potency, long life span(permitting intermittent dosing and prolonged pharamcological effects), and general reduction of off-target toxicity makes them the ideal therapeutics. Also monoclonal igG antibodies used in immune suppression which is more use useful in prolonged drug therapy. Using therapeutic IgG antibodies also helps in activating othe immune mediated molecules like cytokines, infusion complex etc.

CONCLUSION- presence of natural anibody in an healthy individual is necessary for maintaining several functions like fight with pathogens also maintaining the homeostasis of cell ,and studies showed that normal antibodies can be changed in an individual's body such naïve antibodies are target for having recombinant function. Despite the fact that only few therapeutic igG are used in pathogen specific diseases, it has been worth mentioning that separate improvement of variable region property are effective in reducing pathological damage . Due to major developments in past decades first in class strategy for finding promising targets is so competitive in nature. An raising number of immunoefficient monoclonal antibodies (mAbs) and IgG Fc modified proteins are either approved or in early-to-late stage clinical trials for the treatment of different conditions like major inflammatory conditions, autoimmune diseases and rejection in organ transplant. During developing and testing therapeutic antibodies the devolping authority needs to consider the subclass properties, especially testing against an infectious disease. Although this field has a promising future but still ongoing researches in this field is slow compared to other drug dvoloping researches . there are so much variety of potential setting in developing therapeutic igG monoclonal antibodies, against infectious diseases, so therefore the pros and cons of applying this method should be carefully assessed.

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Is nucleotide diversity in mitochondrial gene as an early diagnostic of their conservation status ?

A project report

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YEAR: 2022

Introduction: Habitat destruction, climate change, hunting, excessive usage of pesticides and the transition of many rural areas to suburban and urban areas, are the main reason behind different type of conservation status like critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT), least concern (LC).

According to reptile database, total 337 species are reported from India. After separation all the species along with their conservation status, 71 species were enlisted, among them 2 are endangered, 2 are vulnerable, 5 are near threatened and 62 are least concern. For designing phylogenetic tree, we use mitochondrial gene sequences. Because,

• Mitochondrial DNA offers a particularly rich source of markers for the study of closely related taxa because of the very low rate of recombination (Piganeau et al., 2004).

• Maternal inheritance, simple genetic structure, reduced effective population size (Ne), and relatively rapid rates of evolution (Avise et al., 1983).

Methodology: Methodology will describe step by step with few bullets -->

- 1. At first I enlisted total 337 species from "Reptile Database".
- 2. After that according to the IUCN Database, I separate all the species along with their conservation status. And finally I enlisted total 71 species, among them 2 are endangered, 2 are vulnerable, 5 are near threatened and 62 are least concern.
- 3. Then from NCBI Nucleotide Database, I collected total CYT-b and COX1 gene sequence along with their accession Id. of 71 species.
- 4. After that I runed multiple sequence alignment via MEGA for three times. First time I runed total 68 species along with their CYT-b sequence. Second time & third time I runed total 15 species. And those 15 species had both CYT-b & COX1 gene sequence.
 - 5. Then I analysed all three phylogenetic tree and at the end I capable to take a simple decision which have been justified by many scientific journals.
 - Which will be describe later in result & discussion section.

Objective: We were trying to see the correlation between phylogenetic position of Indian snakes along with their conservation status.

List of 15 Snake species along with their Conservation Status :

Name of the Snake	Family	Conservation status
Ophiophagus hannah	Elapidae	VU
Python bivittatus	Pythonidae	VU
Python molurus	Pythonidae	NT
Coelognathus flavolineatus	Colubridae	LC
Coelognathus radiatus	Colubridae	LC
Euprepiophis mandarinus	Colubridae	LC
Gonyosoma oxycephalum	Colubridae	LC
Gonyosoma prasinum	Colubridae	LC
Trimeresurus stejnegeri	Viperidae	LC
Lycodon zawi	Colubridae	LC
Naja kaouthia	Elapidae	LC
Protobothrops jerdonii	Viperidae	LC
Protobothrops mucrosquamatus	Viperidae	LC
Boiga ochracea	Colubridae	LC
Bungarus fasciatus	Elapidae	LC

Result:



Fig1: 68 CYT-b gene sequences alignment based on their conservation status







0.02



Discussion : It's very much clear that, phylogenetic position of different snake species isn't depend upon their conservation status. According to figure1, it depicts that position of all endangered, vulnerable, near to threatened & least concern isn't in a synchronous way. Previous statement also justified by figure 2 & figure 3. Now 2 question arises in mind, i. Why all snake of Pythonidae family facing a critical condition & ii. Why only one Elapidae snake King Cobra facing trouble and characterised as vulnerable species ?

• Reason behind decreasing population trends of Pythonidae family :

i. **Nidoviruses :** The order Nidovirales is a large group of diverse enveloped positivestrand RNA viruses (Gorbalenya A. E. et al., 2006).

Nidoviruses are known to infect a range of vertebrate and invertebrate hosts, several of which have caused serious diseases in both humans and animals. In humans, prominent nidoviruses belong to the family Coronaviridae and infections can result in a wide range of presentations from asymptomatic infections to significant morbidity and mortality associated with severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS-CoV) (Tyrrell D. A. et al., 1965 & Pringle C. et al., 1996). Since their discovery in 2014, reptile nidoviruses (also known as serpentoviruses) have emerged as significant pathogens worldwide. They are known for causing severe and often fatal respiratory disease in various captive snake species, especially pythons. Related viruses have been detected in other reptiles with and without respiratory disease, including captive and wild populations of lizards, and wild populations of freshwater turtles. There are many opportunities to better understand the viral diversity, species susceptibility, and clinical presentation in different species in this relatively new field of research. In captive snake collections, reptile nidoviruses can spread quickly and be associated with high morbidity and mortality, yet the potential disease risk to wild reptile populations remains largely unknown, despite reptile species declining on a global scale. Experimental studies or investigations of disease outbreaks in wild reptile populations are scarce, leaving the available literature limited mostly to exploring findings of naturally infected animals in captivity. Further studies into the pathogenesis of different reptile nidoviruses in a variety of reptile species is required to explore the complexity of disease and routes of transmission. This review focuses on the biology of these viruses, hosts and geographic distribution, clinical signs and pathology, laboratory diagnosis and management of reptile nidovirus infections to better understand nidovirus infections in reptiles. (Parrish, K. et al., 2021)

		Host	Ensease	Country	dowatic	Population	Reference
 _	NC 027199	Bos taurus (Berine nidovirus outgroup)	Y	United States of America	Terrestrial	Captive	(Tokarz et al., 2015)
	MG600028	Pope's keelback (H. popel	NE	Chima	Semi-Aquatic	Wild	(Shi et al., 2018)
100	MN161572	Honduran milk snake H., t. kondurensis	N	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
	KX883638	Snake-associated nematode	NE	China	Terrestrial	Wild	(Shi et al., 2016)
98 100 r	MN161561	Emerald tree hos iC coninus	N	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
	MN161562	Enerald tree has (C canings	N	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
100	MN161566	Reticulated python (M. reticulates	N	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
100	KX883637	Snake-associated nematode	NE	China	Terrestrial	Wild	(Shi et al., 2016)
85	MG600031	Mandorin vat snake (E. mandarings	NE	China	Terrestrial	Wild	(Shi et al., 2018)
100 June	MT997159	Veiled chameleon (C. calentratus	Y	United States of America	Terrestrial	Cantive	(Hoon-Haples et al., 2029)
100 55	MT997160	Veiled chameleon (C. caleptratus)	Y	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2020)
100	MG600030	 Red banded snake (L. rufozonatus) 	NE	China	Terrestrial	Wild	(Shi et al., 2018)
52	MG600029	Chinese water make IM, chinemis	NE	China	Semi-Aquatic	Wild	(Shi et al., 2018)
~ <u>u</u>	KX184715	Shineleback lizard (T. ravosa	Y	Australia	Terrestrial	Wild	(ODca et al., 2016)
	ME685025	Reliever River snapping partie (M. georgesi	Y	Australia	Acuatic	Wild	(Zhang et al., 2018)
100	K1935003	faction methon (P. malores	Y	Germany	Terrestrial	Cantive	(Bodewes et al., 2014)
26	MN161571	Woma python (A. ramsau	Y	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
1004	MG752895	Rall author (P. certins	Y	United States of America	Terrestrial	Cantise	(Hoon-Hanks et al., 2018)
100 100 1	KI541759	Rall pythen (P.regius	Y	United States of America	Terrestrial	Contine	(Stepplein et al. 2014)
	MK722372	Green tree nythen (M. vietelis	Y	Spain	Terrestrial	Captive	(Dervas et al., 2020)
164	ME351880	Green tree outlion (M. viridis	Y	Switzerland	Terrestrial	Contise	(Dervac et al. 2017)
16	MN161563	Green tree withou (M. viridia	Y	United States of America	Terrestrial	Cantive	(Hoon-Hanks et al., 2019)
100 721	MN161560	Green tree nython (M. viridis	Y	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
[~]	MM161558	Green tree woken (ht. virith)	Y	United States of America	Terrestrial	Contine	(Hoon-Hanks et al. 2019)
-	MN161565	Ricod python (P. brownerowai	Y	United States of America	Terrestrial	Contive	(Hoon-Hanks et al. 2019)
	MN161567	Rall methow the restore	N	United States of America	Terrestrial	Contivo	(Hoon-Harles et al., 2019)
- Flow	MN161559	Green tree python (M. viridis	Y	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
99 -	MN161564	Blood arthur (P. benaverma)	Y	United States of America	Terrestrial	Captive	(Hoon-Hanks et al., 2019)
	MK182566	Green tree withou (M. virid).	Y	Germany	Terrestrial	Captive	(Blahak et al., 2020)
100	MK722373	Green tree withon (M. viridis	Y	Switzerland	Torrestrial	Contivo	(Dervas et al., 2020)
	MK722375	Ball onthon (P. repins	NE	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
100	MK722365	Given tree nython (M. viridis	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
100	MK722367	Green tree ryshon (M. virid)s	Y	Switzerland	Terrestrial	Cantise	(Dervas et al., 2020)
94	MK722364	Green tree nythen this visidis.	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
	MK722370	Angolan python (P. anchistor	Y	Switzerland	Terrestrial	Contive	(Dervas et al., 2020)
100	MK722368	Carnet instant fM. mileta	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
100	MK722371	Ball onthon (P. cerrins	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
	MK722260	Grown tree workon (M. viridis	Y	Switzerland	Terrestrial	Captive	(Demas et al., 2020)
	MK722278	Grown tree nython (M. viridis	Y	Switzerland	Terrestrial	Cantive	(Dervas et al. 2020)
50	MK722376	Green tree python iM, viridis	Y	Switzerland	Terrestrial	Contive	(Dervas et al., 2020)
60	MK722262	Cornet aution (M. milain	Y	Switzerland	Terrestrial	Cantive	(Dervas et al., 2020)
	MK722374	Ball untion (P. covins	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
96	MN1161568	Green tree withou (M. viridix	Y	United States of America	Terrestrial	Cantive	(Hoon-Hariks et al. 2019)
	MN161570	Groon tree withou (M. viewlin	Y	United States of America	Terrestrial	Contise	(Hoon-Hanks et al., 2019)
100	MN161560	Grown tree workon (M. viridis	Y	United States of America	Terrestrial	Captive	(Hoop-Hanks et al., 2019)
100	MK722280	Hong wikes M. concerd	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
100	MK722265	Green tree makes (M. virib)	Y	Switzerland	Terrestrial	Captive	(Dervas et al., 2020)
	WIN/ 22303			100000000000000	0.0000000	0.000 0.000	A NEW YORK OF THE OWNER OF THE OWNER

Fig4: Existence of Nidovirus among different species

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Left portion of figure 4 depicts that Nidovirus present not only in Phyton & Boa but also in lizard & turtle. And the right position of this picture depicts that near about all terrestrial, captive pythons are facing this problem and the end result is death.

Another reason for decreasing population trends of Pythonidae family is Inclusion Body Disease (IUB) (Rachel E. et al., 2014). Inclusion body disease (IBD) is caused by reptarenaviruses and constitutes one of the most notorious viral diseases in snakes.

According to a current research report (Simard, J. et al., 2020), A total of 292 snakes (178 boas and 114 pythons) from 40 collections in Belgium were sampled. In each snake, blood and buffy coat smears were evaluated for the presence of IBD inclusion bodies (IB) and whole blood was tested for reptarenavirus RNA by RT-PCR. Of all tested snakes, 16.5% (48/292) were positive for IBD of which all were boa constrictors (34.0%; 48/141) and 17.1% (50/292) were reptarenavirus RT-PCR positive. The presence of IB could not be demonstrated in any of the tested pythons, while 5.3% (6/114) were reptarenavirus positive. In contrast to pythons, the presence of IB in peripheral blood cells in boa constrictors is strongly correlated with reptarenavirus detection by RT-PCR (P<0.0001). Although boa constrictors often show persistent subclinical infection, long-term follow-up indicated that a considerable number (22.2%; 6/27) of IBD/reptarenavirus positive boas eventually develop IBD associated comorbidities.

• <u>Reason behind Vulnerable (VU) status of Ophiophagus hannah :</u>

According to IUCN red list, The world's largest venomous snake, the King Cobra (Ophiophagus hannah), is listed as vulnerable due to loss of habitat and over-exploitation for medicinal purposes.

1. The International Union for Conservation of Nature has listed the king cobra as vulnerable to extinction. These snakes face a variety of threats stemming from human activities. Heavy deforestation in Southeast Asia has destroyed the habitats of many king cobras, while they are also harvested in large numbers for skin, food, and medicinal purposes. They are also collected for the international pet trade. King cobras are also persecuted by humans who fear their menacing reputation.

<u>Comparison of venom composition between Elapidae & Viperidae family</u> <u>based on their conservation status :</u>

The major difference between elapid and viper venoms was the presence of 3FTx in elapid venoms The major difference between elapid and viper venoms was the presence of 3FTx in elapid and the virtual absence of 3FTx in viper venoms. Elapid venoms were also less diverse in the range venoms and the virtual absence of 3FTx in viper venoms. Elapid venoms were also less diverse in the or number of protein families, largely consisting of only PLA2 and 3FTx, although different groups range or number of protein families, largely consisting of only PLA2 and 3FTx, although different were dominated by one or the other (Figure). Elapid venoms were more variable in the amount of groups were dominated by one or the other (Figure). Elapid venoms were more variable in the different protein families compared to viper venoms.



So, from the previous slide it's very much clear that; for King Cobra the amount of neurotoxic venom that means Phospholipase A2 (PLA 2) is near about 4% & hemotoxic venom that means Snake Venom Metalloprotease (SVMP) is near about 15%. This SVMP & PLA 2 help them for hunting. 81% 3-finger Toxic (3FTx) venom also present in King Cobra, which help for showing defensive character.

Along with King Cobra, another snake species of Elapidae family like Naja naja, Naja sagittifera, Bungarus caeruleus have 22%, 28.5%, 72% PLA 2 and 77%, 75%, 20% 3FTx respectively. All three have very little amount of SVMP.

But for Daboia russelii (family Viperidae); the amount of PLA 2 is 50%, SVMP is 38 % and SVSP is 12 %. If I compare all snakes of Elapidae family based on their venom composition, the it's very much clear that King Cobra have very less amount of neurotoxic venom PLA 2 than others but the twist is King Cobra also have a decent amount of hemotoxic venom SVMP whereas another snakes of Elapidae family have very low amount of SVMP.

But still King Cobra is vulnerable and Naja naja, Naja sagittifera , Bungarus caeruleus are least concern, WHY ????



<u>Fig5</u>



Fig6: Structure of PLA2 in different snake

54	splQ2LD49/VM3TM TRIST Zinc metalloproteinase-disintegrin-like TSV-DM QS=Trimeresurus stejnegen QX=39682 PE=1 SV=1	Sequence alignment based on SVMP sequence
92	spiP83912/VM2JT PROJR Zinc metalloproteinase-disintegrin jerdonitin OS=Protobethrops jerdonii OX=242841 PE=1 SV=1	
	spiB8K1W0jVM3DK DABRR Zinc metalkoproteinase-disintegrin-like daborhagin-K OS=Daboia russelii OX=8707 PE=1 SV=1	
	splA8QL48[VM3 BUNFA Zinc metalloproteinase-disintegrin-like B/MP (Fragment) OS=Bungarus fasciatus OX=8613 PE=2 SV=1	
	spIA3R0T9[VM3 OPHHA Zinc metalloproteinase-disintegrin-like ohanin OS=Ophiophagus hannah OX=8665 PE=1 SV=1	

<u>Fig7</u>

Figure 5 depicts that Russell'sViper has more primitive PLA2. King Cobra has also primitive PLA2 but it's slightly modified than Russell'sViper. Figure 6 also justified this statement. Figure 6 depicts that all structure of PLA2 for different snake species is more all less same but the modification and differences present based on the position and number of phosphodiester bond. Very few research article explained that more phosphodiester bond means more complexity and more toxic. So for neurotoxic venom aspect King Cobra facing a huge problem, not only King Cobra but also Russell's Viper. But Viper have a benefit for presence of hemotoxic venom SVMP. According to figure 7 viper have more modified and toxic SVMP than King Cobra, whereas King Cobra has the less toxic and primitive SVMP than others Elapid & Viper. For this less toxicity, may be King Cobra facing very much problem due to time of hunting. It's correct that King Cobra inject higest amount of venom than other snake but may be due the reason of less toxicity, it creating very much problem. So along with all ecological reason, this also a huge and a major point behind vulnerable status of King Cobra.

Reference :

- Reptile Database
- NCBI
- RCSB PDB
- UniProt
- Other articles cited in the text

RAMAKRISHNA MISSION VIVEKANANDA CENTENARY COLLEGE

Rahara, Kolkata - 700118, West Bengal

Department of Zoology

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Evolution of Snake Venom Metalloproteinase (SVMP) in the context of Atrajin from *Naja atra*

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Introduction:

<u>S</u>nake <u>Venom Metalloproteins</u> (SVMPs) constitute about 30 percent for vipers' and pit vipers' venoms. They are also present in elapid snake venoms, but in little amounts (less than ten percent) and make a significant contribution to the haemorrhagic effect on prey following venom delivery. They cause serious damage to the prey's microvasculature, which usually ends in death. Aside from that, they're fibrinogenolytic agents, prothrombin activators, blood coagulation factor X activators, apoptotic agents, platelet inhibitors, pro-inflammatory agents, and blood serine protease inhibitors [8]. The "<u>A Di</u>sintegrin <u>and Metalloproteinase</u>" (ADAM) proteins are neofunctionalized in SVMP. ADAMs are important extracellular cell signalling proteins in mammalian cells [8]. SVMP is thought to have evolved from a duplication event of the ADAM28 gene, which was then neofunctionalized around 60 million years ago on Earth. Those proteins were taken up by a variety of animals, including snakes, who used them to help in the capture of prey. Snake venoms from the Viperidae and Crotalinadae families have an exquisite venom protein. Elapidae venoms, on the other hand, have a lower concentration of them.

The development of SVMP venoms among Elapidae, Viperidae, and Crotalinadae snake venoms was the focus of our early research. We phylogenetically analyzed the SVMP proteins whose solved structures have already been deposited in the RCSB PDB. We found that VAP1 from Crotalus atrox (Viperidae) and K-like & Atragin from *Naja atra* (Elapidae) belong to the same monophyletic group when analyzing the sequences. The phylogenetic analysis of cyt b sequences for each species was in discrete positions since they are from separate families. After that, we looked at their geographical distributions. *Crotalus atrox* was found in the United States and Mexico, whereas *Naja atra* was found in China (Guizhou, Hainan, Hubei, Hunan, Zhejiang, Chongqing, Fujian, Jiangxi, Anhui, Guangdong, Guangxi); Hong Kong; Lao People's Democratic Republic; Macao; Taiwan, Province of China; Viet Nam. Because they were distantly placed in the Pangea formation state, the reasoning based on localization proximities were rejected.

The conclusions may currently be expressed using the dietary specificity of the two snakes [1, 2]. Daltry et al. presented an intriguing article in 1996 in which they looked at the diet of the pitviper *Calloselasma rhodostoma* from different parts of South and North America and associated snake venom evolution. Their research discovered that, even within conspecific groups, food and venom evolution differed substantially across geographical areas. It's worth noting that their research ruled out both contemporaneous gene flow (based on geographical proximity) and phylogenetic linkages based on mitochondrial DNA analysis as explanations for snake venom diversity and evolution [1]. Our present goal is to investigate the diet-related differences between the two snakes to better understand their evolution.

In addition, we aim to expand an Ancestral Sequence Reconstruction approach [9], in which we will underpin the ancestral most protein of SVMP, which was first introduced to snakes, and its leading to the accumulation and modification for other species. The Ancestral Sequence Reconstruction (ASR) is also known as the "retro" approach of protein engineering. Proteins are often modified, and environmental factors result in new protein capabilities.

Metalloproteins are an excellent option for such breakthroughs in evolution. Finding the parent protein, on the other hand, can be challenging since it may not exist in its primordial form. We can locate proteins to fill in the gaps in protein evolution using this "retro" method to protein engineering.

Methods:

Phylogenetic Analysis w.r.t. Mitochondrial gene cytB

FASTA sequences were obtained when an acceptable structure was chosen. For further screening, the FASTA sequences were manually put into the MEGA 11 software (https://www.megasoftware.net/) [7]. For better understanding and presentation of the idea, each sequence was renamed in the following format: "RCSB PDB ID | Name of the Protein | Scientific Name of the Snake species | Family of the Snake species | Protein Class at which that specific SVMP belongs to." The sequences were aligned using the MUSCLE technique and gaps in alignment were

manually trimmed out. Following trimming, the proteins were analyzed using the Neighbor-joining Technique [4] with the exception of setting Test of Phylogeny to "Bootstrap method" and increasing the number of bootstrap replications to 1000 [5]. The phylogeny of the mitochondrial gene cytb was studied using a similar set of techniques. The mitochondrial cytb sequences of snake species previously considered for protein analysis were found in the NCBI Nucleotide database (https://www.ncbi.nlm.nih.gov/nuccore/?term=). [("Scientific Name" AND (Cytb OR cytb)] was created as a search string. We removed the *Crotalus adamanteus* from further study since there was no data available. The findings were reorganized from long to short depending on their sequence lengths. The cytb gene with the longest sequence length was chosen for further investigation. The FASTA format of the finished sequence was obtained, and the set was manually aligned with MEGA 11 software. The MUSCLE algorithm was used to align the DNA. Gaps were minimized and aligned sequences were pruned further. At the earlier given settings, the phylogenetic tree was built using the Neighbour-joining method [4]. After generating the phylogenetic tree, we renamed the sequence entries in the following format "Accession ID Scientific Name of the Snake | SVMP protein it carries (structure already solved) | Two Major Classes that represent its Venom Composition".

The venom composition information came from a previous study that reviewed the proteomic characterisation of venom compositions for diverse Elapidae, Viperidae, and Crotalinae snakes [3]. The conservation status of the indicated species was assessed using the IUCN Red List website (https://www.iucnredlist.org/). There is still no reputable source for diet-related information.

The evolutionary history was inferred using the Neighbor-Joining method [4]. The optimal tree with the sum of branch length = 4.27790847 is shown in Figure 1. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) [5] are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The proportion of sites where at least 1 unambiguous base is present in at least 1 sequence for each descendent clade is shown next to each internal node in the tree. This analysis involved 16 amino acid sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There was a total of 198 positions in the final dataset.

There is a clear distinction between the Class P III and Class P I SVMP proteins in the phylogenetic tree. However, the Acutolysin C from *Deinagkistrodon acutus* which belongs to class P I is in the middle of other P-III proteins. Same thing applies for the RVV-X from *Daboia russelii* that lies in between other class P III proteins. Such results are often confusing. The reasonings behind such results are either a strong correlation of evolution from P-III to P-I class proteins or a pruning error that puts distinct proteins into related phylogenies. Further review of the literature might clarify such points.

The evolutionary history was inferred using the Neighbor-Joining method [4]. The optimal tree is shown in figure 2. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) [5] are shown above the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [6] and are in the units of the number of base substitutions per site. The proportion of sites where at least 1 unambiguous base is present in at least 1 sequence for each descendent clade is shown next to each internal node in the tree. This analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There was a total of 609 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [7].

While Vipers have SVMP as their main venom component, Elapids prefer PLA₂ and 3FTx as their ultimate weapons. However, proteomic characterization of venom components reveals that a significant proportion of SVMP is present in some Elapid snakes (such as, *Naja haze*) and vice versa. Therefore, there is a strong need to look for their evolutionary ancestral sequences. Later studies on the same analysis resulted on significant correlation between the venom complexity and mitochondrial gene diversity.

Conservation Analysis

The Protein Data Bank (PDB) files for Atrajin (3K7L, 2.5 angstroms) and K-line (3K7N, 2.3 angstroms) of *Naja atra* were downloaded from RCSB PDB database (<u>https://www.rcsb.org/</u>). The PDB files was uploaded on the Consurf

database (<u>https://consurf.tau.ac.il/</u>) to perform the conservation analysis. The settings applied are briefed in the following table.

Table: Consurf Database Settings used:

Parameters to homolog search algorithm					
Homolog Search Algorithm	HMMER				
Number of iterations	1				
E-value cut-off	0.0001				
Protein database	NR (This database is maintained by the NCBI and comprised of				
	non-redundant sequences from GenBank CDS translations, PDB,				
	SwissProt, PIR, and PRF, excluding environmental samples from				
	WGS projects.)				
Select homologs for Consurf analysis	Automatic				
Parameters to select the sequences for	the analysis out of homolog search algorithm results				
Select <u>150</u> sequences	that sample the list of homologues to reference sequence				
Maximal %ID between sequences	100				
Minimal %ID for homologs	75				
Alignment method to build the Multiple Sequence Alignment (MSA)					
Alignment method	CLUSTALW				
Calculation method	Maximum Likelihood (ML)				
Evolutionary substitution model	Best model (default)				
Phylogenetic Tree	Neighbor Joining with ML distance				

Ancestral Sequence Reconstruction

The Atrajin 3K7L PDB file was uploaded to the FireProtASR (<u>https://loschmidt.chemi.muni.cz/fireprotasr/</u>) webserver. The default settings were used. The results can be viewed using the link: <u>https://loschmidt.chemi.muni.cz/fireprotasr/?action=calculation&job=lmujva_636&</u>. The protocol for the ASR is described below.



Structural Analysis

The predicted structures (obtained through Homology Modelling) and the experimental structures were subjected to further analysis for the Disulphide bridge patterns in PyMol. The structure colours were set using proper RGB codes from HTML colour palette. The codes are mentioned in the Table.

Table: Details of Experimentally Predicted Structures.

Protein PDB ID		Experimental/Predicted	Colour code
	(If		
	available)		
Atrajin	3K7L	Experimental	168, 38, 99
K-like	3K7N	Experimental	82, 111,134
C. mydas SVMP	-	Predicted (Homology Modelling)	103, 158, 47
L. s. domestica SVMP	-	Predicted (Homology Modelling)	49, 154, 237
O. hannah SVMP	-	Predicted (AlphaFold database)	32, 95, 143

Homology Modelling of the Predicted Proteins

Since the predicted proteins for *C. mydas*, *L. s. domestica* and *O. hannah* did not have any experimental structures submitted in the protein databases, we went for structural prediction using Homology modelling approach. We uploaded their respective sequences on the Swiss-model server (put link). The details of the templates used for homology modelling is mentioned in the Table.

Table: Homology Modelling

Protein	Template	Sequence	GMQE	Q-mean
		Similarity		
C. mydas SVMP	3k7l.1: Structures of two elapid snake venom	51.79 %	0.40	0.61 ± 0.05
	metalloproteases with distinct activities			
	highlight the disulphide patterns in the D			
	domain of ADAMalysin family proteins			
L. s. domestica SVMP	2dw0.2: Crystal structure of VAP2 from	49.03 %	0.51	0.71 ± 0.05
	Crotalus atrox venom (Form 2-1 crystal)			

The protein structures were further validated by deriving their respective Ramachandran Plots from the UCLA Saves server (https://saves.mbi.ucla.edu/).

Results:

No significant correlation between Venom complexity and Mitochondrial gene cytB diversity: Our study found no significant correlation between venom complexity and mitochondrial gene cytB diversity. Although it was expected by us as earlier studies reported the same results in this context.

Ancestral Sequence Reconstruction of Atrajin from Naja atra:



Figure: Phylogenetic Tree derived from the Ancestral Sequence Reconstruction in the MEGA 11 software.

Automated ASR studies using the Fireprot ASR server resulted in a detailed phylogenetic tree that covered the total aspect of SVMP. A total of 150 sequences successfully represented the entire background of the evolutionary module. The SVMP homolog from Green Sea Turtle is suspected to be the primitive versions of these snake proteins. It is important to note that, the first appearance of SVMP has taken place in the Elapid snakes, namely *Thamnophis sirtalis*. *Ophiophagus hannah* served as a link between the SVMP of Vipers and Elapids. Protein structure obtained from the AlphaFold Database has shown an unusual structure profile for the protein that revolves another important aspect of further research in this theme.

Analysis of the Experimental Structures:

The two experimental structures of Atrajin and K-like respectively, both from *Naja atra* was downloaded as .pdb format from RCSB PDB Database. The structures were uploaded in UCLA Saves server for Ramachandran Plot generation. The visualization processes were performed using the PyMol software. Images produced are set in 300 DPI settings, without the transparent background while using the "Draw" option in command box.





Plot statistics

lesidues in most favoured regions [A,B,L]	289	80.7%
esidues in additional allowed regions [a,b,l,p]	62	17.3%
tesidues in generously allowed regions [~a,~b,~l,~p]	5	1.4%
lesidues in disallowed regions	2	0.6%
lumber of non-glycine and non-proline residues	358	100.0%
lumber of end-residues (excl. Gly and Pro)	4	
lumber of glycine residues (shown as triangles)	28	
lumber of proline residues	19	
otal number of residues	409	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Figure: Surface, Electrostatics, Ramachandran Plot and its Statistics for the SVMP Protein Atrajin (PDB ID: 3K7L) from *Naja atra*.







Figure: Surface, Electrostatics, Ramachandran Plot and its Statistics for the SVMP Protein K-like (PDB ID: 3K7N) from *Naja atra*.

Homology Modelling of the Predicted Proteins

Homology modelling using the Swissprot server resulted in two protein structures. The server successfully modelled the proteins obtained from *C. mydas* and *L. s. domestica*. However, the *T. sirtalis* protein obtained no such models.



Figure: Homologs of SVMP: Predicted Structures from C. mydas, L. s. domestica, and O. hannah.

Structural Analysis:



Figure: Electrostatic Surface Representation of K-like, SHOH, Atrajin, SHLS, and SHCM.

The experimental and predicted structures were subjected for further analysis in the visualization software PyMol. The patterns of disulfide bonds were focused. The details of the structural analysis were described in the Table. The disulfide bond patterns significantly contributed to the venom complexity. This disulfide bond patterns, or the "Molecular Stitching" patterns were highly diverse among the proteins. Further docking studies will confirm if the predicted structures have different substrate specificities or not.

The experimental structures were aligned against each other to obtain their RMSD vale, by which we can define the protein structural similarity attributes. The RMSD value for the alignment of Atrajin-K-like was 18.453, which is very high w.r.t. the similarity parameters. It is quite expected as there are distinct structural differences among the two proteins, already documented in their structure report paper.

The predicted structures were aligned against the Atrajin protein to obtain their RMSD values for the similar set up. The RMSD values (shown in the table) clearly demonstrates that the C. mydas SVMP honolog closely resembles the Atrajin, while others are quite different in structure. By structural similarity with Atrajin, the proteins can be arranged in the following sequence: SVMP Homolog from *C. mydas*>SVMP Homolog from *L. s. domestica>* SVMP Homolog from *O. hannah*. However, the same task was not performed for K-like since, by visual means it is quite evident that the K-like structure is quite different from the predicted proteins, while Atrajin is closer in structural relation.

Sl.	Protein 1	Protein 2	RMSD Values	Order of Similarity
No.				w.r.t. Atrajin
01	Atrajin	K-like	18.943	SHCM > SHLSD >
02	Atrajin	SVMP Homolog from C. mydas (SHCM)	0.145	SHOH > K-like
03	Atrajin	SVMP Homolog from L. s. domestica (SHLSD)	3.444	
04	Atrajin	SVMP Homolog from O. hannah (SHOH)	8.045	

Table: RMSD Value Calculations.



Figure: Experimental Structures of Atrajin and K-like. The Alignment of Atrajin-K-like protein (RMSD = 18.943).



Figure: Alignment of Atrajin against the *C. mydas* protein (RMSD = 0.145), *L. s. domestica* protein (RMSD = 3.444), and *O. hannah* protein (RMSD = 8.045).

Discussion:

Snake Venom Metalloproteins significantly contribute to the venom complexity of all Vipers, Pitvipers, and some Elapid snakes. These proteins are important to understand since they are the neo-functionalized versions of ADAM and ADAMTS proteins, that play a critical role in extracellular cell signaling. Additionally, these proteins serve as important cues for antivenom development against Viper venoms.

Previous literatures reported ADAM28 as the most primitive non venom protein precursor for SVMPs. About 60 million years ago, a duplication and insertion deletion event resulted in the P-III subclass SVMPs. About 32 million years later, the P-II SVMP was derived from the P-III SVMPs. It is important to note that, SVMP first appeared in Elapid snakes and the Vipers took them up to upgrade their venom arsenal. However, the Elapid snakes did not take up SVMP as their main venom component.

We delved through the proteome comparisons of Elapid snakes and found *Naja haze* having the highest percentage of SVMP among the Elapids. We progressed with the *Naja atra* since it has a validated experimental structure to back up our bioinformatic studies. We processed with the .pdb files and conducted Ancestral Sequence Reconstruction of the Atrajin protein. SVMP Homolog from the C. mydas is found out to be the most ancestral version of the protein family. However, how these proteins came up to the snakes is still under investigation.

Future Directions:

- The predicted proteins will be docked against an array of small molecule substrates to obtain their biochemical characteristics and activity profiles.
- Further analysis of the *O. hannah* SMVP protein will be performed using computationally validated models to retrospect the unusual structure of the protein.
- A conservation analysis study will be performed parallel to this study, and it will look if venom complexity is related to the organism survival or not.
- An activation path modeling study has been proposed to investigate the activation pathways of the respective proteins.

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Observation of pollinators vitis Vitis triflorum:

Objective of the study:

Pollination is the act of transferring pollen grains from the male anther of a flower to the female stigma. The goal of every living organism including plants is to create offsprings for the generation.... Seeds can only be produced when pollen is transferred between flowers of the same species. Pollination is very interesting subject. How pollinators come and visit the flower, take the pollen from the flowers. Pollination can be occurred by different types of pollinator in different species or one species.

- ✤ At the first, we shall observe the flower at different times.
- We will observe the time in which the pollinators coming and how long they visit the flowers and note the time into notebook.
- Then recognise the pollinator's species.

Study site:

Ramakrishna Mission Vivekananda Centenary College, garden.

Collection methodology:

At first I visit the garden to choose the flowering plant. I took help of our teacher to choose the flower. I choose the flower name <u>Vitis triflorum</u>.

I visit the flower in the noon at 1:30-2pm and has been waiting for the pollinators. At first I saw the ants came to the flower. I took the pictures of those ants using my mobile camera.

Then another day I had gone to visit the flower again and this time at 1:30 -2:00 pm. I saw the ants came again and I saw a new species came to the flower. The next two days I could not visit the flower because of heavy raining.

Results:

Day	Pollinator	Time of arrival
1	Ants	1:30-2pm
2	Ants and	1:30-2pm
	insects	

Discussion:

At the first day saw the ants were coming most of the time but I could not find out the reason behind it. When I went to the garden the other day I saw a different insect which had a disease on their skin .what is the disease and how it occur? I could not find.

Pictures:



1

2













Pollinator observation on Hibiscus

Shaibal Mondal

Roll no - 510

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- **Objective** To gain the knowledge about the various pollinator and their interaction with hibiscus plant in my locality.
- **Study Site** The study was conducted at Mira Kadamtala Para, Plassey in Nadia district of West Bengal. The insect species on *Hibiscus rosa sinensis* during its blooming phase was recorded from September 26, 2021 to
- Latitude & Longitude 23.77 & 88.28
- **Habitat** The study site was a garden in front of my house. The tree was surrounded by various small & big trees, and under the tree was covered with patchy grasses. The flower visitors were observed for an interval of each 2 minutes for approximate 1 hour

per day.



• Description of the Flant (Flower)

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
Red	Trumped shaped	6 – 10 cm in diameter	No	5.0ft – 5.6ft	Inside the calyx	Bottom of the flower

• **Collection methodology** – Collection of flower visitors was made by live observing the flower and clicking some pictures by mobile. Flower visitors were observed for 1 hour per day.

• DAY 1 – 26/09/21: Time – 11.15am to 12.15pm

• Temp – 31°C, Humidity – 60%, Wind – 9.8km/h, Partly sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying	Sitting time on flower
Odonata			26/09/202111	-	3 minute approx

• <u>DAY 2 – 27/09/21:</u> Time - 8.30am to 9.15am

 $\circ~$ Temp – 34°C , Humidity – 40% , Wind – 6.7km/h , Sunny weather.



Lepidoptera	Papilionidae	Papilio	On the	-	5 sec
		clytia	style		approx
		(common			
		mime)			

• <u>DAY 3 – 28/09/21:</u> Time – 12.00pm to 12.40pm

 $\circ~$ Temp – 30°C , Humidity – 71% , Wind – 14km/h , Partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• Not a single visitors observed.

• <u>DAY 4 – 29/09/21:</u> Time –

 $\circ~$ Temp – 29°C , Humidity – 92% , Wind – 11.2 km/h , Light rainy weather.

Order	Family	Genus/	Posture	Pollen	Sitting
		Species	of sitting	carrying	time on
				parts	flower

-	-	-	-	-	-

• Due to rain fall since all day no data collected.

• <u>DAY 5 – 30/09/21:</u> Time – 4.00pm to 5.10pm

 \circ Temp -32°C, Humidity - 81%, Wind - 3.6 km/h, Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	-	Approx. 6 sec

• Not able to capture image.

• <u>DAY 6 – 07/10/21:</u> Time – 2.45pm to 3.15pm

 $\circ~$ Temp – 33°C , Humidity – 70% , Wind – 4.9 km/h , partly cloudy weather.
Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No flower visitor found.

• <u>DAY 7 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No flower visitor observed.

• <u>DAY 8 – 18/10/21:</u> Time – 4.30pm to 5.05pm

 $\circ~$ Temp – 29°C , Humidity – 55% , Wind – 3.4 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	-	3 sec.

• <u>DAY 9 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No data found.

• <u>DAY 10 – 04/11/21:</u> Time – 9.10am to 9.50am

 $\circ~$ Temp – 28°C , Humidity – 43% , Wind – 5.6 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Roaming around stamen	Leg, wings	3-4 sec

- **Result** As a result I recorded an observation chart of 10 days on flower visitor or pollinator of *Hibiscus rosa sinensis* at a garden of my house which is located in Plassey, Nadia. Here -
- 1. Anisoptera sp (order belongs to Odonata), seen 1 time
- 2. Papilio clytia or common mime (order belongs to Lepidoptera), seen 1 time
- 3. *Apis indica* (order belongs to Hymenoptera) seen **3 times** are observed as flower visitor.
- **Discussion** Though Hibiscus is very attractive plant for pollinator but I got 3 flower visitors which is not good at all. Most flower visitors are often seen at morning and afternoon time. No visitors found at the time of mid-noon and rainy days. Due to a moderate pollution in this area and low amount of flowers in the tree, flower visitors are seen very rarely and also low individual. So, it indicates the low rate of pollination and also less crop or flower production.

Pollinator observation on Hibiscus

Manas Saha Roll - 513 Department of zoology, Ramakrishna Mission Vivekananda Centenary Collage, Rahara, Kolkata -700118

- **Objective** To gain the knowledge about the various pollinator and their interaction with hibiscus plant in my locality.
- **Study Site** The study was conducted at Mira Kadamtala Para, Plassey in Nadia district of West Bengal. The insect species on *Hibiscus rosa sinensis* during its blooming phase was recorded from September 26, 2021 to
- Latitude & Longitude 23.77 & 88.28
- **Habitat** The study site was a garden in front of my house. The tree was surrounded by various small & big trees, and under the tree was covered with patchy grasses. The flower visitors were observed for an interval of each 2 minutes for approximate 1 hour



• Description of the Plant (Flower)

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
Red	Trumped shaped	6 – 10 cm in diameter	No	5.0ft – 5.6ft	Inside the calyx	Bottom of the flower

• **Collection methodology** – Collection of flower visitors was made by live observing the flower and clicking some pictures by mobile. Flower visitors were observed for 1 hour per day.

4 <u>DAY 1 – 26/09/21:</u> Time – 11.15am to 12.15pm

 \circ Temp – 31°C, Humidity – 60%, Wind – 9.8km/h, Partly sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Odonata	-	Anisoptera sp	In front	-	3 minute
			upper		approx
			portion of		
			petal		



↓ <u>DAY 2 – 27/09/21:</u> Time - 8.30am to 9.15am

 $\circ \quad Temp-34^{\circ}C$, Humidity -40% , Wind -6.7 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Lepidoptera	Papilionidae	Papilio clytia (common mime)	On the style	-	5 sec approx



↓ <u>DAY 3 – 28/09/21:</u> Time – 12.00pm to 12.40pm

 $\circ \quad Temp-30^{\circ}C$, Humidity -71% , Wind -14 km/h , Partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• Not a single visitors observed.

↓ <u>DAY 4 – 29/09/21:</u> Time –

 \circ Temp – 29°C, Humidity – 92%, Wind – 11.2 km/h, Light rainy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• Due to rain fall since all day no data collected.

↓ <u>DAY 5 – 30/09/21:</u> Time – 4.00pm to 5.10pm

 \circ Temp -32°C, Humidity - 81%, Wind - 3.6 km/h, Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	_	Approx. 6 sec

• Not able to capture image.

↓ <u>DAY 6 – 07/10/21:</u> Time – 2.45pm to 3.15pm

 $\circ~$ Temp – 33°C , Humidity – 70% , Wind – 4.9 km/h , partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No flower visitor found.

↓ <u>DAY 7 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	_

• No flower visitor observed.

↓ <u>DAY 8 – 18/10/21:</u> Time – 4.30pm to 5.05pm

 $\circ~$ Temp – 29°C , Humidity – 55% , Wind – 3.4 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	-	3 sec.

↓ <u>DAY 9 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	_	-	-	_

• No data found.

↓ <u>DAY 10 – 04/11/21:</u> Time – 9.10am to 9.50am

 $\circ~$ Temp – 28°C , Humidity – 43% , Wind – 5.6 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Roaming around stamen	Leg, wings	3-4 sec

- **Result** As a result I recorded an observation chart of 10 days on flower visitor or pollinator of *Hibiscus rosa sinensis* at a garden of my house which is located in Plassey, Nadia. Here -
- 1. Anisoptera sp (order belongs to Odonata), seen 1 time
- 2. *Papilio clytia* or common mime (order belongs to Lepidoptera), seen 1 time
- 3. *Apis indica* (order belongs to Hymenoptera) seen **3 times** are observed as flower visitor.
- **Discussion** Though Hibiscus is very attractive plant for pollinator but I got 3 flower visitors which is not good at all. Most flower visitors are often seen at morning and afternoon time. No visitors found at the time of mid-noon and rainy days. Due to a moderate pollution in this area and low amount of flowers in the tree, flower visitors are seen very rarely and also low individual. So, it indicates the low rate of pollination and also less crop or flower production.

A OBSERVATION REPORT ON THE POLLINATORS OF

Ixora coccinea

Submitted by,

SANMITRA BISWAS

Registration No.: A01-1112-115-009-2019 of 2019-2020

Semester-V

of

RAMAKRISHNA MISSION VIVEKANANDA CENTENARY COLLEGE RAHARA, KOLKATA-700118



(AFFILIATED TO WEST BENGAL STATE UNIVERSITY) DEPARTMENT OF ZOOLOGY YEAR: 2021

~ Pollinator observation of *Ixora coccinea* ~

- **Objective** To gain the knowledge about the various pollinator and their interaction with **Jungle Geranium** plant in my locality.
- Study Site The study was conducted at Ultadanga at Kolkata, the Capital of West Bengal. The pollinator species *Ixora coccinea* during September 29th, 2021 to October 7th, 2021.
- Latitude & Longitude 22.592772,88.387433
- Habitat The study site was a very small patch of trees in front of our building. The tree was surrounded by some shrubs like Crepe Jasmine, and under the tree was covered with patchy grasses. The flower visitors were observed very rarely.



• **Description of the Flower**

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
Red	The body is stick type	5 – 6 cm in height	No	3 ft – 4 ft	In the middle of the petals	Bottom of the inflorescence

• **Collection methodology** – Collection of flower visitors was done by live observation and taking photographs with the smartrphone. Flower visitors were observed for 1 hour per day.

↓ <u>DAY 1 – 29/09/21:</u> Time –

 \circ Temp – 27 °C, Humidity – 81%, Wind – 8.3 km/h, mild rain fall.

• Insect visitor :

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• Due to rainfall data not collected.

↓ <u>DAY 2 – 30/09/21:</u> Time – 2:30 pm to 3:30 pm

 \circ Temp – 30 °C, Humidity – 78 %, Wind – 9.1 km/h, partly cloudy weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Formicidae	Lasius niger	Roaming on the petals & the base of the inflorescence	-	Didn't sit

• Insect visitor : Diurnal

• Not able to capture image.

4 <u>DAY 3–01/10/21:</u> Time – 2:00 pm to 3:00 pm

 $\circ~$ Temp – 33 °C, Humidity – 75 %, Wind – 7.8 km/h, partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
_	_	_	_	_	_

• No visitor found.

↓ <u>DAY 4 – 02/10/21:</u> Time – 2:30 pm to 3:30 pm

 \circ Temp – 33 °C, Humidity – 76%, Wind – 7.9 km/h, partly cloudy weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
_	_	_	_	-	_

• No visitor found.

↓ <u>DAY 5 – 03/10/21:</u> Time – 11:15 am to 12:15 pm

 $\circ~$ Temp – 30° C, Humidity – 77%, Wind – 8.1 km/h, partly cloudy weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Formicidae	Solenopsis sp.	Roaming on the petals & the base of the inflorescence	_	Didn't sit



↓ <u>DAY 6 – 04/10/21:</u> Time – 11:30 am to 12:30 pm

 \circ Temp – 29 °C, Humidity – 78 %, Wind – 7.9 km/h, normal sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No visitor found.

DAY 7 – 05/10/21: Time – 01:15 pm to 02:15 pm

 \circ Temp – 32 °C, Humidity – 79%, Wind – 9.1 km/h, normal sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
_	_	_	_	-	_

• No visitor found.

DAY 8 – 06/10/21: Time – 1:45 pm to 2:45 pm

 \circ Temp – 31 °C, Humidity – 79%, Wind – 8.6 km/h, normal sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrving	Sitting time on
			~8	parts	flower
Lepidoptera	Papilionidae	Papilio polytes	On the style	-	Max. 4-5
					seconds



↓ <u>DAY 9 – 07/10/21:</u> Time – 11:15 am to 12:15 pm

 $\circ~$ Temp – 30 °C, Humidity – 78%, Wind – 8.4 km/h, normal sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No visitor found.

Result & Discussion :

According to the Results of this observation on the pollinators of the Jungle Geranium plant, it can be said there are very few number of pollinators that could be seen during this observation period.

Although, the observation period was 9 days long and observed minimum 1 hour daily, the timing varied also; but only some ants as visitors and a Common Mormon as pollinator can be seen.

From these observation results, it can be said that the arrival of the visitors or pollinators are very rare to the taken plant. As, the plant is situated in a proper city area so the main reason behind the lack of visitors can be anthropogenic activities and interferences such as sounds, pollutions, disturbances etc. Human developments around the plant area is the main cause for the rare arrival of the visitors (butterfly could be seen only once.) During the afternoon time (01:45 PM to 02:45 PM) when the anthropogenic activity is much less the visitor Common Mormon could be seen. This is a reference to discussion done as the inference of this series of observations.

Review on the advance floral morphology and pollination syndrome in various plants

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Abstract: - Study of advance floral morphology is a very important aspect of pollination biology. Many varieties of advance floral morphology are seen across various plant families and orders. Though most of the advance morphology is related with pollination of the plant, *i.e.* for attracting pollinators and complete pollination efficiently, pollination is not only its sole purpose, some also serves for preying, defense, mutualism, symbiotic relation and other purposes. Orchids (Orchidaceae) have most variety among the advance morphology- from conspicuous "star of Bethlehem" to little *Epipactis*, they show extensive variety in both advance floral morphology and in pollination syndrome. Other genus like, *Arisaema, Salvia* etc. also shows various advance floral morphology is evolved, modified and controlled by many factors like specific pollinator/s, abundance of pollinators, coevolution with the pollinator, habitat, environmental factors and stress from surrounding, mutualism or symbiotic relation of the pollinators with the plant etc.

Keywords: - Pollinator flower relation, Coevolution, Competitive selection.

Introduction: - Floral morphology differs in various flowering plants with respect to its habitat, reproductive strategies, pollination syndrome and types of pollinators associated with the plant or flower. Floral morphology consists of a large number of parameters, including the number and shape of petals, number of stamens, petal size and the number and arrangement of styles and ovaries. The pollen grains of insect pollinated flowers are sticky due to pollen kit. The surface of stigma of flowers is rough. Some of the plants develop special adaptation for insect pollination. Many flowers show advance floral morphology for different pollinators. Study of advance floral morphology is important to understand relation of pollinator and plant, and also the co-evolutionary aspect of these two.

Discussion: - Through years of observation, it is a well-established fact that angiosperm flowers and its insect pollinators have influenced each other's evolution a lot, but it is not quite understood that is coevolution is a major process to form diversification among these groups. Coevolution is most likely when interacting organisms have strong effects on each other's fitness (Thompson 1994). This criterion is clearly met for pollination mutualisms in which the insects that pollinate plants also depend on them as brood sites (Thompson 1994). Classic examples of such coevolved brood-site pollination mutualisms are the relationships between figs and Agaonid fig-wasps and between Yuccas and Tegiticula moths (Pellmyr *et al.* 1996; Sakai 2002; Weiblen 2002).

Co-evolution: - One of the great examples of this kind of coevolution is Darwin's orchid (*Macroplectrum sesquipedale*) and its only pollinator the Hawk moth or *Xanthophane morganii* praedicta.

In hypothesizing, how the Malagasy star orchid might have evolved it's extraordinarily long (30 centimeters) nectar spur, Darwin (1862) proposed the first mechanistic model of the coevolutionary process. He did refer to "a race in gaining length between the nectary of Angraecum and the proboscis of certain moths" (Darwin 1862). He noticed that the Malagasy star orchid, which is endemic to Madagascar, have an unusual long spur and have nectar at the very bottom of long spur. In fact, to reach the nectar of the orchid requires a 30cm (11inch) long proboscis to penetrate the long nectar spur. Darwin and Alfred Wallace (Father of principle of evolution) predicted that the pollinator of this long spur flower must have to be some long-tongued moth. Hawk moth, also called sphinx moth or hummingbird moth, any of a group of sleek-looking moths that are named for their hovering, swift flight patterns. These moths have stout bullet-shaped bodies with long, narrow forewings and shorter hind-wings. Wingspans range from 5 to 20 cm. Later, after discovery of the moth, it was also observed that the fittest moths in a population would then be those with long tongues that could access the nectar in even the deepest flowers, whereas the shorter-tongued moths would access less nectar (Fig.1). Thus, moths would be expected to be under strong directional selection and should evolve greater tongue lengths (Fig. 1). This is a fine example of both adaptive floral morphology of Darwin's orchid, which have almost 30cm long spur and their coevolutionary significance with giant hawk moth who also have almost 30cm long proboscis and is the only pollinator of that orchid.



Mimicry in orchids: -

Prey mimic: - Orchids show enormous types of adaptive or advance unique floral morphology to attract its pollinators. One of the finest examples is Helleborines, *Epipactis veratrifolia* (*Orchidaceae*). This flower has structure that looks like aphid. This aphid mimicry is a kind of prey mimicry as aphidophagous hoverflies lay eggs on false brood sites on their flowers as its larvae eats aphids during its developmental stage-



Fig 2.1- Prey Mimic by Epipactis (Ref- bmcplantbio.biomedcentral.com)

Aggressive Mimic: - Another example from orchid genus is *Oncidium*. *Oncidium* species have bright yellow color flower and it situates at the ends of stalks that sway in breeze, it mimics an antagonist- a male bee. An aggressive Centris bee always try to drive other bees or specifically males out of their territory. So, the bee mistakenly attacks the flower as male competitor and strikes it, eventually the pollinia attaches to its head. When it attacks a second flower, the pollinia presses into the stigma and pollination occurs-



Fig 2.2- Oncidium mimicking male bee (Ref- researchgate.net)

Another fine example of using adaptive floral morphology as mimic is ophrys. In *Ophrys sphegodes* orchid chemical mimicry was first proposed by Kullenberg (1961). Beside of the fact that the flower exactly looks like a female bee, BergstroÈm (1978) discusses mainly two possibilities concerning the biologically active volatiles involved in the chemical mimicry of Ophrys orchids:

(1) the orchid mimics an aphrodisiac produced by the females, and (2) *Ophrys* orchids make use of "extranormal stimuli", i.e., compounds usually not produced by a female, which hit existing receptors associated with sexual behavior. Borg-Karlson and TengoÈ (1986) first suggested presence of aliphatic primary alcohols and methyl carbinols as well as several terpenes, occurring in flowers and bee secretions, to be the key components in *O. lutea* pollinated by Andrena-bees., the alkenes of the orchid and bee cuticle proved to be behaviorally more active than the alkanes. The specific adaptation of *O. sphegodes* flowers for pollinator attraction seems therefore to be a higher production of specific isomers of alkenes. The evolution of the pollination mechanism of sexual deception, which involves a mimicry of the pollinator's sex pheromone, has apparently been mediated by a change in the hydrocarbon pattern in the wax layer of the flowers-



Fig 2.3- *Ophrys* flower mimicking female bee, also producing odor that resembles pheromone released by female bees. (Ref- Researchgate.net)

Lever mechanism: -

Another very complex advance floral morphology is seen in Salvia, a family of shrubs (*Salvia pratensis*). Salvia pratensis is a gynodioecious species featured by its modified stamens that act as a lever mechanism in pollination. (Gynodioecy, a sexual system with hermaphrodite and female individuals in a population, raises the question how the two sexual morphs are maintained).

Floral traits significantly differ between two sexual morphs in the population of *S. pratensis*. The female has on average a shorter corolla and tube, a smaller platform (i.e., flower mouth), and a stigma closer to the platform than hermaphrodite flowers. Style exertion, flower production and stalk diameter do not significantly differ between two morphs. The floral traits (e.g., corolla, tube length and stigma height) are significantly larger in hermaphrodites than in females of S. pratensis. The flowers of salvia have bilabiate corolla tube.

The connective of stamen is long. The anterior anther lobe of connective is fertile while posterior lobe is sterile. When the insect lands on the lower lip, the fertile lobe automatically comes down to touch the back of insect and thus depositing the pollen grains there on.





Another example of advance floral morphology that is very common in various species of orchids as well as other families is nectar guide, which are the specific patterns or markings on some flowers that guide a pollinator to its reward which is a nectar and elicit the pollination. It is proven that flowers with these special markings have more chance to achieve pollination than the flowers that don't have this kind of markings. Nectar is a sugar rich compound that is produced by gland nectaries. Nectar is one of the most abundant and common reward used for attracting pollinators. But sometime it is hard for the pollinators to find the exact position of nectaries or nectar. Here comes the role of nectar guides, these are markings or patterns seen in flowers of some angiosperm species, that guide pollinators to their rewards. Rewards commonly take the form of nectar, pollen, or both, but various plants produce oil, resins, scents, or waxes. Such patterns also are known as "pollen guides" and "honey guides". Here are some examples of nectar guides (both normal and uvvisible)-



Fig 4- Nectar guide in different flowers (Ref-journal.plos.org)

Another fine and complex example of advance floral morphology in sake of pollination is Cobra Lily, also known as Jack-in-the-pulpit (Arisaema triphyllum). It is named for its resemblance with a preacher (jack) in its hanging pulpit. The flowers are simple: male flowers are comprised of only four stamens, and female flowers of a fuzzy stigma atop an ovary. Jack-in-the-pulpit is pollinated by fungus gnats. A total of 16 fungus gnat genera comprising 47 identified species were observed. Usually, members of more than one taxon are attracted per Arisaema species, and both sexes of gnats are involved. Attraction is deceptive by mimicking olfactory, visual and tactile cues characteristic of fungi where the gnat sexes normally meet and females oviposit. Odours produced by osmophores play the most important part. The gnats visit to lay their eggs on what they are duped to believe is a fungus. Fungus gnats normally lay their eggs on fungi so that when the eggs hatch the larvae will have a readily available food source. When they mistakenly fall into the preacher, they are unable to crawl out of the spathe due to its slippery interior, nor can they fly straight up to escape in that way. However, if the plant is a male, they may eventually notice a small opening at the base of the spathe through which they can escape. By this time, they are dusted with pollen. They eventually enter a female plant where the pollen that they are carrying brushes off on the fuzzy stigmas, thereby effecting pollination. This time there is no escape since the spathes of female plants have no opening in the base of their spathes, and the gnats die within the spathe-



Fig 5- Preacher and pulpit like structure of spathe of Cobra lily (Arisaema) (Ref-Gardenia.com)

Another example can be cited by *Titan arum*, infamous as corpse flower. It is known for its massive foul-smelling inflorescence (cluster of flowers). The plant is endemic to the steep hillsides of rainforests in western Sumatra. This flower has a very conspicuous unbranched inflorescence and it smells like rotting flesh to attract flies and beetles. The massive inflorescence of the titan arum consists of an inner flower spike, known as a spadix, surrounded by a petal-like collar known as a spathe-



Fig 6- A conspicuous Corpse flower (Titan aurum) (Ref- Britanica.com)

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We also want to thank our principal Swami Kamalasthananda & Vice principal Swami Vedanuragananda for providing us facilities that have helped me during our work.

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Pollination in Holy basil (ocimum tenuiflorum

Presented by - Sayonil sen, roll no.-518, sem-V

*Study site: Shyamnagar, near Annapurna Bazar

- Locality: Shyamnagar, near Annapurna Bazar, Allahabad Bank building
- Habitat: Tropical Semi-Evergreen Forest
- Date & time:- D:-17/9/21, T:- 12.43PM
- Lat: 22.8239, Lng: 88.3856



1 Photograph description:-

The exact location of the sight is my house, the Tulsi plant is located on the roof of my house and the time was 12.43PM when I noticed an hymenopteran insect came and it belonged to the family "Apidae" and the order "Hymenoptera".

So, here's the conclusion is Holy basil (ocimum tenuiflorum) has a pollination called digger need, from the bee family.

2 Description of plants

Colour	Shape	Size	Odour	Height from GL	Position of the nectarine	Position of the ovaries
White	Small funnel shaped, and star shaped from the bird's eye view.	0.6 cm in length and 0.4 cm in width	Sweet and strong aroma		Flower base	Inside the flower. At the last part of the style, above the disc, thalamus and pedicel.

Insect visitors:- Diurnal / Nocturnal

Insect visitors	(Digger bees)			
<u>Order</u> Hymenoptera	<u>Family</u> Apidae	Genus/species Andrena	Posture of sitting Ventral part was towards the flower and was enjoying nectar by digging it's head inside the flower	Pollen carrying parts - body and legs

Foraging activities			Foraging caught on this period		
6AM - 8PM	8AM - 10AM	10AM -12PM	12PM - 2PM	2PM - 4PM	4PM - 6PM

Foraging speed				
Sitting on flower head	Time of foraging and sitting - hardly 1min	Flower touching (per minute) - hardly 3 - 4 times	At a stretch visiting the flowers of same plant species? Ans:- Well yes, there's two of them and the fly was like visiting	Time spent in the field - hardly 40 mins

	flowers from both trees.	

Date:- 18/9/21

Visited the location for 2 hours, 12PM to 2PM, but no such pollination activities caught.

Date:- 19/9/21

*Study site:- Shyamnagar, near Annapurna Bazar

- Locality: Shyamnagar, near Annapurna Bazar, Allahabad Bank building
- Habitat:
- Date & Time:- D:- 19/9/21, T:- 1:06:46PM



Description with photographs:-

The photograph was taken in the afternoon time, the fly is again the "digger bee", it belongs to the family"Apidae" and the order is "Hymenoptera". The Hymenoptera came for foraging at 1:06:46PM

2 Description of the plants

Flower Tulsi (<u>Ocimum tenuiflorum</u>) *(Described previously)**

Insect visitors:- Diurnal ✓ / nocturnal

**Described previously

Foraging activities			Chosen time period		
6AM - 8AM	8PM - 10AM	10AM - 12PM	12PM - 2PM	2PM - 4PM	4PM - 6PM

Foraging speed				
Sitting on flower head	Time of sitting and foraging - hardly 1.30min	Flower touching (per minute) - 4 to 5 minutes	At a stretch visiting the flowers of same plant sp.? Ans:- yes, the fly was visiting two plants at a time.	Time spent on the location - 20min.

* At the same day there was also another pollinator arrived and it was ants, let's take a view about this insect



🔟 Insect visitors:- Diurnal 🗹 / nocturnal

Insect visitors	Small black ants		

<u>Order</u> Hymenoptera	<u>Family</u> Formicidae	<u>Genus/species</u> Monomorium	Posture of sitting Walking rapidly throughout the plant also walking over the flower.	Pollen carrying part Mouth, ventral side of the body and legs
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Foraging activities			Time was 1:06:38PM, watched during this time period		
6AM - 8AM	8AM - 10AM	10AM - 12PM	12PM - 2PM	2PM - 4PM	4PM - 6PM

Foraging speed				
Sitting on flower head	Time of foraging - almost about 10-20 mins.	Flower touching (per minute) - many times not less than 50 times	At a stretch visiting the flowers of same plant species? Ans:- yes	Time spent at the spot - almost 30min



** Other visitors like Damselflies were also present there and it was sitting on a leaf of "Sambic jasmine" for almost 5mins then it was flown away.

here are "Damselflies"
 Order - Odonata
 Sub order - Zygoptera
 They are predatory in nature both nymphs and adults eat other insects.

Date:- 20/9/21 * Nothing special happened, only the same small black ants showed up at 12.48 PM where I went to check the pollinators on the time period of 12PM - 2PM. They stayed for 30 mins.

Date:- 21/9/21



No Hymenopteran showed up but a visitor came and it was "Dark grass blue" butterfly. "Dark grass blue" butterfly

- Order: Lepidoptera
- Class: Insecta
- Family: Lycaenidae
- Genus: Zizeeria

It was sitting on several plant leaves nearby the holy basil and didn't visiting for almost 30mins but didn't go for the Basil

Date:- 22/9/21

Nothing special, Though visited the spot for 2 hours, 12PM to 2PM

Date:- 23/9/21

*Again a hymenopteran digger bee showed up on 2PM and the Pollination was quick. Lasted for about 5mins. Flying from flower to flower of two basil plants for 5min.

Here are some other pollinators/visitors sighted on different random days of the year

<u>2021</u>

Date:- 25/9/21

A damselfly showed up on 4.09 PM, stayed for 2 mins.



It was sitting on the plant and roamed for sometimes. This time it was pollinating

Insect visitors	Damselfly			
<u>Order</u>	<u>Family</u>	G <u>enus/species</u>	Posture of sitting	Pollen carrying parts
Odonata	Coenagrionidae	Nehalennia	Ventral part was towards the flower	Legs

• Foraging activity :- time slot – 12PM to 2PM

Foraging speed				
Sitting on flower Dura head fora	ration of aging – 1min	Flower touching (per minute) - 1	At a stretch visiting the flower of same plant species -	Time spent in the field – Hardy 5 mins

Date:- 27/9/21

*A Hawk moth showed up, was perfectly pollinating the neighbouring Tabarnaemontana and passed Swiftly within 2 sec.
Description of Hawk moth-

 <u>Scientific classification</u> Kingdom: Animalia Phylum: Arthropoda Class: Insecta Order: Lepidoptera Superfamily: Bombycoidea Family: **Sphingidae**, Latreille, 1802

Diet – Flower nectar is the main food for hawk moths, fragments also affect their foraging activity.

Date:- 1/10/21 A house fly showed up and was perfectly pollinating the holy basil, stayed for almost 2 minutes.



Description of the pollinator

Insect pollinator	House fly			
<u>Order</u>	<u>Family</u>	<u>Genus/species</u>	Posture of sitting	Pollen carrying parts
Diptera	Muscidae	Musca/M.domestica	Ventral part was towards the flowers	Legs

• Foraging activity:- time slot – 5.29 PM (5PM to 6PM)

Foraging speed				
Sitting on flower	Duration of	Flower touching	At a stretch	Time spent in
head	foraging – 2 min	(per minute) - 1	visiting the	the field –
			same plant	hardly 5
			species - 1	minutes

Date :- 8/11/21

A lime butter fly showed up, pollination performed for almost 5 minutes. Description of the pollinator



Insect pollinator	Lime butterfly			
Order	Family	Genus/species	Posture of	Pollen carrying
			sitting	parts
Lepidoptera	Papilionidae	Papilio	Ventral part	Legs
			was towards	
			the flowers	

• Foraging activity:- time slot – 11.08 AM (11AM to 12PM)

Foraging speed				
Sitting on flower	Duration of	Flower touching	At a stretch	Time spent in
head	foraging – 10	(per minute) - 1	visiting the	the field –
	minutes		same plant	hardly 15
			species - 1	minutes

Date:- 6/10/21

A lime blue butterfly showed up twice as a visitor, stayed almost 5 minutes simultaneously



Description of the pollinator

Insect visitor	Lime blue			
Order	Family	Genus/species	Posture of	Pollen carrying
			sitting	parts
Lepidoptera	Lycaenidae	Chilades	Ventral part	None
			was towards	
			the leaf of the	
			lemon tree	

• Foraging activity:- time slot – 7.57 AM and 8.20 AM (7AM to 9AM)

Flower visiting on Tulsi (Ocimum tenuiflorum)

SAFIKUL ALAM

Δ Objectives of the study

1.To document the status and trends of pollinator.

2.To determine and analysis the multiple pressure that are driving changes in pollinator and animal pollinated plant .

3. To analyse and improve the interface between the scientific knowledge base on pollinator change assessment and policy instruments to reduce pollinator loss and mitigates it's effect.

4. To develop communication and education link with a wide range of stakeholders and the general public.

Δ Study site; villege -Sashpara, near primary school , Kandi, Murshidabad.

 Δ Collection methodology;

Day1: Date- 27/9/2021, Time – 8 Am to 10 Am

The location of the site our primary school garden .The Tulsi plant is located baside the wall and the time was 8 am to 10 am i.e 2 hours but I can't noticed any insect came there.

Day2, Date- 7/10/2021, Time-12pm to 2 pm

This was mid day time .I wating for 3 hours .Some time there was visitor arrived and it was Ant.This ant Shaw in the tob wall.

Day3 Date- 18/10/2021, Time- 4pm to 5 pm.

This was evening time .I waiting till 1 hour but there no insect found.

ΔDiscussion; Morphology of this flower is ---

Holy basil (*ocimum tenuiflorum*)

Colour	Shape	Size	Odour	Height from GL	Position of the nectarine	Position of the ovaries
White	 Small funnel	 0.5 cm in	 Sweet and strong		Flower base	Inside the flower. At

shaped, and leng star shaped from the bird's eye view.	gth and aroma cm in th			the last part of the style, above the disc, thalamus and pedicel.
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Only one visitor we can found that's back Ant .In the following we can describe the morphology of the ant---

Insect visitors	Small black ants			
<u>Order</u>	<u>Family</u>	Genus/species	Posture of sitting	Pollen carrying
Hymenoptera	Formicidae	Monomorium	Walking rapidly throughout the plant also walking over the tob.	<u>part</u> Mouth, ventral side of the body and legs

Foraging speed				
Sitting on flower head	Time of foraging - almost about 10- 20 mins.	Flower touching (per minute) - many times not less than 50 times	At a stretch visiting the flowers of same plant species? Ans:- yes	Time spent at the spot - almost 30min

 Δ Photo plate with number or identified name;

Day-1



Day-2

Day-3



ANTIGEN PRESENTATION of MHC CLASS II

Priyanshu Saha

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Introduction:

In contrast to antibodies or B-cell receptors, which can recognize an antigen alone, T-cell receptors only recognize pieces of antigen that are positioned on the surface of other cells. These antigen pieces are held within the binding groove of a cell surface protein called the major histocompatibility complex (MHC) molecule, encoded by a cluster of genes collectively called the MHC locus. MHC molecules act as a cell surface vessel for holding and displaying fragments of antigen so that approaching T cells can engage with this molecular complex via their T-cell receptors. There are two main types of MHC protein molecules—class I and class II. Class I and class II MHC molecules are membrane-bound Glycoproteins that are closely related in both structure and function.

Antigen presentation is an important immune process that is essential for T cell immune response. Because T cells recognize only fragmented antigens displayed on cell surfaces, antigen processing must occur before the antigen fragment, now bound to the MHC, is transported to the surface of the cell, a process known as presentation, where it can be recognized by a T-cell receptor.MHC class II molecules are critical for the initiation of the antigen-specific immune response.

Objective:

Antigen presentation with MHC class II is essential for the activation of T cells. MHC class II molecules at the cell surface of antigen presenting cells present antigenic peptides to CD4+ T helper cells. MHC class II molecules bind to peptides that are derived from proteins degraded in the endocytic pathway. In this review, the process of antigen presentation of MHC class II is discussed.

Discussion:

T cell receptor (TCR) can recognize only antigen that in associated to MHC molecules. T helper cells (Th cells) recognize antigen with MHC class II molecules on antigen presenting cells (APCs). In general, endogenous protein antigens are presented in MHC class I molecules to cytotoxic T cells (Tc cells) and exogenous protein antigens are presented in MHC class II molecules to Th cells. Antigen processing and presentation in both endogenous and exogenous pathway show these steps – 1.acquisition of antigen; 2.proteolysis; 3.delivery of peptides to MHC molecules and 4.display of the peptide-loaded MHC molecule on the surface of the cell. Here, the discussion is on the exogenous pathway.

MHC class II molecules are expressed by APCs - dendritic cells (DC), macrophages and B cells (and,under IFNγ stimuli, by mesenchymal stromal cells, fibroblasts and endothelial cells, and by epithelial cells, enteric glial cells). After internalization, antigen degrades into peptides within compartments of endocytic pathway. In each compartment, internalized antigen encounters hydrolytic enzymes and a lower pH. Final protein degradation and peptide loading in MHC class II proteins occurs in the **MHC class II-containing compartment** (**MIIC**), APCs' unique form of late endosome. Within the compartments antigen is degraded into oligopeptides of 13–18 residues that bind to class II MHC molecules in late endosomes, as the hydrolytic enzymes are more active under low pH. As the movement mechanism of internalized antigen from one endocytic compartment to the next is not clarified, some ideas are suggested that early endosomes from the periphery move inward to become late endosomes or small transport vesicles may carry antigen through the compartments. The portions of endocytic compartments return to where they fuse with the plasma membrane to recycle the surface receptors.

Some mechanism exist to prevent MHC class II molecules from binding with the antigenic peptides destined for MHC class I molecules. When class II MHC molecules are synthesized within rough endoplasmic reticulum (RER), they interact with a non-MHC encoded protein named the **invariant chain** (**Ii** or **CD74**) that serves as a chaperon and interacts with the MHC class II peptide-binding groove preventing any endogenous peptide to bind when MHC class II molecule is in the RER. The invarient chain (Ii or CD74) carries sorting signals that direct the transport of the MHC class II molecules from the trans-Golgi network to the endocytic compartments.

Some experiment shows that most of class II MHC-invariant chain are transported from RER through the Golgi complex and trans-Golgi network, then through the endocytic pathway, moving from early endosomes to the MIIC late endosomal compartment. The proteolytic activity increases in the successive compartment, the invariant chain goes through degradation. Somehow, a short fragment of the invariant chain named **CLIP** (for class II-associated invariant chain peptide) remains bound to the class II MHC molecule aft er the majority of the invariant chain has been degraded within the endosomal compartment. CLIP physically occupies the peptide-binding groove of the MHC class II molecule, like antigenic peptide. It prevents any premature binding of antigen-derived peptide.

A nonclassical class II MHC molecule named **HLA-DM** is required to catalyze the exchange of CLIP with antigenic peptide. The DM-alpha and DM-beta genes are located close to the TAP and LMP genes in the MHC complex of humans, with similar genes in mice. Like other class II MHC molecules, HLA-DM is a heterodimer of alpha and beta chains. Somehow, unlike other class II molecules it's relatively nonpolymorphic and isn't normally expressed at the cell wall but is found predominantly in the endosomal compartment.HLA-DM has been found to associate with the class II MHC beta chain and to serve in removing or editing peptides, including CLIP, that associate transiently with the binding groove of class II molecules. Peptides that make especially strong molecular relations with class II MHC, creating long-lived complexes, are harder for HLA-DM to displace, and therefore

become the repertoire of peptides that in the end make it to the cell surface as MHC-peptide complexes.

Another nonclassical MHC class II molecule, **HLA-DO**, like HLA-DM, is relatively nonpolymorphic class II MHC molecule. Unlike other class II molecules, HLA-DO has been found to act as a negative regulator of antigen binding. It modulates the function of HLA-DM and changes the repertoire of peptides that preferentially bind to classical Class II molecules. In cells that express both DO and DM, these two molecules strongly associate in the endoplasmic reticulum and maintain this interaction to the endosomal compartments. Although this interaction has been recognized for years, the function of this negative regulator (HLA-DO) and the impact of this changed peptide repertoire is only now being resolved. HLA-DO only observed in B cells and the thymus and recently has been expanded to dendritic cells (DCs).

After the process of CLIP exchanging for an antigenic peptide obtained from a protein degraded in the endosomal pathway, MHC Class II molecules binded with foreign peptide are then carried to the cell surface to present their cargo to CD4+ T cells. This is the process of antigen presentation by MHC class II molecules which is opposed to MHC class I as MHC class II molecules don't dissociate at the plasma membrane. The mechanism of MHC class II degradation have not been established but it can be ubiquitinised.



Figure: The MHC class II antigen presentation pathway (Source: Antigen Processing and Presentation; Pavel Nesmiyanov; Volgograd State Medical University, Volgograd, Russia)

Conclusion:

Unlike MHC class I, MHC II presents extracellular pathogens rather than intracellular. The first step is to accumulate pathogen through phagocytosis. The pathogen is then broken down and a desired component is then acquired and loaded onto a MHC II molecule. The MHC II molecule then travels to the cell surface to present the antigen to a Th cell. MHC II active Th cells which help release cytokines and other things which can help induce other cells which help to combat the pathogens outside the cells.

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Department of Zoology

Title: Parental Care and swimming behaviour of black Swan

Project report done by : Mrinmoy Ghosh

Roll:524

Introduction:

The black a Species of Swan is a large water bird, which breeds mainly in southeast and

Within south west regions of Australia. Australia, the black swan is nomadic, with erratic migration patterns dependent upon climatic Conditions. It is large bird with mostly black plumage and a red bill. It is monogamous breeder, with both parents sharing incubation and egg net- rearing duties. They swim with their feet and collect food with the help of their bill.



observation:

we Saw towards the a water group of black swan is going for swimming. In this group there are two parents and five ducklings. The parents are guarding the new-borns and moves slowly towards water. The new-borns feather are woolly and white but parents are totally black in colour. At last the parents jumped into water and new-borns jumped water and one after another. Among them 4 were diving well. The parents were catching food for feeding them.

Interpretation:

In this video we get a very wonderful example of learning behaviour. As the new-borns are little and their feet are not fully developed and their wings are not completly overdo with feathers they had a fear of swim water so, their parents encourages and teached how to jump slowly in waters and how to swim.

Here we also learn feeding behaviour of swan. As the new-borns' bill are too small to catch food, the parents were catching food for their babies and feeding them with the help of their bill.

RAMAKRISHNA MISSION VIVEKANANDA CENTENARY COLLEGE

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DSE 2C Project Report (End Semester), September-January 2021

PHYLOGENETIC STUDY OF DIFFERENT SNAKE SPECIES WITH RESPECT TO THEIR GEOGRAPHIC VARIATION BY USING MITOCHONDRIAL GENE CYT-B AND FINDING THE ANOMALOUS ORIGIN BY USING MULTIPLE SEQUENCE ALIGNMENT.

Submitted by

Dhruba Datta

UG | Semester: V | Roll No.: 526

Examination roll number-2022151161

Registration Number: A01-1112-115-018-2019 of 2019-2020

under the supervision of

Dr. Ajoy Mallik

Asst. Professor, Department of Zoology

RKMVCC Rahara

Introduction-

Mitochondrial DNA is the most useful evident to study phylogenetic relation among different species or organisms as it lacks recombination, it doesn't mutate faster it has a very low recombination rate in a constant manner it gets mutated, it inherited maternally. That's why it has massive use in determining phylogeny over three decades[1]. It do not follow Mendelian law of inheritance as it has different inheritance nature and evolutionary characteristics , comparison between mt-DNA and genomic phylogenies is an important tool to represent the speciation process of complexity[2]. So from the above discussion we may conclude that it is uni-parental only inherited from mother and no recombination occurs that's why it is most conserved than any other genetic material for ancestry study purpose.

Gene flow occur due to movement of individual organisms that reproduce in their new population or because of movement of gametes. When the isolated population reach secondary contact this is expected that these gene flow will get restore but genetic exchange between the populations shows a directional movement that is usually not symmetrical[3,4]. But as the migration or drift changes occur among the populations it is not necessary to reflect this effect to the whole genome[5,6]. That indicates though drift occurs and location change arise their genomic sequence will not get change and they show a common ancestry. So in this study this is our motto to see whether same individuals of same species in different location conserve their genomic sequence and their common ancestry or not. Or their is different common ancestry among same species in same area.

So many studies were done on the systematics of Asian pit vipers of *Trimeresurus* complex [7,8].

Except Antarctica everywhere this limbless reptiles are present about more than 3000 species till now[9]. Of the total snake species one third resides in Asia which is a large amount. Indonesia has 128 endemic snake species, India 112, China 54, Papua New Guinea 42, Sri Lanka 41, and the Philippines has 32 endemic species.

In a previous study they showed that species from same origin don't occupy monophyletic origin in phylogenetic tree. Rather they show some variation in their origins of same species of Corso-Sardinian grass snakes (*Natrix cetti*) with respect to their mitochondria genes. This study was done with respect to time by using relaxed molecular clock calibrated with fossil evidence[10].

cytochrome b (Cyt-b) and cytochrome c oxidase subunit 1 (Co-1) show largest variation among the all mitochondrial genes in animal's phylogenetic study. It was studied among five groups compared: populations within species; subspecies, semi-species, or/and sibling species; species within a genus; species from different genera within a family; and species from separate families within an order. By calculating the p-distance using ANOVA[11].

Species identification using DNA is a very effective tool for systemic research, biodiversity study or forensic analysis[12]. These molecular techniques are used for the identification of the snakes of different regions of different country all over the world [13].

Objective -

The main aim is to find the relations among the geographical origins (different countries or same country of different regions), if the same species of different snakes of different origins are connected phylogenetically(in monophyletic or paraphyletic group) or not and what is the relation among them with their ancestors by using mitochondrial DNA (cytochrome b).

So in this study this is our motto to see whether same individuals of same species in different location conserve their genomic sequence and show common ancestry or not. Or their is any different phylogenetic group among same species of the same area. And if this deviates then why the deviation occur by studying their gene sequence and base substitution through Multiple Sequence Alignment of DNA.

Materials And Methods-

Sampling -

Total 7 samples representing the genus *Trimeresurus* and other species has been selected for studying the phylogenetic relationship among them . These are *Trimeresurus stejnegeri*, *Trimeresurus gramineus*, *Trimeresurus albolabris*, *Trimeresurus popeiorum*, *Naja naja*, *Echis carinatus*, *Ophiophagus hannah*. In the above table it has been depicted with country name and the accession number of cytb.

Data Collection-

At first with all the desired species of desired snake species were documented in an excel file. Then by using NCBI nucleotide database we have collected the accession number for cytb gene for all respective species. After that by using all the accession number we did blast on NCBI nucleotide blast and collected the result of full gene bank data from where all the country names were collected and put on the table some of the rest which were not founded in the full gene bank data were collected from some research paper.

Sequence Analysis-

The sequence of the mitochondrial DNA (cytb) were aligned with MEGA11 software. First the FASTA sequence was downloaded for the respective species by doing blast of the selected accession number from NCBI. The BLAST results were filtered with 75 to 100 percent identity and 80 to 100 query coverage. Then we have analyzed the sequence on MEGA11 software this sequence were sorted by removing the gap in between them. To draw the phylogenetic tree for those selected species we used Construct/test neighbour joining tree option and all the phylogenetic trees were downloaded in PDF format for further use.

Schematic diagram of methodology-



<u>Result-</u>

	GeneBank	
Species Name	Accession ID(cyt b)	Geograpgical Origin
Trimeresurus albolabris	AF171887.1	East Java
Trimeresurus albolabris	AF171909.1	Nepal
Trimeresurus albolabris	AF171910.1	North Thailand
Trimeresurus albolabris	AF171894.1	South Thailand
Trimeresurus albolabris	KT216375.1	China: Yunnan
Trimeresurus albolabris	KP999432.1	Viet Nam: Gia Lai
Trimeresurus albolabris	AY352770.1	Viet Nam
Trimeresurus albolabris	AF171886.1	West Java
Trimeresurus albolabris	AF171891.1	West Java
Trimeresurus albolabris	AF171893.1	Northeast Thailand
Trimeresurus albolabris	KP999380.1	China: Qinzhou, Guangxi
Trimeresurus albolabris	KP999378.1	China: Qinzhou, Guangxi
Trimeresurus albolabris	KP999377.1	China: Qinzhou, Guangxi
Trimeresurus albolabris	KP999376.1	China: Qinzhou, Guangxi
Trimeresurus albolabris	KP999423.1	China: Hainan
Trimeresurus albolabris	KP999433.1	Viet Nam: Gia Lai
Trimeresurus albolabris	KP999372.1	China: Zhanjiang, Guangdong
Trimeresurus albolabris	KP999438.1	Viet Nam: Cao Bang
Trimeresurus albolabris	KP999430.1	Viet Nam: Vinh Phuc
Trimeresurus albolabris	KP999363.1	China: Cenxi, Guangxi
Trimeresurus albolabris	KP999405.1	China: Quanzhou, Fujian

Table 1. Accession IDs of cytochrome-b of Trimeresurus albolabris with their country names.



Figure-1: Phylogenetic tree of *Trimeresurus albolabris* based on cytochrome b mtDNA sequence data with respect to their geographical origin.

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 21 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 546 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Here we have taken total 21 accession IDs of cytochrome b as we have got their geographical origin against them. After aligned then in MEGA we got the above phylogenetic relationship between different origin. All the results shows more than 50% bootstrap support value. That means they shows a high posterior probabilities . Here we just found a very interesting data from the first relation that though distance of Nepal from East Java is more than 5000km and there is barrier of sea(figure-2) they occupy the monophyletic group and show a close relationship with 86% high posterior probability that indicates ancestry relation between them though it is little far from the origin of this tree but show relation between different geographic region. East Java, Nepal, North Thailand and South Thailand, China's Trimeresurus albolabris show paraphyletic group with the bootstrap value 86,66,68,98 respectively. Species of China: Qinzhou, Guangxi are close to the origin with bootstrap value 62% and they show monophyletic and paraphyletic relation among them. And the second interesting data we have found that though both species have same origin in Viet Nam: Gia Lai with accession ID KP999432.1 and KP999433.1 that show neither monophyletic nor paraphyletic relation that indicates divergence of them but have the common origin. Here accession ID KP999432.1 of origin Viet Nam: Gia Lai show monophyletic relation with AY352770.1 accession ID of the same geographic location Viet Nam but accession ID KP999432.1 of origin Viet Nam: Gia Lai show monophyletic relation with KP999372.1 accession ID of different location China: Hainan. China: Zhanjiang, Guangdong

Viet Nam: Cao Bang, Viet Nam: Vinh Phuc, China: Cenxi, Guangxi, China: Quanzhou, Fujian's species show paraphyletic relation with a low bootstrap value 21%, 12%, 16%, 24%.



5,003 km Distance from East Java to Nepal

Figure-2: Distance of Nepal from East Java(source: google)

Napal_AF171909.1 East_Java_AF171887.1 China_Hainan_KP999423.1 Viet_Nam_Gia_KP999423.1 China_Fujian_KP999405.1 China_Guangxi_KP999363.1 China_Guangxi_KP999372.1 Viet_Nam_Cao_KP999343.1 China_Guangxi_KP999376.1 China_Guangxi_KP999376.1 China_Guangxi_KP999378.1 China_Guangxi_KP999378.1 China_Guangxi_KP999378.1 China_Guangxi_KP999380.1 Northeast_Thailand_AF171893.1 Viet_Nam_Gia_KP999380.1 Viet_Nam_Gia_KP999380.1 West_Java_AF171886.1 West_Java_AF171886.1 West_Java_AF171891.1 North_Thailand_AF171910.1 China_Yunnan_KT216375.1 South_Thailand_AF171894.1

TAGCAATCA
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TACCAATICA
TACCALTCCA
TAGGARTINGA
TAGCARTUCA
TAGCAATICCA
TAGCAATCCA
TAGCAATICA
TAGCALTCCA
TRACABUCA
TAGGAR TOGA
TAGUNATUCA
TAGCAATUCA
TAGCARTICA
TAGCAAT <mark>C</mark> CA
TAGCAATCCA
TAGCAATCCA
TTTTTT

Nepal AF171909.1
East Java AF171887.1
China_Hainan_KP999423.1
Viet Nam Gia KP999433.1
China Fujian KP999405.1
China_Guangxi_KP999363.1
China Guangdong KP999372.1
Viet Nam Vinh KP999430.1
Viet_Nam-Cao_KP999438.1
China Guangxi_KP999376.1
China_Guangxi_KP999377.1
China Guangxi_KP999378.1
China Guangxi KP999380.1
Northeast Thailand AF171893.1
Viet_Nam_Gia_KP999432.1
Viet Nam AY352770.1
West_Java_AF171886.1
West_Java_AF171891.1
North_Thailand_AF171910.1
China_Yunnan_KT216375.1
South_Thailand_AF171894.1

10	80	30	100	110	130
CTAMACOCCAA	CATCGACCTAGC	CTTCTCATC	ATEATECATA	TCTCCCGAGA	TGTGCC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATC	ATTATTCACA	TCTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGE	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATTATECACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCI	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCALCCTACC	CITCICATCI	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCI	ATEATECAEA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATC	ATCATCCACA	TTTCTCGAGA	TGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	TGTACE
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	TGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCT	ATCATCCACA	TTTCTCGAGA	TGTACC
CTATACAGCCAA	CATCALCCTACC	CTTCTCATC	ATCATCCACA	TTTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCC	ATCATICACA	TTCTCGAGA	CGTACC
CTATACAGCCAA	CATCAACCTAGC	CTTCTCATCC	ATCATACACA	TTTCTCGAGA	CGTACC
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CTATACAGCCAA	CATCGACCTAGE	CITCICATCI	ATCATCCACA	TCTCTCCAGA	CGUYGG
CTATACAGCCAA	CATCGACCTAGC	CTTCTCATCT	ATCATCCACA	TCTCTCGAGA	CGTACC
CTAMACAGCCAA	CATCMACCTAGE	CTTCTCATC	ATEATECAEA	TETCHCGAGA	TGTACE

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East Java AF171887.1
China Hainan KP999423.1
Viet_Nam_Gia_KP999433.1
China Fujian KP999405.1
China Guangxi_KP999363.1
China Guangdong KP999372.1
Viet Nam Vinh KP999430.1
Viet_Nam-Cao_KP999438.1
China_Guangxi_KP999376.1
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Northeast Thailand AF171893.1
Viet_Nam_Gia_KP999432.1
Viet_Nam_AY352770.1
West_Java_AF171886.1
West_Java_AF171891.1
North_Thailand_AF171910.1
China_Yunnan_KT216375.1
South Thailand AF171894.1

130	140	150	160	170	180
CTACGGCTGAGTC	ATACAAAATAC	ACATGCCATT	GGCGCATCCA	TATTCTTTAT	TGCAT
ATACGGCTGAATT	ATACAAAACAC	GCATGCTATC	GGGGGCATCEA	TATTCTTTATC	TGCAT
ATACGGCTGAATC	ATACAAAACAC	GCATGCTATT	GGCGCATCTA	TATTCTTTAT	TGCAT
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ATACGGCTGAATC	ATACAAAACAC	GCATGCTATT	GGCGCATCTA	TATTCTTTAT	TGCAT
ATACGGCTGAATC	ATACAAAACAC ATACAAAACAC	GCATCOTATE	GGCGCATCTA	TATTCTTTAT	TGCAT
ATACGGCTGAATC	ATACAAAACAC	GCATGCTATT	GGCGCATCTA	TATTCTTTATT	TGCAT
ATACGGCTGAATC	ATACAAAACAC ATACAAAACAC	GCATGOTATI	GGCGCATCTA GGCGCATCTA	TATTCTTTAT	TGCAT
ATACGGCTGAATC	ATACAAAACAC	GCATGCTATT	GGCGCATCTA	TATTCTTTAT	TGCAT
ATACGGCTGAATT ATACGGCTGAATT	ATACAAAACAC ATACAAAATAC	GCATGOTATT GCATGOTATT	GGCGCATCTA	TATTCTTTATC	TGCAT
ATACGGCTGAAT	ATACAAAATAC	GCATGCTATT	GGCGCATCTA	TATTCTTTAT	TGNAT
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ATACGGCTGAATT	ATACAAAACAC	GCATGC CATT	GGCGCATCTA	TATTCTTTAT	TGEAT
CTACCCCCCCCAATT	ATACAAAACAC	GCATGCCATT	GGCGCATCTA	TATTCTTTAT	TGCAT

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CTACACCCACATC	GCACGAGGACTT	TACTACGG <mark>C</mark> 7	CCTATCTTA	CAAAGAAGT	ATGACT
CTACATCCACATC	GCACGAGGACTT	TACTACGEC	CCTATOTTA)	CAAAGAAGT	ATGACT
CTACATCCACAT	GCACGGGGGCTC	TACTACGGC	CCTATCTTAL	CRAAGAAGT.	ATGACT
CTACATCCACAT	GCACGAGGGCTC	TACTACGGC	CCTATCTTAL	CAAAGAAGT.	ATGACT
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CTACATCCACATT	GCACGAGGCTC	TACTACGGCI	CCTATCTTAL	CAAAGAAGT	ATGACT
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CTACATCCACAT	GCACGAGGCTC	TACTACGG	CCTATCTTAJ	CARAGAAGT	ATGACT
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CTACATCCACATC	GCACGAGGACTC	TACTACGE	CCTATETTAL	CAAAGAAGT	ATGACT
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CTACATCCACATC	GCACGAGGACTC	TACTACGG	CCTATCTTAL	CAARGAAGT	ATGACT
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CTACATCCACATC	GCACGAGGACTT	TACTACGGT	CCTATCTTAL	CAAAGAAGT	ATGACT
CTACATCCACATC	GCACGAGGACTT	TACTACEGAT	CCTATCTTAL	CAAAGAAGT	ATGACT
CTACANCCACATC	CACCACACAC	TACTACCOT	CCTATCTTA	CASAGAGT	ATGACT

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250	260	270	280	290 300
CTOAGGCACAACCCTT	TTAATTATEC	TAATAGECACA	GOGTACTAC	GETATGTACTOC
CTCAGGCACAACCCTT	TTAATTATCC	TAATAGCCACA	GCCTTCTTC	GTTATGTACTAC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTTC	GCTATGTACTACC
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CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTTC	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTTC	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTT	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGECACA	GCCTTCTTTG	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTG	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTTC	GCTATGTACTACC
CTCAGGCACAACCCTT	TTARTCATCT	TAATAGCCACA	GCCTTCTTTG	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTC	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTT	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGECACA	GCCTTCTTT	GCTATGTACTACC
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CTCAGGCACAACCCTT	TTAATTATCC	TAATAGCCACA	GCCTTCTT	GTTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATAT	TAATAGCCACA	GCCTTCTT	GCTATGTACTACC
CTCAGGCACAACCCTT	TTAATCATCT	TAATAGCCACA	GCCTTCTTC	GCTATGTACTACC

Nepal AF171909.1
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China Guangxi_KP999363.1
China Guangdong KP999372.1
Viet Nam Vinh KP999430.1
Viet_Nam-Cao_KP999438.1
China Guangxi KP999376.1
China_Guangxi_KP999377.1
China_Guangxi_KP999378.1
China Guangxi KP999380.1
Northeast Thailand AF171893.1
Viet_Nam_Gia_KP999432.1
Vist_Nam_AY352770.1
West_Java_AF171886.1
West_Java_AF171891.1
North Thailand AF171910.1
China_Yunnan_KT216375.1
South Thailand AF171894.1

310	320	330	340	350	360
ATGAGGCCAAATAT	CCTTCTGAGC.	AGCAACAGT	ATTACAAAC	TCC TAACCGC	CATTCC
ATGGGGGCCAAATAT	COTTOTGAGO	AGCAACAGT	ATTACAAAC	TTOCTARCOGC	CATECC
ATGAGGACAAATAT	CCTTCTGGGC.	AGCAACAGT	ATTACAAAC	TOTTAACCGC	CATCCC
ATGAGGACAAATAT	CCTTCTG <mark>G</mark> GC	AGCAACAGTI	LATTACAAAC	TCTTAACCGC	CATCCC
ATGAGGACAAATAT	CETTETGEGE	AGCAACAGT	ATTACAAAC	TOTTAACCGC	CATCCC
ATGAGGACAAATAT	CETTETEGEC	AGCAACAGT	ATTACAAAC	TUTTAACCGC	CATCCC
ATGAGGACAAATAT	CCTTCTG <mark>G</mark> GC	AGCAACAGT	LATTACAAAC	CTCTTAACCGC	CATCCC
ATGAGGACAAATAT	CCTTCTGGGC	AGCAACAGT	ATTACAAAC	TETTAACCGC	CATCOO
ATGAGGACAAATAT	CCITCIGGC	AGCAACAGT	ATTACAAAC	CTOTTAACCGC	CATCCC
ATGAGGACAAATAT	CCTTCTGGGC	AGCAACAGT	ATTACAAAC	TTCTTAACCGC	CATCCC
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ATGAGGCCAAATAT	CCTTCTGGGC	AGCAACAGT	ATTACAAAC	TCCTAACCGC	CATCCC
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ATGAGGCCAAATAT	CCTTCTGGGC	AGCAACAGT	AATTACAAAC	TCCTAACCGC	CATTCO
ATGRCCCAAATAT	CCTTCTGGGC	AGCAACAGT	ATTACAAAC	CTOCTARCOGO	CANTOO
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370	380	390	400	410	420
ATACTTAGGAACA	ACCCTCACCAC	GTGACTATC	GGGGGGTTTC	CAATCAACG	ACCCAAC
ATACCTAGGAATA	ACCETCACCAC	ATGCTATG	AGGGGGCTTC:	GCAATCAACG	ACCCAAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATE	GGAGGCTTC	CAATCAACG.	ACCCTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATE	GGAGGCTTC	GCAATCAACG	ACCCTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	GGAGGCTTC	CAATCAACG	ACCCTAC
TACCTAGGAACA	ACCCTCACCAC	ADGACTATG	AGGAGGCTTC	CAATCAACG	ACCCTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	GCRATCARCG	ACCOTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	CAATCAACG	ACCCTAC
TTACCTACGAACA	ACCCTCACCAC	AUGACIADG	AGGAGGCTTC	CANTCANCE	ACCOTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	CAATCAACG	ACCOTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	GCAATCAACG	ACCCTAC
TTACCTACCA	ACCCTCACCAC	ATCACTATE	AGGAGGCTTC	CAATCAACG	ACCOTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	CAATCAACG	ACCOTAC
TTACCTAGGAACA	ACCETCACCAC	ATGACTATG	AGGAGGCTTC	GCRATCAACG	ACCCTAC
TTACCTAGGAACA	ACCCTCACCAC	ATCACTACCI	AGGAGGCTTC	CAATCAACG	ACCOTAC
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TTACCTAGGAACA	ACCCTCACCAC	ATGACTATG	AGGAGGCTTC	GCAATCAACG	ACCCTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTATE	AGGAGGCTTC	CAATCAACG	ACCOTAC
TTACCTAGGNACA	ACCETCACCAC	ATGACTATG	AGGAGGCTTN	CAATCAACG	ACCOTAC
TTACCTAGGAACA	ACCCTCACCAC	ATGACTGTG	AGGAGGCTTC	CAATCAACG	ACCOTAC
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Nepal_AF171909.1
East Java AF171887.1
China Hainan KP999423.1
Viet Nam Gia KP999433.1
China Fujian KP999405.1
China Guangxi KP999363.1
China Guangdong KP999372.1
Viet Nam Vinh KP999430.1
Viet_Nam-Cao_KP999438.1
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China_Guangxi_KP999377.1
China Guangxi KP999378.1
China Guangxi_KP999380.1
Northeast Thailand AF171893.1
Viet_Nam_Gia_KP999432.1
Viet Nam AY352770.1
West_Java_AF171886.1
West Java AF171891.1
North Thailand AF171910.1
China_Yunnan_KT216375.1

Nepal_AF171909.1 East_Java_AF171887.1 China Hainan KP999423.1 Viet_Nam_Gia_KP999433.1 China_Fujian_KP999405.1 China_Guangxi_KP999363.1 China_Guangdong_KP999372.1 Viet_Nam_Vinh_KP999430.1 Viet_Nam-Cao_KP999438.1 China_Guangxi_KP999376.1 China_Guangxi_KP999377.1 China_Guangxi_KP999378.1 China_Guangxi_KP999380.1 Northeast Thailand AF171893.1 Viet_Nam_Gia_KP999432.1 Viet_Nam_AY352770.1 West_Java_AF171886.1 West_Java_AF171891.1 North_Thailand_AF171910.1 China_Yunnan_KT216375.1 South_Thailand_AF171894.1

430	440	450	460	470	480
ACTARCCCGTTTCTT	GCCCTACAC	TTATCCTCCC	ATTCACTATC	ATCTCCTTA	TCTTC
ACTAACCCGCTTCTT	GCCCTACAC	TTATCCTCCC?	ATTCGCTATCI	ATCTCCCTA	TOTIC
ACTAACCCGTTTCTT	GCCCTACAT	ITCATECT TCC!	ATTCACTATC:	ATCTCCCTA	TCCTC
GCTAACCCGTTTCTT	GCCCTACAT	ITCATCCTTCC/	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTTC	GECCTACAT	TTCATCCTTCC3	ATTCACTATCI	ATCTCC TTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	ITCATCCTTCC!	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	TTCATCCTTCC/	ATTCACTATES	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTTC	GCCCTACAT	TTCATCCTTCC!	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	TTCATCCTTCC3	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	TTCATECTTCC!	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	TTCATECTTCC:	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	ITCATCCTTCCI	ATTCACTATC:	ATCTCCTTA	TCCTC
ACTAACCCGTTTCTT	GCCCTACAT	ITCATCCTTCC.	ATTCACTATES	ATCTCCTTA	TCCTC
ACTAACCCGCTTCTT	GCCCTACAT	TTCATCCTTCCI	ATTCGCTATC	TCTCCTTA	TOTTO
ACTAACCCGTTTCTT	GCCCTACAN	TTCATCCTTCCI	ATTCCCTATC	ATCTCCTTA	TOTTO
ACTAACCCGTTTCTT	GCCCTACAT	TEATECTICCI	ATTCCCTATC	TCTCCTA	TCTTC
ACTAACCCGCTTCTTC	GCCCTACAT	TTCATCCTTCC?	ATTCGCTATC	TCTCCTTA	TOTTO
AGTAACCCGCTTCTT	RECETACAT	THEATCOTTCC!	ATTCCCTATC	TCTCCTTA	TOTTO
GTANGCOGTATCTT	GECCTACAC	TTCATECTTCC	ATTCGCTATE	TCTCCTA	TOTTO
ACTAACCCGTTTCTTC	GECCTACAC	TTCATCCTTCC	ATTCCCTATC	TCTCCTTA	TOTIC
ACTAACCCGTTTCTT	GECCTACAC	TCATCCTTCC	ATTOGCTATO	TCTCCTTA	TOTAL
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490	300	910	0.40	330	340
AATCCATATCCT	GCTACTACATA	CGACGCCTC	AGCAAGCCC	TAGGCACAAA	TCAGA
AATTCATATCCT	CCTACT GCATA	CGAAGGTTC	TACAACCOAT	TAGGAACAAI	CTCAGA
AATTCACATCCT	CCTACTACATA	CGAAGGTTC	AGCAACCCC	TAGGAACAAI	CTCAGA
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AATHCABATCCT	CORRECTACATA	CONACCUTC	AGCAACCOG	TAGGAACAA	CTCAGA
AATTCACATCOT	COTACTACATA	CONSCERED	AGOANCOGC!	TAGGAACAA	CHCACA
AATTCACATCCT	CTACTACATA	CAACCETC	A COMPOSE	TACCALCAL	GTCACA
AATTCACATCCT	CTACTACATA	CGAAGGTTC	AGCAACCOCT	TAGGAACAA	CTCAGA
AATECACATCCT	CETACTACATA	CGAAGGTTC	AGCAACCCC	TAGGAACAA	CTCAGA
AATTCACATCCT	CCTACTACATA	CGAAGGTTC	AGCAACCCC	TAGGAACAA	CTCAGA
AATTCACATCCT	CCTACTACATG	CGAAGGTTC	AGCAACCOCT	TAGGNNNAA	CTCAGA
AATTCACATCCT	CCTACTACATA	CGAAGGTTC	AGCAACCCC	TAGGAACAAA	CTCAGA
AATTCACATECT	CCTACTACATA	CGAAGGTTC	AGCAACCCC	TAGGAACAAI	CTCAGA
AATTCACATCCT	CCTACTACATA	CGAAGGTTC	AAGCAACCCC	TAGG GACAA!	CTCAGA
AATTCACATCCT	CCTACTACATA	CGAAGGTTC	AGCAACCCE	FTAGGAACAA/	ETCAGA
AATHCATATCCT	CCTACTACATA	CGANEGTTCI	AGCAACCCC	TAGEAACAA	TCAGA
AATTCAGATCCT	CEVACUACIANA	EGHARCTINE!	ABGCAACCOC	TAGGGACAA	ACTICAGA



Figure-3: Multiple sequence alignment of phylogenetic tree.

Species Name	Accessio n ID	Geographic Location	graphic T tion Base Substituion a						Tot al	Percentag e substituti on(%)		
			Т >С	C >T	A >G	G >A	T >A	A >C	C >A	A >T		
Trimeresurus albolabris	AF1718 87.1	<mark>East Java</mark>	13	13	7	5	2	2	0	1	42	7.70
Trimeresurus albolabris	AF1719 09.1	<mark>Nepal</mark>	11	10	8	4	2	2	0	0	37	6.77
Trimeresurus albolabris	AF1719 10.1	North Thailand	4	8	4	2	0	1	1	0	20	3.66
Trimeresurus albolabris	AF1718 94.1	South Thailand	6	7	1	2	0	2	0	0	18	3.3
Trimeresurus albolabris	KT21637 5.1	China: Yunnan	4	5	4	2	0	1	1	0	17	3.11
Trimeresurus albolabris	KP9994 32.1	<mark>Viet Nam: Gia</mark> Lai	3	5	1	2	0	1	0	0	12	2.2
Trimeresurus albolabris	AY3527 70.1	Viet Nam	3	4	1	2	0	1	0	0	11	2.01
Trimeresurus albolabris	AF1718 86.1	West Java	4	6	1	2	0	1	1	0	15	2.75
Trimeresurus albolabris	AF1718 91.1	West Java	3	5	1	2	0	1	1	0	13	2.4
Trimeresurus albolabris	AF1718 93.1	Northeast Thailand	2	3	0	2	0	1	0	0	8	1.47
Trimeresurus albolabris	KP9993 80.1	China: Qinzhou, Guangxi	0	1	0	0	0	0	0	0	1	0.18
Trimeresurus albolabris	KP9993 78.1	China: Qinzhou, Guangxi	0	1	0	0	0	0	0	0	1	0.18
Trimeresurus albolabris	KP9993 77.1	China: Qinzhou, Guangxi	0	1	0	0	0	0	0	0	1	0.18
Trimeresurus albolabris	KP9993 76.1	China: Qinzhou, Guangxi	0	1	0	0	0	0	0	0	1	0.18
Trimeresurus albolabris	KP9994 23.1	<mark>China: Hainan</mark>	1	0	1	0	0	0	0	0	2	0.37
Trimeresurus albolabris	KP9994 33.1	<mark>Viet Nam: Gia</mark> Lai	0	0	2	0	0	0	0	0	2	0.37
Trimeresurus albolabris	KP9993 72.1	China: Zhanjiang, Guangdong	0	0	0	0	0	0	0	0	0	0
Trimeresurus albolabris	KP9994 38.1	Viet Nam: Cao Bang	0	0	0	0	0	0	0	0	0	0
Trimeresurus albolabris	KP9994 30.1	Viet Nam: Vinh Phuc	0	0	0	0	0	0	0	0	0	0
Trimeresurus albolabris	KP9993 63.1	China: Cenxi, Guangxi	0	0	0	0	0	0	0	0	0	0
Trimeresurus albolabris	KP9994 05.1	China: Quanzhou, Fujian	0	1	0	0	0	0	0	0	1	0.18

Table-2: Multiple sequence alignment's discussion on base substitution.



Figure 4: Geographical distribution of Trimeresurus albolabris.

In total 19 positions species of East Java and Nepal have shown similar base substitution and none of the region which indicates why they are showing monophyletic origin.

Species of Viet Nam Gia Lai don't show any similar base substitution rather they have shown different base substitution from each other and they also shown percentage substitution of 2.2 and 0.37 respectively which is not neither similar nor close. That's why though they are from same origin don't show monophyletic or paraphyletic origin rather it is showing the same percentage base substitution with species of China: Hainan species that is 0.37% from this result we can conclude their monophyletic nature. Here up to 546th position conserved region is located. And which species are in monophyletic origin they showing similar type of percentage base substitution.

Table-3: Accession IDs of cytochrome-b of Trimeresurus gramineus with their country names.

	GeneBank Accession ID(cyt	
Species Name	b)	Geograpgical Origin
Trimeresurus gramineus	MG995812	India: Odisha
Trimeresurus gramineus	MG995810	India: Odisha
Trimeresurus gramineus	MG995808	India: Odisha
Trimeresurus gramineus	AY352762	India
Trimeresurus gramineus	AY352761	India
Trimeresurus gramineus	AF171905	South India



Figure-5: Phylogenetic tree of Indian snake(viper) *Trimeresurus gramineus* based on cytochrome b mtDNA sequence data with respect to their geographical origin with bootstrap value >50%.

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the

bootstrap test (500 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 6 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 711 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

From the above phylogenetic tree we can interpret that *Trimeresurus gramineus* of Odisha show monophyletic origin with the highest bootstrap value 100%. And rest regions show paraphyletic origin. South Indian origin species shows the closest relation with the origin. And Odisha regions species show farthest with respect to the origin.

Table-4: Accession IDs of cytochrome-b of Trimeresurus popeiorum with their country names.

Species Name	Accession ID	Country
Trimeresurus popeiorum	AF171888.1	West Malaysia
Trimeresurus popeiorum	AF171904.1	South Thailand
Trimeresurus popeiorum	AF171902.1	North Thailand
Trimeresurus popeiorum	KT216370.1	China: Yunnan
Trimeresurus popeiorum	KT216359.1	China: Yunnan
Trimeresurus popeiorum	KT216361.1	China: Yunnan
Trimeresurus popeiorum	KT216368.1	China: Yunnan



Figure-6: Phylogenetic tree of Indian snake(viper) *Trimeresurus popeiorum* based on cytochrome b mtDNA sequence data with respect to their geographical origin .

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 7 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 610 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Here West Malaysia and South Thailand's species shows monophyletic relation among them with bootstrap value 100% and both show paraphyletic relation with North Thailand and

China Yunnan's species. China Yunnan's species show closest relation to origin with accession ID KT216368.1 and West Malayasia's species show farthest relation with origin. And both the China Yunnan's species shows monophyletic relations and with another China Yunnan's species show paraphyletic relation with bootstrap value 74 and 76 respectively.

Table-5: Accession IDs of cytochrome-b of Trimeresurus stejnegeri with their country names.

Species Name	Accession ID	Geographic Origin
Trimeresurus stejnegeri	KX019087	China: Guangdong
Trimeresurus stejnegeri	KX019144	China: Hunan
Trimeresurus stejnegeri	KX019148	China: Jiangxi
Trimeresurus stejnegeri	KX019068	China: Fujian
Trimeresurus stejnegeri	KX019140	China: Fujian
Trimeresurus stejnegeri	KX019143	China: Jiangxi
Trimeresurus stejnegeri	KX019121	China: Jiangxi
Trimeresurus stejnegeri	KX019106	China: Anhui
Trimeresurus stejnegeri	KX019137	China: Anhui
Trimeresurus stejnegeri	KX019155	China: Zhejiang
Trimeresurus stejnegeri	KX019126	China: Zhejiang
Trimeresurus stejnegeri	KX019104	China: Hainan
Trimeresurus stejnegeri	KX019139	China: Hainan
Trimeresurus stejnegeri	KT216408	Viet Nam
Trimeresurus stejnegeri	KX019147	Viet Nam
Trimeresurus stejnegeri	KX019160	Viet Nam
Trimeresurus stejnegeri	KX019159	Viet Nam
Trimeresurus stejnegeri	KX019152	China: Guangxi
Trimeresurus stejnegeri	KX019154	China: Guangxi
Trimeresurus stejnegeri	KX019037	China: Chongqing
Trimeresurus stejnegeri	KX019071	China: Guizhou
Trimeresurus stejnegeri	KX019008	China: Chongqing
Trimeresurus stejnegeri	KX019110	China: Sichuan
Trimeresurus stejnegeri	KX019141	China: Guizhou
Trimeresurus stejnegeri	KX019053	China: Guizhou
Trimeresurus stejnegeri	KX019124	China: Guangxi
Trimeresurus stejnegeri	KX019053	China: Guizhou
Trimeresurus stejnegeri	KX019158	China: Guangdong
Trimeresurus stejnegeri	KX019149	China: Guangxi
Trimeresurus stejnegeri	KX019157	China: Hunan
Trimeresurus stejnegeri	KX019156	China: Guangxi



Figure-7: Phylogenetic tree of *Trimeresurus stejnegeri* based on cytochrome b mtDNA sequence data with respect to their geographical origin with bootstrap value >50%.

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of

the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 30 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1040 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Here we have taken total 31 accession IDs of cytochrome b as we have got their geographical origin against them and which IDs shows common origins we haven taken only one or two from them as all of them are showing monophyletic origins. After aligned then in MEGA we got the above phylogenetic relationship between different origin. All the results shows more than 50% bootstrap support value. That means they shows a high posterior probabilities. Closest relation from the origin are shown by accession id KX019037 China:Chongqing's species and their monophyletic species. Same origin species shows monophyletic origin and paraphyletic origins. China: Anhui, China: Zhejiang, China: Hainan, China: Guangxi, China: Guizhou and China: Chongqing shows maximum bootstrap value 100.

Table-6: Accession IDs of cytochrome-b of *Echis carinatus* with their country names.

Species Name	Accession ID MG995822	Geographic origin India: Tamilnadu,
Echis carinatus		Vadanemmeli
Echis carinatus	MG995811	India: Odisha, Talcher
Echis carinatus	MH646094	Iran
Echis carinatus	GQ359441	Pakistan
Echis carinatus	GQ359440	Pakistan
Echis carinatus	GQ359439	India
Echis carinatus	GQ359438	Pakistan
Echis carinatus	GQ359437	United Arab Emirates
	GQ359436	United Arab Emirates
Echis carinatus	00250425	India: Tamilandu
Echis carinatus	GQ359435	
Echis carinatus	GQ359434	India: Rajasthan
Echis carinatus	GQ359433	India
Echis carinatus	AJ275706	Pakistan





Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown above the branches [2]. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 13 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 554 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Echis carinatus common name is saw-scaled viper shows Asiatic origin and all resides in a same phylogenetic tree without showing any exceptions. Total 13 accession IDs were selected and put them with species name against their origin after aligned in MEGA11. Monophyletic origin shown by the species from Pakistan origin with bootstrap value 80 and their accession numbers are GQ359441.1 and AJ275796.1 respectively and another monophyletic origin shown by Indian species with bootstrap value 63 and their accession numbers are GQ359439.1 and MG995811.1 respectively. And rest of the origins shows paraphyletic origin with others.

Table-7: Accession IDs of cytochrome-b of Ophiophagus hannah with their country names.

Species Name	Accession ID	Geographic Location
Ophiophagus hannah	MT346766.1	Viet Nam
Ophiophagus hannah	MT346773.1	China
Ophiophagus hannah	MT346767.1	Indonesia
Ophiophagus hannah	MT346770.1	Malaysia
Ophiophagus hannah	MT346771.1	Malaysia
Ophiophagus hannah	MT346765.1	Malaysia
Ophiophagus hannah	MT346764.1	Malaysia
Ophiophagus hannah	MT346768.1	Philippines
Ophiophagus hannah	MT346769.1	Indonesia
Ophiophagus hannah	MT346772.1	Indonesia


Figure-9: Phylogenetic tree of *Ophiophagus hannah* based on cytochrome b mtDNA sequence data with respect to their geographical origin with bootstrap value >50%.

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. This analysis involved 10 nucleotide sequences. All ambiguous positions were removed for each sequence pair

(pairwise deletion option). There were a total of 427 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Ophiophagus hannah or commonly known as king kobra shows paraphyletic origin and no monophyletic origin with respect to all the countries and all the countries are of Asiatic origin. Total 10 accession IDs were selected to construct the phylogenetic tree. We have put the respective country name with their accession IDs as founded from the NCBI database. From this tree we cannot conclude the origin and which country species was originated first and which has the highest distance from the origin.

Table-8: Accession IDs of cytochrome-b of *Naja naja* with their country names.

Species Name	Accession ID	Geographic Location
Naja naja	MT346711.1	Nepal
Naja naja	AY13376.1	Nepal
Naja naja	MZ029431.1	India: Tamil Nadu
Naja naja	GQ359506.1	Nepal
Naja naja	DQ272477.1	Hong Kong
Naja naja	MH337569.1	Sri Lanka
Naja naja	EU547039.1	Australia
Naja naja	MT346712.1	Sri Lanka





Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The evolutionary distances were computed using the Maximum Composite Likelihood method

and are in the units of the number of base substitutions per site. This analysis involved 8 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 264 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Total 8 accession IDs were selected to construct the tree as we have found the origin nmes from NCBI database of this 8. From the above tree of Naja naja we can say that Nepal and hong Kong origin shows the closest relation to the original with accession IDs GQ359506.1 and DQ272477.1 respectively. And a interesting relation we habe found here that Sri Lanka and Australia's Naja species shows monophyletic origin with a high bootstrap value of 96 though there are no connection between two places.



Figure -11: Multiple sequence alignment of Naja Naja phylogenetic tree.

Species Name	Accession ID	Geographic Location			Base Su	Ibstituion			Total	Percentage substitutio n(%)
			T>C	C >T	A>G	G>A	T>A	A >C		
Naja naja	MT346711. 1	Nepal	2	3	1	1	0	0	7	2.46
Naja naia	AY13376.1	Nepal	2	3	1	1	0	0	7	2.46
Naja naja	MZ029431. 1	India: Tamil Nadu	3	2	1	1	0	0	7	2.46
Naja naja	GQ359506. 1	Nepal	2	3	1	1	0	0	7	2.46
Naja naja	DQ272477. 1	Hong Kong	7	7	6	1	1	4	26	9.12
Naja naja	MH337569. 1	Sri Lanka	2	5	3	2	1	0	13	4.56
Naja naja	EU547039.1	Australia	2	6	3	2	1	0	14	4.91
Naja naja	MT346712. 1	Sri Lanka	2	5	3	2	1	0	13	4.56

Table-9: Multiple sequence alignment's discussion on base substitution.

From the above multiple sequence alignment(MSP) it is clearly seeing that base substitution in all positions except 132nd position is same between the two same species of *Naja naja* of two different regions of Australia and Sri Lanka. So from this result we can interpret the cause why they are showing monophyletic origin.

From the table of base substitution it Hong Kong's Naja species shows the highest base substitution rate of 9.12%. And Australia and Sri Lanka shows approximately same type of base substitution rate that also indicates their monophyletic nature.

Species of Nepal(total 3) and India showing similar percentage base substitution of 2.46% that's why they all are located in same group. Here up to 285th position conserved region is located. And which species are in monophyletic and paraphyletic origin they showing similar type of percentage base substitution.

Discussion-

From the above results we can conclude that in the same region all the species may not stay in monophyletic or paraphyletic group and the vice versa different region's same species may occupy monophyletic position. So not only the same region's species occupy monophyletic group but also others show similar category which interpret about their common ancestry and previous relation among them from which they became diverge. By analyzing Multiple Sequence Alignment(MSA) from base pair substitution we can conclude the reason that why they are showing monophyletic origin though they are very far apart from each other. Due to

common change in base substitution they showing common ancestry. And same origin don't showing monophyletic or polyphyletic origin due to different base substitution in same or different positions. The regions which are in same group showing same percentage base substitution.

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A Brief Review on Exposing Rate of IHS (Anaphylaxis) after Vaccination at Male and Female.

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Introduction:

Females have an immune adversity response to vaccinations.(2) Basically after vaccination at this stage men and women have different responses due to hormonal reasons, whereas in women it's much more active. But looking at the random evidence, it's clear that women have much higher risk of side effects or hypersensitivity than men after vaccination. Some of the post-hypersensitivity outcomes are dyspnea, anaphylaxis, wheezing, syncope, dizziness etc. After vaccination anaphylaxis is rare because there have been very few cases reported. It can be one in every 100,000,(negligible). But in terms of gender classification, women are more likely to be reported as anaphylactic after the vaccination. Post-vaccine anaphylaxis is more common in men and women at different stages of life.(2) Evidence suggests that anaphylaxis is more common in men during puberty and in women after puberty. Many subsequent reviews highlighted that females have a higher frequency of hypersensitivity than male(passive surveillance and rarity of events). A comprehensive population study shows that there are many vaccines in the world that are more likely to infect men than most. Larger population studies will clarify the difference rate on the basis of gender and related biological studies. Studies on reviewing based on anaphylaxis in emergency room reports shows that 58% and 60% of women are suffering and when it comes For non food related anaphylaxis hospitalization the cases of women found 57%. For food allergies 65% in women.

Objective:

The chances of IHS(majorly I'm highlighting here anaphylaxis) increase mainly after vaccination, and in each case gender and age have become a major factor.Because women and men have not been exposed to IHS equally, in some cases after vaccination, men are more prone to anaphylaxis, in other words, the ratio of males to females is getting heavier in males and vice versa in some vaccinations.So here are some of the VAERS(vaccine adverse event reporting system, a US spontaneous reporting system) experimental vaccination trials conducted from 1987 to 2010 and its impact on a large population. Here data on five vaccine trials have been collected and presented in a comparative manner.

Discussion:



Figure 1: Anaphylactic reaction(IHS) after vaccination

Anaphylaxis: Anaphylaxis is a sudden, potentially life-threatening allergic reaction that involves multiple system dysfunction. It's caused by massive release of inflammatory mediators from mast cells and basophils into the circulation. These mediators are normally responsible for the body's protective response against infections or injuries. In case of anaphylaxis this is mainly due to the severity of the gender. Female hormonal factors like estrogen play a special role but evidence says, it's still not certain that only women will respond immediately to ier, in some cases this tendency has been observed in men after specific vaccination. Only some experimental research is able to address the gender issue in anaphylaxis.(2)

Immediate Hypersensitivity Reactions Following Vaccines by Gender:

Anthrax vaccine: More than 500,000 US military personnel are given safety assessments for the AVA vaccine trial through review and medical evaluation of adverse events(AEs) reported to the Vaccine Adverse Event Reporting System(VAERS) by some review and medical evaluation of adverse events(AEs) reported to the vaccine Adverse Event Reporting System(VAERS). And it was seen as a result that 1841 reports describing 3991 AEs(9.4 reports/10,000 doses of AVA) were reviewed by AVEC that were submitted to VAERS(from 1Q1998 through 4Q2001). 147 form that particular participants reports told about SAE or OMIAE, from there 26 were tentatively rated as possible, probable or certain consequences of vaccination probable cause or effect anaphylactic-like reaction, injection-site reaction, or eight other systemic AEs. (3)

Result overview :

Population : N=2 million doses in 500000 vaccines $F\approx51,546$, M $\approx448,454$ (Estimated from report 8.7:1 M/F)

Outcome: Anaphylactic like reaction

Gender ratio: F=1,M=4 where F/M incidence ratio is 2.17

AVA causes significant local inflammation and should be directed as the ulnar nerve and initially reported that females had higher AEs than males, but after vaccination it was found that transient articular reactions were more prevalent in male.(3)

Japanese encephalitis(JE) vaccine: From 1999 to 2009, VAERS's Adverse Event Report on the inactivated Japanese Encephalitis Vaccine extracted from the Mouse's Brain was published. During this time, VAERS also collected more information, including 300 Adverse events that complied with the JE vaccination, where basically 24 per 100,000 doses were distributed and were seen after classifying. As a result 8.4 per 100,000 doses were classified as hypersensitivity (106 or 35 percent) and 1.8 per 100,000 doses that mean 23 or 8% were reported serious adverse events and 0.3 per 100,000 doses that mean 4 or 1% reported as neurological events. When they were immunised, hypersensitivity responses were noted as a common symptom. Women, on the other hand, are thought to be more likely than males. (4)

<u>Result overview</u> : Population: N = 1.26 million doses distributed . Outcome : Anaphylaxis Gender ratio: F=10, M=1, F/M ratio: 10:1

Rabies vaccine: The rabies immunoglobulin vaccine was experimentally administered from 1987 to 2005 on 72132 patients at Queen Saovabha memorial institute in Bangkok . Report says 59.56% patients(42965 patients) were given equine rabies immunoglobulin(ERIG) and 49.44% patients(29167) were given rabies immunoglobulin(HRIG). The data show that a total of 812 people from both groups have been the victims of advanced reactions where top part of which came from ERIG .

ERIG - male (43.13%), female (56.87%)

HRIG - male (34.62%), female (65.38%)

The result says that women were at higher risk of developing ERIG and HRIG hypersensitivity than men. (5)

Result overview:-

Population: N=72,132 vaccines F=35,893 M=36,239 Outcome: Anaphylaxis Gender ratio: F=1, M=0

Yellow fever(YF) vaccine : Although the vaccine has been administered in about 500 million doses since 1937.Yet the VAERS produced a report between 2000-2006, keeping in mind the safety of the vaccine. So they used approximately of age sex distribution of administered doses wih a report from, a 2006 survey of how reactions such as SAE(serious adverse events), anaphylaxis. The tendency of SAEs is much higher in men, especially in adults over 60 years of age. These results strengthen the generally accepted safety profile of the YF vaccine.(6)

<u>Result overview</u> : Population: N=1,534,170 vaccines F=790,865 M=743,305 Gender ratio: F=1.3, M=2.3 per 100,000 doses F/M incidence ratio: 0.61.

Influenza A(H1N1) 2009 monovalent vaccines: This vaccination program was launched in October 2009 named The United States(US) influenza A(H1N1) 2009 monovalent(2009-H1N1) vaccination program and reports to the vaccine adverse event reporting system(VAERS).

<u>Result overview :</u> Population: N=82.4 million vaccines Outcome: Anaphylaxis Gender ratio: F=80, M=36 F/M ratio: 2.2:1

Conclusion:

I have briefly discussed sex gender aspect that characterize risk of developing anaphylaxis like reaction after vaccination. Where vaccination trials 'reports from VAERs' data show that IHS development is much higher in girls than in men. Women are more prone to allergic reactions because the amount of estrogen in the body is much higher than in men.However, there are exceptions. Some vaccines, such as the anthrax vaccine, have been shown to cause after-vaccination in men who are more likely to suffer from anaphylaxis than women in their sixties.

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Pollinator observation on Hibiscus

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- **Objective** To gain the knowledge about the various pollinator and their interaction with hibiscus plant in my locality.
- **Study Site** The study was conducted at Mira Kadamtala Para, Plassey in Nadia district of West Bengal. The insect species on *Hibiscus rosa sinensis* during its blooming phase was recorded from September 26, 2021 to
- Latitude & Longitude 23.77 & 88.28
- **Habitat** The study site was a garden in front of my house. The tree was surrounded by various small & big trees, and under the tree was covered with patchy grasses. The flower visitors were observed for an interval of each 2 minutes for approximate 1 hour



• Description of the Flant (Flower)

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
Red	Trumped shaped	6 – 10 cm in diameter	No	5.0ft – 5.6ft	Inside the calyx	Bottom of the flower

• **Collection methodology** – Collection of flower visitors was made by live observing the flower and clicking some pictures by mobile. Flower visitors were observed for 1 hour per day.

• <u>DAY 1 – 26/09/21:</u> Time – 11.15am to 12.15pm

 \circ Temp – 31°C, Humidity – 60%, Wind – 9.8km/h, Partly sunny weather.

Order	Family	Genus/	Posture of	Pollen	Sitting
		Species	sitting	carrying	time on
		-		parts	flower
Odonata		Anisontera sn	In front 26/09/2021 11:36		3 minute approx

• Insect visitor : Diurnal

• <u>DAY 2 – 27/09/21:</u> Time - 8.30am to 9.15am

 $\circ \quad Temp-34^{\circ}C$, Humidity -40% , Wind -6.7 km/h , Sunny weather.

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Lepidoptera	Papilionidae	Papilio clytia (common mime)	On the style	-	5 sec approx

• Insect visitor : Diurnal



• <u>DAY 3 – 28/09/21:</u> Time – 12.00pm to 12.40pm

 $\circ~$ Temp - 30°C , Humidity - 71% , Wind - 14km/h , Partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• Not a single visitors observed.

• <u>DAY 4 – 29/09/21:</u> Time –

 $\circ~$ Temp – 29°C , Humidity – 92% , Wind – 11.2 km/h , Light rainy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
_	-	-	-	-	-

• Due to rain fall since all day no data collected.

• <u>DAY 5 – 30/09/21:</u> Time – 4.00pm to 5.10pm

 $\circ~$ Temp –32°C , Humidity – 81% , Wind – 3.6 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	-	Approx. 6 sec

• Not able to capture image.

• <u>DAY 6 – 07/10/21:</u> Time – 2.45pm to 3.15pm

 $\circ~$ Temp – 33°C , Humidity – 70% , Wind – 4.9 km/h , partly cloudy weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No flower visitor found.

• <u>DAY 7 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No flower visitor observed.

• <u>DAY 8 – 18/10/21:</u> Time – 4.30pm to 5.05pm

 $\circ \quad Temp-29^{\circ}C$, Humidity – 55% , Wind – 3.4 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Around the petal	-	3 sec.

• <u>DAY 9 – 08/10/21:</u> Time – 10.00am to 10.30am

 $\circ~$ Temp – 31°C , Humidity – 50% , Wind – 4.1 km/h , Sunny weather.

• Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
-	-	-	-	-	-

• No data found.

• <u>DAY 10 – 04/11/21:</u> Time – 9.10am to 9.50am

- $\circ~$ Temp 28°C , Humidity 43% , Wind 5.6 km/h , Sunny weather.
- Insect visitor : Diurnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenoptera	Apidae	Apis indica	Roaming around stamen	Leg, wings	3-4 sec

- **Result** As a result I recorded an observation chart of 10 days on flower visitor or pollinator of *Hibiscus rosa sinensis* at a garden of my house which is located in Plassey, Nadia. Here -
- 1. Anisoptera sp (order belongs to Odonata), seen 1 time
- 2. Papilio clytia or common mime (order belongs to Lepidoptera), seen 1 time
- 3. *Apis indica* (order belongs to Hymenoptera) seen **3 times** are observed as flower visitor.
- **Discussion** Though Hibiscus is very attractive plant for pollinator but I got 3 flower visitors which is not good at all. Most flower visitors are often seen at morning and afternoon time. No visitors found at the time of mid-noon and rainy days. Due to a moderate pollution in this area and low amount of flowers in the tree, flower visitors are seen very rarely and also low individual. So, it indicates the low rate of pollination and also less crop or flower production.

RAMAKRISHNA MISSION VIVEKANANDA CENTENARY COLLEGE

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Department of Zoology

DSE 2C Project Report, September 2021 – January 2022

Annotations and Analysis of Whole Mitochondrial Genome of Snake Species of India

Submitted by,

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Introduction-

Mitochondrial genome is the sum of the genetic information contained in the chromosome of the mitochondrion, a structure located in the cytoplasm outside the nucleus of the cell. The mitochondrial genome is composed of mitochondrial DNA (mtDNA), a double-stranded circular molecule that contains a limited number of genes. It has only 16,500 or so base pairs in it and it encodes different proteins that are specific for the mitochondrial.

A typical vertebrate mitochondrial gnome has one control region (CR), two ribosomal RNAs (rRNA), 13 protein-coding genes, and 22 transfer RNAs (tRNA). Compared to the typical vertebrate mtDNA, snake mtDNAs have many unusual features, including two duplicated CRs, a compact genome, and an elevated evolutionary rate (Kumazawa et al. 1996, 1998). Based on the correlation resulting from the asymmetric replication of mtDNA, the usage of control regions (CRs) was inferred to be species specific. In snake mitochondrial DNA, the rate acceleration varied considerably among genes and over time, and it appears that these changes at the nucleotide and protein level co-occurred with snake mitochondrial DNA incurring a reduction in size and a duplication of the control region.

The mitochondrial genome (mtDNA) represents a favored genetic source for evolutionary studies due to four valuable features: a) a faster evolutionary rate than nuclear genome, and this provides higher resolution in phylogenies of closely related species; b) a mechanism of maternal inheritance and lack of recombination, which introduces fewer errors into the phylogenetic reconstructions; c) a compact genome, which allows easier DNA sequence determination and computational analyses than would nuclear genomes; d) the presence of various protein-coding genes, which provide an evolutionary context of the genome.

ATP8 – ATP8 is a mitochondrial gene with the full name 'mitochondrially encoded ATP synthase membrane subunit 8' that encodes a subunit of mitochondrial ATP synthase, ATP synthase Fo subunit 8 (or subunit A6L). This subunit belongs to the Fo complex of the large, transmembrane F-type ATP synthase. This enzyme, which is also known as complex V, is responsible for the final step of oxidative phosphorylation in the electron transport chain. Specifically, one segment of ATP synthase allows positively charged ions, called protons, to flow across a specialized membrane inside mitochondria. Another segment of the enzyme uses the energy created by this proton flow to convert a molecule called adenosine diphosphate (ADP) to ATP.

COX1 – MT-COX1 is a gene that is often used as a DNA barcode to identify animal species. The MT-COX1 gene sequence is suitable for this role because its mutation rate is often fast enough to distinguish closely related species and also because its sequence is conserved among conspecifics.

NAD1 – MT-ND1 or NAD1 is a gene of the mitochondrial genome coding for the NADHubiquinone oxidoreductase chain 1 (ND1) protein.

CYT B – The MT-CYTB gene provides instructions for making a protein called cytochrome b. This protein plays a key role in structures called mitochondria, which convert the energy from food into a form that cells can use. Cytochrome b is one of 11 components of a group of proteins called complex III.

Objective-

The main objective of this study is to identify and find the evolutionary trend, evolutionary relationship among the closely related species by interpreting the phylogenetic tree and the graphic summary of the complete genomes of these snake species of India. Annotation, gene identification, multiple sequence alignment of the complete mitochondrial genomes of snakes to study the molecular changes among those species. Phylogenetic relation also be established in this study.

Material and Method-

In this study we focused only on snake species of regions of India.

So at first all the scientific name of snake species of India were collected from Reptile Database (https://reptile-database.reptarium.cz/). At advanced search snakes were considered as higher taxa and India as the place of distribution. Total 337 species were reported which distributed in India. Then we select 7 mitochondrial gene to study further. These are Cytochrome-b, COX-1, 12s rRNA, 16s rRNA, ND-1, ND-4 and D loop. Now in NCBI (https://www.ncbi.nlm.nih.gov/), these nucleotides were searched against all of those 337 snake species. The accession id, distribution of the species, title of the reference paper of the various previous studies on those species were collected from the NCBI database and put those data on a Excel sheet. Now I further studied my topic of study- whole mitochondrial genomes of snake species of India. So then the accession id of the whole mitochondrial genomes were collected form NCBI databases. This databases of NCBI shown that there is only 24 snake species have the complete mitochondrial gene sequence and the total accession id of those species are 51 in number.

Now, the sequences were to be aligned in NCBI BLAST. As we took complete mitochondrial sequence we did the BLASTn

(https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LIN K_LOC=blasthome) for nucleotide sequences. The accession id of *Daboia russellii* (Accession id-EU913478) was put in the query sequence and all the 51 accession ids were put in subject sequence. Now the BLAST was done. The BLAST result was the filtered with 75 to 100 percent identity and 80 to 100 query coverage. Then FASTA (complete sequence) was downloaded and the Graphics of the BLAST result and the BLAST tree view was thoroughly studied for further development of this study.

Then the further study was done mainly on MEGA 11 software (Molecular Evolution Genetics Analysis). In the MEGA, the FASTA complete sequence was converted into MEGA files after the muscle algorithm run, trimming of unmatched sequences and alignment of the genome sequences. Then neighbor joining phylogenetic tree of complete mitochondrial genome as well as 4 genes atp8, cox1, nad1 and cyt b was drawn by using Bootstrap method. Now the interpretation was done from this Phylogenetic tree.

Annotations of the sequence using MITOS http://mitos.bioinf.uni-leipzig.de/help.py

Multiple sequence alignment was done using ClustralW, Clustral Omega and ESPript

[https://www.ebi.ac.uk/Tools/msa/clustalo/, https://espript.ibcp.fr/ESPript/ESPript/]





Establishment of Phylogenetic tree of atp8, cox1, nad1 and cyt b complete CDS of those species

Results and Discussion- The results are mainly based on the finding of interpretation of the constructed phylogenetic tree of the whole mitochondrial genome of snake species.

Alignment Scores
ribution of the top 158 Blast Hits on 36 subject sequences

Fig-1: Graphic summary of BLAST result against the accession number of complete genome of *Daboia russelli*.

https://www.ncbi.nlm.nih.gov/projects/sviewer/?rkey=NCID_1_29891540_130.14.18.128_9147 _1638639648_2283183770_0MetA0__S_NC_PhyloTree&appname=ncbiblast&link_loc=fromD escr&tracks=%5Bkey%3Asequence_track%2CShowLabel%3Atrue%5D&v=%3A&id=EU9134 _78.1#

From this graphic summary we can interpret that these complete mitochondrial genome shows some important points. The BLAST mitochondrial genome of *Daboia russellii* show most similarities with *Protobothrops jerdonii* as only 174 unaligned regions present between them. Protobothrops mucrosqumatus and Protobothrops jerdonii have dissimilarities from 173 to 177 base pairs with the genome sequence of Daboia russellii. Their unaligned regions present between 3551 to 3689th sequence. But the species Protobothrops himalayanus and Protobothrops kaulbacki under genus Protobothrops have unaligned regions between 3551-3689 as well as 4538-4658th sequence. This dissimilarities among species of the same genus Protobothrops reflects that there

was some evolutionary divergence may be present. Again Viridovipera stejnegeri stejnegeri and Trimeresurus albolabris show more or less same dissimilarities like Protobothrops mucrosqumatus and Protobothrops jerdonii .The sequence of Naja naja shows unaligned sequence about 185 basepairs with the genome sequence of Daboia russellii at 3 regions. Elaphe poryphyracea and Ptyas mucosa show about 200 unaligned base pairs at 2 regions. Whereas Naja kaouthia and Sibynophis collaris differs at 3 different regions on the sequence. Ophiophagus hannah shows some different unaligned regions than the other species. So, this graphic summary have shown a significant relationship between the unaligned regions and the dissimilarities among the genome sequence of the species at a glance.

	Species name	Accession id	Unaligned	Mismatches
			regions	
1.	Protobothrops jerdonii	KC112560.1	174	2989
2.	Protobothrops jerdonii	NC_021402.1	174	2989
3.	Protobothros mucrosquamatus	NC_021412.1	177	3055
4.	Protobothros mucrosquamatus	KC438281.1	177	3055
5.	Protobothros mucrosquamatus	KT447436.1	173	3070
6.	Protobothros kaulbacki	KY695463.1	158	3027
7.	Protobothros kaulbacki	NC_029166.1	158	3026
8.	Protobothros kaulbacki	KJ689382.1	158	3026
9.	Protobothros himalayanus	NC_029165.1	130	3021
10.	Protobothros himalayanus	KJ689381.1	130	3021
11.	Trimeresurus albolabris	NC_022820.1	175	3098
12.	Trimeresurus albolabris	KF31110.1	175	3098
13.	Viridovipera stejnegeri stejnegeri	FJ752492.1	186	3019
14.	Viridovipera stejnegeri stejnegeri	NC_012146.1	186	3019
15.	Daboia russellii	NC_011391.1	0	0
16.	Ophiophagus hannah	AZIM01009253.1	146	2422
17.	Ophiophagus hannah	AZIM01009253.1	61	611
18.	Sibynophis collaris	JN211315.1	151	2567
19.	Naja naja	DQ343648.1	185	2634
20.	Naja kaouthia	LC431744.1	179	2701
21.	Elaphe poryphyracea	GQ181130.1	179	3005
22.	Bungarus fasciatus	EU579523.1	210	2978
23.	Ptyas mucosa	NC_030041.1	200	2975
24.	Gonyosoma frenatum	NC_057467.1	191	3031
25.	Sinomicrurus macclenllandi	MT547176.1	199	3118
26.	Ophiophagus hannah	EU921899.1	212	3235
27.	Sibynophis collaris	NC_016424.1	151	2568
28.	Sinomicrurus macclenllandi	NC_054255.1	201	3264
29.	Orthriophis taeniurus	NC_025275.1	169	2888

Table 1. : The comparison of Unaligned regions and Mismatches in the genome sequences from the graphic summary.



Fig-2: Phylogenetic tree of Indian snake species with respect to complete mitochondrial genome

Caption of the Phylogenetic Tree-

Evolutionary relationships of taxa-

The evolutionary history was inherited during the Neighbor-Joining method [1]. The bootstrap consensus tree inferred from 500 replicates [2] is taken to represent the evolutionary history of the taxa analyzed [2]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of trees in which the associated taxa clustered together in the bootstrap test(500 replicates) are shown next to the branches [2]. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. This analysis involved 35 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pair-wise deletion option). There were a total of 16349 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [4].

- 1. Sailou N. and Nei M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution **4**:406-425.
- 2. Felsenstein J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. Evolution **39**;783-791.
- 3. Tamura K. Nei M. and Kumar S. (2004). Prospects for inferring very large phylogenies by using the neighbor-joining method. Proceedings of the National Academy of Sciences (USA) **101**:11030-11035.
- 4. Tamura K. Stecher G. and Kumar S. (2021). MEGA 11: Molecular Evolutionary Genetics Analysis Version 11; Molecular Biology and Evolution <u>https://doi.org/10.1093/molbev/msab120</u>.

Phylogenetic tree interpretation-

Protobothrops mucrosquamatus and Protobothrops jerdonii have monophyletic relationship as they are originated from same ancestor. Protobothrops himalayanus and Protobothrops kaulbacki are also monophyletic group. Viridovipera stejnegeri stejnegeri and Trimeresurus albolabris have a monophyletic relationship. But the genus Protobothrops, Viridovipera and Trimeresurus have a paraphyletic relationship between them. There is common ancestor between these 3 genus. Daboia russellii also diverged from the same common ancestor. Ophiophagus hannah, Naja kaouthia and Naja naja are put in a monophyletic group. These 7 species are in the family Viperidae.

Now in the family Colubridae, the deepest diverging lineage is Orthriophis taeniurus. Viperidae and Colubridae diverged from the same ancestor. The species of family Elapidae (except Bungarus fasciatus) and the common ancestor of Viperidae and Colubridae diverged from the same common ancestor. But the species Bungarus fasciatus is outgrouped from the common ancestor of family Elapidae. So this phylogenetic tree shown a relation between these three families of snake.



Fig 3.: Summary phylogeny of 761 colubroid snake species based on a concatenated maximum likelihood analysis of five genes (5814 bp). Pyron et al. 2011

Traditionally, colubroids have been divided into groups based on their tooth morphology: those with fixed fangs were placed into Elapidae, those with folding fangs into Viperidae, and those without fangs lumped into Colubridae. The first two of these groups have proven to be for the most part monophyletic, certain exceptions notwithstanding (Pyron et al. 2011)

This previously studied phylogenetic tree shows that Viperidae and Elapidae are closely placed but our constructed phylogenetic tree shows that Viperidae closely related with Colubridae not with Elapidae.

Pyron et al. 2011 constructed this tree on the basis of conserved regions like CytB, ND1 and ND4 but our constructed tree is on the basis of complete mt genome. So we can conclude that the evolutionary trend is different with respect to conserved regions and complete genome.

Multiple sequence alignment using ClustralW, Clustral Omega and ESPript-

Multiple Sequence Alignment (MSA) is equencelly the alignment of three or more biological sequences (protein or nucleic acid) of similar length. From the output, homology can be inferred and the evolutionary relationships between the sequences studied.

Here, at first the total gene region of atp8, Cox1,cyt b and nad1 cut form the complete mitochondrial genome sequence as data collected from Genome annotations. Then the MSA was performed using Clustral omega and ESPript web server.



Fig 4 : MSA with respect to ATP8

This MSA of ATP8 gene shows that there is conserved region present in between 1 to 80 base pairs. But base substitution occurs very random and frequently in this region. 80 to 156 base pair region is highly variable.

ATP8						Base S	ubstitution					
Species name	A>T	A>C	A>G	C>T	C>A	C>G	T>C	T>G	T>A	G>T	Total	Percentage substitution
Ramphotyphlops braminus	7	2	2			1		1 :	1		12	15.58
Acrochordusgranulatus	5	5 1	. 2		2	2		2	1	. 1	16	20.77
Pythonmolurusmolurus	1	L	3		1			2			7	9.09
Xenopeltisunicolor		1			2			1			4	5.19
Malayopython	1	L	3					1			5	6.49
Gonyosomafrenatum	1	L	1					1			3	3.89
Orthriophistaeniurus	2	2			1			2			5	6.49
Elapheporyphyracea	2	2						2			4	5.19
Ptyasmucosa		1			2			1			4	5.19
Daboiarussellii	3	3 1		3	3	1		:	1		9	11.68
Trimeresurusalbolabris	1		2		2	1					6	7.79
Viridoviperastejnegeristejnegeri			1		1			1			3	3.89
Protobothropsmucrosquamatus	6		2								2	2.59
Protobothropsjerdonii											0	0
Protobothropshimalayanus		1									1	1.29
Protobothropskaulbacki			1								1	1.29
Hydrophiscyanocinctus	1	. 1	. 3								5	6.49
Sinomicrurusmacclellandi			2	:	2						4	5.19
Bungarusfasciatus			1		2						3	3.89
Najanaja			7					1			8	10.38
Najakaouthia			7					1			8	10.38
Laticaudacolubrina		2	2 2		2						6	7.79
Sibynophiscollaris		1	. 6		1			1			9	11.68

Base substitution analysis of ATP8 gene-

	1 10	20	30	40	50	60
NC 010196 1 Ramphotyphlops braminus	TCCTTGGAC CC	ACTINTAT	Bec BA Bec B	ANGC STRATTO	COCHET CHILDREN	ccile
NC 046795.1 Hydrophis cyanocinctus	TCACTAACTAAC	ACHARACANCE	ACALCON	ATTECCT	GCATTTTAAC	CCTT
EU913478.1 Daboia russellii NAD1	TCATCAACCECT	TCHCHACANCO	CCCCC TOT	ATTOCACTO	OCCUTTCTTAC	CCLA
NC_022820.1_Trimeresurus_albolabris	TCATAAACCECC	ACEACCARCO	ACALCC	ATCOCAGT	GCATTICTIAC	CCEA
FJ752492.1_Viridovipera_stejnegeri_stejnegeri	TCATAAACCECC	GCHARACANTO	BACETABCICES	ATCCCCCT	GCATTCCTCAC	TCOC
NC_029165.1_Protobothrops_himalayanus	TCATCAACCAAC	ACHARACARCO	ACALTCON	ARCEGACIE	SCATTTCTTAC	ACA
NC_029166.1_Protobothrops_kaulbacki	TCATCAACCEAC	ACHARACANCO	ACALECCES	ARCSCAST	GCATTTCTTAC	ACTA
NC_021402.1_Protobothrops_jerdonii	TCATTAACC CC	ACHARICARCO	TCCCTTCC	ATCHOUT	SCATTICTCAC	CCEC
NC_021412.1_Protobothrops_mucrosquamatus	TCATAAACCOCC	ACHARATARCO	CCOTOTOTO	ATCOCAGT	SCATTCCTCAC	CC
NC_016424.1 Sibynophis collaris	CTATTAACTAAC	ACTORACOTO	ATCALTON	ATAGCOT	ACATTCC TCAC	CTOA
NC_057467.1 Gonyosoma_frenatum	TATCALCT	ACTOR ACCES	BAT BAADCORT	ATCOCCUT	GCATTCICTCAC	CORA
NC_012770.1_Elaphe_poryphyracea	TTACTAACTCC	TACTOTACATCO	ATTANCE	ATTOCCOT!	ACATTCCTCAC	CCEA
NC 025275.1 Orthriophis taeniurus	TTACCAACTOCC	AARTELCARCO	OT A TOT	ATACCTOT	OCATTTCTTAC	COBA
NC_030041.1_Ptyas_mucosa	TCACAAACTETT	BACHTEACANTO	ATCALETCE	ATCCCCUT	GGATTCCTCAC	TCHA
NC_036054.1_Laticauda_colubrina	TTACTAATT AC	BACHCHARCARCO	BACGALTIC	ATTOCTOT	OCCUTTCTARC	CCOT
NC 011393.1 Bungarus fasciatus	TCATCAATCAAC	ACHCHARCE	ACALCO	ATTOCAGT	SCATTC: TCAC	CCA
NC_054255.1_Sinomicrurus_macclellandi	CTATTAACCOC	ACCOLTACTO	TTC T CC	ATTOCOT	GCATTOTTANC	CC CC
DQ343648.1_Naja_naja	TAATCAACCAC	ACCALLACO	atcocker at the second	ATTOCAST	GCAPTICTAAC	CTOA
LC431744.1_Naja_kaouthia	TTATCAACCEAC	ACTACATO	GTC GT GCC GC	CATTOCAGTO	GGATTTCEAAC	CTEA
NC_007400.1_Acrochordus_granulatus	TACTASTCAA	TACHCERCARTS	TCOTATT	ATCECAGE	SOCTOTATATAAA	CCEA
NC_007402.1_Xenopeltis_unicolor	TCATTAACCTC	ACETERCAETA	CT GG CCC	ATTROCAT	SCOT TTTTAAC	CCA
NC_042397.1_Malayopython_reticulatus	TTATTAACCAC	TACHARACARCA	TTOCASCO .	ATTOCACTO	GOOTICGTAAC	CCA
NC_015812.1_Python_molurus_molurus	TTATCAACCAC	BACHCHACABCA	CT CC CC CC	ATCOCAGE!	SCC21CT2AAC	CTEC

	70	80 91	100	110	120
NC_010196.1_Ramphotyphlops_braminus	COOL GOALA CAA	ATTACATO	CTTCCANCO	BATT OF A THE	CERA
EU911478 1 Daboia russellii NADI	CONTACT PRIMACINE T	A DOWNARD AND	CTACOANALOAL	CONTRACTOR DE LA CONTRACTOR	0.33
NC 022820 1 Trimeresurus albolabris	CHARACTARIA CHAC	ADDATATATACA	CTCCCAMAADOC	COLACITACIACI	- 4 C
FJ752492.1 Viridovipera stejnegeri stejnegeri	CTAGAACGAAAACTAT	AGGATATATALA	CTACGAAAAOOTC	CALACITYAGTAGE	COT
NC_029165 1_Protobothrops_himalayanus	CTAGAACGAAAACTAT	ADDATATATADA	CTACOARASOCC	CCAACCTAGTAG	ceec
NC_029166.1_Protobothrops_kaulbacki	CTACAACCAAAACTAC	AGGATATACA	CTACCALA SOCC	CTARCCTACTACC	CECC
NC_021402.1_Protobothrops_jerdonii	CTAGAACGAAAACTAC	ABGATCTATGEA	ACTACGTALA DOCC	CTAACTTACTACC	GCCT
NC_021412.1_Protobothrops_mucrosquamatus	TTAGAACGARAA CTAC	AGGATACATOCA	CTACOTALACOC	GTAACCT GOTACO	CO C
NC_016424.1_Sibynophis_collaris	E TAD AACOADAA CEAC	A DIATAC TASA	CATCOTINASION	TANK TRACES	Cit in
NC_057467.1_Gonyosona_Frenatum	C AND A CONTRACTOR OF C	G OTAC LAR	CACCUARTA	Charles and the second	C
NC 012770.1 Elaphe poryphyradea			CATCOC		CORE:
NC 010041 1 Pryas mucosa	CHARTER TARGET		CACCOTTANA	CONTRACTOR OF LOT	CHER
NC 016054 1 Laticauda colubrica	THAT AND A CHACKAC	A DOT A TANAL	CTCCCAMALOG	CONTRACTOR OF	61.57
NC 011393 1 Bungarus fasciatus	CTAGAACGAAAACTCT	ADDATATATA A	CTACCARAGO	CANACCTACTAC	ACCT
NC_054255.1_Sinomicrurus_macclellandi	CTAGAACGAAAACTCT	GOOCTACATACA	TTCCCCANACCAC	CTAACCTAGTAG (TCCT
DQ343648.1_Naja_naja	CTGCAACGAAAACTCC	AGGC7ATATACA	CTTGACALAGGAC	CALACCTACTICO	CCCA
LC431744.1_Naja_kaouthia	CTAGAACGAAAACTCC	ADDCTACATACA	ACTICC CCANAGOAC	CAAACCTACTTCC	TCCA
NC_007400.1_Acrochordus_granulatus	CHADAACCCAAACCCC	ADDACACATACA	CTACGCALAGOTE	CALACICICUTADO	TOPC
NC_007402 1_Xenopeltis_unicolor	THANKA MUNICIPAL A ALLA T	A DOME AND A DATA	TTACGALASSOC	CALLSTING STREET	CHAT
NC 015813 1 Pathon solution solution					100
MC_019812.1_Python_Bolurus_Bolurus	C Electron Geological S Elect	ALL ALL ALL ALL ALL	A FALL SALES AND A DATE OF	Contraction of the second	- 33 A

Fig 5 : Portion of MSA with respect to NAD1

The average length of nad 1 gene of these studied species is about 936 base pairs. The MSA of this gene shows a conserved region between 1 to 930 base pairs. This suggests that the evolutionary divergence is less with respect to nad1 gene region among those studied snake species.

NO ALALAS I Branchetunklans brandaus
NC_010196.1_Ramphocyphiops_Draminus
NC_007400.1_Acrochordus_granulatus
NC_015812.1_Python_molurus_molurus
NC_007402.1_Xenopeltis_unicolor
NC 042397.1 Malayopython reticulatus
EU913478.1 Daboia russellii
NC 022820,1 Trimeresurus albolabris
NC_029165.1 Protobothrops_himalayanus
NC_029166.1_Protobothrops_kaulbacki
FJ752492.1_Viridovipera_stejnegeri_stejnegeri
NC_021402.1_Protobothrops_jerdonii
NC_021412.1_Protobothrops_mucrosquamatus
NC_036054.1_Laticauda_colubrina
NC 016424.1 Sibynophis collaris
NC 057467.1 Gonyosoma frenatum
NC 012770.1 Elaphe poryphyracea
NC 025275.1 Orthriophis taeniurus
NC 030041.1 Ptyas mucosa
NC_011393.1_Bungarus_fasciatus
NC 046795.1 Hydrophis cyanocinctus
NC_054255.1_Sinomicrurus_macclellandi
DQ343648.1_Naja_naja
LC431744 1 Nata kaouthia

91	0	920	930	940	950	960
TACTACTTT	AACC	ATTCTACET	ACCTGAATAGO	AAGCAAAGG	GRAGATAC	CCA1
CAAGAATTA	CALCATT	GTTATCC	ACCTOGGCCOC	CTGAMACC	TOTAGOATCT	0077
ACCOGATT	CAACATTC	ATTCCCAT	ACATGAGCCGG	CACAMAACC	AGHACTT	EGAR
CATTAGTTT	CARCATTC	GCAACCARC	ACATEACCAGE	CACANAACC	CONACCE	COAR
CACUAGTCT	CCACTTTT	ATTACTACC	ACATOACCO	TACAAAACC	CONAGROCCIC	COT D
CCTACTA	CTATCGTT	ATTATTATC	ACCTGAACAGO	CARTAARCI	CONCERNANCIC	COAR
CCTCACAA	CTACATT	ATTATCATT	ACCEPTACCE	CASTAAASS	GUTGHACCC	5543
CTT CACTO	TCACATET	ATCATTANT	ACTICANCER	ANCANGES	AGHAGHACCC	2 2 4 2
TTCACCG	TTACATTT	ATCATTANT	ACTICANCTOS	CARCANARS	AGHAGHACCC	an cu
CT TACGA	CTATTC	ATCATCANT	A THE ACCONT	CARTANAR	LG TG GCCT	
CTACCA	CTCATTC	ATAATTAHC	AUCHAACCH	CARTAARS	AGE AGE ACCO	44^H
TINIATIA		ACTATIANC.		18.44.88	A DECEMBER	33.4
ATTAATTO		ATTACT OF		1 B. A. B.	LA COLACCO	49° 9
CC CCATE	COLOR NOR	ATTACA A		CARL NO. BO	CHACCO	99°. M
AC ACTAC	Contraction of the	a meria a same			CONCERCION OF	
CCHAGTCO	COLATTO	ATAACTAC	A DA DA DA DA	- 8-01.83	AGUAGUACCO	
AT ACTAC	CHARTC	ATCATAARC	ACA BOARCOR	CAR ANA BO	A CHARDACCA	94 . H
ATAATCT	CALCETT	ATTATTATT	ACATOACA	TARCHIARG	CONAGRATCA	22.0
TTAATTG	TAACCTTT	ATTACTANT	ACATGATCASC	CANTANACO	GRAGAACCA	a di
ACAATCA	COCCTTT	ATCACCACC	ACATGAACAGO	CTOTALACC	GAGACCT	CONT
ATAATTG	CTACTTTC	GTTACCANT	ACATGAACTCO	CTOTALACC	GRAGAACCA	CONT
ATAATCO	CTACTITC	ATTACCANT	ACATGAACCCC	CTOTALACO	GRAGMACCA	CCAT
	and a second a second a second	and a second sec				

NC 010196.1 Ramphotyphlops braminus
NC_007400.1 Acrochordus granulatus
NC 015812.1 Python molurus molurus
NC 007402.1 Xenopeltis unicolor
NC 042397.1 Malayopython reticulatus
EU913478.1 Daboia russellii
NC 022820.1 Trimeresurus albolabris
NC 029165,1 Protobothrops himalayanus
NC 029166.1 Protobothrops kaulbacki
FJ752492.1 Viridovipera stejnegeri stejnegeri
NC_021402.1_Protobothrops_jerdonii
NC 021412.1 Protobothrops mucrosquamatus
NC 036054,1 Laticauda colubrina
NC_016424.1_Sibynophis_collaris
NC_057467.1_Gonyosoma_frenatum
NC_012770.1_Elaphe_poryphyracea
NC_025275.1_Orthriophis_taeniurus
NC_030041.1_Ptyas_mucosa
NC_011393.1_Bungarus_fasciatus
NC_046795.1_Hydrophis_cyanocinctus
NC_054255.1_Sinomicrurus_macclellandi
DQ343648.1_Naja_naja
LC431744.1 Naja kaouthia

970	980	990	1000	1010	1020
TATCACAATAGGCCAU	CTAGECTCAC	TCCTCTATT	TTCAATTTT	TACAATCCTT	CTAC
TATCACCATTAGTCAL	ATAGCCTCAA	CCATATATT	TTCTATTCTT	TATTAT	TAA.
CATCATTAACAGCCAI	TCAACTACAA	CGTTACACT	CAACTTCTT	TATCCAGACA	ADDD
TTACCGCAATT	GCCAGGCAGC	CTCCGTCAC	CTACTICACA	TATTTTGCCT	CAAA
TTATCACTATT	GTCAAGTAAC	TTCAACACT	TATTTCACA	TTCTTCATCT	CCAT
CACAGAAATTAGCCAI	CTTGCCTCAA	TTCTATACT	CATGTTCTT	TATCTC	TAA
CACAGAAATTAGTCA	TTOOCOTCAN	TTCTATACT	COTATTOTT	CATAAC	644
CACAGAAATTAGTCA	CTEGCCTCAA	TTTTATACT	CATATICTT	CATGAC	TAA
CACAGAAATCGGCCAJ	CTEGETTCAN	TCCTATACT	TCACGTTCTT	CATAGC	CAA
CACAGAAATTGOCCAJ	CTAGCCTCAG	TCCTATATT	CATGTTCTT	CATAAC	AAT .
CACAGAAATCGGACAC	ICTA GCCTCAA	TTCTATACT	TCATATTCTT	TGTAGC	CAA
CCTCCTTATTAGTCAL	ACAACCTCAA	TCCTGTACT	TCTCCITTTT	CATTAT	AAA.
CACAATTATTGGACA	ACAACGTCAA	TTCTATACT	CREATER	CATTAT	
CGTCCTAATTGGTCA	TCAACCTCCA	CCCTATACT	TCTCATTCTT	TATTAT	AAA
TAATACTATCGGCCAL	GTAACCGCCA	TTCTATACT	TCTCATTCTT	CATTAT	AAA
TACTATCATTGGACAJ	ACAACTGCTA	TTCTATATT	TCTCATTCTT	CATTAT	AAA
CATCTCTATCAGCCAI	ATAACTTCGA	TTATCTATT	TOTOCTTOTT	CATTAT	TAA
TATCTTTATTAGCCAI	ACAGCCTCAA	TTATCTACT	TOTCOTTOTT	CATTAT	TAA
CATCATTATCAGCCAI	ATAACCTCAA	TCCTCTACT	TTTCATTCTT	CATTAT	AAA
TATTACTATCAGTCAG	ACAACATCAA	THE REAL	CTCCTTCTT	TATCTT	AAC

NC 010196.1 Ramphotyphlops braminus	CAC.
NC 007400.1 Acrochordus granulatus	cccc
NC 015812.1 Python molurus molurus	CTTC
NC 007402.1 Xenopeltis unicolor	CCCA
NC 042397.1 Malayopython reticulatus	CCCA
EU913478.1 Daboia russellii	CCCT
NC 022820.1 Trimeresurus albolabris	TCCC
NC 029165.1 Protobothrops himalayanus	TCCT
NC 029166.1 Protobothrops kaulbacki	CCCT
FJ752492.1 Viridovipera stejnegeri stejnegeri	cccc
NC 021402.1 Protobothrops jerdonii	CCCA
NC 021412.1 Protobothrops mucrosquamatus	TCCA
NC 036054.1 Laticauda colubrina	CCCA
NC 016424.1 Sibynophis collaris	CCCT
NC 057467.1 Gonyosoma frenatum	cccc
NC 012770.1 Elaphe poryphyracea	CCCA
NC 025275.1 Orthriophis taeniurus	CCCA
NC 030041.1 Ptyas mucosa	TCCA
NC 011393.1 Bungarus fasciatus	TCCT
NC 046795.1 Hydrophis cyanocinctus	cccc
NC 054255.1 Sinomicrurus macclellandi	cccc
DQ343648.1 Naja naja	CCCT
LC431744 1 Nata kaouthia	CCCT

	1030	1040
CAC	TACATTATTA	GAGMITMAAATC
CCCCCTTC	AGGCTGAATA	GARAACAAAATT
CTTCAGGG	GATTTGAAAA	CGGAATA
CCCAATCC	COOCTGAACT	GAAAACAAAATA
CCCATTCC	AGGCTGAATA	GAAAACAAAATA
CCCTCTCC	AGGACTCTTA	GANAATAAGATC
TCCCTTAT	CGGTATAACA	GAAAATAAGATC
TCCTGCACE	AGGCCTAGCG	GAAAACAAAATC
CCCTGTACE	AGGCCTGGCG	GALAACAAAATC
CCCCCCCCC	AGGCCTAACA	SAMAACMAAATC
CCCAATACT	GGGCCTAGCC	GAANACIMAAATIC
TCCAATAC	GGGCCTAACA	GAAAACAAAATC
CCCAGTCCH	CGGACTAGTA	GAGAATATAATA
CCCTATTT	AGGCTGGTCA	GAAAATAAAATT
CCCCCTAC	TGGCTGACTA	GANANTAAAATT
CCCACTGC	CGGTTGACTA	GAAGCMAAATC
CCCACTAA	TOGCTGATTA	UAAATTAAAATC
TCCATTAC	TUGACAATTA	GAAATC
TCCTCTAC	COGCTGAATC	GAAAATABAAATT
CCCCCTTCH	AUGATEGETC	GAAAATT
CCCCCTACH	TOGCTGAACC	GAAGTTAAAATT
CONCEACE	COUCTGAACC	AAATA
CCCTCTACE	COOCTGAACC	GAAMATAAAATA

Fig 6 : Portion of MSA with respect to Cyt B

The MSA of cyt b shows a conserved region between 1 to 1041 base pairs, but from 960 to 1024 base pair region shows high variability.

NC010196. 1Ramphotyphlopsbraminus ATAAACC TTGACTA TTC ACTAATCACAAAGACA TG C NC007400.1Acrochordusgranulatus ATTACTC TTGACTA TTC ACAAACCACAAAGACA CG C 20913478. 1Daboiarussellii NC042397. 1Malayopythonreticulatus ATTACTC TTGACTA TCC ACAAACCACAAAGATA CG A NC0229165. 1Protobothropskaulbacki ATTACTC TTGACTA TTC ACAAACCACAAAGATA CG A NC021402. 1Protobothropskuubacki ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021402. 1Protobothropsicrosquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021402. 1Viridoviperastcjnegeristejnegeri ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG G NC024820. 1Trimersurusmacclellandi ATCACCC TTGACTG TTC ACCAACCACAAAGACA CG A NC014095. 1Nydrophiscyanocinctus ATTACCC TTGACTG TTC ACCAAACACACAAAGACA CG A NC016054. 1Laticaudacclubrina ATCACCC TTGACTG TTC ACCAAACACACAAAGACA CG A NC016054. 1Laticaudacclubrina ATCACCC TTGACTG TTC ACCAAACCACAAAGACA CG A NC016054. 1Laticaudacclubrina ATCACCC TTGACTG TTC ACCAAACCACAAAGACA CG A NC016054. 1Laticaudacclubrina ATCACCC TTGACTG TTC ACAAACCACAAAGATA CG A NC02575. 10orthriophiscyanocinctus ATTACCC TTGACTA TCCC ACAAACCACAAAGATA CG A NC02575. 10orthriophiscyanocinctus ATTACCC TTGACTA TCCC ACAAACCACAAAGATA CG A NC02575. 10orthriophiscyanocinctus ATCACCACAAAGATA CG A NC02575. 10orthriophiscyanocinctus ATTACCC TTGACTA TCCC ACAAACCACAAAGATA CG A NC02770. 1Elapheporyphyracea ATCACCACAAAGATA TG A NC02770. 1Elapheporyphyracea ATCGCCCC TTGACTG CCCCC CCCCCCCCCCCCCCCC				1	10	20	30	40
NC007400 LACTOCHOROUSGTANUISUS DEDI3378 LDaboisrussellii NC042397 LMalayopythonreticulatus NC029166 lProtobothropshulbacki NC029166 lProtobothropskulbacki NC029166 lProtobothropskulbacki NC021402 lProtobothropsjerdonii NC021402 lViridoviperastejnegeristejnegeristejnegeriste NC02400 lTrimeresurussalbolabris NC044795 lNijanja NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016054 llaticaudacolubria NC016074 llapheporyphysacea NC02770 lElapheporyphysacea NC015612 lPytomolurussolurus NC016624 llapheporyphysacea NC015612 lPytomolurussolurus NC01652 lPytomolurussolurus NC016624 llapheporyphysacea NC015612 lPytomolurussolurus NC016624 lPy	NC010196.1Ramphotyphlopsbraminus			ATAAAC	COTTGACT	ATTTCAC	TAATCACAAA	GACANTGOC
DO14103118 ATTACCC TTGACTA CCC ACAAACCACAAAGATA CG A NC023165 1Protobothropshimalayanus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC023165 1Protobothropshimalayanus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021402 1Protobothropsicrosquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021412 1Protobothropsmucrosquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021412 1Protobothropsmucrosquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC022420 1Viridoviperaste jnegeriste jnegeri ATTACCC TTGACTA TTC ACAAACCACACAAAGATA CG A NC054255 1Sinomicrurusmacclellandi ATCACCC TTGACTA TTC ACCAACCACAAAGACA CG A NC054257 1Sinomicrurusmaccleus ATTACCC TTGACTA TTC ACCAACCACAAAGACA CG A NC01433 ATCGCCC TTGACTA TTC ACCAACCAACAAGACA CG A NC0146795 1Hydrophiscyanocinctus ATTACCC TTGACTA TTC ACAAACCAACAAGACA CG A NC036054 Laticaudacolubrina ATCACCC TTGACTA TTC ACAAACCAACAAGATA CG A NC036054 Laticaudacolubrina ATCACCC TTGACTA TTC ACTAACCAAAAGATA CG A NC036054 Laticaudacolubrina ATCACCC TTG	FIG13478 1Dabaiarussellii			ATTACT	CHITCHEI	A TOTOMO	ANACCACANA	CATADOOR
NC029165 IProtobothropshimalayanus ATTACCC TTGACTA CTTC ACAAACCACAAAGATA CG A NC029166 IProtobothropskuubacki ATTACCC TTGACTA CTTC ACAAACCACAAAGATA CG A NC021402 IProtobothropsmucroquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC021412 IProtobothropsmucroquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC02220 ITrimeresurusalbolabris ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC022420 IViridoviperastejnegeristejnegeri ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC024252 IViridoviperastejnegeristejnegeri ATTACCC TTGACTA TTC ACAAACCACAAAGATA CG A NC054255 ISinomicrurusmacclellandi ATCACCC TTGACTA CTTC ACAAACCACAAAGACA CG A NC054255 ISinomicrurusmacclellandi ATCACCC TTGACTA CTTC ACCAACCACAAAGACA CG A LC431744 INajakaouthia ATCGCCC TTGACTG TTC ACCAACCACAAAGACA CG A NC014795 INydrophiscyanocinctus ATTACCC TTGACTA CTTC ACAAACCAAAGACA CG A NC036054 ILaticaudacolubrina ATCACCC TTGACTA TTC ACAAACCAAAGACA CG A NC036054 Ilaticaudacolubrina ATCACCC TTGACTA TTC ACAAACCAAAGATA CG A NC036054 Ilaticaudacolubrina ATCACCC TTGACTA TTC ACAAACCAAAGATA CG A NC0362575 IOrthriophiscaeniurus ATTACCC TTGACTA TCTC ACAAACCAAAGATA CG A NC030041 IPtyasmucosa ATTACCC TTGACTA TCTC ACAAACCAAAGATA CG A NC037070 IElapheporyphyracea ATCGCCC TTGACTA TCTC ACAAACCAAAGACA TG A NC03770 IElapheporyphyracea ATCGCCC TTGACTA TCTC ACAAACCAAAGACA TG A NC03770 IElapheporyphyracea CAGG ATCGC CTGCCCA TGACTA TCTC ACAAACCAAAGACA TG A NC03770 IElapheporyphyracea ATCGCCC TTGACTA TCTC ACAAACCAAAGACA TG A NC03770 IElapheporyphyracea CG ATCGCCCCTATACCTTATTCG CGCACGAAACCAAAACCAAAGACA TG A	NC042397 1Malayonythonraticulatus			ATTACT	COTTGACT	THECTCHAC	AAACCACAAAA	CATADOORT
NC029166. Protobothropskaulbacki ATTACCC TTGACTA TTC ACAAACCACAAAGATA CC AAAGATA CC AAAACCAACAAAGATA CC AAAGATA CC AAACCAACAAAGATA CC AAACCAACAAAGATA CC AAACCAACAACAAAACAA	NC029165.1Protobothropshimalayanus			ATTACC	COTTGACT	ANTITCHAC	AAACCACAAA	GATALCOLA
NC021402. IProtobothropsjerdonii ATTACCC TTGACTA TTC ACAAACCACAAAGATA CGAA NC021412. IProtobothropsmucrosquamatus ATTACCC TTGACTA TTC ACAAACCACAAAGATA CGA SUC022820. ITrimersurusalbolabris ATTACCC TTGACTA TTC ACAAACCACAAAGATA CGA NC022820. IViridoviperastejnegeristejnegeri ATTACCC TTGACTA TTC ACAAACCACAAAGATA CGA NC054255. Isinomicrurusmacclellandi ATCGCCC TTGACTA TTC ACCAACCACAAAGACA CGA NC054255. Isinomicrurusmacclellandi ATCGCCC TTGACTG TTC ACCAACCACAAAGACA CGA ATTACCC TTGACTG TTC ACCAACAACACACGA ACCACCCCAAAGACA CGA ATCGCCC TTGACTG TTC ACCAACAACAACACACGA ACCACCAACAAACAACAACACACGA ATCGCCC TTGACTG TTC ACCAACAACAACACACGA NC013133. Ibungarusfasciatus ATTACCC TTGACTG TTC ACCAACAACAACAACAACACA NC046795. IHydrophiscyanocinctus ATTAACC TTGGTTG TTC ACCAACCAAAGACAACGA NC046795. IHydrophiscyanocinctus ATTAACC TTGGTTG TTC ACAAACCAACAAAGACAACGA NC046795. Ihydrophiscyanocinctus ATTAACC TTGGTTG TTC ACAAACCAACAAAGACAACGA NC046795. Ihydrophiscyanocinctus ATTAACC TTGGTTG TTC ACAAACCAACAAAGATA CGA NC036054. Llaticaudacolubrina ATCACCC TTGACTA TTC ACAAACCAACAAAGATA CGA NC0362575. JOrthriophistaeniurus ATTACCC TTGACTA TCC ACAAACCAAAGATA CGA NC030041. Ibtyasmucosa ATCACTC TTGACTA TCCC ACAAACCAAAAGATA CGA NC03700. Iklapheporyphyracea NC03707. Iklapheporyphyracea NC03707. Iklapheporyphyracea NC03707. Iklapheporyphyracea ATCGCCCCTTGACCTA TCCC ACAAACCAACAAAGATA TC A NC015812. IPythonmolurusmolurus CTGGCACCCCTTGACCCC TTGACTC TCCCCAAAACCAAAGATA TC A	NC029166.1Protobothropskaulbacki			ATTACC	CGTTGACT	AUTTICAL	AAACCACAAA	GATACCOA
NC021412. JProtobothropsmucrosquamatus ATTACCC TTGACTA TTCACCAAAACCACAAAAACCACAAAAACCACAAAAACCACA	NC021402.1Protobothropsjerdonii			ATTACC	COTTGACT	ANTITCAAC	AAACCACAAA	GATANCERA
NC022820.1Trimeresurusalbolabris ATTACCC TTGACTA TTCACAAAGTACCCG G FJ752422.1Viridoviperastejnegeristejnegeri ATTACCC TTGACTA TTCACAAAGTACCCG G NC054255.1Sinomicrurusmacclellandi ATCACCCC TTGACTG TTCCACAAAGACACCG G DQ343648.1Najanaja ATCGCCC TTGACTG TTCCACAAAGACACCG G LC431744.1Najakaouthia ATCGCCC TTGACTG TTCCACAAAGACACCG G NC01505.1Nydcophiscyanocinctus ATTACCC TTGACTA TTCCACAAAGACACCG G NC016054.1Laticaudacolubrina ATCACCCC TTGACTG TTCCACAAAGACAACGG G NC01624.1Sibynophiscollaris ATCACCC TTGACTG TTCCACAAAGACAATG G NC02575.1Orthriophistaeniurus ATTACCC TTGACTA TCCCACAAAGACATG G NC030041.1Ptyasmucosa ATTACTC TTGACTA TCCCACAAAGACATG G NC0157457.10onyonafrenatum ATTACTC TTGACTA TCCCACAAAGACATG G NC01700.1Lapheporyphyracea ATCGGCACCCTTATCCC TTGACTA TCCCA AAAGACATA TG A NC01521.2.Pythonmolurusmolurus GTGTACCCCCCTTGACTA TCCCA ACAAACCACAAGATA TG A	NC021412.1Protobothropsmucrosquamatus			ATTACC	COTTGACT	ATTTCAC	ANACCACAAA	GATARCORA
F3/52452.1virlaoviperastejnegeri ATTACCC TTGACTA TTCCACCAAGCACACAAGCACAAGCACACAAGCACAAGCACACAAGCACACAAGCACACAAGCACACGACACGACG	NC022820.lTrimeresurusalbolabris			ATTACC	CHITGACT	ANTITCHAC	AAATCACAAA	GATANCONG
NC034233.110mlCrU19maCc1a1and1 ATCGCCC TTGACTA CCACAAGACA CGAA DQ143648.1Najanaja ATCGCCC TTGACTG CTTCACCACAAGACA CGAA LC431744.1Najakaouthia ATCGCCC TTGACTG TTCACCACAAGACA CGAA NC011333.1Bungarusfasciatus ATTACCC TTGACTG TTCA ACCAACAACACA CGAA NC046795.1Hydrophiscyanocinctus ATTAACCC TTGACTG TTCA ACCAACAACACACACAA NC046795.1Hydrophiscyanocinctus ATTAACCC TTGACTG TTCA ACAAACCACAAGATA CGA NC046795.1Hydrophiscyanocinctus ATTAACCC TTGACTA TTCA ACAAACCAACAAAGATA CGA NC046795.1Hydrophiscyanocinctus ATTAACC TTGACTA TTCA ACAAACCAACAAAGATA CGA NC016424.1Sibynophiscollaris ATCACTC TTGACTA TCTCA ACAAACCAAAGATA CGA NC030041.1Ptyasmucosa ATTACTC TTGACTA TCTCA ACAAACCAAAGATA CGA NC057467.1Gonyosmafrenatum ATTACTC TTGACTA TCTCA ACAAACCAAAGATA TGAA NC01707.1Elapheporyphyracea ATCGGCACCCTATACCTC TTGACTA TCTCA ACAAACCAAAGATA TGAA NC015612.1Pythonnolurusmolurus GTGTACACCACCC TTGACTC TCACAAAACCAAAGATA TGAACAAACCAAAGATA TCACAAAACCAAAAACAAAAC	FJ/52492.1Viridoviperastejnegeristejnegeri			ATTACE	CETTGACT	ANTITCHAC	AAACCACAAA	CACANCORA
LC431744.1Najakaouthia ATCGCCC TTGACTG TTTC ACTAACCACAAAGACA CG A NC011393.1Bungarusfasciatus ATTACCC TTGACTA TTTC ACCAATCATAAAGATA TG A NC046795.1Nydrophiscyanocinctus ATTACCC TTGACTA TTTC ACCAATCATAAAGATA TG A NC036054.1Laticaudacolubrina ATCACCC TTGACTA TTTC ACTAACCACAAGATA TG A NC036054.1Laticaudacolubrina ATCACCC TTGACTA TTTC ACTAACCACAAGATA TG A NC025275.1Orthriophiscaniurus ATCACCC TTGACTA TCTC ACTAACCACAAGATA TG A NC030041.1Ptyasmucosa ATCACTC TTGACTA TCTC ACAAAGCACATGA TG A NC030041.1Ptyasmucosa ATTACTC TTGACTA TCTC ACAAAGCACATGA TG A NC037071.1Elapheporyphyracea ATCACCC TTGACTA TCTC ACAAATCACAAAGATA TG A NC00702.1Xenopeltisunicolor ATCGGCACCCATACCTTATTCG CGCATGA CAGACCACCAAAGATA TG A	DO343648 INajanaja		* * * * *	ATCGCC	CHTTGACT	GHTTTCHAC	TAATCACAAA	GACANCORA
NC011393.1Bungarusfasciatus ATTACCC TTGACTA TTTC ACCAATCATAAAGATA TC A NC046795.1Hydrophiscyanocinctus ATTACCC TTGACTA CTTC ACCAAAGATA TC A NC036054.1Laticaudacolubrina ATCACCC TTGACTA TTTC ACCAAAGATA TC A NC016424.1Sibynophiscollaris ATTACCC TTGACTA TCTC ACTAACGATA TC A NC025275.1Orthriophistaeniurus ATCACTC TTGACTA TCTC ACCAAAGATA TC A NC030041.1Ptysmucosa ATTACTC TTGACTA TCTC ACAAACCACAAAGATA TC A NC057467.1Gonyosomafrenatum ATTACTC TTGACTA TCTC ACAAAACCACAAAGATA TC A NC02770.1Elapheporyphyracea ATCACCC TTGACTA TCTC ACAAAACCACAAAGATA TC A NC015812.1Pythonmolurusmolurus ATCGCCACCCTATACCACCAAAGATA TCAC	LC431744, 1Najakaouthia			ATCGCC	COTTGACT	GUTTTCHAC	TAACCACAAA	GACALCGEA
NC046795.1Hydrophiscyanocinctus ATTACCCTTGACTAGTTGTTGACAAACCACAAAGATAGCGCA NC036054.1Laticaudacolubrina ATCACCCTTGACTAGTTGACTAGCCACAAAGATAGCGCA NC01624.1Sibynophiscollaris ATCACTCGTTGACTAGTCCCACAAAGATAGCGCAAAGATAGCGCA NC02005275.1Orthriophistaeniurus ATCACTCGTTGACTAGTCCCACAAAGATAGCGCAAAGATAGCGCA NC030041.1Ptyasmucosa ATTACTCGTTGACTAGTCCCACAAAGATAGCGCAAAGATAGCGCA NC057467.1Gonyosonafrenatum ATTACTCGTTGACTAGTCCCACAAAGATAGTGCA NC012770.1Elapheporyphyracea ATCACTCGTTGACTAGTCCCACAAAGATAGTGCA NC007402.1kenopeltisunicolor ATCGGCACCCCTATACTCGTGACTAGTCACACAAACCACAAAGATAGCA NC015812.1Pythonmolurusmolurus GTGTACACCACCCCTTGACTCGTCACAAACCAAAACCACAAAGATAGCGC	NC011393.1Bungarusfasciatus			ATTACC	COTTGACT	AUTTTCAAC	CANTCATAAA	GATATTOTA
NC036054.laticaudacolubrina ATCACCCTTGACTACTACCTAACCTAACCATAAGATATCGA NC016424.lSibynophiscollaris ATCACCCTTGACTATCTCAACTAACCATAAGATATCGA NC035275.lOrthriophistaeniurus ATCACCCCTTGACTATCTCAACAAACCAAAGATATCGA NC030041.lPtyasmucosa ATCACTCCTTGACTATCCCAACAAACCAACAATATCGA NC057467.lGonyosomafrenatum ATTACTCCTTGACTATCCCAACAAACCAATGAAACCAATGAAACCAATGAAACCAATGAAACCAATGAAAACCAATGAAAACCAATGAAAACCAAAAACCAAAAACCAAAAACCAAAAAACCAAAAA	NC046795.1Hydrophiscyanocinctus			ATTAAC	CGTTGGTT	GUTTTCAAC	AAACCACAAA	GATACCOA
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NC012770.1Elapheporyphyracea ATCACCCCTTGACTACTCCACAAAGATATTGGA NC007402.1Xenopeltisunicolor ATCGGCACCCTATACCTCTTATCGCGCATGATCAGGATTAGTTGGCGCCTGCCAAAGA NC015812.1Pythonmolurusmolurus GTGTACACCACCCCTTGACCCCCCCCAAAGATACCOCC	NC057467.1Gonvosomafrenatum			ATTACT	CATTGACT	ANTOTODAC	AAATCACAAA	GACANTONA
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NC015812.1Pythonmolurusmolurus GTGTACACCCCTTGACCCTCCCCCCCCCCCCCACAAAGATACCACACACA	NC007402.1Xenopeltisunicolor	ATCGGCACCCTAT	ACCTC	TTATTO	GCGCATG	ACAGGATT	AGTTGGCGCC	TOCCANC
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NC010196 IRamphotyphlopsbraminus	ICTTTATACCTCC	TOTTTGGTGCC	TGATCCOG	AATCTTAGGC	GCAACCCT	AGTATAARA
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EU913478 1Daboiarussellii	ACCCTATATTTAA	TATTTGGCGCT	TGATCIGG	GTTAGTCGGA	GCCTGCTT	AGCATCO
NC042397 1Malayopythonreticulatus	ACATTATATCTTT	TATTTGGCGCJ	TGGTCCGG	ATTAGTAGGT	GCCTGCCT	AGCGTACUT
NC029165.1Protobothropshimalayanus	ACCCTATACCTTA	TATTCGGCGCJ	TGATCOGG	CCTTATCGGG	GCCTGCCT	AGCATTC
NC029166.1Protobothropskaulbacki	ACCICTATATCTCA	TATTCGGCGC	TEGTCCGG	CCTTATCGGG	GCCTGCCT	AGTATCC
NC021402.1Protobothropsjerdonii	ACCCTATACCTTA	TATTIGGCGC	TGATCOGG	CCTCATCOGG	SCCTSCCT	AGCATTC
NC021412.1Protobothropsmucrosquamatus	ACCCTATACCTTA	TATTTGGTGCI	TGATCCGG	TCTTATCGGG	SCCTSCCT.	AGCATTCA
NC022820.1Trimeresurusalbolabris	ACCCTATACCTCA	TATTCGGGGC	TGAGCIGG	TCTAACCGGA	GCCTGCCT/	AGCATCC
FJ752492.1Viridoviperastejnegeristejnegeri	ACCCTATACCTAA	TATTCGGCGCJ	TGGTCCGG	CCTTATCGGA	SCCTSCCT!	AGCATCONA
NC054255.1Sinomicrurusmacclellandi	ACTOTOTATCTTC	TATTIGGGGC	TTGGTCCGG	CCTAATTGGA	GCATGCCT	AGCGTACEA
DQ343648.1Najanaja	ACCCTCTACCTTC	TGTTTGGTGCC	TGATCCGG	CCTAATCGGA	GCCTGCCT?	AGCATAC
LC431744.1Najakaouthia	ACCCTCTACCTTC	TGTTTGGTGCC	TGATCCGG	TCTAATIGGG	GCCTGCCT?	AGTATGC
NC011393.1Bungarusfasciatus	ACCITIGTACCTAC	TGTTTGGGGCC	TGGTCAGG	TTTAATTGGA	GCCTGCCT	AGTATTC
NC046795.1Hydrophiscyanocinctus	ACCTTGTACCTTC	TATTCGGCGCC	TGATCIEG	TCTTATCGGG	GCTTGTTT	AGTATAA
NC036054.1Laticaudacolubrina	ACCITTATATCTTC	TATTCGGAGCC	TGATCCGG	TCTTACCGGA	GCATECCT	AGCCTATEG
NC016424.1Sibynophiscollaris	ACCCTTTACCTCC	TGTTTGGGGCC	TGATCCGG	CCTAATTGGG	GCCTGCCT	TAGCATCO
NC025275.10rthriophistaeniurus	ACCICITATACCTAC	TATTTGGCGC	TOGTCTOG	CCTAATCGGA	GCCTGCCTC	AGCATTCHT
NC030041.1Ptyasmucosa	CCCTATACCTAC	TATTTGGCGC	TGATCTOG	CCTAATCOGA	actractio	AGCATTT
NC057467.1Gonyosomarrenatum	ACCCTATACCTAC	TATTTGGAGC	TGATCITGG	CTTGATCOOG	OCCTOCCTO	AGCATCONC
NC012770, 1Elaphoporyphyracea	COCTATACCTAC	TATTTGGCGC	TGATCAGO	CCTAATTOGT	accrection.	AGCATCONA
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Fig 7 : Portion of MSA with respect to COX1

The conserved region present in between 8 to 1517 base pairs as shown in the MSA of Cox 1 gene. 44 to 100 base pairs show a highly base transition. The most variable regions present at the starting bases of the gene sequences.

Analysis of Annotations-

Total 13 conserved regions are present in the mitochondrial genome of snakes. These are nad1, nad2, cox1, cox2, atp8, atp6, cox3, nad3, nad4l, nad4, nad5, nad6 and cob(cytochrome B) along the length of the complete mitochondrial genome.

Daboia russellii has a special region atp6-1 of 186 base pairs at 16973 to 17158 base pair of the complete mitochondrial genome. This region located at the end of the complete mitochondrial genome of Daboia russellii.





Genes like atp6-0, cox3 are of same length in all 23 species [atp6=675, cox3=783].

Now if we compare the 2 species of the same genus Naja that is Naja naja and Naja kaouthia, we found that all the length of the conserved genes are same but the location of these genes in the whole mitochondrial genome is slightly different with respect to their start and stop bases [nad1 2572-3519 and 2566-3513

cox1 6227-7753 and 6219-7745

atp8 8696-8857 and 8688-8849

cob 14993-16042 and 14986-16035 for Naja naja and Naja kaouthia respectively]

2 species of family Pythonidae [Malayopython reticulatus, Python molurus] have significant differences in lengths of nad1, nad2, cox1, atp8, nad3, nad5, nad6. In nad6 the lengths are 468 and 504 respectively. But the lengths of other gene regions[cox2, atp6, cox3, nad4l, nad4 and cob] are same in both species.

4 species of family Viperidae of same genus Protobothrops - Protobothrops himalayanus, Protobothrops jerdonii, Protobothrops kaulbacki, Protobothrops mucrosquamatus the lengths cox2 are 672, 669, 672, 669 respectively.

Lengths of nad5 are 1773, 1776, 1755, 1755 respectively.

But in case of nad6, only Protobothrops mucrosquamatus has different length of 501 base pairs whereas other 3 species show a same length of 513 base pairs.

5 species of family Colubridae - Gonyosoma frenatum, Orthriophis taeniurus, Elaphe poryphyracea, Ptyas mucosa, Sibynophis collaris

Cob or CytB of , Sibynophis collaris is 1080 base in length but others 1047.

tRNA gene rRNA gene protein coding gene

 EU913478.1_ Daboia russellii mitochondrion, complete genome (gi_195549244_gb_EU913478.1_)



2. DQ343648.1_ Naja naja mitochondrion, complete genome (gi_84371449_gb_DQ343648.1_)



 LC431744.1_ Naja kaouthia mitochondrion, complete genome (gi_1644970594_dbj_LC431744.1_)



4. NC_022820.1_ Trimeresurus albolabris mitochondrion, complete genome (gi_558603225_ref_NC_022820.1_)



 NC_025275.1_ Orthriophis taeniurus mitochondrion, complete genome (gi_699256358_ref_NC_025275.1_)



 NC_057467.1_ Gonyosoma frenatum voucher LSU20200812JZF01 mitochondrion, complete genome (gi_2091526104_ref_NC_057467.1_)


FJ752492.1_ Viridovipera stejnegeri stejnegeri mitochondrion, complete genome (gi_224037274_gb_FJ752492.1_)



 NC_007402.1_ Xenopeltis unicolor mitochondrion, complete genome (gi_74310600_ref_NC_007402.1_)



9. NC_042397.1_ Malayopython reticulatus mitochondrion, complete genome (gi_1678641010_ref_NC_042397.1_)



 NC_012770.1_ Elaphe poryphyracea mitochondrion, complete genome (gi_238866932_ref_NC_012770.1_)



11. NC_029165.1_ Protobothrops himalayanus isolate KIZ 012736 mitochondrion, complete genome (gi_992329443_ref_NC_029165.1_)



 NC_021402.1_ Protobothrops jerdonii mitochondrion, complete genome (gi_511348019_ref_NC_021402.1_)



 NC_029166.1_ Protobothrops kaulbacki mitochondrion, complete genome (gi_992329457_ref_NC_029166.1_)



14. NC_030041.1_ Ptyas mucosa mitochondrion, complete genome (gi_1025805876_ref_NC_030041.1_)



15. NC_021412.1_ Protobothrops mucrosquamatus mitochondrion, complete genome (gi_511348159_ref_NC_021412.1_)



16. NC_015812.1_ Python molurus molurus mitochondrion, complete genome (gi_339906613_ref_NC_015812.1_)



17. NC_016424.1_ Sibynophis collaris mitochondrion, complete genome (gi_359422038_ref_NC_016424.1_)



18. NC_054255.1_ Sinomicrurus macclellandi voucher HS2020001 mitochondrion, complete genome (gi_2026155312_ref_NC_054255.1_)



19. NC_010196.1_ Ramphotyphlops braminus mitochondrion, complete genome (gi_164420879_ref_NC_010196.1_)



20. NC_011393.1_ Bungarus fasciatus mitochondrion, complete genome (gi_209886953_ref_NC_011393.1_)



21. NC_046795.1_ Hydrophis cyanocinctus mitochondrion, complete genome (gi_1829769152_ref_NC_046795. 1_)



22. NC_036054.1_ Laticauda colubrina mitochondrion, complete genome (gi_1267170684_ref_NC_036054.1_)



23. NC_007400.1_ Acrochordus granulatus mitochondrion, complete genome (gi_74310558_ref_NC_007400.1_)



Comparative analysis of the phylogenetic trees constructed on the basis of complete sequence of specific mt gene region-

Family	Species name						
Viperidae	Daboia russellii						
	Viridovipera stejnegeri						
	Trimeresurus albolabris						
	Protobothrops himalayanus						
	Protobothrops jerdonii						
	Protobothrops kaulbacki						
	Protobothrops mucrosquamatus						
Elapidae	Naja naja						
1	Naja kaouthia						
	Sinomicrurus macclellandi						
	Bungarus fasciatus						
	Hydrophis cyanocinctus						
	Laticauda colubrina						
Colubridae	Gonyosoma frenatum						
Contoniduo	Orthriophis taeniurus						
	Elaphe poryphyracea						
	Ptvas mucosa						
	Sibynophis collaris						
Varianaltidaa	Vananaltia unicalan						
Xenopelfidae,	Xenopeitis unicolor						
Pythonidae	Malayopython reticulatus						
	Python molurus						
Typhlopidae	Ramphotyphlops braminus						
Acrochordidae	Acrochordus granulatus						



Fig 9 : Phylogenetic Tree with respect to nad1

Here, Colubridae family is outgrouped. Elapidae and Viperidae shows a common ancestor. Xenopeltidae, Pythonidae, Typhlopidae, Acrochordidae show very close evolutionary relationship as they are under a common monophyletic group.

Viridovipera stejnegeri, Trimeresurus albolabris have a common ancestor which is monophyletic with the common ancestor of Protobothrops. But in cyt b there is no such so much closely related common ancestor between Viridovipera stejnegeri and Trimeresurus albolabris.



Fig 10 : Phylogenetic Tree with respect to atp 8

All the species of family Viperidae, are in a monophyletic group [which is different from others].

Here, family Viperidae and the common ancestor of Xenopeltidae and Pythonidae share a common ancestor. In family Colubridae, Sibynophis collaris shows a distant evolutionary relationship with other species of this family. The rate of evolution with respect to atp8 gene is slow in Sibynophis collaris than other species of the family Colubridae.

Hydrophis cyanocinctus, Laticauda colubrina of family Elapidae show the most closely relation with the most common ancestor of the phylogenetic tree with respect to atp8 gene.



Fig 11 : Phylogenetic Tree with respect to cox 1

But in case of cox 1, all species of family Viperidae, are not in a monophyletic group. 4 species of genus Protobothrops possess a same common ancestor.

Acrochordus granulatus (family- Acrochordidae), Ramphotyphlops braminus (family-Typhlopidae), Xenopeltis unicolor(family- Xenopeltidae), Malayopython reticulatus and Python molurus (family- Pythonidae) belong to different genus but present in a same monophyletic group [also same in case of nad1 as well as cyt b]. Common ancestor of families Xenopeltidae, Pythonidae, Typhlopidae, Acrochordidae show very less relation [35 score] with the common ancestor of other 3 families.

Family Elapidae and Colubridae possess a common ancestor. And this common ancestor and the common ancestor of family Viperidae originated from a same common ancestor.



Fig 12 : Phylogenetic tree with respect to cyt b

In phylogenetic tree of cyt b families Viperidae and Colubridae possess a common ancestor. But in case of cox 1 families Elapidae and Colubridae are closely related and possess a common ancestor. It shows that the evolutionary pattern depends on specific gene region changes.

Though Sinomicrurus macclellandi is belongs to family Elapidae, it is outgrouped and distantly related with other species of family Elapidae but is closely related with the most common ancestor.



Fig 13 : Phylogenetic tree with respect to complete mitochondrial genome

Here, Viperidae and Colubridae posses a same common ancestor which is similar to that of Cyt B. This suggests that the rate of evolution of whole mitochondrial genome is very much associated with the rate of evolution with respect to Cyt B gene region of the complete mitochondrial genome. Sinomicrurus macclellandi is also very much closely related with the most common ancestor which is nearly same as Cyt B phylogenetic tree.

Conclusion-

Based on the phylogenetic relationships among the tested snakes and the comparisons of their gene organizations, we estimated the processes of evolutionary events occurred in snake mitochondrial genomes.

Snake mitochondrial genomes present a rare opportunity to investigate the evolutionary interactions and ramifications that link genome architecture, molecular evolution, and multi-level molecular function Previous studies have suggested that snake mt genomes have an accelerated rate of evolution. The above study shows that the rates of snake mitochondrial genome evolution incorporate broad temporal (Branch specific and depend on Family of snake species) and spatial (gene and gene-region specific) dynamics.

In support of a hypothesis involving selection for overall oxidative metabolic function, the accelerated rates of molecular evolution in snakes appear to depend greatly on gene function, with most ATP subunits and COX3 accelerating only slightly and occasionally, while COX, ND, CytB, and rRNA evolutionary accelerations are more fast (on the basis of annotation and length of genes) The roles of these proteins (and the mitochondria in general) in energetics via oxidative phosphorylation are well known, and it may be that a single causative agent accompanying the diversification of snakes that dramatically altered metabolic demand, or led to a fluctuation in metabolic demand, was responsible for large-scale changes in selective pressure on these proteins[2].

However, a more comprehensive sampling of snake mitochondrial genomes is necessary to further refine the phylogenetic relationships among major groups of snakes.

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Review on the advance floral morphology and pollination syndrome in various plants

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Abstract: - Study of advance floral morphology is a very important aspect of pollination biology. Many varieties of advance floral morphology are seen across various plant families and orders. Though most of the advance morphology is related with pollination of the plant, *i.e.* for attracting pollinators and complete pollination efficiently, pollination is not only its sole purpose, some also serves for preying, defense, mutualism, symbiotic relation and other purposes. Orchids (Orchidaceae) have most variety among the advance morphology- from conspicuous "star of Bethlehem" to little *Epipactis*, they show extensive variety in both advance floral morphology and in pollination syndrome. Other genus like, *Arisaema, Salvia* etc. also shows various advance floral morphology is evolved, modified and controlled by many factors like specific pollinator/s, abundance of pollinators, coevolution with the pollinator, habitat, environmental factors and stress from surrounding, mutualism or symbiotic relation of the pollinators with the plant etc.

Keywords: - Pollinator flower relation, Coevolution, Competitive selection.

Introduction: - Floral morphology differs in various flowering plants with respect to its habitat, reproductive strategies, pollination syndrome and types of pollinators associated with the plant or flower. Floral morphology consists of a large number of parameters, including the number and shape of petals, number of stamens, petal size and the number and arrangement of styles and ovaries. The pollen grains of insect pollinated flowers are sticky due to pollen kit. The surface of stigma of flowers is rough. Some of the plants develop special adaptation for insect pollination. Many flowers show advance floral morphology for different pollinators. Study of advance floral morphology is important to understand relation of pollinator and plant, and also the co-evolutionary aspect of these two.

Discussion: - Through years of observation, it is a well-established fact that angiosperm flowers and its insect pollinators have influenced each other's evolution a lot, but it is not quite understood that is coevolution is a major process to form diversification among these groups. Coevolution is most likely when interacting organisms have strong effects on each other's fitness (Thompson 1994). This criterion is clearly met for pollination mutualisms in which the insects that pollinate plants also depend on them as brood sites (Thompson 1994). Classic examples of such coevolved brood-site pollination mutualisms are the relationships between figs and Agaonid fig-wasps and between Yuccas and Tegiticula moths (Pellmyr *et al.* 1996; Sakai 2002; Weiblen 2002).

Co-evolution: - One of the great examples of this kind of coevolution is Darwin's orchid (*Macroplectrum sesquipedale*) and its only pollinator the Hawk moth or *Xanthophane morganii* praedicta.

In hypothesizing, how the Malagasy star orchid might have evolved it's extraordinarily long (30 centimeters) nectar spur, Darwin (1862) proposed the first mechanistic model of the coevolutionary process. He did refer to "a race in gaining length between the nectary of Angraecum and the proboscis of certain moths" (Darwin 1862). He noticed that the Malagasy star orchid, which is endemic to Madagascar, have an unusual long spur and have nectar at the very bottom of long spur. In fact, to reach the nectar of the orchid requires a 30cm (11inch) long proboscis to penetrate the long nectar spur. Darwin and Alfred Wallace (Father of principle of evolution) predicted that the pollinator of this long spur flower must have to be some long-tongued moth. Hawk moth, also called sphinx moth or hummingbird moth, any of a group of sleek-looking moths that are named for their hovering, swift flight patterns. These moths have stout bullet-shaped bodies with long, narrow forewings and shorter hind-wings. Wingspans range from 5 to 20 cm. Later, after discovery of the moth, it was also observed that the fittest moths in a population would then be those with long tongues that could access the nectar in even the deepest flowers, whereas the shorter-tongued moths would access less nectar (Fig.1). Thus, moths would be expected to be under strong directional selection and should evolve greater tongue lengths (Fig. 1). This is a fine example of both adaptive floral morphology of Darwin's orchid, which have almost 30cm long spur and their coevolutionary significance with giant hawk moth who also have almost 30cm long proboscis and is the only pollinator of that orchid.



Mimicry in orchids: -

Prey mimic: - Orchids show enormous types of adaptive or advance unique floral morphology to attract its pollinators. One of the finest examples is Helleborines, *Epipactis veratrifolia* (*Orchidaceae*). This flower has structure that looks like aphid. This aphid mimicry is a kind of prey mimicry as aphidophagous hoverflies lay eggs on false brood sites on their flowers as its larvae eats aphids during its developmental stage-



Fig 2.1- Prey Mimic by Epipactis (Ref- bmcplantbio.biomedcentral.com)

Aggressive Mimic: - Another example from orchid genus is *Oncidium*. *Oncidium* species have bright yellow color flower and it situates at the ends of stalks that sway in breeze, it mimics an antagonist- a male bee. An aggressive Centris bee always try to drive other bees or specifically males out of their territory. So, the bee mistakenly attacks the flower as male competitor and strikes it, eventually the pollinia attaches to its head. When it attacks a second flower, the pollinia presses into the stigma and pollination occurs-



Fig 2.2- Oncidium mimicking male bee (Ref- researchgate.net)

Another fine example of using adaptive floral morphology as mimic is ophrys. In *Ophrys sphegodes* orchid chemical mimicry was first proposed by Kullenberg (1961). Beside of the fact that the flower exactly looks like a female bee, BergstroÈm (1978) discusses mainly two possibilities concerning the biologically active volatiles involved in the chemical mimicry of Ophrys orchids:

(1) the orchid mimics an aphrodisiac produced by the females, and (2) *Ophrys* orchids make use of "extranormal stimuli", i.e., compounds usually not produced by a female, which hit existing receptors associated with sexual behavior. Borg-Karlson and TengoÈ (1986) first suggested presence of aliphatic primary alcohols and methyl carbinols as well as several terpenes, occurring in flowers and bee secretions, to be the key components in *O. lutea* pollinated by Andrena-bees., the alkenes of the orchid and bee cuticle proved to be behaviorally more active than the alkanes. The specific adaptation of *O. sphegodes* flowers for pollinator attraction seems therefore to be a higher production of specific isomers of alkenes. The evolution of the pollination mechanism of sexual deception, which involves a mimicry of the pollinator's sex pheromone, has apparently been mediated by a change in the hydrocarbon pattern in the wax layer of the flowers-



Fig 2.3- *Ophrys* flower mimicking female bee, also producing odor that resembles pheromone released by female bees. (Ref- Researchgate.net)

Lever mechanism: -

Another very complex advance floral morphology is seen in Salvia, a family of shrubs (*Salvia pratensis*). Salvia pratensis is a gynodioecious species featured by its modified stamens that act as a lever mechanism in pollination. (Gynodioecy, a sexual system with hermaphrodite and female individuals in a population, raises the question how the two sexual morphs are maintained).

Floral traits significantly differ between two sexual morphs in the population of *S. pratensis*. The female has on average a shorter corolla and tube, a smaller platform (i.e., flower mouth), and a stigma closer to the platform than hermaphrodite flowers. Style exertion, flower production and stalk diameter do not significantly differ between two morphs. The floral traits (e.g., corolla, tube length and stigma height) are significantly larger in hermaphrodites than in females of S. pratensis. The flowers of salvia have bilabiate corolla tube.

The connective of stamen is long. The anterior anther lobe of connective is fertile while posterior lobe is sterile. When the insect lands on the lower lip, the fertile lobe automatically comes down to touch the back of insect and thus depositing the pollen grains there on.





Another example of advance floral morphology that is very common in various species of orchids as well as other families is nectar guide, which are the specific patterns or markings on some flowers that guide a pollinator to its reward which is a nectar and elicit the pollination. It is proven that flowers with these special markings have more chance to achieve pollination than the flowers that don't have this kind of markings. Nectar is a sugar rich compound that is produced by gland nectaries. Nectar is one of the most abundant and common reward used for attracting pollinators. But sometime it is hard for the pollinators to find the exact position of nectaries or nectar. Here comes the role of nectar guides, these are markings or patterns seen in flowers of some angiosperm species, that guide pollinators to their rewards. Rewards commonly take the form of nectar, pollen, or both, but various plants produce oil, resins, scents, or waxes. Such patterns also are known as "pollen guides" and "honey guides". Here are some examples of nectar guides (both normal and uvvisible)-



Fig 4- Nectar guide in different flowers (Ref-journal.plos.org)

Another fine and complex example of advance floral morphology in sake of pollination is Cobra Lily, also known as Jack-in-the-pulpit (Arisaema triphyllum). It is named for its resemblance with a preacher (jack) in its hanging pulpit. The flowers are simple: male flowers are comprised of only four stamens, and female flowers of a fuzzy stigma atop an ovary. Jack-in-the-pulpit is pollinated by fungus gnats. A total of 16 fungus gnat genera comprising 47 identified species were observed. Usually, members of more than one taxon are attracted per Arisaema species, and both sexes of gnats are involved. Attraction is deceptive by mimicking olfactory, visual and tactile cues characteristic of fungi where the gnat sexes normally meet and females oviposit. Odours produced by osmophores play the most important part. The gnats visit to lay their eggs on what they are duped to believe is a fungus. Fungus gnats normally lay their eggs on fungi so that when the eggs hatch the larvae will have a readily available food source. When they mistakenly fall into the preacher, they are unable to crawl out of the spathe due to its slippery interior, nor can they fly straight up to escape in that way. However, if the plant is a male, they may eventually notice a small opening at the base of the spathe through which they can escape. By this time, they are dusted with pollen. They eventually enter a female plant where the pollen that they are carrying brushes off on the fuzzy stigmas, thereby effecting pollination. This time there is no escape since the spathes of female plants have no opening in the base of their spathes, and the gnats die within the spathe-



Fig 5- Preacher and pulpit like structure of spathe of Cobra lily (Arisaema) (Ref-Gardenia.com)

Another example can be cited by *Titan arum*, infamous as corpse flower. It is known for its massive foul-smelling inflorescence (cluster of flowers). The plant is endemic to the steep hillsides of rainforests in western Sumatra. This flower has a very conspicuous unbranched inflorescence and it smells like rotting flesh to attract flies and beetles. The massive inflorescence of the titan arum consists of an inner flower spike, known as a spadix, surrounded by a petal-like collar known as a spathe-



Fig 6- A conspicuous Corpse flower (*Titan aurum*) (Ref- Britanica.com)

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EXPERIMENTAL OBSERVATION ON SOME LOCAL DRAGON FLIES IN THE AREA OF RIVER AND CANAL OF NAWAB GANJ GANGA GHAT ,24pgs NORTH.

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<u>ABSTRACT</u>: A dragonfly is a flying insect belonging to the order Odonata, infraorder Anisoptera (from Greek ἄνισος anisos, "unequal" and πτερόν pteron, "wing", because the hindwing is broader than the forewing). Adult dragonflies are characterized by a pair of large, multifaceted compound eyes, two pairs of strong, transparent wings, sometimes with coloured patches, and an elongated body. Dragonflies can be mistaken for the closely related damselflies, which make up the other odonatan infraorder (Zygoptera) and are similar in body plan though usually lighter in build; however, the wings of most dragonflies are held flat and away from the body, while damselflies hold their wings folded at rest, along or above the abdomen. Dragonflies are agile fliers, while damselflies have a weaker, fluttery flight. Many dragonflies have brilliant iridescent or metallic colours produced by structural colouration, making them conspicuous in flight. An adult dragonfly's compound eyes have nearly 24,000 ommatidia each. The order Odonata contains the dragonflies and damselflies and is one of the most popular insect groups. Odonates are popular with both the amateur and professional because they are large, colorful, easily observable and have exceptionally charismatic behaviors. In recent years dragonflies in particular have been popular with birders as many dragonflies rival birds in wingspan, color, gregariousness, and predictability. As a result of their popularity with the public, they have become the focus of many conservation efforts in North America, Europe, and Asia.

Odonata was until recently composed of three suborders: Anisoptera, commonly known as dragonflies; Zygoptera, commonly known as damselflies; and Anisozyoptera, as the name denotes, a morphological composite of the previous two suborders. However, the suborder Anisozygoptera has been abandoned, as current research shows that Anisozygoptera is not a natural group, and is paraphyletic (Rehn 2003, Lohman 1996). Thus, the group has been combined with the suborder Anisoptera, which does form a natural group in a new suborder called Epiprocta (Bechly 1996). To facilitate the discussion of North American odonates it is useful to use the names Zygoptera and Anisoptera when discussing differences between the damselflies and dragonflies, as there are no extant Anisozygoptera in North America.

KEY WORDS :- Dragonfly ,flight mechanism, area.

INTRODUCTION :- Dragonfly is a flying insect belonging to the order Odonata, infraorder Anisoptera.Adult dragonflies are characterized by a pair of large, multifaceted compound eyes, two pairs of strong, transparent wings, sometimes with coloured patches, and an elongated body. Dragonflies can be mistaken for the closely related damselflies, which make up the other

odonatan infraorder (Zygoptera) and are similar in body plan though usually lighter in build; however, the wings of most dragonflies are held flat and away from the body, while damselflies hold their wings folded at rest, along or above the abdomen. Dragonflies are agile fliers, while damselflies have a weaker, fluttery flight. Many dragonflies have brilliant iridescent or metallic colours produced by structural colouration, making them conspicuous in flight. An adult dragonfly's compound eyes have nearly 24,000 ommatidia each.

MATERIAL AND METHOD :- Material like mobile phone to capture picture of the dragonfly observed with GPS location ,date,time .Method involve visit to local area for the collection of data .

OBSERVATION :- Four types of dragonflies are observed in the area of palta park (nawab ganj ganga ghat) in different day, these are – *Ictinogomphus rapax*, and other are under family *Odonata*. The weather condition on 16/12/21 mostly clear and foggy at early morning, 18/12/21 clear weather and foggy early morning, 19/12/21 clear, foggy early morning, 20/12/21 and 21/12/21 clear day and foggy early morning. All the dragonfly are near the plant and water side. They also try to hide themselves from birds and other predators in the side of plant and water or river side. They come to collect food for survive.











DISCUSSION:- Fossils of very large dragonfly-like insects, sometimes called griffinflies, are found from 325 million years ago (mya) in Upper Carboniferous rocks; these had wingspans up to about 750 mm (30 in), but were only distant ancestors, not true dragonflies. About 3,000 extant species of true dragonfly are known. Most are tropical, with fewer species in temperate regions. Loss of wetland habitat threatens dragonfly populations around the world.Dragonflies are predatory insects, both in their aquatic nymphs stage (also known as naiads) and as adults. In some species, the nymphal stage lasts for up to five years, and the adult stage may be as long as ten weeks, but most species have an adult lifespan in the order of five weeks or less, and some survive for only a few days. They are fast, agile fliers capable of highly accurate aerial ambush, sometimes migrating across oceans, and often live near water. They have a uniquely complex mode of reproduction involving indirect insemination, delayed fertilization, and sperm competition. During mating, the male grasps the female at the back of the head, and the female curls her abdomen under her body to pick up sperm from the male's secondary genitalia at the front of his abdomen, forming the "heart" or "wheel" posture.

Dragonflies are represented in human culture on artefacts such as pottery, rock paintings, statues and Art Nouveau jewellery. They are used in traditional medicine in Japan and China, and caught for food in Indonesia. They are symbols of courage, strength, and happiness in Japan, but seen as sinister in European folklore. Their bright colours and agile flight are admired in the poetry of Lord Tennyson and the prose of H. E. Bates.

Although dragonflies are swift and agile fliers, some predators are fast enough to catch them. These include falcons such as the American kestrel, the merlin and the hobby;nighthawks, swifts, flycatchers and swallows also take some adults; some species of wasps, too, prey on dragonflies, using them to provision their nests, laying an egg on each captured insect. In the water, various species of ducks and herons eat dragonfly nymphs and they are also preyed on by newts, frogs, fish, and water spiders. Amur falcons, which migrate over the Indian Ocean at a period that coincides with the migration of the globe skimmer dragonfly, Pantala flavescens, may actually be feeding on them while on the wing. Dragonflies live on every continent except Antarctica. In contrast to the damselflies (Zygoptera), which tend to have restricted distributions, some genera and species are spread across continents. For example, the blue-eyed darner Rhionaeschna multicolor lives all across North America, and in Central America emperors Anax live throughout the Americas from as far north as Newfoundland to as far south as Bahia Blanca in Argentina, across Europe to central Asia, North Africa, and the Middle East. The globe skimmer Pantala flavescens is probably the most widespread dragonfly species in the world; it is cosmopolitan, occurring on all continents in the warmer regions. Most Anisoptera species are tropical, with far fewer species in temperate regions.

Some dragonflies, including libellulids and aeshnids, live in desert pools, for example in the Mojave Desert, where they are active in shade temperatures between 18 and 45 °C (64.4 to 113 °F); these insects were able to survive body temperatures above the thermal death point of

insects of the same species in cooler places.Dragonflies live from sea level up to the mountains, decreasing in species diversity with altitude. Their altitudinal limit is about 3700 m, represented by a species of Aeshna in the Pamirs.Dragonflies become scarce at higher latitudes. They are not native to Iceland, but individuals are occasionally swept in by strong winds, including a Hemianax ephippiger native to North Africa, and an unidentified darter species. In Kamchatka, only a few species of dragonfly including the treeline emerald Somatochlora arctica and some aeshnids such as Aeshna subarctica are found, possibly because of the low temperature of the lakes there. The treeline emerald also lives in northern Alaska, within the Arctic Circle, making it the most northerly of all dragonflies.

Flight performance of a dragonfly:-The dragonfly, Anaxparthenope Julius (Brauer) was observed in free flight, and a theoretical analysis of flight performance at various speeds was carried out. The variation with time of forces and moments acting on wings and body in steady trimmed flight was calculated by the local circulation method. Measures of flight performance, such as top speed, cruising speed and maximum endurance speed, were estimated from a necessary power curve required in steady flight and from the estimated available power. The results show that without using any novel unsteady aerodynamic force generated by a separated flow over the wings, the dragonfly can make steady trimmed flight at various flight speeds, from hovering to top speed.The steady slow climbing flight of a dragonfly, Sympetrum frequens, was filmed and analysed. By using the observed data, the mechanical characteristics of the beating wings were carefully analysed by a simple method based on the momentum theory and the blade element theory, and with a numerical method modified from the local circulation method (LCM), which has been developed for analysing the aerodynamic characteristics of rotary wings.

The results of calculations based on the observed data show that the dragonfly performs low speed flight with ordinary airfoil characteristics, instead of adopting an abnormally large lift coefficient. The observed phase advance of the hindwing, $\Delta\delta 1 \simeq 80^{\circ}$ can be fully explained by the present theoretical calculation. Similarly, the spanwise variation of the airloading and the time variations of the horizontal force, vertical force, pitching moment and torque or power can be definitely estimated within a reasonable range of accuracy in comparison with the flight data. The distribution of loading between the fore and hind pairs of wings is also clarified by the calculations.

The dragonfly, Anaxparthenope Julius (Brauer) was observed in free flight, and a theoretical analysis of flight performance at various speeds was carried out. The variation with time of forces and moments acting on wings and body in steady trimmed flight was calculated by the local circulation method. Measures of flight performance, such as top speed, cruising speed and maximum endurance speed, were estimated from a necessary power curve required in steady flight and from the estimated available power. The results show that without using any novel unsteady aerodynamic force generated by a separated flow over the wings, the dragonfly can make steady trimmed flight at various flight speeds, from hovering to top speed.

Dragonfly wings are highly corrugated, which increases the stiffness and strength of the wing significantly, and results in a lightweight structure with good aerodynamic performance. How insect wings carry aerodynamic and inertial loads, and how the resonant frequency of the flapping wings is tuned for carrying these loads, is however not fully understood. To study this we made a three-dimensional scan of a dragonfly (Sympetrum vulgatum) fore- and hindwing with a micro-CT scanner. The scans contain the complete venation pattern including thickness variations throughout both wings. We subsequently approximated the forewing architecture with an efficient three-dimensional beam and shell model.

<u>CONCLUSION</u> :- From the various resorce and help of the teachers and books ,get many information about dragonflies . Various types of dragon flies get observed during early morning .

<u>ACKNOWLEDEMENT</u> :- I would like to express my special thanks of gratitude to our professor DD for his guidance and complete my project.

I would also like to express my gratitude to Partho Ganguly.

<u>REFERENCE</u> :- 1. E-Book of Project Lifescape_ Centre for Ecological Sciences, Indian Institute of Science and Indian Academy of Sciences, Bangalore, India : pp. 118.

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Department of Zoology

DSE IIC Project Report

A Study to find the Evolutionary Trend of Snake species present in Indian subcontinent in respect of Mitochondrial Genes, Cytochrome B and COX1

Submitted by

Anomitra Neogy

UG || Semester: V || Exam Roll no.: 2022151167 Registration Number: A01-1112-115-024-2019

Study and Analysis of the Phylogenetic Tree to understand the Evolutionary Trend of Snake species present in Indian subcontinent in respect of Mitochondrial Genes, Cytochrome B and COX1

Introduction:

A mitochondrial genome is the sum of the genetic information which are available in the chromosome of the mitochondrion, which is located in the cytoplasm, outside of the cell nucleus. Mitochondrial genome encodes proteins related to the oxidative phosphorylation.

The mitochondrial genome generally represents a favoured genetic source for studying the evolutionary trends due to some of its valuable features:

i) offers a faster evolutionary rate than nuclear genome and provides higher resolution in phylogenesis of the closely related species.

ii) a mechanism of maternal inheritance and lack of recombination, which results into fewer errors into the phylogenetic reconstruction.

iii) being a compact genome, allows an easier determination and computational analysis of the DNA sequence.

iv) the presence of various protein coding genes provides an evolutionary context of the genome.

In a typical vertebrate mitochondrial genome, there is one control region (CR), two ribosomal RNA (rRNA), 13 protein coding genes and 22 transfer RNAs. When compared with the typical vertebrate mitochondrial DNA, the snake mitochondrial DNAs have some unusual features. It includes two duplicated CRs, a compact genome and an elevated evolution rate. The CR in a typical mitochondrial genome is responsible for initiating replication and transcription. Depending upon the correlation resulting from the asymmetric replication of the mitochondrial DNAs, the magnitude of the acceleration rate varied considerably among genes and over time, and it appears that the changes at the nucleotide and protein level cooccurred with the snake mitochondrial DNAs incurring a reduction in the size and duplication of the control region.

Objective:

The main objective of this study is to find and identify the evolutionary relationship and the evolutionary trend among the snake species found in Indian subcontinent by constructing the phylogenetic tree in respect of the cytochrome b and COX1 mitochondrial genes.

Material & Methodology:

For this project, the study is kept limited for the snake species available in the Indian subcontinent.

At first, the required details (scientific name, common name, higher taxa & distribution) for the snake species found in Indian subcontinent was collected from the Reptile Database (link). For obtaining a refined search result advanced search was performed taking Snakes as the higher taxa and India as the place of distribution. A total number of 337 snake species were found under the Indian subcontinent. These obtained data sets were preserved in an excel file.

After the collection of the required data, 7 mitochondrial genes were selected, under which, further study will be conducted. Those 7 mitochondrial genes were Cytochrome B, COX1, 12s rRNA, 16s rRNA, ND-1, ND-4 and D- Loop.

Now, for further study, these nucleotides were searched against the 337 snake species of the Indian subcontinent using NCBI (ff) (link). The obtained results were basically the previous studies performed on those species against the given nucleotides. From these results, the accession id, the title of the paper and species distribution were preserved in a separate spreadsheet of the previously made excel file.

For detailed study the mitochondrial genes Cytochrome B and COX1 were chosen and the accession id of the previous studies performed on these two mitochondrial genes were again collected and was saved as a text document in notepad.

Now, these sequences were likely to be aligned using NCBI BLAST. BLAST for nucleotide sequence is performed twice (once for Cyt b and once for COX1). For, cytochrome b, the accession id of species *Cantoria violacea* (accession id- KX694852) is placed in the query sequence and the total sequence was placed in the subject sequence. For, COX1, the accession id of species *Coelognathus flavolineatus* (accession id- LC075340) is placed in the query sequence and the total sequence is placed in the subject sequence and BLAST is performed.

The result obtained from performing the BLAST function was filtered with the percentage identity ranging between 80- 100% and the query coverage ranging between 90- 100%. The filtered results were downloaded as FASTA aligned sequence for further progress.

The next step was performed in the MEGA X software (Molecular Evolution Genetics Analysis). In MEGA, the FASTA aligned sequence was converted into a MEGA format after performing the muscle algorithm, trimming of the unmatched sequences and aligning the genetic sequences for both cytb and COX1. After this, a maximum likelihood phylogenetic tree is constructed using bootstrap method from the previously saved aligned sequences.

Further interpretation was done by studying and analyzing these phylogenetic trees.

Schematic Representation of methodology:

Collection of data of snake species available in the Indian subcontinent from reptile database







Running the FASTA Alligned sequence of Cytochrome B and COX1 in Clustal Omega and ESPript software and perfroming Multiple Sequence Allignment.

Observations:-



Fig- Phylogenetic Tree of Cytochrome B mtDNA



Fig: Phylogenetic Tree of COX1 mtDNA



Fig: Clustal Omega Report of Cytochrome B

	40	70	80		9 Q	100	110	
MG653605.1:75-778_Sinomicrurus_macclellandi	CATTAC	CHARGE	TTHANAG	ALLA	TATCAC	ACCACACGT	TATAT	CATCAA?
MG002968.1:76-779 Psamnophis schokari	CGTANC	Analesen	2 26	CONC	lel elle	ABGAGACGT	ATAC	TAN TAAT
MG002967.1:76-779_Psannophis_schokari	CGTAALC	ATAGOCT	CTOALCTG	CG C	CATCAC	ACGAGACGT	CCATAC	GATGAA?
MG003027,1:76-776_Psamnophis_schokari	CGTAAT	ABABBBB	CINTE	CALC	CA CAC	ACCACATGT	TATAC	CALCAA:
MGC03026.1:76-776 Psamnophis_schokari	CIGTAR	ATACCE	CTCATCTG	CALC	CAC.	ACGAGATGT	ATAC	CATCAA?
MGC02970.1:76-776_Psannophis_schokari	CGTAAA	ATAGORT	CTCATCTG	CALC:	NONTOAC	ACCACACGT	CCATAC	DOAD GAAS
MGC03010.1:76-776_Psawnophis_schokari	CGTAAT		CTOATCTC	CA C	COLUCAC.	ACCACE CT	ACCATACIAN ACC	COARCAA?
MGC03011.1:76-776 Psammophis schokari	CGTAALT	ALACCE	C TG	CA. C	ICI. CAC	ACCACATOT	ATAC	ALLANT
MG002984.1:76-776_Psamophis_schokari	CGTAAAT	ATACCT	TOTCATOTO	CARCE	CATCAC	ACCAUATOT	CCATAC	CATCAAT
MG003005.1:76-776_Psannophis_schokari	CGTAALT	AUACOCE	CT		CALC CAC	ABCARLET	A DEATAC	CONTRACTOR OF
MG003002.1:76-776_Psannophis_schokari	CGTTA	ADAGCER	CTONTE	CA C	Ich ica c	ACGAGATGT	CCATAC	ICAL BAR
MGC02977.1:76-776_Psamophis_schokari	CIGTAAAT	ABAGGER	TOTENTETG	CALC .	CATCAC	ACGAGATOT	REATAC	CATGAA3
MG003004.1:76-776 Psannophis_schokari	CGTAATT		C. T. TG		Charles Sho	A HERAHET GT	A CATAC	COLUMN A A A
ME476936.1:37-729_Rhabdophis_bindi	TATTACC	CACCOTE	TTEATEAA	CALC	CATCOC	ACGACATOT	ACCTTAT	ALLAR
MR530545.1:66-750_Rhabdophis_himalayanus	TATTATT		TTEATEAA	TATE	CATCAC	ACCACATGT	ACATAC	E ALEAA
M0993850_1:71-773 Herpetoreas secura	CATCARC		TTOLENTA	1.1	Childran.	ADDITION	ATAC	ACC ACT
MN993851.1:59-761_Herpetoreas_xenura	CATCALC	CTOOCAT	TTEATETA	TAT	OATTAC.	COTOATOT.	CCATAC	DOGTOAG?
MN993852.1:57-759_Herpetoreas_menura	CATCANO	C C A	THE R. LEWIS	T) T	CATEAC	ACCTONTOT	ATAC	Concercia da
MK595796.1:83-783 Abastulla laudankia	TATTA	CHADCAR	CT CAL	TA 6	TAC	ACCTONTOT	ATAC	A A I
MH043272.1:85-785_Platyceps_ladacensis	CATCAN	CICSCCT	TTCATCCA	TG	TATAC	ACCOGATOT	COATAC	CCTGAA?
ME322863.1:85-775_Gonyosoma_prasinum	CACCA	CHADETE	C AA	TARC	TABAAC	ACCACACGT	COCTAC	CARCAAS
KF669246.1:91-794 Rhadinophis franatus	TATCA	CHERT	CTHATCAN	TATT	TANAAC	ACCTUNTOT	COATAC	TOT ANT
DQ902110.1:91-794_Gonyosoms_frematum	TATCARC	CHERCET	CECATCAA	TAT	TATAAAC	ACGTGATGT	CCATAC	HOGHEAA7
EF669250.1:91-794_Rhadinophis_frenatus	TATCACC		CTEAL		TATAAC	ACGTOATGT	DATAC	COLUMN AND
DC902121.1:104-794 Coelognathus radiatus	TATTAC	CHAR OF	C. AA	CA A	TAT	ACCAUATOT	ATAC	OTTOAAT
EC347466.1:94-782_Boiga_beddomei	CATTARC	TTACCTY	TCTCATCCAT	CA. C	CATTAC	TCGAGACGT	CCATAC	OCTOAA?
MT733294.1:44-734_Boiga_beddomei	TATCANT	CHTCCC	CTEATETA	문학	CARGAC	CCCCGATGT	ATAC	COCCURA.
MT733290.1:44-734 Boiga beddonel	TATTAT	CHECK	CTOAT CTA	CA T	Charles Charles	CONTONTOT	ATAC	COCHE ANT
MT733291.1:44-734_Boiga_beddomei	TATTATT	GTTOCCT	CTCATCTAT	CART	ICATCAC	CCGTGATGT	CCATAC	DOCTOAA7
MW111469.1:76-779_Lycodon_septentrionalis	CATCALC	CHICAT	TTELTET	CALC	CONTAC.	ABEACACGT	ATAC	CONTONAS -
EC010366.1:91=791_Lycodon_fasciatus	CATCA	CIACCIT	TTCATCTA	CALCO	CARCAC	CCAGATGT	DEATAC	COLLAR?
MT625862.1:58-758_Lycodon_fasciatus	CATCARC	CTACCTT	TTCATCTA	CARCE	NONCOAC	CEGAGATGT	CCATAC	CAREAA1
NW111467.1:75-775_Lycodon_fascistus	CATCARC		TTAL		CA CAC	CHEADATST CHEADATST	CHEATAC	CALL AAT
#C010370.1:92-791_Lycodon_lacensis	TATTAC	TACCT	CTEATEAA	TAC	CATTAC	CCGAGACAT	CCATGO	GATGAA
KX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctus	TATTONO	CARGE	CTOATCAG	TGA	CA CAC	ACGAGATOT	DEATAC	OGEO AAC
MT625846.1:58-758_Lydodon_subcinctus MT625859_1:58-758_Lydodon_subcinctus	TATTO	THACCO	CAL	TON	CALC CALC	ACCADATOT	ATAC	CONTROLAD CONTROLAD
#C733203.1:76-776_Lycodon_subcinctus	TATTO	TTACCT	CTEATECA	TG A	CA CAC	ACCAUSTOT	CCATAC	CATCAA?
LC105630.1:21-724_Coelognathus_flavolineatus	CATCALT	CREECE	CIGALSTA	TG A	CATAT	ACCACCT	CACAC	CALCAR1
00902134.1:91-791 Elaphe bella	CATCANO	CHIERCE	CA.	co A	Chicac.	ACCACACCT	COCTAT	CARDAN
KF669231.1:89-778_Euprepiophis_mandarinus	TATTAAC	TAGOOS	TTCATCAL	CG AL	CATCAC	ACGAGATGT	CATAT	CALCAA?
KF669228.1:92~785_Euprepiophis_mandarinus	CATTANT	CHAROCE	TINALAA	CGAL	CATTAC	ACCAUATOT	ATAT	COGE CAAT
KX782330.1:10-690 Wallophis brachyura	CATCANO	CIACCET	CALLERA	CGA	TATAC	ACGAGATGT	CTAC	GOTGAAT
AY611998.1:99-794_Ptyss_mucosus	CATCARC	CTABCAT	TTCATCAA	CARTO	TATCAC	ACCACAT	CCATAC	CATGAA?
LC105628.1:114-809_Ptyss_mucosa	CATCARC	CEACCAR	TT I A A	CAT	CALCAC.	ACCACACGT	ATAT	ALCOARD AND
D0902132.1:91-794 Orthriophis taeniurus grabowsk	CATCALT	CHADOCT	TTOATETA	TOT	CALCAC.	ACCAGATOT	CATAC	SCITCAN?
RF669249.1:91-794_Orthriophis_taeniurus	CATCANT	CTACCT	TTEATETA	TOT	CA DOAC	ACGAGATOT	CCATAC	IGTTGAA7
XX239646.1:95-792_Hydrophis_platurus	CATCANT		AG AG		THOTT	ABBABABATGT	CAAC	ALC: NO.
KT966116.1:49-746_Hydrophis_platurus	CATCALT	CIACCAT	TICALAG	AAT	TOTT	ACCAGATOT	CAAD	CATCAA?
MM886306.1:103-800_Bydrophis_platurus	CATCANT	CEASCAS	TIPATCAG	AA	TAICTT	ACCACATGT	CAAC	CALCANT
MN8863007.1:103-800_Hydrophis_platurus MN886300.1:103-800 Hydrophis platurus	CATCALL	CHARGE A	AG	A	TOTT	ANDADATOT	CAAC	ALLAN
MT966127.1:85-782_Hydrophis_stokesii	CATCANT	CTACCET	TTOATCAG	GA T	CCT CCT	ACGAGATGT	COLTANC	COLCAA?
JQ217201.1:79-768_Nydrophis_stokesii	CATCANT	CEACOCE	TICAG	AA T	CALCCT	ACCACATGY	TAAC	COLLEANS
ET966054.1:79-779 Rydrophis casrulascens	CATCA	CTACCAT	TICATAG	AATT	C CCT	ACCACATGT	TAAC	COTCAAT
JQ217208 1:79-779 Nydrophis caerulescens	CATCANT	CTABCAT	TTCATCAG	AATT	CLICCT	ACGAGATST	TAAC	DOGE CAAT
KY206890.1:10-710 Gerarda prevostiana	CATTAT	CHADDAT	CAG	GA DT	CALCAC	ACCACATGT	CATAC	COGED AAT
KF395916.1:50-750 Gerarda prevostiana	CATTANT		CT AG	al T	CL CAC	C SALE TOT	ATAC	CALCAAT
KX694852.1:1-704_Cantoria_violaces	TATTAC	CARCAS	TICATCAG	AA T	TATCAT	ACGAGATOT	COTTAC	DOCTOAA7
EF395897.1:50-753_Cantoria_violacea	TATTACC		TTCATAG	A. T	TAUCAT	ACCAUNTOT	TTAC	ECCEPTANT.
MT802711.1:62-747 Homalopsis buccata	CATCANO	CIACLE	TICATOTO	AA C	CANTAC	ACCAGACGT	ATAC	CARGAAT
MTS02704.1:61-747_Homalopsis_buccats	CATCAAC	IC TARCAS	CTCATCTG:	AADE	CATTAC	ACGAGACGT	COGATAT	CAT CAAS
MTE02703.1:61-747_Nomelopsis_buccata	CATCARO	CHERCAT	CTUATUTG	AABC	CHUTAC	ACCACACCT	ATAT	CALCAA7
AF471092.1:91-794 Cerberus rynchops	TATCAN	CTARCAT	CTCATCAG	AA	TABCAC	ACCADICAT	SCATAC	RECERANT
EF395900.1:50-753_Cerberus_rynchops	TATCACO	CHARGA	CIPATEAG	AABC	TATCAC	ACGAGATGT	CATAC	COLLANS
Ex595801.1:30-753_Cerberus_rynchops EX696850.1:1-654 Cerberus_rynchops	TATCAL	C La COAL	CTO AG	AG	CAC CAC	A COACT OF	ATAC	C C C A A I
MT802717.1:1-670_Hypsiscopus_plumbea	CATTAC	CIGOCAT	CTHATCAG	AA C	TATCAT	ACGREACAT	CATAC	CARDAA?
JX463014.1:50-753_Enhydris_dussumieri	TATTAN	C DA COA	CT TATAAG	AGUC	TARCAC	ACCADACICT	CECATAC	CARDAA?
LC105625,1:59-763 Enhydris enhydris	TATCA	TATA	TTOLLAG	AL C	TA TTT	ACCAGACOT	ATAC	Contract of the last
MT802681.1:50-753_Enhydris_enhydris	TATCA	TACCAT	TTCATCAG	AAC	TATTAT	ACGAGACET	CCATAC	GCTGAA
MT802683.1:50-753_Enhydris_enhydris	TATCARC	CHACCAT	TTCATCAG	AADCO	TATAT	AMEAGACGT	GTAC	OCTOAAC
LC105626.1:126-829_Enhydris_enhydris	TTTCA	TIAGCAT	TICATCAG	AAUC	TAT	ACGAGACGT	ATAC	CONTAR A

	120	130	140		150	160	170
MG653605.1:75-778_Sinomicrurus_macclellandi	TATACAAA	TCTT	THEAST	GGCGCA	BECABAR	CHECKECK	GTATT TATACACATAT
MG002973.1:76-779 Psamnophis_schokari	CATRCAAA	ACACACI	COGANTC	GGAGCE	TOACTAR	FORDCASCE	OTATET ACATCLATAT
MG002968.1:76-779 Psannophis schokari	CARACAAA	ACACAC	CHRANTC	GGACCA	HEACHAR	CINCANCE	CTATT ACATOCATAT
MGC02967.1:76-779 Psammophis schokari	CARACAAA	ACACAC	CHANTC	CCACCA	REACHAR	CETCATCI	GTATTE ACATION ATAT
MG003027.1:76-776 Psannophis schokari	CARACAAA	ACACA	COMANTO	GGAGCA	HEACHAR	CHARGE	OTATT ACRECCATAT
MGC03028 1:76-776 Psannophis schokari	CARACAAA	CACAL	CHARTCO ANTO	COA COA	HEACHAR	CONCASES	GRATE ACATOL ADAT
MG003026.1:76-776 Psampophis schokari	CARRICANA	CACAC	CHARTC	GEAGER	REACHAR	CORC ADOR	OTATET ACATOL ATAT
MGC02970.1:76-776 Psannophis schokari	CATACAAA	ACACAC	CHEANTC	BOACCA	ACTAC	CERCANCE	OTATT ACATCE ATAT
MGC03010.1:76-776 Psawnophis schokari	CATACAAA	ACACA	CHARTC	GOADCA	TEACHAR	CERCATCE.	OTAT TTACATCCATAT
MGC03017 1:76-776 Psampophis schokari	CARAGARA	ACACAC	COMANTIC	GGAGCA	REACHAR	TOTAL CANCE	OTATTE ACATOL ATAT
MCC03011.1:76-776 Psasmophis schokari	CATACAAA	ACACAL	COMMENTS	COACEA	THEAR BAR	TOTATOT	OTAT TO ACATOR ATAT
MC002984 1:76-776 Psampophis schokari	CATAGAAA	ACACAL	COLLEMN TO	CCACCA	MACHAR	CHOCKNER	CTATTER ACTOR CONTACT
MG003005.1:76-776 Psampophis schokari	CARADAAA	ACACA	CHARTE	COL COL	THAC HAD	CHARGE	OTATE ACTOR ATAT
MG003008 1:76-776 Paannophis schokari	CENADIAL	ACACAL	CHARTE	CICA CICA	Distant Practic	C DEC DEC D	TATT COT STAT
MG003002 1:76-776 Paannophis schokari	CARACTAN	ACACAL!	Contractive:	COLUMN STATE	THEAD TRACE	CONCERNED.	OTATT ALCOT A DEAD
MGC02977.1:76-776 Psampophis schokari	CARACAAA	ICACAL	CORANTO	STOR GOLA	MACHAR	TOTAL CATION	OTATT ACATOMICS
MG003004 1:76-776 Paannophis schokari	CARACAAA	CACA	COLUMN TO A	GER A CERA	ACHAN	CONCASION	OTATT ACATOMAT
AF471011 1:91-794 Psawnodynastes pulverulentus	CARACAAA	CTTR.	Contra Merce	PERCINE A	THE ADARD	CONTRACTOR OF	DEADERACKCARDEAU
ME476936.1:37-729 Rhabdophis bindi	ACTACAL	TCTT	THETATO	General	THEATAR	TRACTOR	CONTRACTOR ADD
ME530545.1:66-758 Rhabdophis himalayanus	AATALAAA	COTT	TTALTT	COLORA	THE ADAR	CHECKNER	GENTER ACADECATAT
KF200929 1:60-747 Rhabdophis himalayanus	ANDADADA	ACCTT	THEADTH	CICACICA.	THE ADARD	CHOCARCE.	GEATERACKCICCACAT
MN993850 1:71-773 Herpetoreas senura	ANTACAAA	ACACA	COOTATE	o o c s c a	DOAGNAD	TTTTTATCT	GEATERACACCACAT -
MN993851.1:59-761 Herpetoreas senura	ANDADAA	ACACAL	CONTRACT	agegel	TRAGTAR	TTTTATCT	GEATERACAGEAGAT
MN993852 1:57-759 Herpetoreas senura	ANTALANA	ACACA	CONTRACT	adcack	AGAIN	TTOTTALCT	GENTETACACCACAT
KC347453 1:102-794 Ahaetulla nasuta	CATACAAA	ACCTAC	CHARTO	SOCICIA	RECARA	CARGANCE	CEATE ACARGUAGAT
MK595796.1:83-783 Absetulla leudankia	CATCCAAA	ACICITAC	CHRANTC	GGCCCA	RECARAD	CORRECT OF	CENTER ACARDONEAT
MH043272.1:85-785 Platycems ladacensis	CATACASA	TATAL	COLLARC	CCACCA	REALDER	TTTTCATCI	GENTELACHTCC AGAT
ME322863.1:85-775 Gonyosome prasinum	CATACALA	ACTUAL	THEAATC	GGAGCA	CARAN	CTTTATCT	GENTET ABAT/SCACAT
ME122864.1:85-775 Gonyosoma prasinum	CATACAAA	CTTA	THEADTO	GGAGCA	RECATAN	CTTTATCT.	GCATCTACATICCACAT
KF669246.1:91-794 Rhadinophis franatus	CATACANA	ACCTA	THEADTO	GEAGEA	TOCATAR	CTTCATOT	GENTET AGATIGE AGAT
D0902110.1:91-794 Gonyosoma frematum	CATRCAL	CCTA	TREAMTO	GGAGCI	H GCARAD	C. CARCANCE	GENTETACATOCACAT
EF669250 1:91-794 Rhadinophis frenatus	CARACARA	ACCTAC	THEADTO	GGAGON	THEATAN	CORDINATION	GCATCT ACAPOCACAT
00902112.1:92-794 Coelognathus helena	TABACILA	TATA	COGADTO	auche i	DOCA NAM	C C C C C C	OCATES ACRECEMENT
D0902121.1:104-794 Coelognathus radiatus	CALACIAN	TATA	TRACADES	adche i	CALL A	C C C C C C C C C C C C C C C C C C C	CTATCINTATT ACA
EC347466.1:94-782 Boiga beddomei	CATACARA	Accret	COSCIET	GGAGCI	LOCATA	CHECKDOT	GCATCE ACACINE ACAE
MT733294 1:44-734 Boigs beddomei	CATRICAAL	ATCTTC	TRECHTT	GGAGCA	TOTALAN	TTTTATCT	GRADE ACAGE AGAE
MT733292 1:44-734 Boigs beddomei	CATAGAAA	TOTAL	TRACTT	GGRGCI	TABLAR	TTTCATCT	CONTRACTAGE AGAT
MT733290.1:44-734 Boiga beddomei	CATACAAA	ATICTAC	THOTT	OCA CON	TOTATAD	THEATCH	CTATE ACAROLADAT
MT733291 1:44-734 Boiga beddomei	CARACARA	ATCTAL	THOUTT	CON DOM	THE TABLE	TTOCHER	OTATOTACACCACAT
MW111469 1:76-779 Lucodon septentrionalis	CATROARD	ATICIDAL	THE REPORT	COCCORD N	THE R. D. LEW	THEFT	CONTRELACACIÓN ACAT
MW111468 1:75-775 Lycodon fasciatus	CALL AND AND	ACCUT	CHARTCH INC.	Con Con a	Contraction of the local division of the loc	CONTRACT.	OCAL TRACTORY AND AND
ECG10366 1:91=791 Locodon fasciatus	CARADAAA	ACCTT	CONSTRUCTO	PERCENT.	THE ADARD	Contractory of the local division of the loc	CANTER TRATE
MT625862 1:58-758 Longdon faartatus	COMPANIA D	Aciente 1	COLUMN TWO	PERCENT.	THE ATAP	Contractory of the last	CALLED THE TRUTH ALCAN
MW111467.1:75-775 Lucodon fasciatus	CONTRACTOR OF	COTT OF	Contraction of the	COL COL	Marshall B	Contractor of the local division of the loca	CART STREET STREET
ECC10368 1:92-794 Lanadon Isosnata	COLUMN AND A	H-man a	The Local Division	of the state of	ALC: NOT A	Concession of the lateral sectors of the late	COLUMN STATES OF A DESCRIPTION OF A DESC
EC010370 1:92-791 Lynodon lacensis	CONTRACTOR AND	CTTA-	THEATC	CONCOM	THE ADARD	CONTRACT.	CANCELLAR STREET
EX822578 1:72-772 UNVERIFIED: Lynodon submingtu	CARA GALAN	COTA 1	THATT	COLOR DE LA	107314	10000	dealer Achievenes
MT625846 1:58-758 Lonadon aubrightus	COLUMN AND	ATCTAC	Contraction of the second	disches.		IC DO DO DO	TO A CONTRACTOR
MT625859 1 58-758 Lungdon subcinctus	CA DADADA	OTC TAC	Contraction of the second	Contraction in		- C	
#C733203 1-76-776 Laundon aubringtus	- A	Troits	Contra Deve				
trib5630 1-21-724 Conformations Flaunlingatur	Contraction in the	THAT A	The Lot of the last				THE REPORT OF A
DO902128 1:92-788 Coelognathus flavolineatus	CARADARA	TATA	THEGHTT	and clock	CAN HAD		CARLES AND
50902134 1 91-791 Elanha bella	A CONTRACTOR OF	TCUT	THE REAL	and child a		Contractory of the local sectory of the local secto	
EF669231 1 89-778 Eupremionhis mandarinus	COLUMN AND	TCTT	COLUMN TO				COLUMN TO THE REAL
EF669228 1-92-785 Expresionhis mandarinus	COLUMN AND A	DECTE:	THEFT	en en a	THE R P. LEWIS CO., NAMES	11000	COLUMN AND ADDRESS
MIC20426 1-69-772 Coronella brachwura	CONTRACTA D	Aceres	- Carlotter		THE R A DAM	Contraction of the later	CONTRACTOR OF CONTRACTOR
EX782330 1:30-690 Wallophia brachwura	- ALL ALL ALL	Acene	- Caller	CON CON	HOTA HAD	Contraction of the local sector	No. of the State o
AV611998 1-99-794 Dryna muccaus	THEADY	Accest	State of the local division of the local div	COLOR DOLL	Contra Da D	CONTRACTOR OF	No. of the Party of the Add
LC105628 1:114-809 Ptvas mucosa	TABADAGA	ACCTT	COLLARD THE	CICIA CICIA	HOTAN AN	CONTRACT.	CONTRACTOR DALLAR
EFC76709 1:91-794 Orthriophis taeniurus	A DEALERS A.	ACCTT OF	THE R. DOWN	Sector a	ALC: NO.	CONTRACT.	OCASCING ACTING TO A TANK
D0902132 1:91-794 Orthrightis taeniurus grabows	A ALLANDAR	TOTT	THE ALTER	STATISTICS.	THE R. LEWIS	CONTRACTOR OF	TANC A TOTAL STATE
#FE69249 1 91-794 Orthrights tashiurus	ACCORDER NO.	ATC: T	The second street	ALC: NO.	HO ANAL	Contractor of the later	THAT IS A TAKE A DOWN
#X239646.1 95-792 Hydrophia platuros	COLUMN AND	ACCTT 2	TRANTO	COT DO	TOTATA D	TRACING	NEW YORK CHARLES
#7966115 1-70-767 Hydrophia platurus	- BOARDAN	R-CTT-	Transferic		TATAT		
XT966116 1:49-746 Redrombie platurus	Charles and a la	COTT	THE REPORT			THE REAL PROPERTY OF	
MN886306.1:103-800 Hydrophis platurus	CONTRACT	ACCTT	THALTC		TOTADAD	TIMESTOR	CTATTERCOCCATAT
MN886307.1:103-800 Hydrophis platurus	CASTGAL	CCTT	TREAMTO	COT DOC	TOTADAD	TTOCATOT	GTATTTACACCCATAT
MN886308.1:103-800 Hydrophis platurus	CATTCAAA	ACCTTCA	TREAMTC	COTCO	TUTATAT	TREASER	GTATETACACICATAT
MT966127.1:85-782 Hydrophis stokesii	CAECCAAA	ACCTITCA	THEADTC	Gecer	THE TABLE	TTTCATCT	UTATCEATACCEATAT
JC217201.1:79-768 Hydrophia stokesii	CATCOARA	ACCIT	TICANTC	GGCGCA	RETARAD	TTTCATCI	GENTICE AT ACCURATE
EC014431.1:77-777 Hydrophia chacurus	CATTCAAA	ACCUTC	THATC	COCCCA	TOCAHER	THEFT	CONTEXADAGECATAT
ET966054.1:79-779 Rydrophis caerulescens	TATTCAAA	CCTT-	THATC	GEAGEA	TETANGE	TTTTCATCT	GCATTTACACCCATAT
J0217208.1:79-779 Hydrophis caerulescens	TATTCHAN	ACCTTC	TREAMTC	GGAGCA	TOTANGE	TETCATCE	GCATTERACACCATAT
EV206890.1:10-710 Gerards prevostians	TATACAAA	ATATT	Jos Galard	SGCSCA	BECABAR	ICT TATCT	GOATE ATATCALCA
KY206891 1:19-719 Gerarda prevostiana	TATACARA	ATATTC	CRECKTC	agegen	TOCATAR	TOTO TATCT	GEATTEATATECACAT
EF395916.1 50-750 Gerarda prevostiana	TATACAAA	ATATTC	TREAME	adcaca.	TOCATAN	CONTANCE	GENTETATATIC ACAT
KX694852 1:1-704 Cantoria violacea	CATAGAAA	ACC'TT C	CHARTO	BACREA	HOCAHAR	CONCASCS	CONTRELACADOLAGAT
EF395897.1:50-753 Cantoria violacea	CARACASA	ACCITE	COLLET T	GECCUA	CARA P	CHECKNOR	CONTRACTOR ADD.
MT802706.1:62-747 Homaloosis buccata	TAUNGAL	Acete	THEADTO	Geclen	TOCATAN	COLUMN AND	GTAILCTACATCCATAT
MT802711.1:62-747 Homalopsis buccata	TABBORN	Acie rel	TRANTO	Gersen	RECARA	CONTRACT.	GTAICTACATIC ATAT
MTS02704.1:61-747 Homalopsis buccata	TABAGALA	CCTT V	THANTO	GGAGCI	TOCATA	for chief	GENTERALSTIC ACAT
MT802703.1:61-747_Homelopsis buccata	TATACARA	ACCTT	THEADTO	GGCGCA	THCATAN	CTTCATCT.	GEATETACATOCATAT
MTS02658,1:50-753 Cerberns rynchops	CATACAAA	CATT	COCALTC	GGCGCA	TATA DAT	CTRCA TT	GCATCT ACATOC AVAT
AF471092.1:91-794 Cerberus rynchops	CACACARA	ACATT	CSGARTC	GGCGCA	TOTATAT	CONCAST.	GCATCE ACATION AND
EF395900.1:50-753 Cerberus rynchops	CATACAAA	CACT	CSCARTC	GGC GGL	EGCANAN	TC TO TRUTT	CATCURCET ON THE
EF395901.1:50-753_Cerberus_rynchops	CATACAAA	CATTO	COCANTO	GGCSCA	ECTADAD	CTTCATT	GCATCTACATCCATAT
EX694850.1:1-654 Cerbergs rynchops	CATACALA	CATT	CHEADTO	GGCGCA	BETABAR	CURCANT	GCATCTACATICATAT
MT802717.1:1-670_Hypsiscopus_plumbea	CATACAAA	CCTT	COGARCO	GGCSCN	TGTATAS	TOTTTATOT	GCATCE ATATICC ACAT
JX463014.1:50-753_Ephydris dussumieri	CATACAAA	CCTAC	CSCANTC	99CSCI	TOCATAN	TOTO CATCE	GUATCTAGACISCATAT
JX463015.1:50-753 Enhydris dossumieri	CATACAAA	COTAC	COGANTO	o de a c h	TOCATAN	TOTT CATCE	OCATOT AGAGINC ATAT
LC105625.1:59-763_Enhydris_enhydris	CATACARA	CCCTC	COCARTE	00 COCA	TOTADAD	ICED CATCE	GTATCTACATCCACAT
MT802681.1:50-753_Enhydris_enhydris	CATACAAA	ATCTTC	COCANTE	GGC GC N	TOTATAN	ICTICATCI	GEATCTAGATOCACAT
MT802683.1:50-753_Enhydris_enhydris	CATACAAA	ACCITCA	COCABTT	GECGCA	BOTABAD	TOTTCATCT	GTATCTAGATCCACAT
LC105627.1:132-835_Enhydris_enhydris	CATACAAA	ACCTTC	COCARTE	GGCGCA	BOTABAT	TCTTCATCI	GTATCTACATCCACAT
LC105626.1:126-829_Enhydris_snhydris	CATACANA	ACCUTC	CHARTE	GECEEN	BETABAB	CORCATOR	UTABCE ACAT/CCACAE

	180	190	2	αœ	210	320		\$30	
MG653605.1:75-778 Sinomicrurus macclellandi	COGACO	CERACE	ATTAT	ACTAC	TTOA	AATAAAAGTG	ATGACE	CTE	GEGACTAC
MC002973.1:76-779_Psamnophis_schokari	TOCACO	cascic	ACACIACI	ATCCT	CARA	AACAAAGAAG	CICACI	AT SI	CEAGTTAC
MG002968.1:76-779_Psannophis_schokari	TCCAEC	CCCCC	ACACIEC(HATCOT	CARA	AACAAAGAAG	CIGACI	ATE	EGGGTTAC
MGC02967.1:76-779_Psammophis_schokari	TGENEG	CERCIC	ALACIAC	BRATCET	CALL	ARCHARGARG	CHEACE	A 22.5	GEGGTTAC
MG003027.1:76-776_Psannophis_schokari	TGCACG		AUNCIAC	ATOET	CARA	ALCHARGARC	TICACI	ATO	BEAGTTAC
MG003028.1:76-776_Psampophis_schokari	THEADE		ALC: LET C.	a manufactory	CARA	THC AAGAAG	CHANNE	10.20	HEAGTTAC
MCC02020 1-16-776 Psamnophis schokari			Contraction (ALC: NOT A	100	A REAL PROPERTY.	CHAR	1228	AND AGT TAC
M0002010 1:76-776 Passagetta schokari	100.00			A resident	1.00	COLUMN A DATA	1000	12.18	COLOR PAC
M0003017 1/16-776 Psammonhis achokari	-	charles a		ATCOT	100.00	ANCIAN CANAGE	Sec.	ATE	MAGTTAC
MCC03011.1:76-776 Psasmophis schokari	TREACO	CHARGE C	ATACIDACI	ATCOT	CALLA	ACAAGAACA	THAC	ATE	HEAGTTAC
MG002984.1:76-776 Psamophis schokari	TECALC	caecca	ALACINAC	ATOOT	CALA	AACAAAGAAG	TIGACT	ATE	GEAGTTAC
MG003005.1:76-776_Psamophis_schokari	TOCACO	CHECK	ATACTACI	GATCOT	CA A	AACAAAGAAG	TEACT	ATO	GGAGTTAC
MG003008.1:76-776_Psannophis_schokari	TGGACG	c a cic	ATACTAC	ATOCT	CALA	ANCHARGAAC	TIGACI	ATE	GAGTTAC
MG003002.1:76-776_Fsamnophis_schokari	TGEACE	CEECC	ATACTAC	ATCCT	CABA	AACAAAGAAG	TEACE	ATER	GEAGTTAC
MGC02977.1:76-776_Psamophis_schokari	TGCACG	C C C C C C	ATACTAC	ATOCT	CARA	AACAAAGAAG	TGAC	ATES	GEAGTTAC
MG003004.1:76-776_Psannophis_schokari	TERNED	Cardoc	ATACIAC	TATOOT	CALA	ANCIARGRAG	FOVO	942.01	GEAGTTAC
AF471031.1:91-794 Psawnodynastes pulverulentus	CERTITION	A DACE	CLARK T		CC IC	CAAGGAC	면 이상의	15.23	MARCAC
ME%10525 1-66-758 Dishdowhis himslawarus	100.00					THE REAL OF		C18	CONTRACTOR OF
EFECCEDE 1.60-747 Bhabdophis himslevenus	100.00			and the second	C. B.	A REAL PROPERTY.			CELACARC.
MN993850 1:71-771 Herpetoreas secura	THEATEN	a da a		and com	TCHA	THE ALCARD	ADDACE	A 10	TRAACASC
MN993851.1:59-761 Hernetoreas senura	TOCACO	dadalen	CTACTAC	incr.com	TCHA	ANTIAAGAAG	ATGACH	ATEL	CRAACASC.
MN993852.1:57-759 Herpetoreas menura	TOCACO	cadalca	CTACTAC	CTCCT	TCA	AATAAAAAG	TGACT	ATEL	GGAACAAC
XC347453.1:102-794_Ahaetulla_nasuta	COCACO	100071	GTACIAC	CATOCT	CC A	AATAAAAACG	TTGATE	Ato	GGAACAAT
MK595796.1:83~783_Ahaetulla_leudankia	COGACO	TROOT	GTACTAC	TODYAN	TTGG	AATAAAAACG	CTATE	ATE	DEAACAAT
MH043272.1:85-785_Platyceps_ladacensis	TGGACE	ACCAC	ACCORD	ATCAT	TCHT	AACBAAAACG	ATGACT	ATE	BEAACCAT
ME322863.1:85-775_Gonyosoma_presinum	TGEACE	ASCACT	APACEAC(ATOCT	ACC BA	AACAAAATG	ATCATE	ATE	BAACCAT
ME322864.1:85-775_Gonyosoma_prasinum	TOCACC	ACCACE		ATODI	CORA	ARCHARAATG	ATOATE	ATE	THAACCAT
KF669246.1:91-794_Rhadinophis_frenatus	CITEVES	ALC OF		AND COLL	12211	THE AAAATG	CHACK STREET	121	HEAACCAC
PECOSA 1-91-794 Bondiscola Frenatus			A COLUMN	THE R. LEWIS CO.	1.24	N. N.	G	12.18	PER ACCAC
D0902112 1:92-794 Coelognathus balant	THE REAL	- 50	A THE R	Arciel	100	TTT Date and the	George and	G & C	indage Ta
00902121 1:104-794 Coelognathus radiatus				DOT OUT	TCAL	TRANCOL	a lac	1200	MAACTOT
EC347466.1:94-782 Boiga beddomei	TOCADO	ACCAC	ACREME	ATCAT	OC. T	AATAAAACG	ATGAC	ATA	GGAACATC
MT733294.1:44-734 Boiga beddomei	COCACO	CGGACT	ATATTAT	COTOTE	CC 7	AATAAAAATG	COAR	ATS	GGAACATC
MT733292.1:44-734_Boigs_beddomei	COCACO	COGAC	ATATIAT	ATCITIT	CC 7	AATAAAAATG	CTOAN	ATE	GGAACA7C
MT733290.1:44-734_Boiga_beddome1	COCACO	CORACE	ATATTAT	SUATCH	COST	AATAAAAATG	CTGAAT	ATE	GEAACATC
MT733291.1:44-734_Boiga_beddomei	COCACO	COCACT	ATATIAT	ATOTT	CC 7	AATAAAATG	CITAN	ATES	OCAACATC.
MW111469.1:76-779_Lycodon_septentrionalis	COCACO	ap de la	ATATIAT	ATCOT	CCLT	ANTRABANTON	ATCACE	CTU	HEAACCAC
MW111468.1:75-775_Lycodon_fasciatus	THEADY	THE CL	A CHAR	GICAT	- 99 IQ	ANTHANAATG	이가가	ATT I	HEAACCAT
ACG10366.1:91=791_Lycodon_fasciatus	THURSDAY	CHAC		GT CAT	2010	TTAAAATG		120	PRAACCAC
MULLIAR 1-75-775 Longdon fasciatus				and the second	2.4.6.6	THE R & B & TO			COLLACCAC.
EC010368 1:92-794 Lycodon Isoensis	COLUMN TWO		ALL STO	COT OFT	1.00	NT-BAAAATCO	A	5 - B.	SPEAC ARC
EC010370.1:92-791 Lynodon lapensis	COMAINS	oggale.	ATACINAC	INCTOCT.	ACC NO	AATAAAAAG	TRACT	Ato	CAACAAC
EX822579 1:72-772 UNVERIFIED: Lycodon subcinctus	COCACO	COGACI	ATATIAC	ICTOCT	JOCHA	AATBAAAACG	ATGACE	ic b	GGAACCAT
MT625846.1:58-758_Lycodon_subcinctus	TOCACO	co cialen	ATACTAT	TTCCT	CICHA	AATAAAACG	ATCACT	ATO	OGAACCRC.
MT625859.1:58-758_Lycodon_subcinctus	TOCACO	CCCAC	ATACTAT	SCTTCCT	CODA	ANTAAAAACOT	ATGACT	ATE	GGAACCAC
EC733203.1:76-776_Lycodon_subcinctus	TGGACG	COGACT	ATACTAT	TTOCT	CICIA	AATAAAACG	ATCACT	ATE	GEAACCAC
LC105630.1:21-724_Coelognathus_flavolineatus	CECALE	CERACE	A T C	ATOTT	TCOA	AATRCAAATC	AT TACE	ATE	PEAGTCAC
DQ902128.1:92-788_Coelognathus_flavolinestus	TURAHO	COMACT		GTOCT	COLIN	ANTICARATCI	PLUASI	ATCH	DUAGTAAC
DCF02134.1:91-791_Elaphe_bella				A TOOL	12.84	THANAATG		1.18	ACCAT
#F669231.1:69-776_Exprepionits_mandarinus	- 22			A DECEMPTOR OF A DECEMPTOR OF A DECEMPTOR OF A DECEMPTOR A DECEMPT	1226	A THE A A A A TO	E SAC	12.0	ALCONT.
MIC20426 1-69-772 Coronella brachvura			- B1 - B1-	REPORT	100	ALC: NAME OF COM	A	C-6.	HEASCASC
KN782330.1:10-690 Wallophis brachvura	C PLAN AND	- Alla		OTCAT	CORA.	COLLARD TO	A do	AT ST	
AY611998.1:99-794 Ptyas mucosus	GCACG	Cardeer	ACACTAT	GATCTT	CCHG	AACAAAAACG	CTGACT	ATE	GGAACTAC
LC105628.1:114-809 Ptyas mucosa	CGCACG	TOGACE	ATACTAT	ATCTT	dead	AACAAAAATG	ATGACE	ATE	GGAACTAC
EF076709.1:91-794_Orthriophis_taeniurus	COCACC	AGGACT	AVACTAC	BATCCT	COM	AACAAAAAG	CHGACE	TTO	BEAACCAC
DQ902132.1:91-794_Orthriophis_taeniurus_grabowsk	COCACO	GIGAC	ATACTAC	GATOCT	CC BA	ANCAAAAATG	CTEACE	CTS/	DOAACTAC
<pre>%F669249.1:91-794_Orthriophis_taeniurus</pre>	COCACO	Gardwich	A CHACK	SUATOCT	CCHA	AACAAAAATG	CINACE	CTO	BGAACTAC
XX239646.1:95-792_Hydrophis_platurus	TOWNOD	ALCO	THEFT	ATTCAL	TIMA	TATAACAAG		1.1	HUAACCAC
AT966115.1:70-767_Hydrophis_platurus	THEFT		THE	TTCAT	11 1	ANTINAAGAAGE	CHAR	220	HEAACCAC
Alfootio.1:45"/46_Ayorophis_plathrus	199.99			A DECK OF A DECK	1111	The second second		12.28	AND ARCAL
MW886307.1:103-800 Mydrophis platurus	THURSDA	Artecie	THEFT	Procale	TT	A A A A A A A A A A	CHEAC	A-8	HEAACCAC
MN886308.1:103-800 Hydrophis platurus	TOCACO	ACOCC	TTATTAC	TTCAT	TTA	AATAAAGAAG	CTUACT	ATU	GUAACCAC
MT966127.1:85-782_Hydrophis_stokesii	TOCACO	ABGCC	TTACTAC	CTCAT	TTA	AATAAAGAAG	ATCAC	AT	CAACTAT
JQ217201.1:79-768_Hydrophis_stokesii	TEGACE	ABBAC	TRACERCO	CTCAT	TICA	AATAAAGAAG	ATGACE	ATE	DEAACTAT
EC014431.1:77-777_Hydrophis_obscurus	TGENEG	AGGACI	TTACTAT	TATTTE	A DTO A	ARTRAAGAAG	ATEATE	ATE	CCAACTAT
RT966054.1:79-779_Rydrophis_casrulescens	TGEACG	ALAC	The state	TTCAT	TTAL	ATASAGAAG	ACCO	ATO	CAACTAT
JQ217208.1:79-779_Rydrophis_caerulescens	THEFT	ALC: N	T MARKED C	TTTCAT	TIME	ANTINAAGAAG	ALC: CO	ATE	THAACTAT
RT206890.1:10-/10 Gerarda prevostiana				ATCAT	1200	A REAL PROPERTY OF	CHARTE	1218	THE GATCAC
FF195916 1 50-750 Gerards prevottions			A DR. How	A CAL	TC			1.0	CONC.
Exegence 1 1-704 Cantoria violacea	200.00	100	HALL HALL	APCAR		A BOARD		24 M	ANA ATCAC
EF395897.1.50-753 Cantoria violacea	COMAND			ATCAT	100.11	MC AAGAAG	G 174	et l	TRAATCAC
MT802706.1:62-747_Homalopsis buccata	COCNER	ASSCC	TOTTOT	CTTAT	OCA	AACHAAGAAG	TIGAT	TT	GAATCAC
MT802711.1:62-747_Homalopsis_buccata	CECADE	ABBCIC	TTATTAC	CTTAT	ACC A	AACAAAGAAG	THEAT	TTE	CAATCAC
MTS02704.1:61-747_Homalopsis_buccats	TOCACE	ASSCC	TUTTUTC	TTTAT	COTA	AACAAGAAG	TIGAT	TIM	CAATTAC
MTE02703.1:61-747_Homalopsis_buccata	CGGACG	AGGCC	TTATISAC	TTTGT	CCEA	AACAAAGAAC	THEATE	TTO	PEAATTAC
MTS02655.1:50-753_Cerberus_rynchops	COCACO	Castoric	C C C C C	ATCAT	CCUA	AATAAGGAAC	PARA T	0101	MAATCAC
AF471092.1:91-794 Cerberus_rynchops	COLLAGO	CHARGE C		ATCAT	1 12	AGGAAG	CHINA TO	STOR	MAATCAC
reission 1:50-753 Cerberus runchons				A COLUMN		THE REAL		1.1	AATCAC
EX694850 1:1-654 Cerberge reactions	100.000			TATCAL	1.28	Tona aleasa		1.18	CELATOR.
MT802717.1:1-670 Hypsiscopus nlumbes	THUNKER	and an	C. 71- 31-	TATOOR	Sec	MCRUACE ACT	Corace	A	FRANTCAC
JX463014.1:50-753 Enhydrie dussumieri	cochea	Accide	A	ATOTA	oc.e	AATAAAGAAG	ATGAC	AT	AGTCAC
JX463015.1:50-753_Enhydris_dussumieri	COCACO	AGGTIC	ATACTAT	ATCH	dene	ANTAAAGAAG	ATCAC	AT	CAGTCAC
LC105625.1:59-763_Enhydris_enhydris	TOCACC	AGGTIC	CTACTAC	ATCTT	CC A	AACAAAGAA	CTGACT	ATES	GUAGTTAC
MT802681.1:50-753_Enhydris_enhydris	TGCACG	ASSTC	CHACTAC	ATCTT	CCA	AACAACAAC	CIGACI	ATA	COAGTTAC
MT802683.1:50-753_Enhydris_enhydris	TOCACC	ARCICC	ACCORDE	ATCTIC	OC LA	CHARGAAG	CICACI	ATE	CEAGTTAC
LC105627.1:132-835_Enhydris_enhydris	TOCACC	ALC: NO	Contraction of the second	AT CITIT	CCHA	CHARGAAC	CHARAC	110	GAGTTAC
actores. 1:120-029_mnnydris_ennydris	- Caller and		- HACKER	ALCIN	and the	CONTRACTOR OF	-BEACE	A C B	CIDAWITAC
2	240 250 260 270 280 290								
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MG653605.1:75-778_Sinomicrurus_macclellandi	ACTACCAACCUTCCTT TANAAAAAGCCTTTTTTTTTTTATAACCCTAACCAACAACAA								
MC002973.1:76-779_Psamnophis_schokari	CCHATHAAHIATCTHAATAJIAAAHAGHITTICI HTUGAHACUTTIKAAHATGAGUAAAAAT								
MG002965.1:76-779_Psannophis_schokari MG002967.1.76-779 Psannophis_schokari									
MG003027.1:76-776_Psannophis_schokari	CLETCEAASCATCTEAASCATACAACTESCCECCCCCAACTACAACAACAACAACAACAACAACT								
MG003028.1:76-776_Psannophis_schokari	CONTRACTOR A CONTRACTOR A CARGE TO SOUTHOUS GOAT A CONTRACTANA								
MG003026.1:76-776_Psamnophis_schokari	CONTRACTOR TO TO A CARGA A CARGET TO CONTRACT A CONTRACT A SEA CARGA A A A T								
MCCC3010 1:76-776 Psamnophis schokari									
M0003017.1:76-776 Psawnophis schokari	COTTOTAATTATCTTAATLEGAALAGETTTCTTCCTCCCA.ATTGCCCA.CATGACAATAAAATT								
MGC03011.1:76-776_Psannophis_schokari	CCETCEAAETATCTEAATACEAAEACETTCCTTCCCCCCTATCCCCACCACCACCACAAAAA								
MG002984.1:76-776_Psannophis_schokari	CCTTCCAASTTATCTCAATATCAASACTTTCCTCCCCCATTSCCTACCACCACCACAAAAT								
MC003008 1:76-776 Paammophis schokari									
MG003002.1:76-776_Fsampophis_schokari									
MG002977.1:76-776_Psamophis_schokari									
MG003004.1:76-776 Psannophis_schokari	CONTROL ANTIATOTICA TAGGAA AAGGTTTTCH COOCHATIGCCAA CAAGAAGAAAA								
ME476936.1:37-729 Rhabdoohis bindi	CLATHAN TATICCAN AN A CARGE AND CONTRACT A CARGE AND A								
MR530545.1:66-750_Rhabdophis_himalayanus	CCEACE7AETSTCCE2AEAECAEACEAEECEECEECEATESCCEAEAECAECAECAECAECAECAECAECAECAECAECAE								
KF200929.1:60-747_Rhabdophis_himalayanus	CCEACETATTATCCETATATECACACACACACACACACAC								
MN993850 1:12-773_Herpetoreas_xenura									
MN993852 1:57-759 Herpetoreas sepura	CONSTRAINED TO A ALL TARAGETTO TO OCT AT TARAGETTA. CONTRACTANT								
KC347453.1:102-794_Ahaetulla_nasuta	CCHACHAAH HICCHAAHAAGAAHAAGII HICHICHIGHACAHAAAAAAAAAAAAA								
MK595796.1:83~783_Ahastulla_laudankia									
MR043272.1:85=785_Platyceps_ladacensis MR322863.1:85=775 Conventions prasinum	ATTIAAN ANT TO TTO TTO A ANALY OR ALCON ALCONAUCUSATIAN ANALY AND A ANALY AND A ANALY AND A ANALY AND A ANALY A								
ME122864 1:85-775 Gonyosoma prasinum	GUILDERAGE CATCOUCHER AND AN AND THE CONTRACT AT A THE CONTRACT AND AND AN ANALY								
KF669246.1:91-794_Rhadinophis_frenatus	CTEACEAABCATCCETATAEGAABAGACTTCTTCEGCEATESCCEAEGAEGAEGAEGAABAAAT								
DQ902110.1:91-794_Gonyosoma_frenatum	CITRACEAAHCATCCETATAGCAAEAGCCTTCTTCCGGCTATCTCCCCCACGAGGAGACAAAT								
popo2112 1:91-794 Rhadinophis frenatus									
DC902121.1:104-794 Coelognathus radiatus	ACTAT AN TATTO CA ALCAARAGE TO THE ALCATE AT ALCARE AND ALCARE								
EC347466.1:94-782_Boiga_beddomei	CCEACEACECATCCETAEAECAXEAGACETCETECATATATESCTEACCTECACEAECAECAECAECAECAECAECAECAECAECAECAE								
MT733294.1:44-734_Boigs_beddomei									
MT733292.1:44-734_Boiga_beddomei	ACTAC ACTAC AT CONTACTACTACTACTACTACTACTACTACTACTACTACTACT								
MT733291 1:44-734 Boiga heddonei	All and a second s								
MW111469.1:76-779 Lycodon septentrionalis	THE REFERENCE AND THE CASE OF THE TRACE AND THE CONTRACTORS AND THE								
MW111468.1:75-775_Lycodon_fasciatus	CORACEATECACCORCARACEACECECETECCACCECCEACECEACECACECACECAC								
EC010366.1:91-791_Lycodon_fasciatus									
MT525852.1:58-758_Lycodon_fasciatus									
EC010368 1:92-794 Lycodon lacensis	COMPANY ATTACCESS AND A REAL ADDRESS OF A TAXAGE A TAXAGE A REAL ADDRESS AND A REAL ADDREAL ADDRESS AND A REAL ADDRESS AND A RE								
#C010370.1:92-791 Lycodon laoensis	CCSACEATSTATCCEAATAAGAAAAAGCETCETTOGCEATSTCCCAACAAGAAGAAAAA								
EX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctus	CTEACEACETACTACTACTACEACETTTCTCTCTCTCCCACCACCACCACCACCACAAAA								
MT625846.1:58-758_Lycodon_subcinctus	AT ACHACHTATCOMA ANACAST TO THE THE CANADA CAN DAMAAAA								
#1625659.1156-756_Lycodon_subcinctus									
LC105630.1:21-724 Coelognathus flavolineatus	TO BACKART ACCOUNT A TAKEAA CAGOCT TO TTOOT AT DO CTARCOAT CAGOA CAAA T								
DQ902128.1:92-788_Coelognathus_flavolineatus									
DQ902134.1:91-791_Elaphe_bella	ACTAC AATCATTCHTATATAATAATAC BETTCHTATCHTATUTCCTAACGUAATAAAAT								
EF669228 1-92-785 Expressionhis mandarinus									
MIC20426.1:69-772 Coronella brachyura	CC ANTANTANTANCO CATACOALACAGO DI TOTTOCOALACINOTALCOALOACOACALAN								
KN782330.1:10-690_Wallophis_brachyura									
AY611998.1:99-794_Ptyss_mucosus									
EFC26709 1:91-794 Orthrights fastiurus									
DQ902132 1:91-794 Orthriophis taeniurus grabowsk	ACCACTARTERICCETATACCARCACOCTTCETTOCCEACCTCCEACCACCACARCARA								
KF669249.1:91-794_Orthriophis_taeniurus	ACTACTAATCATCCTTATATCAACACTCCTTTCCTTCCCTACCTACCATCAT								
#X239646.1:95-792_Hydrophis_platurus	GOOGGE A ANTINEA GETA DAGECA DA TETETO CERCERTE AT DECEMBER A GARGA GAA ANT								
#T966115.1:70-767_Hydrophia_platurus	GONGCIAR HITATACICA TABLECARATETI TO FICE OT AT INCTIAR CARDAR ANALY								
MN886306.1:103=800 Hydrophis platurus	CONSCIENCES AND A CONSCIENCES								
MN886307.1:103-800_Nydrophis_platurus	GCTGCTAATTATACTCATACCATACCATATTTTCTTCTTCATCTTTACCATCAT								
MNS86308.1:103-800_Hydrophis_platurus	ACCESSION AND TATACHER IN CARACTERISTIC AT LOCATION TO A CARACANA								
RT956127.1:85-782_Hydrophis_stokesii									
EC014431.1:77-777 Hydrophia obscurus	GCTACTAATTATACTCATACTCATATTATCATTATCATTATT								
RT966054.1:79-779_Rydrophis_caerulescens	ACTIVITY AND THE ACTIVITY ACTIVITY ACTIVITY AT A THE ACTIVITY AND A THE ACTIVITY AND A THE ACTIVITY ACTIVITY AND A THE ACTIVITY A THE ACTIVITY AND								
JQ217208.1:79-779_Hydrophis_caerulescens									
KY206990.1:10-710 Gerarda prevostiana	CONTRACTOR ANTATO CONTACTA VALUE ANA CONTRACTOR AND A CONTRACTOR CONTRACTANTA A A A A A A A A A A A A A A A A A								
EF295916 1 50-750 Gerards prevoetians									
KX694852.1:1-704 Cantoria violacea	CANACTARTCATCOTTATACCARCACOTTTCTTCCTTCCTATOCARCACCACARCARA								
EF395897.1:50-753_Cantoria_violacea									
MT802706.1:62-747_Homalopsis_buccata	CANACTAATCATTCHAATAGCAAATAGCCTTCTTTGGCTAT DACCTACCA.GAGGACAAAT								
MTS02704 1:61-747 Remainments huccats									
MTE02703.1:61-747_Romalopsis buccata	TADAC GGECATTONS TARGALASCOL TOTOL ATTACC ATTACC								
MT\$02658.1:50-753_Cerberus_rynchops	CARACEAAETATCCECAEAEAEAAEAGECEEETEECEACEEETEECEACEAECAEEAEEAEEAEEAEEA								
AF471092.1:91-794_Cerberus_rynchops	CARACTAATTATCCTCATATCAASACTCTTCTCTCTCTCTACCATCATAATAAAAAT								
#F195900.1:50-753_Cerberus_rynchopa									
KX694850.1:1-654 Cerbergs rynchops	CATAC AAUTATCCCAALAAAAAAAAAAAACCCCCCCCAATE TCAALAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA								
MT802717.1:1-670_Hypsiscopus_plumbes	TTOATEAAETATCCETAEAECAAEAUEAUECETCETCEGETACEACCAECAEGAEGAEGAAAAE								
JX463014.1:50-753_Enhydrie_dussumieri	COMACHAARSATCOMATANGAABACCTTCTTTCCTTACESCCTTCCARGAGAAAAAA								
JX463015.1:50-753_Enhydris_dussumieri	CONCERNMENT AT COMANY A GAMMA GOOD TO CENTROL ACONCERNO A GOADAAAY								
MT802681 1:50-753 Enhydris enhydris									
MT802683.1:50-753_Enhydris_enhydris	CCTACTARTATICTAATACCTAATACCTTCTTCCCTTATETCCTA.CATGACGACAAAAT								
LC105627.1:132-835_Enhydris_enhydris	CLEACEAATEATCCEAATASCAACACCTSCTTCEGTTATUSCCEACCATGAGACAAAAT								
LCIUSSIE.1:126-629_Enhydris_enhydris	CE DACEA VELOCINATION AND VELOCING CENCERT AND VELOCINATION CONTRACTOR AND VELOCINATION CONT								

	300	310	320	330	240		350
MG653605.1:75-778_Sinomicrurus_macclellandi	ATCCUTT	dagcag	BAGAGIAAT	CACAMATCE	CORCEPTER	AATC	CACCEGEGAC
MG002973.1:76-779_Psamnophis_schokari	ADDAEDCE	DAGGIE	CAACAG TAAT	CACAGACCE	ACOT OCCU	CATTON	ACACTONAAC
MGC02967.1:76-779 Psammophis schokari	ANGALICE	CACCTE	JAC ACTORY	CARAAACCH	GCHT HCH	CAT	ANCANTRAAC
MG003027.1:76~776_Psannophis_schokari	ALCATICE	GAGCEG	CAACAGTAAT	TACAAATCT	ACTTACCO	CGTACC	ACACIGERCICAAC
MG003028.1:76-776_Psannophis_schokari	ALCAREC	GADOTE	CARCAGEAAT	TACAAATCI	ACTINCE	CGTACC	ALACGUACEAAC
MG003026.1:76-776_Psamnophis_schokari MG002870_1-76-776_Psamnophis_schokari		THE REAL PROPERTY.		TACAAATCI	ACUT ACC	CGTA	ALC COMPANY
MGGG3010.1:76-776 Psawnophis schokari	ALCAUCE	CABOTE	CARCAGEAAT	TACANTET	ACTTACED	COA	ACACGUARCIANC
MG003017.1:76-776_Psamnophis_schokari	ATCATTON	dAGCT0	CARCESTANT	TACANATOT	ACTIACCO	COTACO	ATACGUAGAAC
MGC03011.1:76-776_Psannophis_schokari	ADDAESCE	GARCIE	SAAGAD BAAT	TACAALTCT	ACTIACOD	CGTATE	ACCERTICANC
MG003005.1:76-776 Psammophis schokari	ADDATES	CACOTO	TAA CAC TAAT	TABLE	ACT OCH	CCTA	ALCONA PARC
MG003008.1:76-776_Psamnophis_schokari	ATCATECT	CACCEC	CRACAGTRAT	TACAAATCT	ACTTACCO	CGTACC	ACACGUACCAAC
MG003002.1:76-776_Psannophis_schokari	ATCATECT	GAGCIG	CRACAGERAT	TACAAATCT	ACTIACCO	CGTACC	ACCERACEALC
MGC02977.1:76-776_Psammophis_schokari	AUGAUELCE			TABLACT	ACHT CH	CGTA	APPACE MADEA AC
AF471031.1:91-796 Psawnodynastes pulverulentus	ALLANT	abreak	CALCRETAAT	TACTANCET	ACTAACTO	AATCOL	ACACCHER ALC
HE476936.1:37-729_Rhabdophis_bindi	ATCATET	GAGCEG	CRACASTART	TACAAACCT	CCEALCTC	COTICEC	TTACA COGAAA
MR530545.1:66-758_Rhabdophis_himalayanus	V DEVERSE	SAGEAS	CAACAE IGAT	CACAAACCI	CTUALCTU	TOTAC	ANDARCORAAA
MN993850 1:71-773 Herpetoreas secura			CARCES TAKE			A CTARG	TO A DEAL
MN993851.1:59-761 Herpetoreas xenura	ATCATTCT	GAOCAG	CARCAGTAAT	TACANAGET	ACTAACTO	AGTA	TCTADDAAA
MN993852.1:57-759_Herpetoreas_menura	ATCATECT	GAGCAG	CAACAGTAAT	TACAAACCT	ACTAACTO	AGTA	ALATCHASGAAA
KC347453.1:102-794_Ahaetulla_nasuta	AUGALLC	GAGGAG	일하는 일수는 일수 문제	CACARECCE	ACTO ACCOUNT	COTA	ALACALTOGAAC
MH043272.1:85+785 Platycers ladacensis	ATCATECT	A	A CALTRAT	TACALLET	ATTALCA	CGTA	CARCERANC
ME322863.1:85-775_Gonycsoma_prasinum	ATCCTTCT	GAGCAC	CRACASTAAT	TACAAACTT	ACCALCA	GGTA	ATATATTATATAC
MZ322864.1:85-775_Gonyosoma_prasinum	ADOCTOCI	CAGCAC	BACAGTAAT	TACAMACTI	ACHAACAGO	GGTARC	TATTATAC
Arseszes 1:91-794 Rhadinophis frenatus	ADDALL					AGTA	ALL CAC
EF669250.1:91-794 Rhadinophis frenatus	ATCATOO	GARCIAN	-DA CRO-RA	CARACCE	ACTA	AGTA	CALT CAL
DQ902112.1:92-794_Coelognathus_helena	ATCETTET	GAGCAG	CAACAGTAAT	CACAAACCT	ACTIACAGO	CGTA	CARATCARCAC
D0902121.1:104-794_Coelognathus_radiatus	ATCALLCT	GAGCAG	CAACAGTAAT	TROTADOGI	ACTAACAC	CATC	TATTOTCAT
NCJ47468.1:94-782_Bolgs_beddomei WT713294.1:44-734 Roigs beddomei	ALC: NOT A	Calco Ca			ACCORD NO.	TAT	C. ALCONDINA C.
MT733292.1:44-734_Boigs_beddomei	ATCATECT	GAGCO	TACAGTAAT	TACAAACCT	ACTTACAGE	TATT	CTATSCOGAAC
MT733290.1:44-734_Boiga_beddome1	ACCAUCE	CV0000	CTACASTAAT	TACAAACCT	ACTINA	TATTOO	CATGOCOGANC
MT733291.1:44-734_Boiga_beddome1	ADDALLC			TACAAACCT	ACHTAN	TATE	TOPCHEARC
MN111468.1:75-775 Lycodon fasciatus	ANAAAA	CACCE	CHACKGTRAT	CARCHARON	TIA	ACTA	CANCEPTAC
EC010366.1:91-791_Lycodon_fasciatus	ATCATTCE	GAGCEG	CRACEGURAT	CACCARCEL	ATTAACAGE	AGTACO	CATABOSTAC
MT625862.1:58-758_Lycodon_fasciatus	ACALIC	GGGGCCG	CAACAGTAAT	CACCARCET	ATTAALAD	AGTACO	CATACCOUTAC
HW111467.1:15-775_Lycodon_Isscistus	ALC: NO DECK		CALCULATION OF		A THAT IS A	AGTA	A CONCEPTION AC
KC010370.1:92-791_Lycodon_lacensis	ATCATTCT	GAGCO	CARGAGINAT	CACTAATT	ACTAACAG	AGTACC	ATACCOGOGTAC
KX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctu		GVCCC	CAACASTAAT	CACTARCOT	ATTAXCAGO	AGTACO	GENCARCOCCAC
MT625846.1:38-758_Lydodon_subcingtus	ADDALLET					AGTA	CALCOLOAT
RC733203.1:76-776_Lycodon_subcinctus	ADDALLCT	GACCEL	CHACKGTAT	TACCALCOT	ATTGACACE	AGTA	CA C CAT
LC105630.1:21-724_Coelognathus_flavolineatus	ATCALLCT	GAGCAG	CRACAGIAAT	TACTARCOL	ATTGACAGO	CATTCO	TATALCOCAAC
DQ902128.1:92-788 Coelognathus flavolineatus				TACTARCCI		CATT	TANTOGAAC
KF669231.1:89-778 Euprepiophis mandarinus	ADDATEC	ALCA	CRACACTART	CECAMOCH	ACTTACAD	COTA	ALACARCORCAC
KF669228.1:92+785_Euprepiophis_mandarinus	AUCAUTCE	GACCAC	CARCAGTAAT	CACABACCT	ACTTACAGE	CGTAC	ATACALCOCAC
MIC20426.1:69-772_Coronella_brachyura	VERVER	Geeeg	CAACAGEAAT	CACAAACCI	ACHALCAL	CATT	ALCARCERARC
AY611998.1:99-794 Ptvas mucosus	ANGAINCH	CARCER	CARGACITART	CACAMACCH	ACHT	TATT	ADANCHICAC
LC105628.1:114-809_Ptyas_mucosa	ATCATTCE	GAGCCG	CAACAGTAAT	CACABARCET	ACTTACAGE	TATACC	ATACANCASCAC
EF076709.1:91-794_Orthriophis_taeniurus	ADDADIC	GNOCAG	CANCAGEAAT	TACARACCT	ACTAACAGE	TGCALCO	TARCOUCAC
PERSONAL TOTAL STATES AND A CONTRACT OF A CO	K ADDALL	DARCER .		CACHA ACCT		7010	TARCHICAC
KX239646.1:95-792 Hydrophis platurus	ATCATECT	GOSC ALC	CARCAGTAAT	CACCAACCT	TOTALCOU	AATC	ALACCHOOMAC
MT966115.1:70-767_Hydrophis_platurus	ATCATTCI	GGGGAG	CARCASTAAT	CACCAACCT	TOTALCOO	AATCOC	ACADODODAAC
KT966116.1:49-746_Hydrophis_platurus	VERVER	GECCAR	CARCAGUAAT	CACCARCOT	TCHARGE	AATC	ALL COCHOHOMANC
MREEGIGE.1:103-800 Hydrophis platurus	ANDAL	CRECIAL	de a da conta a se	ette ette ett	TCHARGE	AATC	ALL CONCEPTANC
MN886308.1:103-800_Hydrophis_platurus	AUGAZICI	GGEGAG	CAACAGTMAT	CACCALCET	TCLARGE	AATC	ATACCOCCAAC
NY966127.1:85-782_Hydrophis_stokesii	ALCALICE	ACCAC	DAGAGTAAT	TACCARCON	CELARCED	AATIC	T COG AAC
JQ217201.1:79=768_Nydrophis_stokesii 80014431.1:72=377 Hadrophis_stokesii	ALCONTRACT	COLOR AND				AATC	THE OCCUPANCE AND
RT966054.1:79-779_Rydrophis_caerulescens	ADCARTCH	GAGCAG	CARCAGTAAT	CACTABOOT	TTHAACCO	AATCCC	ALACTARCAAC
JQ217208.1:79-779_Nydrophis_caerulescens	ARCARTCH	GAGCAG	CARCAGEAAT	CACTAACOT	TTTAACCO	AATC	ATACT TACEAAC
EY206890.1:10-710 Gerarda prevostiana	AFCATICE	GAGGAG	CAACACTAAT	TACCASCIT	ATCALCC	AATC	CARCOLLGA
EF195916.1.50-750 Gerarda prevostiana	AND	ALC: NO	ALC: NO.	TARCAL		AATC	ANCINGA
KX694852.1:1-704_Cantoria_violacea	ATCATTCI	CAGCTO	CAACAGTAAT	TACCARCCT	ATTGACTO	AATC	ATACATCOGANA
EF395897.1:50-753_Cantoria_violacea	ADDARDO	GAGCTO	CARCACEAAT	TACCARCCT	ATTGACTOR	AATC	ATACABCOBAAA
MISC2705.1:52-747_Homalopsis_Buccata	ALCO ALCO T		CALLS AND AND A	TACCAACCT	ACHA IT I	AATC	THE OTHER ANA
MTH02704.1:61-747 Homalopsis buccata	ANALATI	CARCEL	CALL TALL	TRACKSCOM	ACHARCE	AATC	TACTATIANA
MT802703.1:61-747_Romalopsis_buccata	AUCAUT	GAGECG	CAACAGTAAT	TACCARCET	ACTAACCO	AATC	CHACTENCOARA
MT\$02658.1:50-753_Cerberus_rynchops	AFCARTCH	CACCC	CARCAGINAT	TACCALCC	ACTENCE	AATT	CTUACOLAR
EF395900.1:50-753 Cerberus rynchops	ANDAL					AATT	CTUR DA
EF395901.1:50-753_Cerberus_rynchops	ATCATIC	GAGGE	CAACEGTAAT	TACTARCCT	ATTAXOCO	AATT	ATACTTACCAR
EX694850.1:1-654_Cerberus_rynchops	ATCARECT	GADOCC	CAACGSTAAT	TACCARCOT	ATTAXCOU	AATT	ALLA CTURACEARA
MTS02717.1:1-670 Hypsiscopus plumbes	ABCARST	ABOTO	ACAGE TADAY		A TOMA OCO	AATT	ACCESSION AN
JX463015.1:50-753 Enhydris dossumieri	ATCAL	Alloc	Chacks They	CROWNED TH	No a T	AATC	ACCUASICANA
LC105625.1:59-763_Enhydris_enhydris	ATCATTO	GAGCEG	CARCAUTAAT	CACCARCOT	ATTALOCOL	AATC	ATATCTACCANA
MT802681.1:50-753_Enhydris_enhydris	AUCATICI	CARCE	CRACEGURAT	CACCANCET	ATTAACCOO	AATC	ALATCHASSAAA
MISU2083.1:50-753_Enhydris_enhydris LC105627.1:132-835 Enhydris_enhydris	ANDALSCI	ACCEL			AUC	AATC	TCHANAAA
LC105626.1:126-829_Enhydris_enhydris	ADCATEC	GACCO	CHACHGTRAT	CACCARCCT	ATTAACCO	AA C	ATATCHASCARA
	La contrato	- 10-20-VIC	Service Press	South States of	- January and	al sure	at AG BASE

	160	370	21	i ç		90	400	410	_
MG653605.1:75-778_Sinonicrurus_macclellandi	TGCAAT	CAACC	PACETE		COCCT		ATTACT CAT	COMACCOLCACCOURT	
MC002958 1-16-779 Psammophis_schokari	AACAAHA	CALCE	CALCULATION OF	101			R.T. Realle		-
MG002967.1:76-779 Psamnophis schokari	AACAA	CALCT	ACHA	CCC	GEGAT	STOCA.	TARCANC	COACCOTANCESCA	1
MG003027.1:76-776_Psannophis_schokari	AACAA	CAACA	Gacilia	GAGG	GGGGI	TTTCA	ATTANCA CO	CCAACCCTAACCCGA	12
MG003028.1:76-776_Psannophis_schokari	AACAA	CARCA	Geo Bei	E AGE	GEGET	OT DOA	TARCANC		22
MGC03026.1:76-776_Psamnophis_schokari	AACAA	CAACA	act of		Gina	E CHAR	TALCARC		44
MICO3010.1:76-776 Psassophis schokari	ABCAN	CALCA	ac a	dala a	G		No. R. A.	and decision of the	
MG003017.1:76-776_Psawnophis_schokari	ABCAA	CARCA	de la	dAGO	AGGGT	TTTCA	ATTANCA AT	COALCOUTAACCOGA	
MGC03011.1:76-776_Psannophis_schokari	AACAA	CAACA	ec a	d A a d	6666	TREA	ATTANCANT	CCAACCCEAACCCEA	22
MG002984.1:76-776_Psannophis_schokari	AACAAHA	CAACA	eac ag	골·길의	ACCOL	DE LEA	TACAT		4
MC003005.1.76-776_Paamophis_schokari	AACAAMA	CALCA		1.4			Rev Bran		1
MG003002.1:76-776_Psannophis_schokari	AACAA	CALCA	Gachar	- calc c	ACCO	TTTA	PETABCANT.	CORACCOTNACCORA	22
MGC02977.1:76-776_Psamophis_schokari	AACAA	CARCA	Geoge	EG A GG	AGGGI	TTTTA	TABCAST	COARCCOTARCCOGA	11
MG003004.1:76-776 Psannophis_schokari	AACAA	CAACA	Sec le		A G	OT DOA	TACAST		
ME476936 1-37-729 Babdophis bindi	CACCOUNT	CAACA	A COMPANY OF A COMPANY	8.4			Real Provide		
MR530545.1:66-750_Rhabdophis_himalayanus	CACCOLC	CCACT	ac a	GAGO	CEGAT	TOTOA	ATTACTORY.	COCACCOTARCESA	
KF200929.1:60-747_Rhabdophis_himalayanus	CACCC	CCACT	ACOT	GAGG	COGAT	TOTOA	ATTANTONT .	COCACCOTARCOSA	
MN993850.1:71-773_Herpetozeas_senura	TATACHT	CAACT	PACET	9999	TERAT		TANTONT	SCALETCHTA SCHOOL	
MN993851 1:57-761 Herpetoreas secura	TATACHT	CALCE	CALCUTE				No. No. No.		-
XC347453.1:102-794 Ahaetulla nasuta	ATCAC A	CCACT	OACHT	GAGO	a a.	TOTCA	ATTARTORY	CCCACACZGACACGA	-
MK595796.1:83-783_Ahaetulla_laudankia	AGCAC	CACA	ACTO	e c c c c	CEOGI	TOTOA	ATARTONT.	COALCACTAACACCA	
MH043272.1:85-785_Platyceps_ladadensis	ATCGC T	CAACA	CHCHC!	C C	GHCAT	ALC: NO.	CARCINE	CEARCICE AND CEGA	
ME122864 1:85-775 Gonvosoma prasinum	AACAC	CCGTC	PACE		G C		Real Real	A CHARMEN	
KF669246.1:91-794_Rhadinophis_frenatus	AACAC	CCACC	CACUT	GACC	Geoc	TOTOL	ATCALTONE	CCCACACTAACTCCA	
DQ902110.1:91-794_Gonyosoma_frematum	AACACTA	COACC	CAC DE	GAGG	GGGCT	TC TCA	ATCANTICAC	CCAGACTAAGTCGA	12
EF669250.1:91-794_Rhadinophie_frenatue	AACAC	CCACC	ACOT		GOOGT	HERE A	CANTER OF	SECONDACE AND TODAY	
D0902121 1 104-794 Coelognathus radiatus	AACAC	CICIACE	Age Le	1.00	T		NOT ANT ON		4
EC347466.1:94-782 Boiga beddomei	TOCCC 7	CCACT	ACUE	o de la c	GLOGI	10100	ATCANCORE	E CANCELETAN FRANK	
MT733294.1:44-734_Boiga_beddomei	TACCT	CCACT	BACEA	r G G G G	csact	BORGA	ATTA TONT	COALCCCCCACCCCA	
MT733292.1:44-734_Boigs_beddome1	TACCCHA	CCACT	EACEAL		COUCT	RED RA	A TANTON		
MT733290.1.44-734_Bolga_beddomet	TACCCHA	CCACT	ACC DO			N 197	Real Property in the	STATE STATE	-
MW111469.1:76-779_Lycodon_septentrionalis	AACOCA	CCAAT	AC T	dad	GCCTT	TOTO	ATTAL TOAT	CEAACACTCACCCCA	11
MW111468.1:75-775_Lycodon_fasciatus	AACAC	CALAC	CACHER	GGGG	GCGTT	TOTOA	ATTANTONT	CCAACCCTTACCCCA	72
EC010366.1:91=791_Lycodon_fasciatus	AACAC	CTAGE	GCOT	CADO	GGGTT	EC EL A	A STARTCAC	CORACA COCACCEDA	-
MT525852.1:58-758_Lycodon_fasciatus	AACACHA	TAGT	ACCURATE ON THE				REAL REAL		4
ECC10368.1:92-794 Lycodon laoensis	AACATA	CCAAC	ACHT	and	TEGET	TOTICA	TOTAL TICKO	COALCOCTALCOCT	-
#C010370.1:92-791_Lycodon_lacensis	AACAC	CCAAT	DACOT	a a a a	CSGET	TOTOA	ATTACTORC.	COALCCCTAACCCCA	2.2
MX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctus	AACAC	CTAAC	CACHC.	GAGG	66661	TOTOA	ATTAACCAC	CONTONCOLOGIA	
MT625846.1:58-758 Lycodon_subcinctus	AACACHT	CCAAC	ACHO			N	A TARTORS		4
#C733203.1:76-776 Loondon subcinctus	AACACUT	COMAC	ALC: NO		CHUCK		North Profile	COAL CAPTURE OF CA	
LC105630.1:21-724_Coelognathus_flavolineatus	AACTCA	CCACC	CACUT	e de c	CGGAT	TCTCA	ATTART CRO	CORACCOZIACCOGA	11
DQ902128.1:92-788_Coelognathus_flavolineatus	AACTCA	CCACC	OACET	d ∧ a a	COGAT	TOTOA	ATCANTON?	CCCRCCCARCCCAR	
DQ902134.1:91-791_Elapho_bella	AGCACHT	CCACT	THE	en en	G		TANCONC	STATE THAT STATE	-
KF669228 1 92-785 Euprepiophis mandarinus	AACAC A	TCACT	Jac in	ales	GCOTT		NTARTON-	THE ADDRESS TO A DECK	1
MIC20426.1:69-772_Coronalla_bracbyura	ATCACHA	CAACC	CACHA	GGGG	TEGAT	TOTOA	Ancal colic	COALCCCTAACCCCA	
KN782330.1:10-690_Wallophis_brachyura	ATCACHA	CAACC	GACEA	6666	TGGAT	TOTOA	A CANCIPAC	COALCCCARCEEA	-
AY611998.1:99-794_Ptyas_mucosus	AACACHA	CCACC	CATE A		ACCCI	HCE14A	TANTONT	HUMAN TCHRANCEDA	32
EFC76709.1:91-794 Orthriophis taeniurus	AATACHA	CAACC	- A CHICK	10	A A	1.00	Real Colle	COCK OT COALS - CA	-
DQ902132.1:91-794_Orthriophis_taeniurus_grabowsk	AACAC	CANCE	GACHE	a a a a	GGGCT	TOTOA	A TALCORE	CCCACCCTAACTCCA	
KF669249.1:91-794_Orthriophis_taeniurus	AACAC	CALCO	BACHC	G AGG	06007	TOTOA	TANCOAC	COCACCOMACTOR	
XX239646.1:95-792_Hydrophis_platurus	CATTLA	CAACA	CACES!	000			TOCATO		4
KT966116,1:49-746 Hydrophia platurus	CATTINA	CALCA	-In cluster	C C C C C	C C		R TGRCARE	CONTRACTOR OF	-
MN886306.1:103-800_Bydrophis_platurus	CATTLA	CRACA	GACING	C C C C	CCCCT	TOTOA	ATTGACASC	CCCACCOTACCCCA	11
MW886307.1:103-800_Hydrophis_platurus	CATTTA	CARCA	PACHE	BODE	GEGET	READA	TGCAC		
MNSU63UE.1:103-SUG_Hydrophis_platurus	CATTIN	CALCA	SACES!				TO TO CARO		-
JQ217201.1:79-768_Hydrophis_stokesii	CATTLA	CAACO	ATIA		A		TGACANC	STATE COMMENT	
EC014431.1:77-777_Hydrophis_obscurus	CATTTA	CASCO	CATHO	GAGO	GGGGI	TCTCA	ATTGACARC	CCAACCCTAACTCGA	11
KT966054.1:79-779_Hydrophis_caexulescens	CATTLA	CALCE	Sex lies		ACCG	C C C A	TGCCACC		
J0217208.1:79-779_Hydrophis_cserulescens	CATTIN	CALCE	COLUMN ST			N-141	CALC NO.		
KY206891 1:19-719 Gerarda prevostiana	CACACHT	CALCO	CACOT	da lete	G G G		ALCANTCH:	COTACCOTCACCOCA	
KF395916.1:50-750_Gerarda_prevostiana	CACACIT	CAACC	ACT	abaa	decar	TOTEA	ATCAL TOBC	CCACCCZCACCCGA	
KX694852.1:1-704_Cantoria_violaces	CATATIC	COTOT	OVCIC	GAGG	COORT	ECZGA	A DODATA	GGCAGCCZAAGCZGA	77
EF395897.1:50-753_Cantoria_violacea	CATATIG	CCTCT	ACTER 1	e Age			TACOLA		4
MT802711.1:62=747 Homalopsis_buccata	CACACHT	CALCE	AL STREET				NicaReche		
MTS02704.1:61-747_Homalopsis_buccats	CACAC	CAACT	GACOT	GACC	CECC	TCTCA	Arcaleche	CONCECTANCEEDA	11
MT802703.1:61-747_Homelopsis_buccata	CACAC	CARCTI	ACET	GACC	CCCCT	TOTOA	A CANCIS NO	COCACCE AACCEEAS	4
MTSU2658.1:50-753 Cerberus rynchops	CACACHT	CALCO	AC DO		T L C T T		Per al conto		1
EF195900.1:50-753 Cerberus rynchops	CACAC	CALCO	HACING	A	T COL	18476	Percalice Ar	acolor contraction	÷
EF395901.1:50-753_Cerberus_rynchops	CACAC	CAATC	GAC	GAGG	TOOCT	TOTOS	STCAL CORC	SECRECCIARCCERA	1
#X694850.1:1-654_Cerberus_rynchops	CACAC	CAACAT	CACHT	Geleic	CECC	EC IZEA	ATCARCORE	COLOCIER ACCESA	1
MTS02717.1:1-670 Hypsiscopus plumbes	CACATOA	CAACCE			A A	RECEIPTAN		A DEALER AND A DEA	
JX463015.1:50-753 Enhydrie docamieri	CCALA	COACC	CAC	dialara	a		R. A. A.	CONCEPTABLE A	-
LC105625.1:59-763 Enhydris enhydris	CITCAC	CAACC	GATOR	0000	couc	TOTOL	ATCAR TORC	COCACCOTTACCOL	
MT802681.1:50-753_Enhydris_enhydris	CTCACTT	CAACC	ATA	GC GG	TUCCI	TOTOA	CAPTORC	CCCACE CT TACCCCA	11
MTS02683.1:50-753_Enhydris_enhydris	CECACET	CAACC	ATOA	Gene	E E E E E	HERE'S	CALL COL	NOT AND CARE AND ADDRESS	
LC105626.1:126-829_Enhydris enhydris	CTCAC	CAACC	CATIN	C G C C	e c c c i	1 1 1 1	ALL AL	COLOR MECHAN	
10 N N N N N N N N N N N N N N N N N N N	15 - 17 M			-	Concert?				

	420		430		4.4	ē.		450		44	ę	2	470		
MG653605.1:75-778_Sinomicrurus_macclellandi	TIM	c ac	CORACI	-	TAUCC	T C	CASE	CACTA	C 171	T SA	TRAT	CEC	AA	CACA	CAT
MCC02973.1:76-779_Psannophis_schokari	1	TOC	CCHAC		CAUCIC	TGC	CATE	CATCA	TCT	ABA	AGAI	A	AAP	CATA	201
MG002968.1:76-779_Fsamnophis_schokari	C	TEE	CCAR		CAUCE	5		CATCA	TACT	A BA	ATAT	Phillips	125		TOR
MGC02967.1:75-779_Psamnophis_schokari	214	C a	CONTRACT	- 10	CVHCC	95		CATCA	E CI	A	The second	1.144	442		ECH.
Musully 1, 1: 16-116_Feannophis_schokars		1.00		1.14	CALL CO			TATUA	2.1	080	10.1	1.14	228	100.0	12.78
MCC03026 1:76-776 Passcophia schokari	- 18	-88		488		-01-		TATCA	- 11	080	16.1			100.0	1.18
MG002970 1:76-776 Psannophis schokari		- 11	66 8 1		71.00	- A		CATCA	-11-1		10. 1	a - 1	A &	CONC N	1.26
M0003010.1:76-776 Psawnophis schokari	C.	THE	de al a	E .	TALCC	A.	CATT	CATCA	THOT	A DA	ANT	A	AAA	CACA	1.1
MG003017.1:76-776 Psammophis schokari	c	TOC	CONACI	c	TALCC	A.	CATT	CATCA	TLCT	A N	ADAT	A	h A a	CACA	TA
MCC03011.1:76-776_Psannophis_schokari	CEL	TRC	CCHAR	CIRC	TARCC	A.	CAUT	CATCA	TOCT	ABN	ABATS	ALC	AAC	CACA	TAT
MG002984.1:76-776_Psannophis_schokari	Cal	Tac	COMARIA	c 📰	TABCC	- A.	CASE	CATCA	TACT	ABN	ADATE	ACC	AA	CACA.	TAT
MG003005.1:76-776_Psannophis_schokari	C	THE	CCHACE		TANCC	- A	CAPT	CATCA	TACT	ABA	ABAT	ALC	AAT	CACA	TAT
MG003008.1:76-776_Psannophis_schokari	C	THE	CCHAG		TARCC	TAC	CAPE	CATCA	TACT	ASA.	ADAT	100	AAE	CACA	TAB
MG003002.1:76-776_Psampophis_schokari	- 244	Citta	CCHAR	200	TANCC	201		CATCA	E 63	-8°.	18° I 1	194	24E	10.3	E^E
MCCC3004 1-76-775 Presecoble schokari	- 18	466		(- HE)		-0-		CARCA	A	080	8.4	C H	110	R 1	1.2
AF471011.1:91-794 Psampodynastes pulverulentus	2	- 68	di la la		CA CC	14	CATT	CACCA	- N	H	1.7	G 1	1.1.1	ALC: N	CC.
ME476936.1:37-729 Rhabdophis bindi	č	666	center (-	CAUTC	-8-	CALL	CGCTA	TITC	-8-	CHAT I	8.1	A 8 0	CAC A	CAT
MR530545.1:66-758_Rhabdophis_himalayanus	CT	TEC	CONTRA	C 220	CAUTT	a.	CARE	CACTA	TATE	: Oct	THAT	100	AAC	CACA	CAL
KF200929.1:60-747_Rhabdophis_himalayanus	CER	100	CONTRA	0.00	CANTT	EA.C	GARE	CACTA	1071	1234	TEAT	1726	AAG	CACA	TAT
MN993850.1:71-773_Herpetoreas_senura	C	0.00	ACTOR	C 25	TACC	TAC.	CADE	COCCV	1.21	TEN	CEAT	0.00	CAR	CATA	TAT
MN993851.1:59-761_Herpetoreas_xenura	C	C arc	ACTION		TAUCC	TAP	GARE	CGCCA	TATT	TEN	CEATS	9	CAR	CATA	100
MN993852.1:57-759_Herpetoreas_wenura	244	222	ACHER A	2	TALCC		C A LED	CECCA	E 11	100		9-1	CAL	and a	E AL
MCSE/653.1:102-796_Anaetolia_nasuta	2	C 194		1	TABOO	15.	12.12	TTTAN	100		10.1		ang.	100	12.2
MR043973 1:85-785 Blatucons ladatensis	1	C 68		1.122			122.5	CACCA	-	181	- Bi - I		20H	100 1	201
ME322863 1:85-775 Convesome prasinum		G 88	90 B		CALCO	- A	Cales.	CGCTA	1.0	-8.	A T		A 3 44	- A	- 2
ME322864.1:85-775 Gonyosoma prasinum	- Chi	TRO	2000	C.	CANCO	i de	CALT	CGCTA	C 70	TEN	ADAT		44.	CAC A	-CA
XF669246.1:91-794 Rhadinophis frenatus	C	cac	ochece.	CIT	CALCC	rcc	CATT	CACCA	TATC	TEN	GRATE	100	AAT	T CAT A	TAT
DQ902110.1:91-794_Gonyosoms_frematum	CE	ic ac	CC CC	1 B	CANCC	rce	CATT	CACCA	TATC	TEN	GEAT	1.00	2.4.7	CATA	10.0
EF669250.1:91-794_Rhadinophis_frenatus	C	cac	CC CC	10 20	CADCC	1 C C	GARE	CACCA	TREC	TEN	GEAT	725	2.4.0	CAT N	141
DQ902112.1:92-794_Coelognathus_helena	C	Tac	actices.		TAUTC	T T C	CATE	CACCA	CATC	T BC	ALLA		***	CACA.	CAT
DQ902121.1:104-794_Coelognathus_radiatus	14	100	TCHAC	C III	TAUTC	19.	SAUL	TACTA	0.21		10.4 2 2	100	AA	EACA	三方目
MUTITION 1 44-714 Boigs beddonel	264	C H		1.12	ALC: C	1	ALC: NO	TACCA	CR.S	1	HAT I		1.1	100	101
MT/JJ294.1:44-734 Bolgs_beddone1	- 28	C 11			TARTIC .			TACTA					<u> </u>	BA 1	ECH.
MT133290, 1:44-734 Boiga beddone1	- 28	CHH	83 6 6	(-123	CAUTO			TACTA	ch+c	-80	ALC: N	÷.		101-1	42
MT733291.1:44-734 Boiga beddomei	č.	C III	cc al i		CALTC	d.	Ares	TACTA	chire	- 3.	ALLAT	1.17	1.1.	CACA	1.0
MW111469.1:76-779_Lycodon_septentrionalis	c	cae	CONACI	C TT	CALCC	TCC	COTT	CACTA	TATT	TEA	CTATE		4.4.1	CACA	CAT
MW111468.1:75-775_Lycodon_fasciatus	CER	TEC	OTTACA	0.00	CARCIC	ECC.	CATT	CACTA	CATC	TEN	ABATE	123	AA	CACA	CAR
EC010365.1:91=791_Lycodon_fasciatus	C 13	100	CTHACE	- E	CARCO	TCC	CARE	CACTA	TRIC	184	CHAT	100	2.4.2	CACA	CAT
MT625862.1:58-758_Lycodon_fasciatus	C 11	CBC	CTHAC		CAUCC			CACTA	1.20	TEN	C 697 2 6	100	AND	CACA	CAT
MW111467.1:75-775_Lycodon_fascistus	CIN	C and	CTHAC	E DE	CAHCC	191		CACCA	1.10	224	C A T	- C	A A 2	C D C D	ICAN.
ACUIUSES.1:92-796_Lycodon_Lacensis					TANCC	ш.		CACCA	E 13				~ E	EAC 1	1001
EVE22575 1:72-TT2 UNVERTETED: Lucades subsingto	. 18		3312	(- 199		- H.		TACCA		280	8.4		201	BR 21	201
MT625846 1:58-758 London subcingtus	7 X	Sec.	53 B .	6	71.00		dale -	CACCA	0.00		100.00	R 1		BR A	20
MT625859.1:58-758 Lycodon subcinctus	č.	Second	GG A		TALCC	al.	CATT	CACCA	COTO	TEN	ALC: N	H 1	14.	CACA	CAR
EC733203.1:76-776 Lycodon subcinctus		E d	cciac a		TALCC	A.	CALC	CACCA	CATC	TEN	ANAT		4.4.4	CACA	CAT
LC105630.1:21-724_Coelognathus_flavolineatus	C CO	TEC	COTTOA	C 22	TARCC	TTC	CALT	TATTA	CLITA		CAT	C	AAD	CATA	TAT
DQ902128.1:92-788_Coelognathus_flavolineatus	C	Tac	OC TO A		TACC	110	CATT	TATTA	CUTA	TET	COAT	0.0	A. A. C.	CACA	TAT
DQ902134.1:91-791_Elaphe_bella	CT	1200	CONTRA		TALCC	ec.	CA DO	TACCA	Chird	TON.	ADATE	01.5	A A 🖸	CVCV	TAT
KF669231.1:89-778_Euprepiophis_mandarinus	244	E H	CONTRA		TAUCC	18		CACTA	TITC	191	ALL TR	9.1	2.0 <u>0</u>	EAL H	ECH-
MP020426.1:52*785_Exprepiophis_mandarings	- 14	1 111			TACC	10.		CACTA	H-Re		10.10	1.195	с . н		1201
KV182330 1:10-650 Mallophia brachwire	- 18	C (8)			CALCO			CACCA	- A	180	10.4	C 198	<u> </u>		1228
AY611998.1:99-794 Ptvas success	- 18	F H	66 A .	(- He	TANCC	-86	Alter	CATTA	chize		104.7		1.1.1	CACA	6.1
LC105628.1:114-809 Ptyas mucosa	cut	T RC	CC ACL	-	TAUCC	TTC	CATE	TATTA	C. 7 C	TSK	ADATE	8.1	22.0	CACA	CAR
EF076709.1:91-794 Orthriophis taeniurus	TT	cac	COTTON	ici an	TACC	TTC	CATT	TACTA	TATO	724	ADATE	0.0	AAT	CACA	CAR
DQ902132.1:91-794_Orthriophis_taeniurus_grabows	k T	Tac	TCHCCA	100	TACC	r cic	CATT	TACTA	TATC	TSN:	ABATS	id 3	A A 20	CACA	CAR
<pre>KF669249.1:91-794_Orthriophis_taeniurus</pre>	TIT	TOC	TORCEN	1	TARCC	n cir	CART	TACTA	TNEC	T N.	ADAT	ici -	A A P	CACN	CAL
XX239646.1:95-792_Hydrophis_platurus	- 544	七日日	CCHAP		CALTC	12	C T D D	CATAA	CATC	TON	ALC: N	E 144	AA 24	ENC N	EAU
ATS66115.1:70-767_Hydrophia_platurus	244	CH	69 6	2.44	CANTC	н.	E LA	CATAA		190	10.11	T 144	- - -		ECH-
MERESON 1-103-800 Budershis slaturus	18	1.68		1.128	CALL TO	220		CAPES	-	180	1.4		1.1		100
MN886307.1:103-800 Hydrophis platurus		计标识	66 A .		CANTC			CATAA	Chie	- 6.	1.1			Dia a	1.78
MN886308.1:103-800_Hydrophis_platurus	- C	TOP	COMAC	C III	CAUTO	TIC	CITT	CATAA	CUTC	TEN	ALAT	T.	AA	CACA	TAT
MT966127.1:85-782_Hydrophis_stokesii	C	T ac	TTBACA		TATTC	TTC	CAST	CATAN	e rie	TEN	TEAT	- 23	A.A.2	CACA	CAL
JQ217201.1:79-768_Hydrophis_stokesii	CIT	TOP	TTA		TANTC	TTC	CAIN	CATAA	CUTC	TEA	THAT	100	440	CACK!	CAT
RC014431.1:77-777_Hydrophis_obscurus	C	TBC	TABA	TE	TARTC		CASE	CATAN	CATC	TEA	THAT	100	AAZ C		STAT:
KT966054.1:79-779_Rydrophis_caerulescens	95	TEC	TCHEN	Test	TANTC	- F		CATAA	0.20		THAT	100	AAE		TANK .
J0217208.1:79-779_Rydrophis_cserulescens	5 1	C		199	TAUTC	12.		CATAR	5.55		THAT I		2 M (ECH.
W206891 1-19-710 Gerarda prevostiana	2 H	CHE					1000	TTCCA		180			228	- B.	1408
FF195916 1 50-750 Gerards prevoetians	- 28	CH	22 B A	1288		8 H K		CTCCA	1.1	180			2210	80.1	
KX694852 1:1-704 Cantoria violacea		ι÷.	66 B.		TA CC	- H.	CA.	CTCTC	ALTO	1.5	C 7 A	8 1	4.3.1	CACA.	CA
EF395897.1:50-753 Cantoria violacea	- C	Tale	oc A	C TE	CALCC	A.	CATT	CTCTC	A TO	100	CITA	8.1	AAC	CACA	CA
MT802706.1:62-747_Homalopsis_buccata	CEL	c as	OT A	C	CALCC	TAC	CART	TTCCC	chirc	TEA	C CT	C	AA	CACA	CAL
MT802711.1:62-747_Homalopsis_buccata	CIT	CEL	CTHACA	10	CANCIC	TAL	CASE	TTCCC	CATC	TEA	c C c t c	C C	AAZ	CIERC A	CAT
MTS02704.1:61-747_Homalopsis_buccats	Cite	C 80	CT A		CARCIC	A.	App	TTCCC	TATO	TBA	CACA	C C	225	CACA.	CAT
MTR02703.1:61-747_Romelopsis_buccata	CLA	1	CT A		CAHCC	TAC.	100	TTCCC	C 10	C PA	CUCA	9	AAZ	CA-	100
ALEVANDE 1:50-753 Cerberus rynchops	200	C H		1.14	CONCC.			CTCCC	CALC:	181		1.14	COM	SAL S	100
EF195900.1:50-753 Cerberus runchons	14	G 14	Sec. 1		Caller	-		CTCTC	E C	-80		3.1			27
EF395901.1:50-753 Cerberus rynchops	200	i la	oct -	C.	TANT	a.	A.	CTCCC	0.70	-	Chical	6	AA	- CA.	A ST
EX694850.1:1-654 Cerberus rynchops	c	c.	CONTRACT	C C	CANTC	TG:	CATT	CTCCC	Chite	- 31	CACA	c.	4.4.	EXCO	AL
MT802717.1:1-670_Hypsiscopus_plumbes	C	cac	CC CC	C	CANTC	TTC	CATT	TACCC	Chitc	TEA	TEAT	C. P	TAR	CACA	TAT
JX463014.1:50-753_Enhydris_dussumieri	CIT	TOC	GCT GC/		TAUCC	1	CATE	CACCC	0.70	TBA	COAT	C C	AAE	CACA.	CAT
JX463015.1:50-753_Enhydris_doseumieri	COL	Eac	CC CC	1	TAUCC	T	ALC: N	CACCC	0.70	E BA	CUAT	1914	AAU	CA.	CAL
LC105e25.1:59-763_Enhydris_enhydris	CL	Citt	SCHER !!	1	TAUCC	19	AU	TACCC	5 19	1.0	DO T	21		E.C.A	SSL
MIGUZGEL 1:50-753 EMBYGELS embydels	200	1.1		C-141	ABIC			TACCC				14	1.1		
LC105627 1:132-835 Enhydria anhydria	- 64	-	22.0		TANK			TACCC		18.		-	2.4		100
LC105626.1:126-829 Enhydria enhydria	200	1	CONTRACTOR		TANCC	-ch	Cale-	TACCC	chire.	- 2.	Cinc +		4.3.	EN-N	CAR
		-	-	-		-		-	-	and the second second	-	-	-		-

12	486	490	500	510	520	220
MG653605.1:75-778 Sinomicrurus macclellandi	CTHAT	ANGRACALAR	BORGORACING	ALCETGOC	ANT ANT TOAL	ACR TRACKASA
MCC002973.1:76-779 Psamnophis schokari	AC OC	TACOATCAAS	COTCARACAAC	Achelolie	ANT MACTINA.	INTRODUCED AND
MC002968 1:76-779 Psampophis schokari	Acriacia	TALCHATCAAH	OCTOBERCASO	CACHCOPT.	ACT BACTERA	TREATERINA
MG002967 1:76-779 Psampophis schokari	Acade	TOACAATGAAG	COLORADA CARD	ACCORDENT	ACT ANO DOM	THOMAS AND
MC003027 1:76-176 Passmoohis schokari	ALC: NOT	TATICACE	CONTRACTOR OF	A DACE TO ST	ALC: NO.	Man All All All All All All All All All Al
MCD03028 1:76-776 Passmophis schokari	ALTRACT	CONTRACTOR	opposite and a closed	A CONTRACTOR	State of the state	Stand and a sta
MCC03026 1:76-776 Pearmonhis schokari	A CONTRACTOR	CONTRACTOR OF	COLUMN ADDR SAL-	ALC: NOT OTHER	No. 191	THE REAL PROPERTY OF
MCCD2078 1-76-776 Brannophis schokari		CONTRACTOR OF THE OWNER OWNER OF THE OWNER O				Manager Provention
MCCC2010 1-76-776 Peanmonhis schokavi						The second s
MUCUSUID I 16-176 PRANNOPHIA SCHOKAFI	AC DAC D	CONTRATONOUS		ALC NEW PLANE		A CARLES AND A CARLES
MUCUJULT.1:16-776_PSammophia_schokars	AL DALL	CHILDRIGAN	Contraction of the second	ACCESSION OF		
MGC03011.1:76-776_Fsammophis_schokari	AL DAL U	CENTANTGAAS	CIT CLACING	REVENUEL		THE ALL AND AND
MG202984.1:76-776_Psannophis_schokari	ACHACH	CONTRATGAND	COLOGANCE C	REACHTONC	ACTRACTOR	TATACACACAAAAT
MG003005.1:76~776_Psammophis_schokari	ACAC	CONTRATGAAS	CGT CGT ACT AC	SHACHTCHC	ACTRACTOR	ATRCACACAAAT
MGC03008.1:76~776_Psamnophis_schokari	ACHACH	CONTRATGAAS	COTOGNACIAC	CHACHEGHE	ACTRACTER	INTICAC ACA AAA
MG003002.1:76-776_Fsamnophis_schokari	ACOACO	CONTRATOAGO	GGTEGAACAAC	CONCERTION C	ACTARCTON	TATACACACAAABT
MGC02977.1:76-776_Psamnophis_schokari	ACOACO	CONTANTIGAGO	GGTCGAACAAC	CACHTGRO	ACTARCTICAS	TATACAGAGABART
MG003004 1:76-776 Fsannophis_schokari	ACHACH	CONTRATOAGE	GGTCGAAGAAS	BRACETOSC	ACTANCIENS	ATACACACAAAAT
AF471031.1:91-794 Psawnodynastes pulverulentus	ACTIC	ACALCHACHAA	GGTCANGCAAC	EGACECOSIC	ACARACTCA	TATATTGACAAAAT
ME476936.1:37-729 Rhabdophis bindi	ACCCC	CONCRETEAAS	GOT CANGE AND	ATACA	ACAAACTCA	ATATTGATAAAAT
MR530545.1:66-758 Rhabdophis himalayanus	ACHCCH	CONCENCTION OF	OCT CANCELAC	CAT BAGEA	ACAAACTCA	ATATTGATAAAAT
KF200929.1:60-747 Rhabdophis himalayanus	ACHCCH	CARCHETGAGE	HER CANGENNE	ATRACEA	ACANACTOR	ATOTTONTA ABAT
MN991850 1:71-771 Herpetoreas secura	ACTIN	A CONTRACTOR	des de la contra da la	o da cina lo da	ACCORD NO.	Contraction of the local division of the
MUDDIDS1 1:50-751 Hernstoress venurs	in the second	AND DESCRIPTION OF		ALC: NO. OF	ALC: NO.	
MACONCEL 1.57 TEL MELPELOLOGIA MEDICA						CALCE CALL
MANJONDA A DI TOT DE DECOEMAS ANNUEA						
KC347455.1:102-794_Anaetolla_nasuta	ALC: UNK	THICHAAGAGE	CEL PROCESS	ATTACIA		
MK595796.1:85°785_Ahsetulla_leudankia	OC DAL D	ACCORACIANT		AT GG A	ALL TRACTERS	
MH043272.1:85-785_Platyceps_ladacensis	ACCACE	TENTACAGAAG	COLCUMPTANCE AND	ACHAGHA	ACARACTER	ACATICACBAABE
ME322883.1:85=775_Gonyosoma_presinum	ATOALO	CAGAAB	GATCANGGAAD	ACHAGEA	AC AAAC TEA	ATALICALAAAAT
ME322864.1:85-775_Gonyosoma_prasinum	ATOACO	TOACHCAGAAB	GAT CANCEARC	CACHAGEA	ACAAACTCA	ATATICACRAAST
KF669246.1:91-794_Rhadinophis_frenatus	AABACB	ACAGAGE	GGTCANGCANT	CCHAGEA	ADARACTEA	ATATCONCARANT
DQ902110.1:91-794_Gonyosoma_frematum	AABACB	ACACAGAGE	GGTCANGCAAT	CCCASEA	ACAAACTEA	ATATCUACAAA
EF669250 1:91-794 Rhadinophis frenatus	AAAAC	ACACAGAGE	GTECANGCANT	CCGAODA	ACAAACTEA	ATATCGACAAAAT
D0902112.1:92-794 Coelognathus helena	ACLAC	TCACALGT	COLCOMACA AC	CAC AGEA	ACAAACTCO	ACATCOACAAAA
DC902121.1:104-794 Coelognathus radiatus	ACUTC	TEACHCAGAAN	OGT OT OGT OTT	TCHACTA	AGA AND THAT	ATATTGACAAAA
EC147466.1:94-782 Boigs beddonei	AC CC	ACRECICACION	GC CC CC CC CC	CTC TCL	ACAMOTICS!	ATATTATAAA
WT113294 1:44-734 Boigs beddomet	ACTOR	AGACATACAAS	Cold Service - Main	Recubación	ACT AND TO A	The Party of the P
METTINGS 1:44-724 Boigs haddonai	A CONTRACTOR	A DOMESTICAN D		and the second second		the second s
WT133260 1:44-724 Boirs haddonal	A COMPANY	A CONTRACTOR OF				A SHORE HAVE A
WEISSER 1.44 734 Bolgs beddones	a la					State of the second s
MINISSESS. 1. 44-734_Bolga_Deddobel		- Change				A REAL PROPERTY OF
MW111665.1:76-779_Lycodom_septentrionalis	AL AL	ACHERCAGAGE	COLUMN STATE	A CLACER	ALC THAT	
NW111468.1:75=775_Lycodon_fasciatus	ATA	ALICECAGAGH	GCT CLAGTAAU		ACARCTCA	A GATIOU ACAAACT
EC010366.1:91=791_Lycodon_fasciatus	ACUACU	ACACACAGAAD	OCT CANGUARC	CCHAGEG	ACC ANCI DA	ACATICACAAAG
MT625862.1:58-758_Lycodon_fasciatus	ACHACH	ACACAGAAB	OCT CAMECANC	RECHAORE	ACAAACTEA	INCHITI UNCARAN
MW111467.1:75-775_Lycodon_fascistus	ACACE	ACACECAGAAG	GCTCANGCANC	COCCEACEC	ACAAACTER	TACATT FACAAAAT
ECC10368.1:92-794_Lycodon_lacensis	ACDACD	CONCREAGANE	GCTCTARTAAS	CONCRACES	ACAAACTEA	INTATIGATAAAAT
#C010370.1:92-791_Lycodon_lacensis	ACAC	CACACAGAAG	OCTOTATAAC	CACEAGEA	ACAAACTCA	INTATTIATAAAA
KX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctus	ACTIC	ACACACAGAAG	GETCENEGAND	COACEACEA	ACGAACTEG)	IACADE CAERAAAT
MT625846.1:58-758_Lycodon_subcingtus	ACAC	CEACACAGAAG	OPT CENEGAND	CACTACEA	A CAANCY CM	JACAPE CACAAAET
MT625859.1:58-758_Lycodon_subcinctus	ACTACE	CARDADADO	CCT CTACCAAC	ACCACCAC	ACAAACTCA	ACAPTOACAAANT
EC733203.1:76-776 Lycodon subcinctus	ACTACO	COACECAGANG	GOT OTAGEAAG	ACAGEA	ACAARCTCA	ACATTCACAAAAT
LC105630.1:21-724 Coelognathus flavolineatus	ACHACH	ACACECAGAAG	GGT GCAACAAC	Rec HAGEA	ACCAACTCA	ACATTGATAAAAT
DO902128 1:92-788 Coelognathus flavolineatus	ACTAC	ACACAGAGAAG	GAT COMACANO	CCC RADORA	ACCANCTON	IACR/TTOACAAAAT
50902134 1 91-791 Elaphe bella	ACHACH	ACACAGAAG	OTTOCH GOMAN	BACHAOSE	AGA MACTON!	ACADE LATA AND
EFE69231 1 89-778 Europeniophis mandarinus	ATTAC	Conche Adams	data ender the	ALC: NO DE COM	ALC: NO. OF TAX	The second s
EF669228 1-92-785 Expressionhis mandarings	AT A	A CREACES.	COLORADA COLORADA	THE COMPANY	And BACTERS	STATE STATE
MT020426 1-69-772 Coronalla brachmina	ALC: NOT OF ICE	CALCACACAC	opposite the state	A CONTRACTOR		
KW182330 1-10-680 Wallowhis brachutes	ALC: NOT	COLLEGE ADAGE	and the second	A CHARTER		
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HUSDBER T. AT THE PUP PLYAS HUGDES		- Change				
metreroy, 1:91-794 Dechriophie teeniurus		C. C. C. A.				
DUPVELSE 1.91-796_OFCHELOPISE_EBENIUEUS_GEADOWSK		COLUMN STORAG		AT BAUMA		A CONTRACTOR OF A
REsearch 1:91-794_Orthriophis_taeniurus	ACTIVE	ACCOUNT ON A		ATTACEA	CALC THE	
WYT228648 T: AD- LAS HAdrobura Distances	CTUAT	GENCINGTGAAD	GERCANACAAE	REACTORNEY	CONCERN.	ACACELAEAAAA
#T966115.1:70-767_Hydrophia_platurus	CTUATU	GENCINGTIGAAB	OT CAMACANT	REACHDONE	ACCARCELA	INCOUTOATAAADT
KT966116.1:49-746_Hydrophis_platurus	CTUATO	GCACINGTGAAS	OTE CALACIANT	SEACHCORD	RECARCEEA)	ACACTERTARAS
MNSE6306.1:103-800_Hydrophis_platurus	CTUATO	GENCINGTGAAS	UTTCAMACAN T	A CHCOSC	CHARLEDA.	ACACTGATAAAAT
MN886307.1:103-800_Nydrophis_platurus	CTATO	GCACAGTGAAG	GTTCANACAAT	REACTORES	ACCARCCE	TACACT GATAAAAT
MN886308.1:103-800_Hydrophis_platurus	CTUAT	GCACAGTGAAG	UTICARACAAT	ACCOSC	ACCANCE HAS	ACACTGATAAAAT
MT966127.1:85-782_Hydrophis_stokes11	CCOGTO	GCACAATGAAG	GTICANACANC	EEVCECCEC	ACCARCELA	ACACTUATAAAAT
JQ217201.1:79-768_Hydrophis_stokesii	CCOAT	GCACHATGAAS	OT TOARACAAC	SEACEC690	ACCANCER	ACACTGATAAAAT
EC014431.1:77-777_Hydrophis_obscurus	CLEATE	GEACHATGAAS	CTTCANAGAAG	CEACECCEC	ACCAACCES	ACACTCATAAAAT
KT966054.1:79-779_Nydrophis_caerulescens	CCHATE	ACACINGTIGAAS	GTECABACRAC	GACECCE	ACCARCERA	ACACTGATAAAAT
J0217208 1:79-779 Rydrophis caerulescens	CCATE	ACACAGTIGAAG	GTTCANACAAC	CACHCOSC	ACCARCERA	ACACTGATAAAAT
KY206890.1:10-710 Gerarda prevostiana	CALAC	TEATAACGAAG	GOLCTAGONA	ACAMPA	ACCALCTON	ATATTCATATAT
KY206891 1:19-719 Gerarda prevostiana	CALAC	TONTALCGAR	GETCTAGEAAS	BOAC BACKA	ACCARCTON	ATATT GATAAAA
EF195916 1 50-750 Gerards prevostians	CANACH	TONTRACIAND	OCT CTAGENAR	A DACEASIA	And Address	AT BUT DATE AS A AT
KX694852 1:1-704 Cantoria vislacea	ATAC	ACRETICACI	dan ochorna.	SGAC BACK	Machine Service	TTTTTTTTTTTTTTT
##395897 1-50-753 Cantoria violance	AT	A CONTRACTOR OF	Ranger Bair Main		The Work of the	THE REPORT OF
WERSTON 1.62-747 Hemployels humple	000000	A STATISTICS IN COMPANY	and and a state			State - Although the second
Magazia 1.62-147 Homelopsis Lucrate	10.00	- Contraction	A DESCRIPTION OF THE OWNER OF THE			
Mission 1.41-242 Real		THE REAL				A CONTRACT OF A
MISCHICK, 1:51-147_HOMELOPEIS_BUCCETE		CUAAH	THE REAL PROPERTY OF	C. C. C.	Contraction of the second	
MINU2/03.1:61-747_HomeLopsis_buccata	CCBCCB	- ATMACGAAR	THE LEAGERAN	C. C. CALCER	C C C C C	A CALCUARAAA
MTSU2658.1:50-753_Cerberus_rynchops	CCETCE	TATGALT	COLUMN STATES	COMAGEC	THEFT	INCRUTE GACKARDE
AF471092.1:91-794 Cerberus_rynchops	CONTON	CATATGAAS	UCT TAGTAAC	CCC ALOSC	TACCUT	ACANTGACAAAAT
EF395900.1:50=753_Cerberus_rynchops	CCBCCB	CHATGAAD	UCTOTAGTAAC	CTHAGEC	A CARCCEC	ATATITCATAAAAT
EF395901.1:50-753_Cerberus_rynchops	CCUTCH	CONTRATGANE	UCTUTNUTARC	CCC GGEC	CANCERC	ATATT GATAAAAT
EX694850.1:1-634_Cerberus_rynchops	COTTO	COACHATGAAT	GTTCTAGTAAC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACCANCER	ATATTCATAAADT
MT802717.1:1-670_Hypsiscopus_plumbea	CTRACE	CALACALAS	GTTCANGICAAD	CAC TODA	ACCARCTER	ATATTGACAAANT
JX463014.1:50-753_Enhydris_dussumieri	CCTTC	TATACAAA	OCTOTAGCAAC	CCCACEA	ACTANCTON	ATACCOATAAAAT
JX463015.1:50-753 Enhydrie dossumieri	CONTON	TALACALAN	OCTOTAGOA AN	CCC RAODA	ACTANCTON	ATACCONTAND
LC105625.1:59-763 Enhydris enhydris	cic cic	CONCEACIONAG	GATCTAGCALC	ACTOR	ACT ALC: THE	ATAZCOACAAA
MT802681.1:50-753 Enhydris enhydris	CC CC	CONCRACCAN	GETETNOCANC	CACTORE	ACTANCTOT	ATATICOACAAAA
MT802683.1:50-753 Enhydria anhydria	cic eco	CONCRACCAL	CAL OT DO	CAC NOR	ACT ADD TO THE	Define the state
LC105627.1:132-835 Enhydris enhydris	CONCE	CONCRACIGASIO	AUTOCIA	A A A A A A A A A A A A A A A A A A A	AGT MACT ST	Transfer of the second second
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MG653605.1:75-778 Sinomicrurus macclellandi	THE	TTTHACK	BC BATT	TTTTTT	Antes	TACACE	3300	ACCACCUTTA	SCOTOTCAC.
MCC02973 1:76-779 Penmonhis schokari	-			TTCCTAC		CACAC	1.1.1	TTAACCATTA	ASHCHCCAC
MCCORES 1.76-770 Beamschie schokari		State State		A REPORT OF	1.6	C. M. C. A. C.		WHERE PARTY AND	as a close
Massager 1.76-779 Beamwohls schoker	100	1120		Descont.cl	ACE.	C. C. C. C.	17.16	AND A COMPANY	A A DECEMP
Metta 201.1.10-112_Familiophia_schokari		and the second	BOH LI	A S COL ENGLISH		a shake	22.5	THE REPORT	ALL DE COME
Massage 1, 1, 10-110_Feamoonis_schokers		11100	Part and a	THE COLUMN COLUMN	101	ALC: NO. OF THE OWNER.	222.	A DESCRIPTION OF THE OWNER OWNER OF THE OWNER OWNER OF THE OWNER O	a shares a
MGGGGGGG, 1: 76-776_FRAMPOPN18_BCNOK811			100	TTLLTAL	10	CONCERCE OF		TTAALLATLA	GARGE CAC
Moon 2018.1: 18-118_Feannophis_schokari	Carter	TTC: ACC	CONTRACT OF	ATTCUTACA	요산문	CACAC	AA24	TIMACEATEA	GALCHUCAC
MUDU2970.1:76-776_PEANNODRIS_SCHOKAF1	CIERN	X T C P ALL	14	ACTOCYACA	202	CACACI	0030	TTAACCATCA	GALICICAC
MUUU3010.1: /6-//6_PSAMNOPALS_SCHOKAT1	CHEA	11CH CC		TTOCTACE	100	CACACI	AATA	THANCEATEA	GALCHCCAC
MOUD3017.1:16-776_Psammophis_Bdbokari	CARA	TICHICK		TTCCTACK	200	CACAC	AATA	TTAACCATCA	GARCICCAC
MG003011.1:76-776_Psammophis_schokar1	CHEA	TTCENCE	A TT	ATTCCTACE.	ALC: N	CACAC	AATA	TTAACCATCA	GARCICCAC
MG002984.1:76-776_Psannophis_schokari	COCA	TTCHICK	14 17	ATICCTACA	지지다	CACACH	AATA	TTAACCATCA	GARCECCAC
MG003005.1:76-775_Psamnophis_schokari	CECA	TTCCACC	TAL TI	TICCIACA	Aab	CACAC	AATA	TTAACCATCA	GALICHCICAC
MG003008.1:76-776_Psannophis_schokari	CECA	TTCEACE	ALAT	ATTCCTACK	A851	CACACE	BATE	TTAACCATCA	GARCICCAC
MG003002.1:76-776_Psannophis_schokari	CERA	TTCHACK	AL TT	TTTCCTACH		CACACH	AATH	TTAACCATCA	GARCICCAC
MG002977.1:76-776_Psampophis_schokari	CINCA	TTCCAC	ALC: TT	ATTCCTACA	ALC: N	CACAC	A.A.71	TTAACCATEA	GANCINCAC
MG003004.1:76-776_Psannophis_schokari	CEREN	TTOPACE	A TT	TTTCCTACK	AAG	CACAC	AATA	TTAACCATCA	GUICHCCAC
AF471031.1:91-794_Psawnodynastes_pulverulentus	THE	TTCEACE	HAL IC:	CICCOCTO	A D	CACAC	TOTAL	CTTACCTCAC	ACHTICAAC
ME475935.1:37=729_Rhabdophis_bindi	CINA	TTCHALL		CTCACAC	100	TTTT	AATA	TTAACTATTA	ATHTICTGC
MR530545.1:66+758_Rhabdophis_himsisyanus	CHEA	TTCHICK	Sense:	CTUTAAL		TTTCC	2020	TTAGCTATTA	AAHCICCAC
KF200929.1:60-747_Rhabdophis_himalsyanus	CLERK	TTCHACE		CTOCARCE	신다보	TTTCL	AATA	TTATCTGTTA	AAHCICCAC
MWW93850.1:11-713_Herpetoreas_xenura	C C C C C C C C C C C C C C C C C C C	STORAGE STOR		CICACATA	100	TATAL	CCT	CITER CITA TAA	ANGULTAT
MN393851.1:59-761_Herpetoreas_Menura	Clean	IIC HC		CTCACATA	100	TATAC	CCY	CTTACTATAA	AADCINCTAT
MN993852.1:57-759_Herpecoreas_wenura	CINA	TIC NO	14 19	CICACAT	100	TATAC	CCI	CITACIATAA	AAUCICIAT
NC347455.1:102-794_AhaeCulla_hasuta	CORD	TICHLOR		CICATACI	100	COCCC	TATE	CTAACTATIT	AAUCICCAC
MK595/96.1:83*785_Absetulia_laudankia	CHEA	TTC COLOR		CTCATAC	100	COCCE	AATA	CTAACTATIT	AADCINCTAC
MNV43272.1:65-765_PistyCeps_ladacensis	- BOAN	LICENCE	C C	CICCTATA		CACCIC	1024	TIGACAATCA	ART CAT
Maiszons, 1:85-775_Gonyonoma_prasinum	C. State	11100	Contract in	TICTCACH	APT	TATCC	ALTA	LITACUTTA	ALUCICICI
PERSONAL 1.81 784 Photo President	- Mark			TELECAL	1.1	TATC: D	100	CALCUTIN	ALCOLTCT
Areeves, 1:91-794 Rhadinophis frenatus	- HARA	THE REAL PROPERTY IN		CTUCTAC	1.1	ATA U	COL	CHEACCATCA	CLOCK CAC
Surveying 1.91-796 wonyosoma frenatum	- HOA	TACK CONCERNING	E Hard	CTOCTAC	1.1	TAL AL	COL	CACCATCA	ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
RF669230 1:91-794 Rhadinophis frenatus	CHARA	TCCCACC	C AC	CTOCTACK	AP	TATACI	0.070	CICACEATCA	ACOCICCAC
byFurire.1.92-796_Coelognathus_helena	C C C A	SECTOR	Contraction of the second	CTOCTACE	1.0	CACCC	0.024	TTAACCATTA	AATTCCCCT
DC902121.1:104-794 Coelognathus_radiatus	CERA	TTTELCE		CICCTATA	AP-	CACOCH	AATA	CTTACTATTA	AAUTICACT
EC347466.1:94-782_Bolga_beddome1	THEA	TECHNOL		CTOCTAC	A P	CACCC	CAT	CTGACAATCC	GALTICCAC
MT733294.1:44-734_Bolga_beddome1	Colora	TTCHACE		CICCOC	AA9	CATAC	AATA	TTAACCATCC	AAATACCAC
MT733292.1:44-734_Bolgs_beddome1	Clean	TTCEACE	A C	CTOCCACE	140	CATAC	AATA	TTAACCATCC	AAHTICCAC
MT733290.1:44-734_Bolga_beddome1	CELEA	TTCCACE		ACT OCCACA	242	CATAC	AATA	TTAACCATCC	AAUTICICAC
MT733291.1:44-734_Boiga_beddomei	CEGA	TTCEACE	CALCO	CTOCACA	240	CATAC	AATA	TTAACCATCC	ARTTICCAC
MW111469.1:76-779_Lycodon_septentrionalis	THER	TTTEACE	ALC:	CTCCCATA	AP	CATTCH	AATA	CTAACCATCA	ATHANCCAC
MW111468.1:75=775_Lycodon_fasciatus	CEEC	TTCCACE	CC AC	ACTUTCATA	AAG	CACCC	AATA	CTAACCACTA	ACTANCET
RC010366.1:91=791_Lycodon_fasciatus	CEC	TTTCACE		ACTOCACA	AAD	CNCCC	AATA	ATAACTATTA	ATTACCCT
MT625862.1:58-758_Lycodon_fasciatus	CECC	TTTEACE		RETUCCACA	지지다	CACCC	AATA	GTAACTATTA	ATTACCCT
MW111467.1:75-775_Lycodon_fasciatus	CEEC	TTTEACE	CCL VC	CICCUCACA	AAG	CACCC	8.8,T.8	ATAACTATCA	ATTACCCT
EC010368.1:92-794_Lycodon_lacensis	CCCA	TTCEACE	CATIC	ACTOCTACA	AAG.	CACCA	9.9.2.9	CTAACACTAA	ACTANCACT
#C010370.1:92-791_Lycodon_lacensis	CEGN	TTCCAC	ON THE	CTOCTACE	APR	CACCA	A.A.T.A	CTARCACTAR	ACTACACT
EX822579.1:72-772_UNVERIFIED:_Lycodon_subcinctu	s CCCA	TTCCAC	CATATO	ACTOCTACA	100	CACTO	AATA	TTAACCATTA	ACCALCCT
MT625846.1:58-758_Lycodon_subcinctus	TEEC	TTOCACE	CATATO	ACTOCTACA	900	CACCC	A A 7 A	TTCACTATIA	ATTACCCT
MT625859.1:58-758_Lycodon_subcinctus	THEC	TTOCACE	CAL TI	ACTOCTACA	2 60)	CVCCC	AATA	TTCACTATTA	ATTACCCT
<pre>%C733203.1:76=776_Lycodon_subcinctus</pre>	TEEC	TTCCACE	CATAT	ACTOCTACA	A60.	CACCC	AATA	TTCACTATTA	ATTARCCCT
LC105630.1:21-724_Coelognathus_flavolineatus	CCCA	TTTCACC	CENC	ACTOTTATA	AAG	CACCC	AATA	CTANTIATIA	AAUARCICAC
DQ902128.1:92-788_Coelognathus_flavolineatus	CECA	TTCCACC	de la	ACTOTTACA	220	CACCT	AATA	CTAACCATTA	AABCECTAT
DQ902134.1:91-791_Elaphe_bella	TECA	TTTCACE	TATAT	CTOCTACA	AAD	TATOO	AATA	CTAACCACTA	AABCACTTT
<pre>KF669231.1:89-778_Euprepiophis_mandarinus</pre>	TEEA	TICENCE	ALC:	CTCTCACE	ALC: N	CATCC	CATA	CTAACTGITA	AAUTICCAC
KF669228.1:92=785_Euprepiophis_mandarinus	TEEA	TTCCCC	CALC:	ACTUTCACA	지지다	CATCICE	AATA	CTARCTATTA	AAHTICCAT
MIC20426.1:69-772_Coronella_bracbyura	TCCA	TTCERCE		ACTOCACA CA	AAG	CATAC	AATA	CTAACAATCA	AABABCCAC
KN782330.1:10-690_Wallophis_brachyura	TCCA	TTCEACE	oct oct	ACTOCACA	시시다.	CATACE	AATA	CTRACARTCA	AABACCAC
AY611998.1:99-794_Ptyas_mucosus	TEEA	TTTEACE	CAL SCI	ACTOTOACA	AAG	TATOCH	AATA	TTAACCCTAT	AANTINCTAT
LC105628.1:114-809_Ptyas_mucosa	TEEG	TTTCACE	ALC:	ACTOTOACE	APE	TATOCH	AA76	CTARCCCTAT	AABTECCAT
EFC76709.1:91-794_Orthriophis_taeniurus	COGY	TTATE	CALC:	ACTOACATA	A NO	CATATI	AATA	CTARCEATER	ACTANCERC
DQ902132.1:91-794_Orthriophis_taeniurus_grabows	K CLEW	TTCHATS	ALC:	ACTOACATA	140	CATACE	A.A.T.A	CTGACTATIA	ACTACICAT
<pre>KF669249.1:91-794_Orthriophis_taeniurus</pre>	CEGV	TTCENTE	ALC:	CTCACATA	AAG.	CATAC	AATA	CTGACTATTA	ACTANCIAT
XX239646.1:95-792_Hydrophis_platurus	CEEA	TECHNOR	CAL ACT	CICATATA	AAC.	TOCCT	AATA	ATCACTACCA	AAUTICTCC
RT966115.1:70-767_Hydrophis_platurus	CEEA	TICENCE	18 10	GTCATATA	220	TACCT	AATA	ATCACTGCCA	AANTICTOC
KT966116.1:49-746_Hydrophis_platurus	CIRCUN	TTCCCC	CALC: NO	CTCATAT	201	TOCOT	AATA	ATCACTGCCA	AAUTHCIGC
AMARCONG. 1:103-800_Hydrophis_platurus	- HEAL	A CONTRACTOR	A C	CTUATAT	ALC: N	TOUCT	1034	ATCALTGCCA	ARTICIEC
www.secore 1.103-sou sudarable platurus	100			ATAT	1	THUCKER P	100	ANDACTOCCA	A A B C T GC
evecting 1. et. 765 Markaronia statutus		ALC: NO.	Hard I	CT CATAIN	1,12	COLCUTE .	1000	A THACEGUCA	L L L L L L L L L L L L L L L L L L L
ALFORNATION TO THE MANAGEMENT ALE AND A		1.1.1	Contraction of the	CHARTER THE	1.1	decer	222	ATTACT ACCT	CCTC
MCG14431 3.72-372 Hadrochia abaasaa	- Hann			CHARTER STATE	1.1	ALC: NOT THE OWNER	172	A THE R OWNER WATER	A A DOT
TTREADSA 1-79-779 Badrochia contrilances	- 198	TTOMA		Circle Barris	A. 15	CACCE		And a come work	A A BOOM
J0217208 1:79-779 Redrochis contributions	C COL	TTCHICK	GALLES	CTCATAT	Gla	CACCIE		ATCACELTCH	A A BOAR
EV206990 1:10-710 Gerards preventians		CON STATE		ICACCOLT.	1216	7172	692 B	CTARCOTTR	111000000
EV206001 1 10-710 Gerards prevotians	100			L'ACCCAT.	126	The state	12.56	PERSONAL PROPERTY.	A A DO COTO
FF195916 1 50-750 Gerards provostians	-	142		CACCOAT		TATAC	A	CTASCOLTES	AANCHCCTC
Ex696852 1:1-704 Cantoria utalacea	C C C	1 1 1 1 1 1 1 1	Contraction Contraction	ACTOCALTA	No. H	CACAL	A	TO A A COLO TIME	AADT
#F195997 1.50-753 Cantoria violanea	-			CTOCTATI		dalcalo.	11-6	TTARCOSTRA	A A Delice PC
MT802706 1:62-747 Honalousia huccata	COL	TT	Cont-1	CAGCOLO	A-L	TATAT	AA-1	CTAACCOTCA	Actichesee
MT802711 1 62-747 Homelonsis buccata				CACCAT		TLTAT	11-1	CTAACCOTCA	AFRENCATO
MTSC2704 1:61-747 Romaloguia buccate	Chica	117.00-0	- 10- E	AGCOL	A. 1	CATAC	AAT	CTARCCATTR	ACHERCATE
MT802703.1:61-747 Romaloguia buccata	Children	117 104-1	Cici Ci	TARCOL	La La	CATAL	AA-B	CTARCOUTES	ACHTRATE
MTR02658 1:50-753 Cerberus rynchons	THE	TTC	CC T	CACCAC	LA.	CATAC	AATE	CTABCCATCA	A ANCHORE
AF471092 1:91-794 Cerberus rynchops	THEFT	TTCMA	Contraction of the	CACCORC	U.C.	CATA	2275	CTARCENTER	AANCH COTC
EF395900.1:50-753 Cerberus rynchops	COOR	TTC	TINT	CACCACO	AAL	CATAC	AATE	TTAACCATTA	AABCOCCTC
EF395901.1:50-753 Cerberus rynchops	CIDEA	TTC	Coc Dog	CACCACA	AAL	CATAC	AATA	TTAACCATTA	AABCRECTC
EX694850 1:1-654 Cerbergs rynchops	CCCA	TTCALC	CCTAT	CACCOLC	AF	CATAC	AATE	TTAACCATTA	AAACACCTC
MT802717.1:1-670 Hypsiscopus plumbea	CEER	TTCAAC	GALINC	CACCOAT	AAR	CATAT	AATA	CTAACAATCA	AABCACCCT
JX463014.1:50-753 Ephydrie dussumieri	COGA	CITCAT	CATAC	OCTOCTACE	Age	TACAC	CAT	CTARCCATTA	AARCOCCTC
JX463015.1:50-753 Enhydris dussumieri	CORA	CTTONT	CATAC	ACTOCTACA	A a l	TACAC	CATE	CTAACCATTA	AABCOCCTC
LC105625.1:59-763 Enhydria enhydria	COOT	TTCBACK	och och	CT CCCAC	1.11	CATAT	TATE	CTAACTATTA	AABABCACT
MT802681.1:50-753 Enhydris enhydris	COOT	TTCCAC	CC C	CTCCCACA	AL	CATAT	TAT	CTAACTATTA	AAGACACT
MT802683.1:50-753_Enhydris_enhydris	CORT	TTCCAC	CCLC	ACTOCCACE	AAL	CATAT	TAT	CTAACTATTA	AABARCACT
LC105627.1:132-835_Enhydris_enhydris	COGT	TTCCAC	CCTAC	ACTOCCACE	AA	CATATA	TATE	CTARCTATTA	AADACACT
LC105626.1:126-829_Enhydris_enhydris	COOT	TTCARC	GCERC	TTOCCACK	AAD	CATATA	TATE	CTAACTATTA	AADABCACT
	-					-			

	aa	610	6.2 (0	630	440	620	
MG653605.1:75-778_Sinomicrurus_macclellandi	ACTAT	CATTAN	COATCAT	TACA	AG TC AT	TATAS	CATAGAACT	GT SHA
MG002968.1:76-779_Psammophis_schokari	ACTAT	CACAR	CADATCAT	CTOC	AGACTAC	TARTER	CAGAAAAT	TOT CARA
MG002967.1:76-779_Paannophis_schokari	ACTAT	CACAA	CARATCAT	CTOC	AGICTAC	TAATEAS	CAGAAAATT	
MG003028.1:76-776_Psamophis_schokari	ACTAT	CGCAA	CADATCAT	CTCC	AGATTAC	CARCERC	TTANANTT	TOTOAAA
MG003026.1:76-776_Psammophis_schokari	ACTAT	GCAA	CADATCAT	C7 C	AG CT AC	CARCERC	CAGAAAATT	TOTAL
MGC02970.1:76-776 Psamophis schokari	AATAT	OCCAN	CADATCAT	CTOC	AG T AC	CANCOAG	COTABAATT	TOTCAAL
M0003017.1:76-776_Psannophis_schokari	AATAT	OCAN	CADATCAT	CTOC	CAGACTTACT	CANCURC	CONTRACT	TOTOANA
MCC03011.1:76-776_Fsammophis_schokari MC002984 1-76-776 Psammophis_schokari	AATAT	COCALL	CADATCAT	CTCC	AGACT AC		CAURAA ATT	
MG003005.1:76-776_Psannophis_schokari	AATAT	GCAAL	CADATCAT	CTCC	AGACTAC	CAACUAC	CAGAAAATT	TCTCARA
MG003008.1:76-776_Paannophis_schokari MG003002_1-76-776_Paannophis_schokari	AATAT	CGCAL	CAMATCAT	CTCC	AGRETIAC		CACADA ATT	
MG002977.1:76-776_Psamophis_schokari	AATAT	GCAA	CADATCAT	CTOC	AGACT AC	CAACGAC	CAGADAATT	CTCARA
MG003004 1:76-776 Psannophis_schokari	AATAT	COCAL	CALATCAT	CTOC	AGOTAC	CANCERC	CAGADAATT	
ME476936.1:37-729_Rhabdophis_bindi	CCTAT	CCTAAL	CADATCAT	TTAC	CG TA A	EAAEGAE	CAUNCANES	TOT BAL
MR530545.1:66-750_Rhabdophis_himalayanus	TCTAT	OCTAIAN	CADATCAT	CAAC	CGTATAT	C C C	CACACACT	
MN993850.1:71-773 Herpetoreas senura	TTTAT	TATCA	CT ATCAT	CTCA	AG CA AT	CARCOLO	CAGAAAACT	TOTORA
MN993851.1:59-761_Herpetoreas_xenura	TTTAT	TATCA	CTRATCAT	CTCA	KG CA AT	CAACCAC	CASAAACT	DOT CANA
KC347453.1:102-794 Ahaetulla nasuta	CATAT	CACAA	ATCAT	TACC	AA CA TT			CH ALL
MK595796.1:83-783_Ahaetulla_Iaudankia	AATAT	ATAN	TATATCAT	TACC	CAANCATCTT	CARCING	COMMANCE	TOTOAAA
MH043272.1:85-785_Platyceps_ladadensis ME322863.1:85-775 Gonvosces prasinum	CATAT	TACCAR	TABATCAT	TACC	AGLICIGI		CACAGA ACT	
ME322864.1:85-775_Gonyosoma_prasinum	TACAC	TATCA	TACATCAT	TACC	CAAACATAT	CAACGAC	CAGAGAST	TOTTARA
KF669246.1:91-794_Rhadinophis_frenatus	CATAT	TACTAC	CABATCAT	TACT	CG TATAT		C C C ANA A CT	
EP669250.1:91-794_Rhadinophis_frenatus	CATAT	TACTA	CARATCAT	TACT	TG TATAT	TANAGAC	CTGANAACT	TTCAAA
DQ902112.1:92-794_Coelognathus_helena	AACCC	CATTA	CADATTCT	CACC	NANTACT	CAATOAS	CONTRACTOR	
EC147466.1:94-792_Boiga_beddomei	AATAT	CATTA	CALATCAT	CACC	AGACATT	TAXE ALS	CAGARANCE	TOTOARA
MT733294.1:44-734_Boiga_beddomei	AATAT	CATCAL	TADATCAT	CACC	CARCE OF	TANCONC	CADAAAACT	TOT TAA A
MT733292.1:44-734_Boiga_beddome1 MT733290.1:44-734_Boiga_beddome1	AATAT	TATTA	TABATCAT	CACC	A			101 - AAA
MT733291.1:44-734_Boiga_beddomei	AATAT	TATTA	TADATCAT	CACC	CARCATCT	TAACOAC	COLGARAACT'	TOTCAAA
MW111469.1:76-779_Lycodon_septentrionalis	AATAT	CATTAC	TAHATCAT	CACC	AA CALCT		CACADA ACT	TICT CARA
#C010366.1:91=791_Lycodon_fasciatus	AATAT	CACCA	TADATCAT	TACC	AACATAT	CAATGAC	COAGAAAACT	CT CAAA
MT625862.1:58-758_Lycodon_fasciatus	AATAT	CACCA	TATATCAT	TACC	AACATAC	CAATCAC	CACARAACT	TO DUARA
EC010368.1:92-794_Lycodon_lacensis	GATAT	ATTA	CADATCAT	TTAC	CALCATTO	TAATGAC	CADADANCT	TOTIAAA
#C010370.1:92-791_Lycodon_lacensis	AATAT	CATTAN	CADATCAT	TTAC	CAA CA TT	TAATTAS	CARAAACT	TOTOAAA
MT625846.1:58-758 Lycodon subcinctus	AATAC	CACTAC	CANARCAT	CACC	AA A T	CAR CAR		TOT CAA
MT625859.1:58-758_Lycodon_subcinctus	AATAT	CACTA	CARACAT	CACC	CAACATTEE	CANTCAC	CAGAGAACT	TOTCARA
EC733203.1:76-776_Lycodon_subcinctus LC105630 1:21-724 Comlognations flavolineatus	CCTGT	CACTAN	CARAACAC	CACC	AA TO OT			
DQ902128.1:92-788_Coelognathus_flavolineatus	CCTAT	CTCTA	TADATCAT	CACC	AATGTGT	TAACGAC	CAGAMANCT	TOTCARA
DQ902134.1:91-791_Elaphe_bella EF669231_1:89-778 Europeniophis mandarinus	ACTAT	CATCO	TADATCAT	TACC	AACA	T C C C		TOT DAA
KF669228.1:92-785_Euprepiophis_mandarinus	ACTAT	CACAS	CADAACAT	CACC	AAACATCT	TANTONC	CAGAGAA	TCTCANA
MIC20426.1:69-772_Coronella_brachyura	ACTAT	CATAA	TABATCTT	CCAC	GGACALGT	CARCERC		
AY611998.1:99-794_Ptyss_mucosus	AATAT	TACTA	TABAGCAT	CACC	AA TATGT	TANTONO	TTANANTA	POTCARA
LC105628.1:114-809_Ptyas_mucosa	AATAT	TACTA	TABAGCAT	CACC	AAACATATT	TAATGAC	CACAAAATT	TOTOAAA
DC902132.1:91-794 Orthriophis taeniurus grabowsk	AATAT	CATTA	TABATCOT	CATC	NA TA CT	TANTONO	CTGANANCT	TOTCARA
KF669249.1:91-794_Orthriophis_taeniurus	AATAT	CATTAN	TADATCOT	CATC	AAATA CTT	TAATGAC	COTOANAACT	TOTCAAA
#X239646.1:95-792_Hydrophis_platurus #T966115_1-70-767_Hydrophis_platurus	CATAC	ATCAL	TABATOTT	TACA	CA CC CT		CALLAR AND	
KT966116.1:49-746_Hydrophis_platurus	CATAC	ATCA	TADATCTT	TACA	CALCOTOT	CANTURC	CAGAAAACT	UCTOCAA
MN886306.1:103-800_Hydrophis_platurus	CATAC	CATCAR	TABATCTT	TACA	CALCCIGT		CAGARIA CT	
MN886308.1:103-800_Hydrophis_platurus	CATAC	CATCA	TADATCTT	TACA	CALCO	CAATGAC	CAGADAACT	TOTOCAA
NT966127.1:85-782 Hydrophis_stokesii 20217201 1:79-768 Hydrophis_stokesii	TATAC	TATTA	TABATCTT	TTCA	CALCOLUTI	CARECAC	CACANA ACT	
EC014431.1:77-777_Hydrophis_obscurus	TATAC	ATCA	TADATCTT	TATA	CANCCTAT	CAATGAC	CAGAGAACT	TCTCCAR
RT966054.1:79-779_Nydrophis_caerulescens	CACAC	CATCAR	TABATOTT	TACA	CALCORT	CARTING	CACAGAS	
KY206890.1:10-710 Gerards prevostians	AATTT	TCTCA	CANATCAC	CTCA	AG TC AT	c c	GANANT	TOTOLAN
KY206891.1:19-719 Gerarda prevostiana	AATTT	TCTCA	CANATCAC	CTCA	AGTCAT	e verve	GGANANCT	TOT CAAA
KX694852.1:1-704 Cantoria violacea	AATTT	OCTTAN	CALATCAC	TTCA	NG CC A		CAUADA AUT	
EF395897.1:50-753_Cantoria_violacea	AATTT	OCTTAN	CALATCAT	TTCA	CAGACCTATE	CAACGAC	CAGAAAACT	TOTOAAA
MT802706.1:62-747_Homalopsis_buccata	AATTT	OCTCAR	TABATCAT	CTCA	AGACCIGT			
MTS02704.1:61-747_Homalopsis_buccata	AATTT	TCTCAR	TADTATA	CTCA	CAGACITIAT	TAACOAC	CACAAAACT	TOTOARA
MTE02703.1:61-747_Homalopsis_buccata	AATTT	TCTCAR	CADATCAT	CTCA	CAGNCT TATE	TAACCAC	CAGANAACT	
AF471092.1:91-794_Cerberus_rynchops	AATCT	CCTCA	ATCAT	TACA	CAGACCTAT	TANTON	CABAMAACT	TOTOBAL
EF395900.1:50+753_Cerberus_rynchopa	AATTI	CCTCA	TATATCAT	TATA	AGACCIGT.	TATAC	CACARAAT	I I I AAA
KX696850.1:1-654_Cerberus_rynchops	AATTT	OCTCAR	TATATCAT	TACA	AGACIC IA	TAXTORS	CASAAAAT	TOTCALL
MT802717.1:1-670_Hypsiscopus_plumbes	AATAT	TCTTA	CALAACCT	AACG	AG CC AT	CAACOAC	CASAAAAC	TTTCAL
JX463015.1:50-753 Enhydris doseumieri	AATTT	ATAA	TALAACCT	CTCC	AGA CHA	CAN CHAR	- N	NOT ON
LC105625.1:59-763_Enhydris_enhydris	AATTT	CTTA	CALATCOT	CTCA	CAGACTTAT	TAACOAC	COMPANANCT	TOTOTAA
MT802681.1:50-753_Enhydris_enhydris MT802683.1:50-753 Enhydris_enhydris	AATTT	CCTTAN	CANATOCT	CTCA	A CALL			TOTO AA
LC105627.1:132-835_Enhydris_wnhydris	AATTT	OCTTAN	CALATCOT	CTICA	CAGACITIAT	TAACOAC	CROADAACT	TOTOTAA
LC105626.1:126-829_Enhydris_enhydris	AATTT	CTTAG	CABATCCT	CTCA	BAG OTBAT	TANCEAC	CAGADAAST	DOLLERAN.

		660	670	680	690 700
MG653605.1	:75-778_Sinomicrurus_macclellandi	AGECAN	CACHAGTT	CACC.	CCRACATATTAAACCAGAATGATA
MQ002973.1	:76-779_Psamnophis_schokari	ADDOAA	SCAREAGTCA	G- 25	ACAACACATCAAACCTCAATCATA
MG002968.1	:76-779_Fsammophis_schokari	ADDCAR	AAHAGTCH	고신감자	ACRACACATCAAACCTGAGTGATA
MG002967.1	:75-779_Psamnophis_schokari	ACCOL	AAHAGTCA	2.22	ACAACACATCAAACCTGAGTGATA
MCD03027.1	76-776 Paamophis schokari		Con Agente Total		ACASCACATCASACCTUSATC
MG003026.1	:76-776 Pearmophis schokari	alter	A A A DA GTOL	alte a	ACRACACATCARACCTGRATG
MG002970.1	76-776 Psamnophis schokari	ADDCAA	CANDAGTON	dicd	ACARCACATCARACCTGARTG.
MG003010.1	76-776 Psawnophis schokari	AGCCAA	CEALBAGTCA	CACC	ACAACACATCAAACCTGAATG
MG003017.1	176-776_Psannophis_schokari	AGCCAA	COANTAGTO	CACC.	ACAACACATCAAACCTGAATG
MG003011.1	:76-776_Psannophis_schokari	AGCCAA	CAABAUTCA	CACC	ACAACACATCAAACCTGAATG.
MC002984.1	:76-776_Psannophis_schokari	ADDCAR	CAABAGTCA	CACC	ACRACACATCAAACCTGAATG.
MG003005.1	:76-776_Psannophis_schokari	AGGCAA	AABAGTCA	CACE	ACAACACATCAAACCTGAATG
MG003008.1	:76-776_Psamnophis_schokari	ACCELLA	AAHAGTC	1.1	ACAACACATCAAACCTGAATG
MCC02977 1	16-776 Parmophis schokari		A ANALGUE	2.63	ACARCACATURARCCTURETU
MC003004 1	76-775 Pressophia schokari		A A DA OTON		ACARCALATICARACLETURATU.
AF471011.1	91-794 Psampodynastes pulverulentus	APTHEND	AARADTCH	died	ACAACACATCAAGCCAGAATGATA
ME476936.1	:37-729 Rhabdophis bindi	ALCONA	AAGTAA	CLCC	ACAACATATTAAGCCAGAATG
MR530545.1	:66-758_Rhabdophis_himalayanus	AGCTAR	CALBAGTAN	GACC	ACRACACATTARGCCAGRATG
KF200929.1	:60-747_Rhabdophis_himalayanus	AGETAA	COANTAGTAN	GACC.	ACAACACAT TAAGCCAGA
MN993850.1	:71-773_Herpetoreas_xenura	AGECAA	CEATERGTAN	GAGG	ACAACACAT CAAACCAGAGTGATA
MN993851.1	:59-761_Herpetoreas_xenura	ABLCARK	ATBAGTA	6-86	ACAACACATCAAACCAGAGTGATA
MN993852.1	157-759_Herpetoreas_wenura	A DECAR	ATHAUTA	경수법의	ACAACACATCAAACCAGAGTGATA
NC347455.1	22-799 Anastulla_nasuta		CCHOUTAN	1.11	ACAGCACATTARACCAGAGTGATA
MUG43033 1	25-795 Anseculia_leusancia		A REAL PROPERTY.	8.68	ACARCATATITARACCAUARIG
ME322863 1	185-775 Gonvosoma prasinum	Girld-Int.	GANACTAL	64.8F	ACAACACATTAGACCAGAATCATA
M2322864 1	:85-775 Gonyosoma prasinum	COLUMN.	GARACTA	CALC P.	ACAACACATTAAACCAGAATCATA
XF669246 1	91-794 Rhadinophis frenatus	AGOCAN	CEACEAGTAN	CACC	TCAACACAT TAAACCAGAATGATA
DQ902110.1	:91-794_Gonyosoms_frematum	AGCCAA	CACEAGTAN	CACC	TCAACACAT TAAACCAGAATGATA
RF669250.1	:91-794_Rhadinophis_frenatus	AGCCAA	AGRAGIA	GADE	TCAACACAT TAAACCAGAATGATA
00902112.1	:92-794_Coelognathus_helena	GOCCAR	COCTENSIAN	GAEG	ACARCACATTARACCAGRATGATA
DQ902121.1	104-794_Coelognathus_radiatus	ACCOAL	CCHACTT	aca a	CCARCATATTAAACCAGAATGATA
AC.347468.1			AAHAUTAA	1.11	CCAUCACATCARACCAUA
MT133294.3	-14-734 Boiga beddonei		A A DA OF A	20.0	ACAUCACATTRAACCAUAATUATA
MT113290.1	44-734 Boiga beddonel	A DECTRONAL	AAHACTAL	10.1	ACAGCACATTAAACCACAATGATA
MT733291.1	44-734 Boiga beddomei	ACCTAN	COARDACTAN	chee	ACAGCACATTAAACCAGAATGATA
MW1111469.1	:76-779 Lycodon septentrionalis	ACCTAN	CCCATCGTAA	chie e	ACAACACATCAAGCCAGAATGATA
MW111468.1	:75-775 Lycodon fasciatus	AGCCAA	CCCCAGTAA	CALC	ACAACACATTAAGCCAGAATG
XC010366.1	:91-791_Lycodon_fasciatus	AGOCAR	CCCRACTAR	CLCC.	ACAACACATCAAGCCAGAATG
MT625862.1	:58-758_Lycodon_fasciatus	AGECAA	COCCHAGTAR	CLEC	ACAACACATCAAGCCAGAATG
HW111467.1	:75-775_Lycodon_fascistus	AGCCAA	COCCEASTAN	CARE	ACAACACATCAAGCCAGAATG.
EC010368.1	:92-794_Lycodon_lacensis	ABUTAA	GCHAGTAN	946.6	ACAACACATTAAACCAGAATGATA
RC010370.1	32-791_Lycodon_lacensis	A SHEAR	ACHAUTAA	A 83	ACAACACATTAAACCADAATU
MPERSON 1	56-750 Lunadan subsignatus		A COLARCE	8.68	ACANCACATERANCCAGARATO
MT625859 1	58-758 Lengdon subringtus		ACHAATCH	an Ca	ACEACATTALACCECERTC.
#C733203.1	76-776 Lycodon subcinctus	AGOCAA	ACHAATCH	CA.C.C.	ACAACACATTABACCAGAATG
LC105630.1	21-724 Coelognathus flavolineatus	GGCTAA	COCCHAGEAA	CACC	ACAACACATTAAACCAGAGTGATA
DQ902128.1	92-788_Coelognathus_flavolinestus	AGCTAA	CCCCCASTAN	CARC	ACAACACATTARACCAGA
00902134.1	:91-791_Elaphe_bella	AUCCAA	CCCRACTAA	GACE	ACAACACATTAAACCAGAATG
XF669231.1	:89-778_Euprepiophis_mandarinus	ACCORA	CARGUTAA	모스템모	ACAACACATTAAACCAGA.
RF669228.1	1:92-785_Euprepiophis_mandarinus	APPROX	CANGUTAA		ACRACACATTAAACCAGAATGATA
KY162330 1	10.650 Wallochia brachuura		A CHACTAL	2,62	AAAALALALALALAAALLAUAUIUAIA
AV611998.1	99-794 Dryna muccaus	A PLACE VI	A AND OTHER	61 B B	ACARCACATTRAACCACAATCATA
LC105628.1	:114-809 Ptyas mucosa	ACCUTON	CARDACTER	ched	ACAACACATTAAACCAGAATGATA
EF076709.1	91-794 Orthriophis taeniurus	AGOCAAS	CACHAGTA	CACC	ACARCACATCARACCAGARTGATA
DQ902132.1	:91-794 Orthriophis taeniurus grabows	K ABCTAA	CCACTAGTAN	CACC	ACAACACATCAAACCAGAATGATA
XF669249.1	91-794_Orthriophis_taeniurus	ACCTAN	CACEAGTAN	GAEC	ACAACACATCAAACCAGAATGATA
XX239646.1	:95-792_Hydrophis_platurus	ACCANA	SOCTIAUTCA	GADE	CCARCACAT CARACCAGA
KT966115.1	:70-767_Hydrophia_platurus	ADCARAC	THAUTCH	GAEG	CCRACACATCRAACCAGA.
KT766116.1	1:49-746_Hydrophis_platurus	A COMPANY	CTHAGTCH	2022	CCARCACATCARACCAGA
MEREGICE 1	-103-800 Budrophis platurus	A PERSONAL PROPERTY.	C TO D C THE	dial and	CARCACATCARACCAGE
MN886308 1	:103-800 Hydrophis platurus	ACCAPT	CTRACTO	CAR-	CCAACACATCAAACCAGA
KT966127.1	:85-782_Hydrophis_stokesii	ACCARA	COCTRACTOR	CALC	TCAACATATCAAACCAGA
30217201.1	:79-768_Hydrophis_stokesii	ACCARA	CTRASTO	GACC	TCAACATATC
RC014431.1	: 77-777_Hydrophis_ohscurus	AGCANA	CTEAGTCA	CA.CC	TCARCACATCARACCAGAATC
RT966054.1	:79-779_Rydrophis_caerulescens	AUCAAA	TTEAATC	일수 된 단	TCAACACATCAAACCAGAATG.
30217208.1	19-779_Hydrophis_caerulescens	ADDA	TTEAATCH		TCARCACATCARACCAGAATG.
A1206890.1	10-710 Gerarda prevostiana		AADGGTAN		ACAACACATTAAGCCAGAATG.
PE395914	11-15 Opravda prevostiana		A A DOTAL	8.88	ACARCACATTAAUCCAUAATG.
KX696953 1	1-704 Castoria violaces	A HELL MARK	POC A PAGE A	8.88	ACAACACCATCAAACCACAAATCA
EF395897 1	50-753 Cantoria violacea	ALLER	CARACTAL	8-88	ACAACACATCAAACCAGAATCATA
MT802706 1	:62-747 Homalopsis huccata	ACCT	CATAGTAL	GCER	ACAACATATTAAACCAGA.
MT802711.1	:62-747_Homalopsis_buccata	ADDITAN	CALAGTAA	EC SE	ACAACATATTAAACCAGA
MT802704.1	:61-747_Homalopsis_buccata	ADCCAR	COCABAGTAN	CCCC	ACAACATATTAAACCAGA
MT802703.1	:61-747_Homalopsis_buccata	AGCCAA	CABAGTAN	CCCC	ACAACATATTAAACCAGA
MT802658.1	:50-753_Cerberus_rynchops	AGCCAR	CARAGTAN	CCCC	ACAACACATCAAACCAGAATGATA
AF471092.1	91-794_Cerberus_rynchops	AGCCAA	CADAGTAN	BCSE	ACAACACATCAAACCAGAATGATA
EF395900.1	.:50-753_Cerberus_rynchopa	AUGUAA	CAUGGTAN		ACAACACATTAAACCAGAATGATA
EF395901.1	1.50-153_Cerberus_rynchops		CARAGEAR		ACAUCACATTAAACCAGAATGATA
A494830.1	1-670 Humstecomus niumbas		CONTRACT OF	8. BE	ACRACACO TO A A OCACE TO A T
38463014	50-753 Echydrie dosemieri	Gild The	CARGACA	deb a	ACAACACATTAAACCACAATTAA
JX463015 1	50-753 Enhydrie dosemieri	GOOT	CARGACA		ACAACACATTAAACCAGAATGATA
LC105625.1	159-763 Ephydria enhydria	ACCOM	CAADACTAL	GA CO	ACAACACATCAAACCAGAATCATA
MT802681 1	:50-753 Enhydris_enhydris	ACCOM	CCAATAGTAA	GARC	ACAACACATCAAACCAGAATCATA
Company of the Print of the	50-753 Enhudris anhudris	AGCCAA	AABAGTAA	CCCC	ACAACACATCARACCAGAATGATA
MIS02083.1					
LC105627.1	:132-835_Enhydris_enhydris	AGCCAR	CCAATAGTAA	CACC	ACAACACATCAAACCAGAATGATI

	1 10	20	3.0	40	50
MT215095.1:20-713_Naja_naja	TTTCAACTAATCAC	AAAGACATCGGA	ACCOTTAC	TTCTGTTT	COTOCCTOATCCCOT
MT215097.1:23-718_Naja_naja	TTTCAACTAATCAC	AAAGACATCOGA	ACCOTTACO	TTCIGTT	FIGGTISCICT GATCCIGGT
MIG11070.1:12-00/_Neja_neje MIG11478.1.1.652 Trimpresurus stainameri	1 1 = 1 1 = 1 + 1 + 1 = 1 + 1 =		ACCOTATATA	TANTATT	COCCEPTER CONTRACTOR
MI031479.1:1-652 Trimeresurus steinegeri			ACCOTATATO	TAATATTO	GOCIGCATOGTCAGOC
MZC31480.1:1-652_Trimeresurus_stejnegeri	+ + = + + = r + + r = - + + - = + + - = + + + - = + + + - = + + + - = + + + - = + + + +		ACCCTATATO	TAATATTC	GOCICATORTCAGOC
LC105603.1:3-697 Enhydris_enhydris	CA CA	CANGACATTOGA	ACCCTATACO	TOCTATT	GGGGCCTGAGCTGGC
LC105601.1:10-716_Enhydris_enhydris	TTCTAACAATCAC	AAAGACA775GA	ACCCTATACO	TOCTATT	TO GOS CICT GAGC TO GC
LC1056C2 1:37-683 Enhydris enhydris	1 1 - 1 1 - 1 1 1 - 1 - 1 - 1 - 1	AAAUACATIGUA	AUGULALAU	10 JALL	and contract the
LC075342.1:27-719_Fowles_flavipunctatue		AAGATATCOGA	ACCOTTTAC	TOCTATTT	FOGTOCCTOATCCOOC
LC075343.1:27-718_Fowles_flavipunctatus	****	AAGATATCGGA	ACCOTTACO	TCCTATT	GOTOCCT GATCCODC
LC105614.1:3-686_Fowles_flavipunctatus		AAGATATCGGA	ACCCTTTAC	TOCTATT	GGTGCCT GATCCGGC
MT215098 1:3-669 Boigs ochraces	ATTTUTUALAACCAC	ARAUALATIUM	TACT	TACIATI	PROFILE TRATCALLA
MT215100.1:3-666 Boigs_ochraces			TAC	TATTATT	GOCICATONTCTOOC
MT215099.1:2-664_Bolga_ochracea	**************		LAAN TACT	TTATTATT	IGGCGCATGATCTIGC
LC075338.1:10-715_Gonyosoma_owycephalum	TTCTCACAACCAC	AAAGATATTGGG	ACACTATACO	TACTATTO	SECECATEATCTEEC
MIG31453 1:1-654 Europaniophia mandarious		AAAGATATIGGG	ACCOTATACI	TACTATO	COCCOCCTOR
MEC31434.1:1-654 Euprepiophis mandarinus			ACCOTATATO	TACTATTO	GOCOCOTOGTCTOGC
MZ031451.1:1-654_Euprepiophis_mandarinus	1 1 2 1 1 2 2 2 2 2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5		ACCOTATATO	TACTATTO	GACACATAGTOTAGC
MZ031452.1:1-654_Euprepiophis_mandarinus			ACCCTATATO	TACTATTO	Gececeresterctesc
MI215095.1:35-722_Lycodon_dullcus	ACAC ACCAC	AAAGATATTGGA	ACCOTATACE	TANTATT	COACCET GAT CAUGE
LC105617.1:10-719 Rhadinophis prasinus	ATTCTCGACAACCAC	AAAGACATTGGA	ACCCTATACT	TACTATTO	GGGGGCCTGATCTGGC
MI031436.1:1-658_Oreocryptophis_porphyraceus	** = * * = * = * * = * * *		ACCCTATACO	TACTATIS	IGGCGCAT GGTCAGGC
MI031437.1:1-658_Oreocryptophis_porphyraceus			ACCCTATACE	TACTATT	FEGCECATGATCAGEC
MC45988 1-1-458 Coalognathus flavolineatus	ATTTCTACAACA	CARGACATUGUA	ACCOUNTATION	TATISTIC	COCOCAT GUTCLUGGC
MZC45969.1:1-658 Coelognathus flavolineatus			ACCOTATATI	TATTOTTO	GOTOCATOGTCOOGC
MEC45960.1:1-658_Coelognathus_flavolineatus	11 - 12 - 2		ACCOTATATS	TATTGTTC	GGTGCA7GGTCGGGC
M2C31450.1:1-658_Elaphe_taeniura			ACCCTATACO	TACTATT	FOOCOCATOGTCTOOC
MIG31465.1:1-657_Ptyas_korros	************		ACCCTATACO	TACIATI	COCCUCATOOTCODOA
MEC31439.1:1-657 Ptvas korros			ACCCTATACO	TACTATTT	GOCOCATOGTCAGEA
MW144274.1:1-671_Ptyas_mucoss			CCTATAC	TATTATTO	GGAGCATGATCAGGA
MT215101.1.9-643_Ptyas_mucosa			********		
MEG31469.111+654_PEyas_mucces		***********	ACCCTATACO	TATTATTC	GOAGCATGATCODGO
LC105608.1:10-715 Ptvas mucosa	TTCTCACAAATCA	CAAGACATTGGA	ACCCTATACO	TATTATTO	GGAGCATGATCGGGG
LC105607.1:4-690_Ptyas_mucoss_mitochondrial	CA	CAAGACATTGGA	ACCCTATACO	TATTATTC	GGAGCATGATCGGGG
MEC45966.1:1-654_Ptyss_muccas			ACCCTATACO	TATTATTO	IGGASCAT GATCAGGG
MIC45970.1:1-634_Ptyss_mucces	1 1 = 1 1 = 1 = 1 + 1 + ± 1 + +		ACCCTATACO	TATIATIC	SGAGCATGATCAGGG
MEC45999 1:1-654 Ptyas muccas			ACCCTATACO	TATTATTO	GGAGCATGATCAGGG
MZC45991.1:1-654_Ptyas_mucosa			ACCOTATACO	TATTATTO	GGASCATGATCAGOS
MT215095.1:20-713_Naja_naja	60 70 CIAARCOCCOCCOC	80 CTACTA	90 ATACCATA	100	
MT215095.1:20-713.Naja_naja MT215097.1:23-718_Naja_naja	60 70 CAAAC COOL COOL CAAAC COOL COOL COOL		90 ATACOCATA	100 ACTOACT	
MT215095.1:20-713.Haja_naja MT215097.1:23-718.Haja_naja MT215096.1:12-667_Haja_naja	60 70 0 4 4 0 0 0 0 0 0 0 0 0 0 0 4 4 1 0 0 0 0 0 0 0 0 0 0 0 4 4 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		90 ATTACOCATA ATACOCATA ATACOCATA	100 ACTOACT ACTOACT	
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LC105608.1:10-715 Ptyas mucosa	CHICK	ASCONC	AAHCTIT	GTACTACTAC	NUCCEACEC	ATTRATAATTTT
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LC105604.1:9-701 Enhydris anhydris	TTCATAGTTAT
LC105602.1:37-683 Enhydris enhydris	TTCATASTTATA
LC075342.1:27-719 Fowles flavipunctatus	TTCATAGTCATE
LC075343.1:27-718 Fowles flavipunctatus	TTCATAGTCATS
LC105614.1:3-686 Fowles flavipunctatus	TTCATAGTCATS
LC105616.1:7-714_Chrysopelea_ornata	TITATOGTCATE
MT215098.1:3-669_Bolga_ochracea	TTTATAGTTATA
MT215100.1:3-666_Boiga_ochraces	TTTATAGTTATE
MT215099.1:2=664_Boiga_ochraces	TTTATAGTTATS
LC075338.1:10-715_Gonyosoms_oxycephalum	TETATA DETATA
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MZ031453.1:1-654_Euprepiophis_mandarinus	TTCATGGTAAT
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ME031451.1:1-654_Euprepiophis_mandarinus	TTCATOGTAATS
M2031452.1:1-654_Ruprepiophis_mandarinus	TTCATGOTAAT
MT215093.1:35-722_Lycodon_aulicus	TTCATCUTATS
LC105618.1:16-713_Rhadinophis_presinus	TITATAGECATS
LCI05617.1:10-719_Rhadinophis_prasinus	TTTATAGTCATS
MIG31436.1:1-658_Oreocryptophis_porphyraceus	TECATOGERATS
MIC31437.1:1-658_Oreocryptophis_porphyraceus	TTCATOGRAATS
LC075340.1:1-705_Coelognathus_flavolineatus	TTTATECTAT
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porphyraceu	BEAGET	COTCACATA	CTTTTCCC	CUTATAAACAA	TATGASCITT	CHOGTHACHAC	CCCA
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aitochondrial	GUAGEA	COACAEA	Concord C	COCATAAACAI	CATHAGTT	CHEATEATIAC	ALGA
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MT215097.1:23=718_Na3a_naja
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M2031478.1:1=652_Trimeresurus_stejnegeri
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MZC31400.1:1-652_Trimeresurus_stejnegeri
LC105603.1:3-697_Enhydris_enhydris
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LC105602.1:37-683_Enhydris_enhydris
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MT215099.1:2-664_Bolga_ochracea
LC075338.1:10-715_Gonyosoma_oxycephalum
LC075338.1:11-717_Gonyosome_oxycephalum
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MT215093.1:35-722_Lycodon_aulicus
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MZC45969.1:1-658_Coelognathus_flavolineatus
MEC45960.1:1-658_Coelognathus_flavolineatus
MSC31450.111-658_Klaphe_taeniura
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MEUSINE 1.1.1-637_PEYAS_KOTTOS
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LC105616.1:7-714_Chrysopelea_ornata
MT215098.1:3~669_Boiga_ochracea
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MT215099.1:2=664_Boiga_ochraces
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LC075339.1:11-717_Gonyosoma_oxycephalum
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LC105617.1:10~719_Rhadinophis_prasinus
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MT215097.1:23-718_Naja_naja
MT215096.1:12-667_Naja_naja
ME031478.1:1-652 Trimeresurus stejnegeri
MEC31479.1:1-652 Trimeresurus_stejnegeri
M2031480.1:1-652 Trimeresurus stejnegeri
LC105603.1:3-697 Enhydris enhydris
LC105601.1:10-716 Enhydria enhydris
LC105604.1:9-701 Enhydris anhydris
LC105602.1:37-683 Enhydris enhydris
LC075342.1:27-719 Fowles flavipunctatus
LC075343.1:27-718_Fowles_flavipunctatus
LC105614.1:3-686_Fowles_flavipunctatus
LC105616.1:7-714_Chrysopelea_ornata
MT215098.1:3-669_Bolga_ochracea
MT215100.1:3-666_Boiga_ochraces
MT215099.1:2-664_Boiga_ochraces
LC075338.1:10-715_Gonyosome_oxycephalum
LC075339.1:11-717_Gonyosoma_oxycephalum
MZ031453.1:1-654 Euprepiophis mandarinus
MEC31434 1:1-654 Ruprepiophis mandarinus
M2031451.1:1-654_Euprepiophis_mandarinus
M2031452.1:1-654_Ruprepiophis_mandarinus
MT215093.1:35-722_Lycodon_aulicus
LC105618.1:16-713_Rhadinophis_presinus
LC105617.1:10-719_Rhadinophis_prasinus
ME031436.1:1-658_Oreocryptophis_porphyraceu
ME031437.1:1-658_Oreocryptophis_porphyraceu
LC075340.1:1-705_Coelognathus_flavolineatus
M2045988.1:1-658_Coelognathus_flavolineatus
MIC45969.1:1-658_Coelognathus_flavolineatus
MIC45960.1:1-658_Coelognathus_flavolineatus
MEC31450.1:1-658_Elaphe_taeniura
M2031466.1:1-657_Ptyas_korros
ME031467.1:1-657_Ptyas_korros
ME031439.1:1-657_Ptyns_korros
MW144274.1:1-671_Ptyas_mucosa
MT215101.1:9-643_Ptyas_mucosa
M2031469.1:1=654_Ptyas_mucosa
LC105605.1:10-715_Ptyas_mucosa
LC105608.1:10=715_Ptyss_mucoss
LC105607.1:4-690_Ptyss_mucoss_mitochondrial
MIC45966.1:1-654_Ptyss_mucces
MEC4597D.1:1-654_Ptyas_muccas
MZ045954.1:1-654_Ptyas_mucoss
MIC45999.1:1-654_Ptyas_mucosa
MZC45391.1:1-654_Ptyas_muccas

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MT215099.1:2-664_Bolga_ochracea
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MT215093.1:35-722 Lycodon aulicus
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LC075340 1:1-785 Coelognathus flavolineatu
MEC45388 1:1-458 Coelognathus flavolineatu
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LC075342.1:27-719_Fowles_flavipunctatus	
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LC105616.1:7-714_Chrysopelea_ornata	
MT215098.1:3-669_Boiga_ochracea	
MT215100.1:3-666_Boiga_ochraces	
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LC075338.1:10-715_Gonyosons_oxycephalum	
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MZ031453.1:1-654_Euprepiophis_mandarinus	
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ME031451.1:1-654_Euprepiophis_mandarinus	
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MT215093.1:35-722_Lycodon_aulicus	
LC105618.1:16-713_Rhadinophis_presinus	
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MEC31437.1:1-658_Oreocryptophis_porphyrace	4
LC075340.1:1-705_Coelognathus_flavolineatu	4
M2C45988.1:1-658_Coelognathus_flavolineatu	8
MIC45969.1:1-658_Coelognathus_flavolineatu	4
MIC45960.1:1-658_Coelognathus_flavolineatu	8
MIC31450.1:1-658_Elaphe_taeniura	
M2C31466.1:1-637_Ptyas_korros	
ME031467.1:1-657_Ptyas_korros	
M2031439.1:1-657_Ptyas_korros	
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M2045954.1:1-654_Ptyas_mucosa	
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215095.1:20-713_Waja_naja	ATAS	CCGACAS	TCGAA	COTALAT	ACATC	CHICKE	CACCE	
215097.1:23+718_Naja_naja	ATTAC	CONCAS	ATCGAA.	RCICTARAT	ACATO	CREATE	다양이 한다.	- COLOR
215096.1:12-667_Naja_naja	ATAC	HCCHGACAG	TCGAA.	ECICTAAAT	AUATO	CULTUC		
31475.1:1=652_Trimeresurus_stejnegeri	ATIGO	COUGACAG	ACCGAA	HCTTANAT	ACAAC	CULLUL		
31479.1:1-652_Trimeresurus_stejnegeri	ALC C	CCHGACAG	CCGAA.	ACTTALAT	REARC	CLEANE		
31480.1:1-652_Trimeresurus_stejnegeri	a ligo	HCCHCACAG	CCGAA.	CTTALAT	ACAAC	CALAR	ENCE C	-0.40 0.0
05603.1:3-697_Enhydris_enhydris	A DAG	HACHCACAG	ACCGAA.	TATCARC	ACCTC	ALC: NO.	CACE IN	1.0
05601.1:10-716_Enhydris_enhydris	ALC: NO	HACHCACAG	ACCGAA	TATCAC	ALC: U	- COLONIA -		- Colored
obece.1:9-701_Ennyaris_ennyaris	ALAS	ACTEACAU	CCGAA.	TATCAL		COLUMN T	HARES!	
05402.1:37-483_Embydris_enhydris	ALC: N	ACHCACAG	CCGAA.	TATCONC		ACCESSION 1		44
/5342.1:27-719_Fowles_flavipunctatus	100	BATBAACAS	TCUTA.	REC ZADAZ		CARLEN -		-
75343.1:27*716_Fowles_flavipunctatus		BATRAACAG	TOUTA	STOTA SAT		- Devening-		- B- B-
US614.1:3-000_FOW148_FISV1punctatus	100	BAT BAACAS	COTAL	Contra Data		- HARANA	10 B B	
15628.1: 7-714_Lnrysopeles_urnsts		STORAL AU	CCUTA.	No. of the last		Constant -	10.68	
15150 1.2 SSE Boigs ochraces	100	Back Cat	COLUMN A	Below Burn		- HARDEN -	N 88	
15750 1:3-566 Bolga ochracea	1000	Concession of the second	CCCCC.	Househaw		- 199299	N 88	
15139 1:10-715 Converses oversets lun	100	THE BLOCK	COGGA.	Belowe Bar				
15338 1-11-112 Converse sevenhalum	100	A COMPANY OF C	Access	Belowie Bar		2		- 194C 198
1411 1-1-614 Europaniophia mandarinus	Ref C	ACT ALOCC	Accoss	Beiczellan			- A - B - B	
11414 1-1-614 Eugraphic mandarinus	Res.	ACT ACC	Access	Receic Hale	10 C	-		
1457 1:1-654 Euprepiophie mandarinus	and a	ACHARCES	Access	Neiczellaic		Contra to 1	chiefe e	
11452 1:1-654 Euprepiophis mandarinus	144	ACCARCES	ACCORA	Decredae		-	distant.	
15093 1 75-722 Iwondon auligue	1000	ATACAS	BCCGAA	Beczellue.			10 C - 1	
Sile 1:16-111 Shadinashia ayaaisma	100	ACRACTO	Beccas	Bernellin	NR 198		N 83	- 1991 - 1993
5617 1-10-719 Shadiwonhis grasing	1000	ACOACTAS	Accarco	AAAT		-	N. 88	
S1436 1-1-658 Orangerantophia aprohuraneus	100 1	ATTARCTO	ACCCAA	Brickie Have	No 6 8	-	-N-86	
1437 1:1-658 Oreocryptophis porphyraceus	A-A-	ATTAACTO	ACCGAA	RECTORAT	A DECK	Contractory 7	Chiefe of Chiefe	
75340 1:1=705 Coelognathus flavolineatus	1 Con	MATHAACCO	FORCA	BECTERAT.	10.0	COLUMN T		
Sills 1:1-418 Coelegnathus flavolinestus	Dista.c	ATAACCO	Accora	BECTERAT	100.00	TRACT	-N-H	
15969.1:1-658 Coelognathus flavolineatus	ATRA C	HATHAACCO	Acceca	TOTTAT	102.70	Contraction of the	chiele e	10-10
45960 1:1-658 Coelognathus flavolineatus	ALC: NO	ATRACCO	ACCECA	MTCTT BAT	100.76	COLUMN T	DACES	THE DE
11450.1:1-658 Elaphe taeniura	a de	ATAACTO	ACCATA	TICTADAC	ACCTC	THICKNE	date of the	76700
1465 1:1-657 Ptyas korros	11111	ATTAACTS	ACCOAL	ATCTT DAC	ACC'10	Witten the	dial circle	of de la
31467.1:1-657 Ptyas korros	ATX:	ATBAACTG	CCGAA	TCTTAC	ACCTC	TRICTIC	TACCO.	- HGC GG
1439 1:1-657 Ptyas korros	ATAT	ATTAACTG	ACCGAA.	TICTITANC	ACCTO	TREESC	CACCO	TGEOG
44274.1:1-671 Ptyas mucosa	ATAC	ATTAACCO	CCGAA.	ACCTITANC	ACCTO	TRACTOR	GARCO	TOTOC
15101.1:9-643_Ptyas_mucosa	ATAC	ATAACTG	ACCGAA	Cictic Ake	ACCTC	TTTCTT	DATES	CT dT CO
31469.1:1-654_Ptyas_mucosa	ATAC	ATOAACTO	ACCGAA.	NCCTTAAC	ACCRC	TTTCTTT	GATCO	of a tac
05605.1:10-715_Ptyas_mucosa	ATAC	ATCAACTG	ACCGAA.	CICTTAAC	ACCTC	TTTCTTT	GALEC	CROTCO
05608.1:10-715_Ptyas_mucosa	ATAC	ATCAACTG	CCGAA.	ACCTT AAC	ACCTC	TTTTTT	CAPECI	CTGTCC
05607.1:4-690_Ptyas_mucosa_mitochondrial	ATAC	BATBAACTO	CCGAA.	COTTRAC	ACCIC	TTTTTTT	CATCO	TGIGC
45966.1:1-654_Ptyas_muccas	ATAC	ATTAACTO	ACCGAA.	COTTAC	ACCIC	TOUGUET	CATCC	TGTOC
45970.1:1-654_Ptyss_mucosa	ATAC	TATEAACTG	CCGAA.	ACCT TAAC	ACC?C	TRICEPT	GATES.	TGICG
45954.1:1-654_Ptyss_mucoss	ATAC	ATTAACTIC	ACCGAA.	ACCTTAAC	ACC7C	TRACTOR	GATCC	TGTCC
45999.1:1-654 Ptyas muccas	ATAC	TATTAACTO	CCGSAA.	ACCTTANC	ACCITE	TRACTOR	GATEC	174140
45991.1:1-654 Ptvas mucosa	ATAC	BATHAACTO	ACCORA.	DCC TTLAC	ACCTC.	THICTT	GATOC	TUTOF

MT215095.1:20-713_Naja_naja
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MT215096.1:12-667_Naja_naja
MIC31478.1:1-652_Trimeresurus_stejnegeri
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LC075338.1:10-715_Gonyosons_oxycephalum
LC075339.1:11-717_Gonyosoma_oxycephalum
MZ031453.1:1-654_Euprepiophis_mandarinus
MEC31434.1:1-654_Euprepiophis_mandarinus
MEG31451.1:1-654_Euprepiophis_mandarinus
M2031452.1:1-624_Euprepiophis_mandarinus
MI215093.1:35-722_Lycodon_aulicus
1/10/01/01/11/20/11/20/00/00/00/00/00/00/00/00/00/00/00/00/
M2031436 1-1-658 Grangrantophis northurson
MEC11437, 1:1-458 Orenoryptophis porphyraceu
LC075340 1:1-705 Coelognathus flavolineatus
M2C45988.1:1-658 Coelognathus flavolineatus
MIC45969.1:1-658_Coelognathus_flavolineatus
MIC45960.1:1-658_Coelognathus_flavolineatus
MEC31450.1:1-658_Elaphe_taeniura
M2031466.1:1-657_Ptyas_korros
ME031467.1:1-657_Ptyas_korros
ME031439.1:1-657_Ptyas_korros
MW144274.1:1-671_Ptyas_mucosa
MT215101.1:9-643_Ptyas_mucosa
MEU31469.1:1=654_Ptyas_mucosa
LC105665.1:10-715_Ptyas_mucosa
LC105602 1.4.600 Phone minore minore
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MEC45999.1:1-654 Ptyas mucosa
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Observations:

By analysing the above phylogenetic trees of mitochondrial genes Cytochrome B and COX 1, it is observed that, many paraphyletic groups are emerging from the same ancestor. As, the species differ from each other by their geographical distribution and habitat, the venomicity of the snakes doesn't depends on the mitochondrial genes. It is observed from the phylogenetic tree that many venomous species emerged from a non- venomous or mildly venomous ancestor. So, the venomicity comes as evolution occurs within the species from time to time.

From the clustal omega results, it is observed that the result of Cytochrome B is more conserved than the COX1 result, it is obtained that the cytochrome B is much diversed than the COX 1 gene.

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Department:- Zoology

Comparison between the Cox1 and Cytb Gene Data of the Common Snake Species Found in India.

> Submitted By:-Shashwata Roy UG | Semester-V | College Roll:- 536 Registration number:-A01-1112-115-026-2019

Under the supervision of Dr. Ajoy Mallik Asst. Professor, Department of Zoology, RKMVCC, Rahara

INTRODUCTION:-

The mitochondrion is a cellular organelle that contains the machinery enabling the production of ATP via the process of oxidative phosphorylation in eukaryotes, thus playing a pivotal role in metabolism, apoptosis, disease, and aging.

Inside this organelle, there is a genome called mitochondrial genome (mtDNA) that encodes proteins related to oxidative phosphorylation, and the genetic content is thought to have been reduced to 37 genes in vertebrates from the original gene content in their ancestor (Lang et al. 1999; Gary et al. 1999). mtDNA is derived from circular genomic DNA of bacteria that became endosymbiotic in the past. For this reason, once released by injured cardiomyocytes, mtDNA is recognized by TLRs as pathogen-associated molecular pattern (PAMP) and elicits inflammationThe mtDNA is small, circular, gene- rich, maternally inherited, and double stranded. During replication, the synthesis of the nascent heavy strand initiates at the origin of heavy strand replication (OH), within the control region (CR). After two thirds of the nascent heavy strand is synthesized, the synthesis of the nascent light strand starts at the origin of light strand replication, located within a tRNA cluster. This tRNA cluster is often referred to as the WANCY region(tRNATrp-tRNAAla-tRNAAsn-tRNACys-tRNATyr), between the NADH dehydrogenase subunit 2 (ND2) and Cytochrome C oxidase subunit 1 (COX1) genes. The asymmetric replication mechanism of mtDNA exposes parts of the heavy strand in a single stranded state for a period of time.

The vertebrate mitochondrial genome has been an important model system for studying molecular evolution, organismal phylogeny, and genome structure. The versatility and prominence of vertebrate mitochondrial genomes stems from their compactness and manageable size for sequencing and analysis, well-characterized replication and transcription processes and the diversity of protein and structural RNA genes that they encode.

The mitochondrial DNAs play an important role in the regulation of cellular metabolism, apoptosis and oxydative stress control. Mitochondrial DNA (mtDNA) has many special features such as a high copy number in cell, maternal inheritance, and a high mutation rate which have made it attractive to scientists from many fields.

The analysis of mitochondrial DNA (mtDNA) fills a vital niche in forensic genetics. It is superior to standard nuclear DNA (nDNA) typing when samples have to be identified that do not contain enough nDNA or need to be evaluated with respect to their maternal relatedness.

OBJECTIVE:-

The main objective of this study is to analyse and compare the phylogenetic tree of the cytb and cox1 gene of the common species. The pattern of branching in a phylogenetic tree reflects how species or other groups evolved from a series of common ancestors. In trees, two species are more related if they have a more recent common ancestor and less related if they have a less recent common ancestor. However, comparison of trees for the purpose of assessing similarity and the quantification of various biological processes remains a significant challenge.

MATERIALS AND METHOD:-

Samples and sequencing:-

We have collected the species from the reptile database (<u>https://reptile-database.reptarium.cz/</u>). Then we choose only the snake species for studying about the mitochondrial genes. We have collected near about 337 snake species from the databases.

Data extraction and arrangement:-

We have searched for the mitochondrial gene (cox1, cytb, ATPase6, ND4, 16s rRNA, 12s r RNA, D - loop) data of the each snake species in the ncbi website (https://www.ncbi.nlm.nih.gov/). Then, I downloaded full gene bank data of each species. From the full gene bank data I have collected the accession id, common name and geographical informations of each species. I arranged these data on a excell file. After that collecting all the accession id of the common species (having more than 2 mitochondrial gene data) and arranged on the notepad. From that choosing only one accession id from each species, I downloaded the FASTA format sequence.

Sequence analysis:-

I merged all the FASTA format sequences of the cytb and cox1. Many software tools exist to visualize DNA sequence data, but in those I used MEGA. Then I changed the FASTA format to MEGA format on the MEGA software. With this MEGA format I run the muscle alogorithm. Then I have trim off the unwanted sequences from the whole sequence. Saving the trim off mega file, I run to construct the maximum likelihood phylogenetic tree. This process worked out for both the cytb and cox1 gene data. After getting the phylogenetic tree of both the gene of the common species, I try to figure out the difference between the cytb gene and cox1 gene of the common species.

After getting the phylogenetic tree of the common species of the cytb and cox1 gene, I found that in the phylogeny of the cytb has more diversity than the cox1. So, usually I started to find the reason behind this changes.

For this, I searched all the data of the common species of the cytb and cox1 gene from the blast results. After that I downloaded all the NCBI data of the all the common species. From those data I marked all the data of complete cds. But due to the shortage of the data, I took partial cds with large (more than 650) gene length. From this I downloaded the FASTA sequences of each selected species. With these FASTA sequences, I created the phylogeny of the cytb and cox1 gene with the help of MEGA software run. I also selected only the complete cds data. And with the accession id of those data I send for annotation on the MITOS Web server. Afterwords, I have performed multiple sequence alignment (MSA) on the Clustal omega software. And I get the sequences.

Flow chart of the methodology:-

Collecting the species from the reptile data base. (<u>https://reptile-database.reptarium.cz/</u>)

Taking each snake species name, searched the data of mtDNA in NCBI website (https://www.ncbi.nlm.nih.gov/).

From the ncbi search, we collected the accession id, distribution of the species as well as the common name of the species. \Box

Collecting those data, we arranged the data in the excel file.

Then selecting all the accession id of the cytb gene of the common species then arranged in a notepad file.

After then I selected all the accession id of the cytb gene.

After that I downloaded the FASTA alligned sequence of each species.

After merging all the FASTA alligned sequence of the cytb gene, I performed a MEGA muscle run.

After trimming the sequences, I created the phylogenetic tree of the cytb gene data.

In the same way, I establish the phylogenetic tree of the cox1.

Analysis of the phylogenetic tree of the common species of the cytb and cox1 gene.

Cytb gene diversity is more than cox1 gene.

I searched all the data of the cytb and cox1 gene from the NCBI blast.

Selection of only complete cds data and partial cds data with large gene length.

Establishing the phylogenetic tree of the cytb and cox1 gene of the selected data.

Annotation of the complete cds data.

After that I took all the FASTA sequences of all the species of cytb and cox 1 gene. \blacksquare

Putting on the Clustal Omega software, then downloaded the alligned sequence.

PHYLOGENETIC TREE-



Fig:- Phylogenetic tree of the cytb of the common species.



Fig:- Phylogenetic tree of the cox1 of the common species.



Fig:- Phylogenetic tree of the cytb gene with complete cds and maximum gene length.



Fig:- Phylogenetic tree of the Cox1 gene with partial cds.

Multiple Sequence Allignment:-

Multiple Sequence Alignment (MSA) is generally the alignment of three or more biological sequences (protein or nucleic acid) of similar length. From the output, homology can be inferred and the evolutionary relationships between the sequences studied.

Clustal is a series of widely used computer programs used in bioinformatics for multiple sequence alignment. There have been many versions of Clustal over the development of the algorithm. Clustal Omega has the widest variety of operating systems out of all the Clustal tools.

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between three or more sequences

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AF471076.1_Daboia_russelii		GTGGGA	TCAAACT	TTCAACCTTGA	AATTTGGA	TCAATACTTCTAGCC
GQ359441.1_Echis_carinatus_isolate_		GTAGGA	TCCAATTO	CTCAACAT <mark>T</mark> G <i>I</i>	AACTTTGGA	T <mark>C</mark> CATAC <mark>T</mark> CTTAGCT
MK193094.1_Protobothrops_mucrosquamatus		GTAGGT	TCAAATTO	CTCAACCTTG <i>I</i>	AACTTTGGA	T <mark>C</mark> AATAC <mark>T</mark> ACTTACT
KX019144.1_Trimeresurus_stejnegeri_		GTAGGA	TCTAACTO	CTCAACTTIGA	AATTTGGA	T <mark>C</mark> AATAC <mark>T</mark> TCTCTCC
HM567533.1_Protobothrops_jerdonii		GTAGGA	TCAAACTO	CTCAACTT T GA	AATTTGGG	T <mark>C</mark> AATAC <mark>T</mark> ACTCTCC
LC094069.1_Sinomicrurus_macclellandi_iwasakii		GTCGGA	TCCAACT	TTCTACCT <mark>T</mark> G <i>I</i>	AATCTTGGC	T <mark>C</mark> TATAC <mark>T</mark> ACTAACC
FR693730.1_Ophiophagus_hannah		GTAGGA	TCTAACT	TTCCACCT <mark>T</mark> GC	AATTTGGT	T <mark>C</mark> AATAC <mark>T</mark> ACTAACT
KU527540.1_Naja_kaouthia		GTTGGA	TCCAACTO	CTCTACCTTGA	AACTTTGGC	T <mark>C</mark> TATAC <mark>T</mark> ACTAGCT
GQ225657.1_Naja_naja_naja_		GTTGGA	TCCAACTO	CTCTACCTTGA	AATTTGGC	TCTATACTAGCT
U69859.1_Python_reticulatus		GTAGCA	ACCAACTO	CTCAACCT <mark>T</mark> G <i>I</i>	AACTTCGGC	T <mark>C</mark> AATAT <mark>T</mark> ACTAACA
JX401136.1_Python_bivittatus		GTAGCA	ACCAACTO	CTCAACATTG <i>I</i>	AACTTCGGC	T <mark>C</mark> AATAC <mark>T</mark> ATTAGCA
AY099983.1_Python_molurus		GTAGCA	ACCAACTO	CTCAACAT T GI	AACTTCGGC	TCAATACTATTAGCA
LC105627.1_Enhydris_enhydris		GGTGGG	TCAAACT	TTCAACCT T GI	AATTTGGGC	TCCATACTCCTCACC
DQ902119.1_Gonyosoma_prasinum_		GTAGGC	TCAAATTO	CTCAACCTTGI	AACTTCGGA	TCTATGT TATTAACC
AF471084.1_Gonyosoma_oxycephalum_		GTAGGC	TCAAACTO	CTCCACCTTGI	AACTTCGGA	TCTATACTAACA
DQ902121.1_Coelognathus_radiatus		GTAGGG	TCTAACTO	CTCAACCTTGA	AATTTTGGA	TCAATATTACTATCC
AY486921.1_Platyceps_rhodorachis_		GTAGGA	TCCAACTO	CTCAACATTG <i>I</i>	AATTTGGA	TCCATATTACTAACC
DQ902128.1_Coelognathus_flavolineatus		GTAGGA	TCAAACTO	CTCAACCTTGI	AATTTTGGA	TCCATGCTACTAGCC
AY486929.1_Ptyas_korros		GTTGGG	TCAAACTO	CTCAACAT T GI	AACTTTGGA	TCCATGCTACTAGCC
AY611998.1_Ptyas_mucosus		GTAGGA	TCAAATTI	TTCAACCTTG <i>I</i>	AACTTTGGA	TCTATGCTATTAACT
AF471054.1_Ptyas_mucosa		GTAGGA	TCAAATTI	TTCAACCT <mark>T</mark> G <i>I</i>	AACTTTGGA	TCCATGCTATTAACT
EF076709.1_Orthriophis_taeniurus		GTAGGG	TTAAATTO	CTCAACCTTGI	AACTTCGGA	TCTATACTTCTAACC
DQ902132.1_Orthriophis_taeniurus		GTAGGG	TCAAACTO	CTCAACCTTG <i>I</i>	AACTTTGGA	TCCATACTACTAACC
DQ902118.1_Oreophis_porphyraceus	GTAGGGTTAAAT	TTTCAA	CCTTGAA <i>I</i>	ACTTCGGA <mark>T</mark> CI	ATACTACTA	ACATGCTTAGCCCTA
DQ902115.1_Euprepiophis_mandarinus		GTAGGA	TCAAACTO	CTCAACCTTG	AACTTTGGA	TCCATACTAACC

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GQ359441.1_Echis_carinatus_isolate_	TGC	CTCTCTATC	CAAA	CCCTTA	CGGAT	TCTTCCTG	GCAATCCAT	TACACAGCCAACATT
MK193094.1_Protobothrops_mucrosquamatus	TGC	TT <mark>A</mark> ATAA <mark>T</mark> C	CAAA	CTGCAA	CTGGGT	TCTTCCTA	GCAATCCAC	TACACAGCCAATATT
KX019144.1_Trimeresurus_stejnegeri_	TGT	CAGTAA <mark>T</mark> C	CAAA	TATAA	CCGGCT	TCTTCCTA	GCAATCCAC	TACACAGCCAACATT
HM567533.1_Protobothrops_jerdonii	TGC	ΓΤ <mark>Α</mark> ΑΤΤΑ <mark>Τ</mark> Ο	CAAA	TACAA	CAGGAT	TCTTCCTA	GCAATCCAC	TATACAGCCAACATC
LC094069.1_Sinomicrurus_macclellandi_iwasakii	TGC	CT <mark>A</mark> ACCC <mark>TA</mark>		FCATAA	CCGGGT	TCTTTCTA	GCAATCCAC	TATACAGCAAACATT
FR693730.1_Ophiophagus_hannah	TGC	CT <mark>A</mark> ACAA <mark>TA</mark>	CAAA	CCTTAA	CCGGAT	TCTTCCTA	GCAATCCAT	TATACAGCCAACATT
KU527540.1_Naja_kaouthia	TGC	CT <mark>A</mark> ATAC <mark>TA</mark>	CAAA	TTATAA	CCGGAT	TCTTCCTA	GCAATTCAC	TACACAGCCAATATC
GQ225657.1_Naja_naja_naja_	TGC	CT <mark>A</mark> ATAC <mark>TA</mark>		TTATAA	CCGGAT	TCTTCCTA	GCAATTCAC	TACACAGCCAACATT
U69859.1_Python_reticulatus	TGT	CT <mark>A</mark> GCCT <mark>TA</mark>		FACTAA	CCGGCT	TTTTCCTA	GCCGTCCAT	TACACAGCAAACAT T
JX401136.1_Python_bivittatus	TGC	TT <mark>A</mark> ACCA <mark>TA</mark>		FATTAA	CGGAT	TCTTCCTA	GCTATCCAC	TACACAGCAAACAT C
AY099983.1_Python_molurus	TGC	TT <mark>A</mark> GCCCTA		FATTAA	CCGGAT	TCTTCCTA	GCCGTCCAC	TACACAGCAAACATC
LC105627.1_Enhydris_enhydris	TGC	CTGGCCCTA		FCCCAA	CAGGAT	TCTTTTA	GCCATCCAC	TATCCAGCCAATATC
DQ902119.1_Gonyosoma_prasinum_	TGC	CAGCCCTA		FCACAA	CGGAT	TCTTCCTA	GCCATTCAC	TATACAGCTAACACC
AF471084.1_Gonyosoma_oxycephalum_	TGC	CT <mark>A</mark> GCACTA		CTACAA	CCGGGT	TTTTCCTA	GCCATCCAC	TACACCGCCAACATC
DQ902121.1_Coelognathus_radiatus	TGC	CC <mark>A</mark> ATCT <mark>TA</mark>		FCATAA	CGGCT	TCTTCCTA	GCCATTCAT	TATACAGCCAATATT
AY486921.1_Platyceps_rhodorachis_	TGC	CAGCCCTA		FCATCA	CAGGAT	TCTTCCTA	GCCATTCAC	TATACTGCCAATATC
DQ902128.1_Coelognathus_flavolineatus	TGC	CT <mark>A</mark> ACCCTA		CTATAA	CCGGAT	TCTTCTTA	GCCATCCAC	TATACAGCCAATATC
AY486929.1_Ptyas_korros	TGC	CAGCCATA		CCCTAA	CCGGTT	TCTTCCTA	GCCATCCAC	TATACAGCTAACATC
AY611998.1_Ptyas_mucosus	AGC:	CAGCCATA	CAAA	TCATAA	CCGGAT	TCTTCCTA	GCTATCCAC	TATACAGCCAACATC
AF471054.1_Ptyas_mucosa	TGC	CAGCCATA		FCATAA	CCGGAT	TCTTCCTA	GCTATCCAC	TATACAGCCAACATC
EF076709.1_Orthriophis_taeniurus	TGTO	CT <mark>A</mark> GCACTA		FCATAA	CCGGCT	TCTTCCTA	GCCATCCAC	TATACAGCCAATATT
DQ902132.1_Orthriophis_taeniurus	TGC	CT <mark>A</mark> GCAC <mark>TA</mark>		FCATAA	C TGGCT	TCTTCCTA	GCCATCCAC	TATACAGCCAACATC
DQ902118.1_Oreophis_porphyraceus	CAA	A. TCATAAC	GGGA	TTCTTC	C T	A	GCAATCCAT	TACACAGCTAACATC
DQ902115.1_Euprepiophis_mandarinus	TGT	CAGCCC <mark>TA</mark> GCCC	CAAA	T T A <mark>T A A</mark>	E AGGCT	TCTTTCTA	GCAATCCAC	TATACAGCAAACATT

	110	120	130	140	150	160
AF471076.1_Daboia_russelii	AATCTAGO	CTTCTCAT	CTATCGTACA	CATTACTCGAG	ATGTCCCA	IATGGC TGAAT TATA
GQ359441.1_Echis_carinatus_isolate_	AACCTGGC	CTTCTCAT	CTATTATCCA	CATCATTCGAG	ACGTACCC	FACGGCTGA<mark>A</mark>TCATA
MK193094.1_Protobothrops_mucrosquamatus	ACCCTGGC	CTTCTCAT	CCATCACCCA	CATCTCCCGAG	ACGTCCCT	FACGGCTGA<mark>A</mark>TCATA
KX019144.1_Trimeresurus_stejnegeri_	AACCTAGO	CTTCTCAI	CCATTATTCA	TATCTCCCGAG	ATGTACCC	FAC<mark>GG</mark>CTGA<mark>A</mark>TTATA
HM567533.1_Protobothrops_jerdonii	AACTTAGC	CTTCTCAI	CCATCACTCA	TATCTCCCGAG	ATGTCCCG	FAC<mark>GG</mark>CTGA<mark>A</mark>TCATA
LC094069.1_Sinomicrurus_macclellandi_iwasakii	AACCTAGO	TTTTCAI	CAGTTATCCA	CATCATGCGAG	ATGTACCA	CAC <mark>GG</mark> G <mark>TG</mark> G <mark>A</mark> TCATA
FR693730.1_Ophiophagus_hannah	AACCKGGC	CTTCTCAT	CCGTAATTCA	CATCACTCGAG	ATGTGCCT	FACGG <mark>A</mark> TGA <mark>A</mark> CCATA
KU527540.1_Naja_kaouthia	AACCTGGC	CTTCTCAT	CAGTAATTCA	CATCACACGGG	ACGTGCCT	FACGGGTGA <mark>A</mark> TCATA
GQ225657.1_Naja_naja_naja_	AACCTAGO	CCTTCTCAT	CAGTGATTCA	CATCACGCGGG	ACGTACCT	FACGGGTGA<mark>A</mark>TCATA
U69859.1_Python_reticulatus	AACCTAGO	CATTTTCAT	CCATCATCCA	CATCACCCGAG	ACGTCCCA	FACGGCTGA <mark>ATA</mark> ATA
JX401136.1_Python_bivittatus	AACCTAGC	C <mark>ATT</mark> CTCAT	CTATCATTCA	CATCACCCGCG	ATGTTCCA	FACGGCTGA <mark>ATA</mark> ATA
AY099983.1_Python_molurus	AACCTAGO	CATTCTCAT	CTATCATTCA	CATCACCCGCG	ATGTTCCA	FACGGCTGAATAATA
LC105627.1_Enhydris_enhydris	A A C T T A G C	CATTTTCAT	CAGTAATCCA	TATTATACGAG	ACGACCCA	FACGGCTGA <mark>A</mark> CCATA
DQ902119.1_Gonyosoma_prasinum_	AACCTAGO	CCTTTTCAT	CAATTATCCA	CATAATACGAG	ACGTTCCT	FATGGGTGAATCATA
AF471084.1_Gonyosoma_oxycephalum_	A A T A T A G C	CTTTTCAI	CAATCGTACA	CATTACACGAG	ACGTCCCA	FATGGGTG<mark>A</mark>ATCATA
DQ902121.1_Coelognathus_radiatus	AACCTAGO	CTTTCTCAI	CAATCATACA	TATTATACGAG	ATGTCCCA	FACGGTTGA <mark>A</mark> TCATA
AY486921.1_Platyceps_rhodorachis_	AACCTTGC	CCTTCTCAT	CTATTGTACA	CATCACACGAG	ACGTCCCG	FACGGGTGA <mark>ATCATA</mark>
DQ902128.1_Coelognathus_flavolineatus	AATCTTGC	CCTTCTCAT	CTATTATACA	CATTATACGAG	ATGTCCCA	CATGGATGAATCATA
AY486929.1_Ptyas_korros	AACCTTGC	CTTTTCAI	CTGTTATCCA	CATAACACGAG	ACGTCCCA	FACGG <mark>atgaatcata</mark>
AY611998.1_Ptyas_mucosus	AACCTAGC	C <mark>ATTT</mark> TCAI	CAATCATTCA	TATCACACGAG	ACGTCCCA	FACGGATGAATTATA
AF471054.1_Ptyas_mucosa	AACCTAGO	CATTTTCAT	CAATCATTCA	CATCACACGAG	ACGTCCCA	FATGGGTGAATTATA
EF076709.1_Orthriophis_taeniurus	AACCTAGO	TTTTCAI	CTATTGTTCA	CATCACACGAG	ATGTACCA	IGC <mark>GGT</mark> TG <mark>A</mark> ATAATA
DQ902132.1_Orthriophis_taeniurus	A A T C T A G C	CTTTTCAT	CTATTGTTCA	CATCACACGAG	ATGTACCA	FACGGTTGAATAATA
DQ902118.1_Oreophis_porphyraceus	AACTTAGO	CTTTCTCAI	CCATTGTGCA	CATCACACGAG	ATGTCCCC	FATGG <mark>ATG</mark> AATCATA
DQ902115.1_Euprepiophis_mandarinus	AACCTAGO	CTTTTCAT	CAATCGTACA	CATCACACGAG	ATGTCCCA	IGT <mark>GG</mark> A <mark>TGAA</mark> TCATA

AF471076.1_Daboia_russelii
GQ359441.1_Echis_carinatus_isolate_
MK193094.1 Protobothrops mucrosquamatus
KX019144.1_Trimeresurus_stejnegeri_
HM567533.1_Protobothrops_jerdonii
LC094069.1_Sinomicrurus_macclellandi_iwasakii
FR693730.1_Ophiophagus_hannah
KU527540.1_Naja_kaouthia
GQ225657.1_Naja_naja_naja_
U69859.1_Python_reticulatus
JX401136.1_Python_bivittatus
AY099983.1_Python_molurus
LC105627.1_Enhydris_enhydris
DQ902119.1_Gonyosoma_prasinum_
AF471084.1_Gonyosoma_oxycephalum_
DQ902121.1_Coelognathus_radiatus
AY486921.1_Platyceps_rhodorachis_
DQ902128.1_Coelognathus_flavolineatus
AY486929.1_Ptyas_korros
AY611998.1_Ptyas_mucosus
AF471054.1_Ptyas_mucosa
EF076709.1_Orthriophis_taeniurus
DQ902132.1_Orthriophis_taeniurus
DQ902118.1_Oreophis_porphyraceus
DQ902115.1_Euprepiophis_mandarinus

170	180	190	200 23	10 2	220
CAAAATTCA	CACGCCATC	GGCGCATCCC	ATTCTTTGTTT	TATCTATAT	ACACATTGCA
CA <mark>AAA</mark> CACA	CACGCCATC	GGCGCTTCCA1	ATTCTTCGTAT	CATCTATA1	CCACATCGGA
CAAAACACA	CACGCCATC	GeceeAletC			CCACATTGCA
CAAAACACA	CACGCCATC	GGCGCATCCC	ATTTTTCATTC	CATCTACA	CCACATTGCA
CAGAACCTC	CACGCAAT T	GGCGCATCCAT	ATTCTTCATCT	CATTTACAC	CCACATCGCA
CAAAACCTT	CACGCAATC	GGCGCATCCA	ATTCTTCATCT	CATTTACAT	ICCACATCGCA
CAAAACCTT	CACACAATC	AGCGCATCCC			CCATATCGCA
CAAAACCTT	CACGCTATC	GGAGCATCCAT	ATTCTTCATCT	CATCTACAT	CCACATCGCA
CA <mark>AAA</mark> CCTA	CACGCCATC	GGCGCATCCA	ATTCTTTATTC	CATCTACAT	TCACATCGCA
CAAAACCTA	CACGCTATC	GGCGCATCCA	ATTCTTCATCT	CATCTACAT	TCACATCGCA
		GGAGCATCTAT	ATTCTTCATCT		
CAAAATCTT	CACGCCATC	GGAGCATCCAT	ATTCTTTATCT	CGTATACT	ACACATCGCA
CA <mark>AAA</mark> TATA	CATGCAATT	GGCGCATCCAT	ATTCTTTATTC	TATCTATA1	T CACATCGCA
CAAAATATA		GGAGCATCAAI		CATCTACAT	TCACATTGCA
CAAAACCTC	CATGCAATT	GGAGCATCCAT	ATTCTTCGTCT	CATTTACAT	CCACATTGCA
CA<mark>GAA</mark>CCT T	CATGCAATT	GGAGCATCTAT	ATTCTTTATCT	CATTTACAT	TCACATTGCA
CAGAACCTT	CACGCAATT	GGAGCATCTA	ATTCTTTATCT	CATTTACAT	TCACATCGCA
	CATGCAATT	GGCGCATCTAL			TCATATCGCA
CAAAACATA	CACGCAATT	GGTGCATCTAT	GTTCTTCATCT	CATCTACAT	TCACATCGCA
CAAAACCT T	CATGCAATC	GGCGCATCAAI	GTTTTTCATCT	CATCTACAT	T <mark>CATGT</mark> C <mark>GC</mark> A

	230	240	250	260	270	280
AF471076.1 Daboia russelii	CGZ	GGCCTCTATTATGGA	TCTTAC	CTAAATAAAG	AAGTTTGACT	TTCAGGAACCACCCTT
GQ359441.1_Echis_carinatus_isolate_	CGZ	GGACTTTACTACGGC	TCCTAC	CTCTACAAAG	AAGTCTGACT	CTCAGGCTCCTCCTC
MK193094.1_Protobothrops_mucrosquamatus	CGG	GGGGGTCTACTACGG A	TCGTAC	CTCAATAAAG	AAGTATGACT	ATCAGGCACCACCCTC
KX019144.1_Trimeresurus_stejnegeri_	CGZ	GGACTTTACTACGG C	TCCTAT	CTTAATAAAG	AAGTA <mark>TG</mark> AC <mark>T</mark>	ATCAGGCACCACCCTT
HM567533.1_Protobothrops_jerdonii	CGZ	GGAATTTACTATGG C	TCATAC	CTTAATAAAG	AAGTCTGACT	ATCAGGCACCACTCTC
LC094069.1_Sinomicrurus_macclellandi_iwasakii	CGC	GGACTTTACTATGGG	TTACAC	CTAAA TAAAA	GTGTG <mark>TG</mark> ACT	CTCAGGAACTACACTA
FR693730.1_Ophiophagus_hannah	CGZ	IGGAATTTACTATGG A	TCCTAC	CTAAACAAAG	AAGTTTGACT	GTCGGGGACTACTCTA
KU527540.1_Naja_kaouthia	CGZ	GGACTCTACTATGG T	TTATAC	CTAAA TAAAG	AAGTTTGACT	ATCAGGAACAGCCCTG
GQ225657.1_Naja_naja_naja_	CGZ	GGACTCTACTATGG T	TTATAC	CTAAATAAAG	AAGT T TGAC T	ATCAGGAACAGCCCTC
U69859.1_Python_reticulatus	CGZ	AGGCCTATACTACGGA	TCATAC	CTCAACAAAG	AAACCTGAAT	ATCAGGCATCACCCTA
JX401136.1_Python_bivittatus	CGZ	AGGACTATACTACGGC	TCCTAT	'CTAAATAAAG	AAACCTGAAT	ATCCGGAATTACACTA
AY099983.1_Python_molurus	CGZ	AGGACTATACTACGGC	TCCTAT	'CTAAA TAAAG	AAACCTGAAT	ATCCGGAATTACACTA
LC105627.1_Enhydris_enhydris	CGZ	AGGTCTCTACTACGGA	TCTTAC	CTAAACAAAG	AAGTCTGACT	ATCAGGAGTTACCCTA
DQ902119.1_Gonyosoma_prasinum_	CGZ	AGGACTGTACTACGGG	TCATAC	CTAAACAAAA	GCGTATGGCT	ATCAGGAACCATAATT
AF471084.1_Gonyosoma_oxycephalum_	CGC	CGGACTATACTACGGA	TCCTAT	TTAAACAAAA	ACGTATGACT	ATCAGGAACCACACTT
DQ902121.1_Coelognathus_radiatus	CGC	CGGACTATACTATGGC	TCGTAI	CTAAA TACAA	ACGTATGGCT	ATCAGGAACTGTACTA
AY486921.1_Platyceps_rhodorachis_	CGZ	AGGACTATACTACGGA	TCATAT	CTCAATAAAA	ACGTATGACT	ATCAGGAACCATATTA
DQ902128.1_Coelognathus_flavolineatus	CGC	CGGACTATACTACGGG	TCCTAC	CTAAA TACAA	ATCTATGACT	ATCAGGAGTAACCCTA
AY486929.1_Ptyas_korros	CGZ	AGGACTATACTATGGA	TCATAC	CATAAACAAAA	ATGTGTGATT	ATCGGGTACCGCTTTA
AY611998.1_Ptyas_mucosus	CGC	GGGCTATACTATGGA	TCTTAC	CTGAACAAAA	ACGTCTGACT	ATCAGGAACTACCCTC
AF471054.1_Ptyas_mucosa	CGI	GGGCTATACTATGGA	TCTTAC	CTGAACAAAA	ACGTCTGACT	ATCAGGAACTACCCTC
EF076709.1_Orthriophis_taeniurus	CGZ	AGGACTATACTACGGA	TCCTAC	CTAAACAAAA	ATGTCTGACT	TTCAGGAACCACATTA
DQ902132.1_Orthriophis_taeniurus	CGG	GGACTATACTACGGA	TCCTAC	CTAAACAAAA	ATGTCTGACT	CTCAGGAACTACACTA
DQ902118.1_Oreophis_porphyraceus	ĊGZ	AGGACTATAT TACGGA	TCCTAC	CTTAATAAAA	ACGTCTGACT	ATCAGGAACCACACTA
DQ902115.1_Euprepiophis_mandarinus	CGZ	GGACTATACTACGGA	TCCTAC	CTAAA TAAAA	ATGTATGACT	ATCAGGGACTATAT <mark>T</mark> A

	290	30 Q	310	320	ззо	340
AF471076.1_Daboia_russelii	ТТАА	CATTCTAATAGCA	ACAGCCTT	TTTCGGTTACG	TCTTCCA	TGAGGACAAATATCA
GQ359441.1_Echis_carinatus_isolate_	СТАА	TATCCTTATAGCCZ	ACCGCCTT	CTTTGGTTACG'	ICCTACCC	T G A G G A C A A A T A T C G
MK193094.1_Protobothrops_mucrosquamatus	TTAA	CATCCTAATAGCCZ	ACTGCTTT	CTTTGGCTACG'	TACTACCA	T G <mark>aggacaaatatc</mark> a
KX019144.1_Trimeresurus_stejnegeri_	СПАА	TATCCTAATAGCT	ACAGCCTT	CTTTGGCTATG	ICCIACCA	TG<mark>A</mark>GG<mark>C</mark>CAAATATCC
HM567533.1_Protobothrops_jerdonii	TTAA	TATCCTAATAGCC	ACCTCCTT	CTTTGGCTATG'	ICTTACCA	TG <mark>GGGC</mark> CAAATATC <mark>A</mark>
LC094069.1_Sinomicrurus_macclellandi_iwasakii	СТАА	CACTCTTATAGCA	ACAGCTTT	CTTTGGTTACG'	ICCTACCC	TG<mark>AGG</mark>ACAAATATCC
FR693730.1_Ophiophagus_hannah	СТАА	TACCCTAATAGCA	ACAGCCTT	CTTTGGCTACG	ICCIACCA	TGAGGCCAAATATC C
KU527540.1_Naja_kaouthia	CTGG	TATCCTTATAGCA	ACAGCCTT	CTTCGGATACG	ICCICCA	TGAGGACAAATATC A
GQ225657.1_Naja_naja_naja_	CTGG	TATCCTTATAGCA	ACAGCCTT	CTTCGGATACG	TCCTCCCA	TGAGGACAAATATC A
U69859.1_Python_reticulatus	CTCA	CACACTAATAGCC2	ACCGCTTT	TTTTGGTTACG'	ICCTTCCA	TGAGGACAAATATCA
JX401136.1_Python_bivittatus	CTCA	CACACTCATAGCA	ACCGCCTT	CTTCGGATATG'	ICCICCA	TGAGGACAAATATCA
AY099983.1_Python_molurus	CICA	CACACTTATGGCA	ACCGCCTT	CTTCGGATATG'	ICCICCA	TGAGGGCAAATATCA
LC105627.1_Enhydris_enhydris	СТАА	TATCCTAATAGCA	ACAGCCTT	CTTCGGTTATG	ICCTACCA	TGAGGACAAATATCA
DQ902119.1_Gonyosoma_prasinum_	CTAA	CACCCTAATAGCA	ACAGCCTT	CTTTGGTTACG	ICCTACCA	TGGGGACAAATATCA
AF471084.1_Gonyosoma_oxycephalum_	CTAA	CACCCTCATAGCA	ACAGCTTT	CTTCGGTTACG	ICCTACCA	TGGGGACAAATATC A
DQ902121.1_Coelognathus_radiatus	TTAA	TATTCTCATAGCA?	ACAGCCTT	T T T T G G A T A T G '	TATTACCA	T G A G G A C A A A T A T C A
AY486921.1_Platyceps_rhodorachis_	ATAA	TATTCTCATAGCA?	ACAGCCTT	CTTCGGATACG	IGCIGCCA	TGAGGACAAATATCC
DQ902128.1_Coelognathus_flavolineatus	СТАА	TACCCTTATAGCA?	ACAGCCTT	CTTTGGCTATG	ICTTACCC	TGAGGACAAATATCA
AY486929.1_Ptyas_korros	СТАА	TATCCTTATAGCA?	ACAGCCTT	CTTTGGTTATG'	ICCTACCG	TGAGGACAAATATCA
AY611998.1_Ptyas_mucosus	CTAA	TACCCTAATAGCA?	ACAGCCTT	CTTCGGCTACG	ICCTACCA	TGAGGACAAATATCA
AF471054.1_Ptyas_mucosa	СТАА	TACCCTAATAGCA	ACAGCCTT	CTTCGGCTACG	ICCIACCA	TGAGGACAAATATCG
EF076709.1_Orthriophis_taeniurus	СТАА	TATCCTCATGGCA?	ACAGCCTT	CTTCGGCTACG	TACTACCA	TGAGGACAAATATCA
DQ902132.1_Orthriophis_taeniurus	CTAA	TATCCTTATAGCA?	ACAGCCTT	CTTTGGCTACG	ICCTACCA	TGAGGACAAATATCA
DQ902118.1_Oreophis_porphyraceus	СТАА	AATCCTTATAGCA?	ACAGCCTT	CTTTGGTTACG	TCCTTCCA	TGAGGACAAATATCA
DQ902115.1_Euprepiophis_mandarinus	TIAA	TATCCTAATAGCG2	ACAGCATT	CTTTGGATACG	TCCTGCCA	TGAGGACAAATATCA

AF471076.1_Daboia_russelii
GQ359441.1_Echis_carinatus_isolate_
MK193094.1 Protobothrops mucrosquamatus
KX019144.1 Trimeresurus stejnegeri
HM567533.1 Protobothrops jerdonii
LC094069.1 Sinomicrurus macclellandi iwasakii
FR693730.1 Ophiophagus hannah
KU527540.1 Naja kaouthia
GQ225657.1 Naja naja naja
U69859.1_Python_reticulatus
JX401136.1_Python_bivittatus
AY099983.1_Python_molurus
LC105627.1_Enhydris_enhydris
DQ902119.1_Gonyosoma_prasinum_
AF471084.1_Gonyosoma_oxycephalum_
DQ902121.1_Coelognathus_radiatus
AY486921.1_Platyceps_rhodorachis_
DQ902128.1_Coelognathus_flavolineatus
AY486929.1_Ptyas_korros
AY611998.1_Ptyas_mucosus
AF471054.1_Ptyas_mucosa
EF076709.1_Orthriophis_taeniurus
DQ902132.1_Orthriophis_taeniurus
DQ902118.1_Oreophis_porphyraceus
DQ902115.1_Euprepiophis_mandarinus

	5 <u>0</u>	360 <u>3</u>	7 Q 3	80 390	400
	I T T T G A G C A	GCAAC <mark>A</mark> GT <mark>A</mark> AT	CACTAACCTC	CTAACAGCAATCCC	ATATCTAGGGACCTCC
TTCTGAGCAGCAACAGTAATTACAAACCTTCTTAACGGCATCCCTTATCGGGGACAACA TTCTGAGCAGCAACAGTAATTACAAACCTCCTAACGGCATCCCTTATCTAGGAACAACC TTCTGGGCGCAACAGTAATCACAAACCTCCTAACGGCATTCCCTATCTAGGAACAACA TTCTGAGCAGCAACAGTAATCACAAATCTCCCTAACGGAATTCCCCTATCTAGGAACTAACA TTCTGAGCAGCAACAGTAATCACAAATCTCCCTTACTGGAATTCCCCTATCTAGGAACTAACA TTCTGAGCGGCAACAGTAATCACAAATCTCCCTAGGAATTCCCCATACTAGGAATTACA TTCTGAGCGCGCAACAGTAATCACCAATCTCCCTACGGAATCCCATACCTAGGAATTACA TTCTGAGCGCGCAACCGTAATTACAAACCTACTCACTGGCGTACCATACTAGGGAATCACA TTCTGAGCGCGCAACCGTAATTACCAACCTACTCACTGCCGTACCATACTAGGGACTCA TTCTGAGCGCGCAACCGTAATTACCAACCTATTAACCGCCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACCGTAATTACCAACCTATTAACCGCGCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACCGTAATTACCAACCTATTAACCGCGCATCCCATATCTAGGCACAACC TTCTGAGCGGCAACAGTAATTACCAACCTATTAACGGCAGTCCCATATCTAGGAAACCCA TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGGCAGTCCCATACTTGGCATACCA TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGCAGTCCCATACTTGGCATACCA TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGCCGTTCCGATACATTGGCAACACC TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGCCATTCCGATACATTGGCAACACC TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGGCATTCCGATACATTGGCAACACC TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGCCATTCCATACATCGCAACACC TTCTGGGCGCAACAGTAATTACTAACCTACTATACAGGCCATTCCATACATCGCAACACC TTCTGAGCCGCAACAGTAATTACTAACCTGATAACAGCCATTCCATACATCGCACACCC TTCTGAGCCGCAACAGTAATTACTAACCTACTACAGGCATTCCATACATCGCACACCC TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACAGCCATTCCATACATCGCCACACCACC TTCTGAGCGCGCAACAGTAATTACAAACCTGTTAACAGCCATTCCATACATCGCCACACCACC TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACAGCTATTCCATACATCGCCACACCACCACCACCACCACCACCACCACCACCACCA		GCAACAGTAA1			TTACCTTGGCACCTCC
TTTTGAGCGGCAACAGTAATCACAAACCTCCTAACCGCATCCCTTATTAGGAACTACA TTCTGAGCAGCAACAGTAATCACAAACCTCCTCACTGGAATCCCCTATCTAGGAACTACA TTCTGAGCAGCAACAGTAATCACAATCTCCTTACTGGAATCCCCATACCTAGGAATCACA TTCTGAGCAGCAACAGTAATCACCAATCTCCTTACTGGAATCCCCATACCTAGGAATCACA TTCTGAGCGCAACAGTAATCACCAATCTCCTTACTGGAATCCCCATACCTAGGAATCACA TTCTGAGCGCAACAGTAATCACAACCTACTGCATGCGATCCCATACCTAGGAATCACA TTCTGAGCGCCAACAGTAATCACCAATCTCCTACTGGAATCCCATACCTAGGAATCACA TTCTGAGCGCCAACAGTAATTACAACCTACTACGCGTACCATACCTAGGAATCAC TTCTGAGCGCCAACAGTAATTACAACCTACTACTGCGCGTACCATACTTAGCCACACC TTCTGAGCGCCAACAGTAATTACAACCTACTAACGCGCGTACCATACTTAGCACAACC TTCTGAGCGCAACAGTAATTACCAACCTATTAACCGCCGTACCATACTTAGCACACA TTCTGAGCGCAACAGTAATTACCAACCTATTAACCGCGCGTACCATACTTAGGCACACA TTCTGAGCGCAACAGTAATTACTAACCTACTAACAGCACTCCCATACATTGGCAACACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCACTCCCATACATTGGCAACACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCCATTCCCATACATTGGCAACACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCCATTCCCATACATTGGCAACACA TTCTGAGCGCCAACAGTAATTACTAACCTACTAACAGCCATTCCCATACATTGGCAACACA TTCTGAGCGCCAACAGTAATTACTAACCTACTAACAGCCATTCCCATACATCGCAACACT TTCTGAGCCGCAACAGTAATTACTAACCTACTAACAGCCATTCCCATACATCGCAACACCA TTCTGAGCCGCAACAGTAATTACAAACCTACTAACAGCCATTCCATACATCGCAACACCA TTCTGAGCCGCAACAGTAATTACAAACCTACTAACAGCCCATTCCATACATCGCACAACC TTCTGAGCCGCAACAGTAATTACAAACCTACTTACACGCCATTCCATACATCGCACAACCA TTCTGAGCGCGCAACAGTAATTACAAACCTACTTAACAGCTGCTATACATCGCCACAACCACCACCACAACCACCACTTCGAACCACACGCAACACACTTTCGAACCGCCAACACACAC		GCAACCGTAA1			
TTC TGGGC GCAAC AGT AATC AC A AACC TTC TC AC TG AATT CC CTA CC TA GG AA CTAC A TTC TGGGC AGCAAC AGT AATC AC AATC TC CTC ACAG CAATT CC CTA CG AA CTAC A TTC TGAGC AGCAAC AGT AATC AC CAATC TC CTT ACT GC AAT CC CC AT AC CTA GG AA TT AC A TTC TGAGC AGCAAC AGT AATC AC CAATC TC CTT ACT GC AT AC CC AT AC CTA GG AATT AC A TTC TGAGC GC AAC AGT AATC AC CAATC TC CTC ACT GC AT AC CC AT AC CTA GG AATT AC A TTC TGAGC AGCAAC AGT AATT AC CAATC TT C TC ACT GC AT AC CC AT AC CTA GG AATT AC A TTC TGAGC TG CAACC GT AATT AC CAACC TAT TAACT GC CGT AC CAT AC TT AG CG C AC AC C TTC TGAGC TG CAACC GT AATT AC CAACC TAT TAACT GC CGT AC CAT AC TT AG CG C AC AC C TTC TGAGC GC AAC AGT AATT AC CAACC TAT TAAC CG CAT AC CAT AC TT AG CG C AC AC C TTC TGAGC GC AAC AGT AATT AC CAACC TAT TAACC GG AGT AC CAT AC TT AG CG C AC AC C TTC TGAGC GC AAC AGT AATT AC CAACC TAT TAAC CG CAT CC CAT AC AT T GG C AC AC C TTC TGAGC AGCAAC AGT AATT AC AAC CTAC TAACAG C AGT CC CAT AC AT T GG C AT AC A TTC TGGGC AGCAAC AGT AATT AC TAACC TAC TAACAG C CAT CC CC TAT AC TT GG C AT AC A TTC TGGGC AGCAAC AGT AATT AC TAACC TAC TAACAG C CAT CC CC TAT AC TT GG C AT AC A TTC TG AGC AGCAAC AGT AATT AC AAACC TAC TAACAG C CAT CC CC TAT AC TT GG C AT AC A TTC TG AGC AGCAAC AGT AATT AC AAACC TAC TAACAG C CAT TC CAT AC AT C GG AA CAT C TTC TG AGC CG CAACAGT AATT AC AAACC TAC TT AC AG C C CAT T CC AT AC AT C GG AA CAT C TTC TG AGC CG CAACAGT AATT AC AAACC TAC TT AC AG C CAT T C CAT AC AT C GG AA CAT C TTC TG AGC CG CAACAGT AATT AC AAACC TAC TT AC AG C TAT TC CAT AC AT C GC AC AAC A TTC TG AGC CG CAACAGT AATT AC AAACC TAC TT AC AG C TAT TAC CAT C GC AC AAC A TTC TG AGC CG CAACAGT AATT AC AAACC TAC TT AC AG C TAT TAC CAT C AT C	TTTGAGCG	GCAACAGTAAT		CTAACCGCCATCC	TTATTTAGGAACAACC
	TTCTGGGCG	GCAACAGTAAT	CACAAACCTI	CTCACTGCAATTCC	CTACCTAGGAACTACA
TTCTGAGCAGCAACAGTAATCACCAATCTCCCTTACTGGAATCCCATACCTAGGAATTACA TTCTGAGCAGCAACAGTAATCACCAATCTCCTCACTGGAATCCCATACCTAGGAATTACA TTCTGAGCCGCAACCGTAATTACCAACCTATTAACTGCCGTACCATACTTAGGCACACC TTCTGAGCCGCAACGTAATTACCAACCTATTAACCGCCGTACCATACTTAGGCACAACC TTCTGAGCCGCAACAGTAATTACCAACCTATTAACCGCCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACAGTAATTACCAACCTATTAACCGCCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACAGTAATTACTAACCTACTAACGGCAGTCCCATACATTGGCAACCACA TTCTGAGCGGCAACAGTAATTACTAACCTACTAACAGCAGTCCCATACATTGGCACACCA TTCTGGGCGGCAACAGTAATTACTAACCTACTAACAGCAGTCCCATACATTGGCAACCACA TTCTGGGCGGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCATACATTGGCAACCACA TTCTGGGCAGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCATACATTGGCATACCAC TTCTGGGCAGCAACAGTAATTACTAACCTACTAACAGCCATCCCCTATATTGGCATACATC TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCCATTCCATACATGGCATACCAC TTCTGGGCAGCAACAGTAATTACTAACCTACTATGGCCGTCCCATACATCGGCATACCAC TTCTGAGCCGCAACAGTAATTACAAACCTACTATAGCGCGTACCATACATCGGCACAACC TTCTGAGCCGCAACAGTAATTACAAACCTGTATAGCGCGTACCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTATACGGCCATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTACAGCTATTCCATACATCGGCACAACACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTATTCCATACATCGGCACAACACA TTCTGAGCGGCAACAGTAATTACAAACCTACTTACAGCTATTACCATACATCGCCACACACA	TTCTGAGCA	GCAAC <mark>A</mark> GT <mark>A</mark> AT	CACAAATCTC	CTCACAGCAATTCC	CTATCTAGGAACAACA
TTCTGAGCAGCAACAGTAATCACCAATCTCCCTCACTGGAATCCCATACCTAGGATTACA TTCTGAGCCGCAACCGTAATTACACAACCTACTAACGCGCGTACCATACTTAGGCACAACC TTCTGAGCGCGCAACCGTAATTACCAACCTATTAACGGCGCGTACCATACTTAGGCACAACC TTCTGAGCGCGCAACAGTAATTACCAACCTATTAACGGCGCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACAGTAATTACCAACCTATTAACCGGCGTACCATACTTAGGCACAACC TTCTGAGCGGCAACAGTAATTACCAACCTATTAACCGGCGTCCCATACATTGGCACAACA TTCTGAGCGGCAACAGTAATTACTAACCACCTACTAACAGGCAGTCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACTACCTACTAACAGGCAGTCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGGCAGTCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGGCGTCCCCATACATCGGCATACCA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGGCCGTCCCATACATCGGAACAACC TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGGCCGTTCCATACATCGGAACAACC TTCTGAGCCGCCAACAGTAATTACAAACCTGTTAACAGGCCGTTCCATACATCGGAACAACC TTCTGAGCCGCCAACAGTAATTACAAACCTGTTAACCTGAATTCCATACATCGGCACAACA TTCTGAGCCGCCAACAGTAATTACAAACCTGTTACAGGCTATCCATACATCGGCACAACA TTCTGAGCCGCCAACAGTAATTACAAACCTGTTACAGGCTGCACATCCATC	I T C T G A G C A	GCAAC <mark>A</mark> GT <mark>A</mark> AI	CACCAATCTC	CTTACTGCAATCCC	ATACCTAGGAATCACA
ITCTGAGCCGCAACCGTAATTACAAACCUACUACUGCCGCGCGCGACACACGCATACTACGGCACAAC TTCTGAGCTGCAACCGTAATTACAAACCUATTAACTGCCGCGTACCATACTTAGGCACAACC TTCTGAGCGCCAACCGTAATTACCAACCUATTAACCGCCGTACCATACTAGGCACAACC TTCTGAGCGGCAACAGTAATTACAACCUACUACUACGCATTCCCATACATTGGCACAACA TTCTGAGCGGCAACAGTAATTACTAACGTACTAACAGCAGTCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACGTACTAACAGCAGTCCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACGTACTAACAGCAGTCCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCATACATTGGCACAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCTACATTGGCACAACA TTCTGGGCAGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCTACATCGGAACACA TTCTGGGCAGCAACAGTAATTACTAACCTACTAACAGCCGTTACCATACATCGGAACACA TTCTGGGCGCAACAGTAATTACTAACCTACTAACAGCCGTTTCCATACATCGGAACACC TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACAGCCGTATTCCATACATCGGAACAACC TTCTGGGCGCAACAGTAATTACAAACCTGTTAACGCTATTCCATACATCGGCACAACA TTCTGGGCGCAACAGTAATTACAAACCTGTTAACGCTATTACCATACATCGCACAACA TTCTGAGCGCGCAACAGTAATTACAAACCTACTTACAGCTGCTTACATCGCACACGCGCACAACA TTCTGAGCGCCAACAGTAATTACAAACCTACTTAACAGCTGCTTACATCGCCACACACGCGCACAACA TTCTGAGCGCCAACAGTAATTACAAACCTACTACAGCTGCTTATACCGCCATACATCGCCACAACA TTCTGAGCGCCAACAGTAATTACAAACCTACTACAGCTGCTCACATACAT	I T C T G A G C A	GCAAC <mark>A</mark> GT <mark>A</mark> AT	CACCAATCTC	CTCACTGCAATCCC	ATACCTAGGAATTACA
TTCTGAGCTGCAACCGTAATTACCAACCTATTAACTGCGCGTACCATACTTAGGCACAACC TTCTGAGCGCGCAACAGTAATTACCAACCTATTAACGCGCGTACCATACTTAGGCACAACC TTCTGAGCGCGCAACAGTAATTACTAACCTACTAAGCGCGTACCATACGATGGCA CAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAAGGCGAGTCCCATACATTGGCA CAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAAGAGCCATCCCCTATATTGGCA CAACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAAGAGCCATCCCCTATATTGGCA CAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCCATTCCATACATCGGA CAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCCCTACATTCCATACATCGGA CAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCCCTACATTCCATACATCGGA CAACA TTCTGAGCGCCAACAGTAATTACAAACCTACTTAACAGCCCTAACTTCCATACATCGGAACAACC TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTCAATTCCATACATCGGAACAACC TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATACCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTACATACA	TTCTGAGCC	GCAAC <mark>CGT</mark> AAT	TACAAACCTA	CTCACTGCCGTACC	ATACCTAGGTACATCA
TTCTGAGCCGCAACAGTAATTACACAACCTACTACAGCCGTACCATACGCAACGCACACA TTCTGAGCCGCAACAGTAATTACACAACCTACTAACAGCAGTACCATACATTGGCAACTCA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCAGTACCATACATTGGCAACACA TTCTGGGCAGCAACAGTAATTACAAACCTACTAACAGCCATACATCGCATACATTGGCATACAT TTCTGGGCAGCAACAGTAATTACAAACTTACTAACAGCCATACCATACATTGGCATACAT TTCTGGGCAGCAACAGTAATTACTAACCTACTAACAGCCATACATCGCATACATTGGCATACAT TTCTGGGCAGCAACAGTAATTACTAACCTATTGACGCGCATTCCATACATTGGAACACA TTCTGGGCGCAACAGTAATTACAAACTTACTAACGCGCATTCCATACATCGGAACAACT TTCTGGGCGCAACAGTAATTACAAACTTACTAACGGCCATTCCATACATCGGAACAACT TTCTGGGCGCAACAGTAATTACAAACCTACTTACAGCGTATTCCATACATCGGCACAACA TTCTGGGCGCCAACAGTAATTACAAACCTACTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCGCGCAACAGTAATTACAAACCTACTTACAGCTGTGCACCTTATATCGGCACAACA TTCTGAGCGCCAACAGTAATTACAAACCTACTACAGCTGCGCACTATATATCGGCACAACA		GCAACCGTAA1			
TTCTGAGCGGCAACAGTAATTACTAACCGACTACGAGTACCATACATTGGCAACAACA TTCTGAGCAGCAACAGTAATTACTAACCGTACTAACAGCAGTACCATACATTGGCAACACA TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGCAGTCCCCATACATTGGCATACACA TTCTGGGCAGCAACAGTAATTACTAACCGTACTAACAGCCGTCCCCTATATTGGCAACAACA TTCTGGGCAGCAACAGTAATTACTAACCGTATTGACGCGCCATTCCATATATTGGAACAACT TTCTGAGCCGCAACAGTAATTACAAACCTGTTAAACCTCAATTCCATACATCGGCAACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTACAACGTATTCCATACATCGGCAACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTACAAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTACAAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTACAAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCCAACAGTAATTACAAACCTACTTACAAGCTACTCCATACATCGGCACAACA TTCTGAGCCGCCAACAGTAATTACAAACCTACTTACAGCTACTACCATACATCGCCACAACA TTCTGAGCGCGCAACAGTAATTACAAACCTACTACAGCTGCGCACCTTATATCGCCACAACA		GCAACCGTAA1			ATACTTAGGCACAACC
TTC TGAGC AGCAAC AGTAATTAC AAACCTACTAACAGCAGTC CCATA CATT GG AAACACA TTCTGAGCAGCAACAGTAATTACTAACGTACTAACAGCCGTCCCCTATAGTGGCATAACA TTCTGGGCAGCAACAGTAATTACTAACTATCGCGCCATTCCATACATCGGAACACT TTCTGAGCGCGCAACAGTAATTACTAACGTATTGACGCCGTTCCATATATTGGACCAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACCTCAATTCCATACATCGGACCAACA TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACCTCAATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTGATACTTACAGCTAATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTAATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGCTACTTACATCGGCACAACCA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTGCACCTTATATCGGCACAACA TTCTGAGCGGCAACAGTAATCACAAACCTACTACAGCTGCGCGTATACCATCGGCACAACA TTCTGGAGCGCAACAGTAATCACAAACCTACTAACAGCTGCTGCCATATATCGGCACAACA	TTCTGAGCG	GCAACAGTAAT	TACTAACCTA	CTAACAGCAGTAC	ATACATTGGCACAACA
TTCTGAGCAGCAACAGTAATTACTAACCTACTAACAGGCATCCCCTATATTGGCATAACA TTCTGGGCAGCAACAGTCATCACAAACTTACTAACAGCGCATACCATCGGAACATCT TTCTGAGCAGCAACAGTAATTACTAACCTATTGACGCATTCCATACATCGGAACAACT TTCTGAGCCGCAACAGTAATTACAAACCTACTTAAGCTCAATTCCATACATCGGAACAACC TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATACCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATACCATACATCGGCACAACA TTCTGAGCGCGCAACAGTAATCACAAACCTACTTACAGCTACCATACATCGGCACAACA TTCTGAGCGCGCAACAGTAATCACAAACCTACTACAGCTGCACCTTATATCGGCACAACA TTCTGAGCGCCAACAGTAATCACAAACCTACTACAGCTGCACCTTATATCGCCACAACA TTCTGAGCGCCAACAGTAATCACAAACCTACTACAGCTGCACCTTATATCGCCACAACA TTCTGAGCGCCAACAGTAATCACAAACCTACTACAGCTGCCACCTTATATCGCCACACA TTCTGAGCAGCAACAGTAATTACAAACCTACTACAGCCGCTACCATATATCGGCACAACA	TTCTGAGCA	GCAACAGTAAT	TACAAACCTA	CTAACAGCAGTCCC	ATACATTGGAAACACA
TTCTGAGCAGCAACAGTCATCACAAACTTACTAACAGGCGTACCATACATCGGAACATCT TTCTGAGCAGCAACAGTAATTACTACTAACTTACTAAGAGGCGTTTCCATACATCGGAACAACT TTCTGAGCCGCAACAGTAATTACAAACCTGTTAAGCTGAATTCCATACATCGGAACAACA TTCTGAGCCGCAACAGTAATTACAAACCTACTTACAGGTATACCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAAACCTACTTACAGGTATACCATACATCGGCACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTTACAGGTTATACCATACATCGGCACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGGTTGTGCCATATATCGCCACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGGTTGTGCCATATATCGCCACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGGTTGTGCCATATATCGCCACACAA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGGTTGTGCCATATATCGCCACACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGGCTGTGCCATATATCGCCACACA TTCTGAGCGGCAACAGTAATTACAAACTACTACAGCCGTACCATATATCGCCACACA TTCTGAGCAGCAACAGTAATTACAAACTACTACTACAGCCGTACCATACATCGCCACAACA	I TCTGAGCA	GCAAC <mark>A</mark> GT <mark>A</mark> AT	TACTAACCTA	CTAACAGCCATCCC	CTATATTGGCATAACA
TTCTGAGCAGCAACAGTAATTACTAACCTATTGACGGCATTCCATATATTGGAACAACT TTCTGAGCCGCAACAGTAATTACAAACCTGTTAACCTCAATTCCATACATCGGAACAAC TTCTGAGCCGCAACAGTAATTACAAACCTGTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATACCATACATCGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTACAGCTGCACCTTTATACGGCACAATA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGCTGCGCCTTATATCGGCACAATA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGCTGCGCCGTATATATCGGCACAATA TTCTGAGCGGCAACAGTAATTACAAACCTACTACAGCTGCGCCATATATCGGCACAATA TTCTGAGCGGCAACAGTAATTCACAAACCTACTACAGCCGTGCCATATATCGGCACAACA TTCTGAGCGGCAACAGTAATTCACAAACTTACTACAGCCGTGCCATATATCGGCACAACA TTCTGAGCGGCAACAGTAATTCACAAACTTACTACAGCCGTACTACCATACATCGCACACA	I T C T G G G C A	GCAAC <mark>A</mark> GT <mark>C</mark> AI	CACAAACTTA	CTAACAGCCGTACC	A <mark>TA</mark> CA <mark>TC</mark> GGAACATCT
TTCTGAGCCGCAACAGTAATTACAAACCHGTHAACCTGAATTTCCATACAHCGGAACAACC TTCTGAGCCGCAACAGTAATCACAAACCHACTTACAGCTATTCCATACATCGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGCTATACCGTATACATCGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCTGCACCTTATATCGGCACAATA TTCTGAGCGGCAACAGTAATTACAAACCTACTAACAGCTGCGCGTATATATCGGCACAATA TTCTGAGCGGCAACAGTAATTACAAACCTACTAACAGCTGTGCGCATATATCGGCACAACA TTCTGAGCGGCAACAGTAATTACAAACCTACTAACAGCTGTGCGCATATATCGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACTTACTAACAGCCGTACGCGTATTATCGGCACAACA TTCTGAGCGCAACAGTAATTACAAACTTACTACAGCCGTACCATATATCGGCACAACA	TTCTGAGCA	GCAAC <mark>A</mark> GT <mark>A</mark> AT	TACTAACCTA	TTGACGGCCATTCC	ATATATTGGAACAACT
TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGGTATTACATCGCACAATGGCACAACA TTCTGAGCCGCAACAGTAATCACAAACCTACTTACAGGTACTACATGGCGCACAACA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGGTGCGCGTATATATCGGCACAAAA TTCTGAGCGGCAACAGTAATCACAAACCTACTAACAGCCGTACCATATATCGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACTTACTACAGCCGTACCATATATCGGCACAACA	TTCTGAGCC	GCAAC <mark>AGT</mark> AAT	TACAAACCTC	TTAACCTCAATTCC	ATACATCGGAACAACC
TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCTATACATCGGCACAAATA TTCTGAGCAGCAACAGTAATTACAAACCTACTAACAGCTGCCCTATATATCGGCACAATA TTCTGAGCGGCAACAGTAATCACAAACCTACTAACAGCTGTGCCGTATATATCGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACTTACTAACAGCCGTACCATATATCGGCACAACA TTCTGAGCAGCAACAGTAATCACAAACCTTACTACAGGCGTACCATACATCGGCACAACA		GCAACAGTAA1			
TTCTGAGCGGCAACAGTAATCACAAACCTACTAACAGCTGTGCGATATATGGGCACAACA TTCTGAGCAGCAACAGTAATTACAAACTTACTAACAGCCGTACCATATATCGGCACAACA TTCTGAGCAGCAACAGTAATCACAAACCTACTTACAGGCGTACCATACATCGGCACAACA		GCAACAGIAAI GCAACAGTAAT		CTACAGCIAIACC	
TTCTGAGCAGCAACAGTAATTACAAACTTACTAACAGCCGTACCATATATC <mark>GGC</mark> ACAACA TT <mark>CTGAGCAGCAACAGTAATCACAAACCTACTTACAGC</mark> CGTA <mark>CCATA</mark> CATC <mark>GGC</mark> A <u>CAAC</u> A	TTCTGAGCG	GCAACAGTAAT	CACAAACCTA	CTAACAGCTGTGC	ATATATCGGCACAACA
TTCTGAGCAGCAACAGTAATCACAAACCTACTTACAGCCGTACCATACATCGGCACAACA	TTCTGAGCA	GCAACAGTAAT	TACAAACTTA	CTAACAGCCGTACC	ATATATCGGCACAACA
	TTCTGAGCA	GCAAC <mark>a</mark> gt <mark>a</mark> at	CACAAACCTA	CTTACAGCCGTACC	ATACATCGGCACAACA

410	420	430	440	450	460
CTAACCACC	TGACTTTGG	GGCGGATTCT	CTATCAACGA	CCCAACCCTT	ACCCGCTTCTTC
CTGACAACC	TGACTCTGG	GGTGGCTTCT	CCATTAACGA	CCCCACGCTT	ACCCGATTCTT
CTAACTACC	TGACTATGA	GGGGGCTTCG	CAATCAGCGA	CCCCACACTG	ACCCGATTCTT
CTTACCACA	TGACTATG A	GGCGGCTTCG	CAATCAACGA	CCCAACACTA	ACTCGCTTCTTT
CTAACAACA	TGATTATG A	GGCGGCTTCG	CAATTAATGA	CCCAACACTA	ACCCGATTTTT
ATTACAACT	TGACTTTGA	GGGGGTTTCT	CCATCAACGA	TCCAACTCTC	ACCCGCTTTTT
CTAACAACC	TGACTATG A	GGGGGTTTCT	CTATCAACGA	CCCAACTCTA	ACCCGTTTCTTC
CTAACAACA	TGACTTTGA	GGGGGGTTCT	CTATTAACGA	CCCAACCCTC	ACCCGATTTTT
CTAACAACA	TGACTTTGA	GGGGGGTTTT	CTATTAACGA	CCCAACCCTC	ACCCGATTTTT
CTAACAACC	TGGCTTTGA	GGCGGATTCG	CAATCAACGA	CCCCACCTA	ACACGATTCTT
CTAACAACC	TGATTATGA	GGAGGATT CG	CAATCAATGA	CCCCACCTC	ACACGATTTTT
CTAACAACC	TGGTTATGA	GGAGGATTC G	C <mark>AAT</mark> CAATGA	T <mark>CC</mark> CACCCTC	ACACGATTTTT
CTTACAACC	TGATTATG G	GGCGGCTTCT	C <mark>aat</mark> caatga	CCCCACCTT	ACCCGATTCTT
CTGACTGTC	TGACTCTGA	GGGGGATTCT	CAATCAACGA	T <mark>CC</mark> C <mark>AC</mark> A <mark>CT</mark> A	ACTCGATTCTTT
TTAACTACA	TGACTGTG A	GGTGGGTTCT	C <mark>AATCAAC</mark> GA	CCCCACACTC	ACCCGATTCTTC
CTTACCACA	TGGCTCTGA	GGTGGGTTCT	C <mark>AAT</mark> TAATGA	T <mark>CC</mark> CACCCTA	ACTCGATTTTT
CTTACAACA	. TGGCTCTG G	GGTGGATTTT	C <mark>AAT</mark> CAACGA	T <mark>CC</mark> A <mark>ACTCT</mark> A	ACCCGATTCTTC
CTAACCACC	TGACTTTGA	GGCGGG <mark>ATT</mark> CT	C <mark>AATCAAT</mark> GA	TCCCACCTA	ACCCGATTCTTT
CTAACTACC	TGACTATGA	GGTGGTTTCT	CAATCAACGA	CCCAACTCTC	ACCCGATTCTTC
CTAACCACC	TGATTATGA	GGAGGCTTCT	C <mark>AAT</mark> TAATGA	T <mark>CC</mark> A <mark>ACTCT</mark> A	ACCCGATTCTTT
CTAACCACC	T G A T T A T G A	GG <mark>A</mark> GGC TTCT	C <mark>AATTAAT</mark> GA	T <mark>CC</mark> AACTCTA	ACCCGATTCTTT
CTAACAACC	TGACTCTGG	GGAGGATTCT	C <mark>AAT</mark> TAACGA	CCCCACTCTA	ACCCGATTTTC
CTAACAACC	TGACTCTGA	GGGGGCTTCT	CAATTAACGA	CCCCACCCTA	ACTCGATTTTT
CTCACTACT	TGATTCTG A	GGGGGT TTCT	CAATTAACGA	CCCCACCTA	ACTCGATTCTTC
CTAATCACT	TGACTCTGA	GGGGGTTTCT	CAATTAATGA	T <mark>CCTAC</mark> CCTT	ACACGATTCTTC
					410 420 430 440 450 CTAACCACCTGACTTTGGGGCGGCGGATTCTCTATCAACGACCCAACCCTT CTGACAACCTGACTGTGGGGTGGCTTCTCCATTAACGACCCCAACGGTT TAACAACGTGACTATGAGGGGGCTTCCGCAATCAACGACCCAACACTA CTAACAACATGACTATGAGGCGGCTTCCGCAATCAACGACCCAACACTA ATTACAACATGATTATGAGGCGGCTTCCCATCAACGACCCAACACTA CTAACAACATGACTATGAGGGGGTTTCTCATCAACGACCCAACACTA CTAACAACATGACTTTGAGGGGGTTTCTCTATTAACGACCCAACACTCT CTAACAACATGACTTTGAGGGGGTTTCTCTATTAACGACCCAACCCTC CTAACAACATGACTTTGAGGGGGGTTTCTCTATTAACGACCCAACCCTC CTAACAACATGACTTGAGGGGGGTTCCCATCAACGACCCAACCCTC CTAACAACATGACTTGAGGGGGGTTCCCAATCAACGACCCAACCCTC CTAACAACCTGACTTGAGGGGGGTTCCGCAATCAACGACCCACCC

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	470	480	490	500	510	520
Li	GCTCT	CACTTCATCO	TACCATTTAT	CATTATCTCA	CTATCATCTA	TTCACATCCTCCTG
s_isolate_	GCCCT	CACTTTATCO	TCCCATTCAC	CATCATCTCC	T <mark>TATCTTC</mark> TA	TCCATATCCTCCTC
mucrosquamatus	GCTCTC	CACTTCATCO	TCCCATTCAC	CATTATCTCT	ATATCTTCAA	TCCATATTCTACTC
stejnegeri_	GCCCTZ	CACTTTATCO	TCCCATTCGC	CATCATCTCT	ATATCTTCAA	TCCACATTCTCCTA
jerdonii	GCTCTC	CACTTCATCO	TCCCATTCAC	CATCATCTCT	ATATCCTCAA	TCCACATCCTACTT
nacclellandi_iwasakii	GCCCTC	CACTTCATCO	TCCCATTTAT	TATCGTCTCG	ТТАТСТТСАА	TCCATGTTATTCTA
annah	GCCCTZ	CATTTTATCO	TCCCATTCAT	CATCATTCA	CTAACCTCAA	TCCACATCATTCTA
	GCCCTZ	CACTTTATT	TACCATTTAT	CATCATCTCA	CTATCCTCAG	TCCATATTATCTTA
a_	GCCCT	CATTTTAT T(TACCATTTAT	CATTATCTCA	CTATCCTCGG	TACATATCATCTTA
us	GCACT/	CATTTAT T	TACCATTCGC	GATTATCTCA	.T <mark>TATCCTC</mark> AT	TACACGTTATCTTA
atus	GCACT7	CATTTCATCO	TACCATTCGC	AATCATCTCT	'A <mark>TATC</mark> AT <mark>C</mark> AC	TACATATCATCCTA
5	GCACT7	CATTTCATCO	TACCATTCGC	AATCATCTCC	ATATCATCAC	TACACATCATCCTA
lris	GCCCTI	CACTTTATCO	CTCCCATTTAC	CCTCATCTCA	.CTCTCTTCAA	TCCACATCATCCTC
sinum_	GCCCTC	CACTTCATCO	TACCATTCGC	TATCATCTCA	.ATATCATCAA	TCCACATTATATTA
cephalum_	GCCCTC	CACTTCATCO	TACCATTCGC	CATTATCTCA	.CTATCCTCAA	TCCACATTATACTT
radiatus	GCTCTZ	CACTTTAT T(CTCCCATTTAC	TATCATTCT	'ATATCTTCAA	TTCACATTATACTT
lorachis_	GCCCTZ	CACTTCATC I	TACCATTCAC	CATTATCTCA	.CTATCCTCAA	TCCACATTATACTA
flavolineatus	GCCCTI	CACTTTATCO	CTTCCATTTAT	TATCATATCT	CTATCCTCAA	TTCACATTATACTA
	GCCCTC	CACTTTATT	TTCCATTCGC	TATCATCTCC	CTATCCACAA	TCCACATTATACTC
	GCCCTZ	CATTTTATCO	CTTCCATTCAT	TATCATCTCA	ATATCCTCAA.	TCCACATCATACTA
	GCCCTZ	CATTTTATCO	CTTCCATTTAT	TATCATCTCA	ATATCCTCAA	TCCACATCATACTA
aeniurus	GCCCT	CACTTTATCO	TTCCATTTAC	TATTATCTCA	ATATCCTCAA	TCCACATCATACTT
aeniurus	GCTCTC	CATTTTATCO	CTCCCATTTAC	TATTATCTCA	ATATCCTCAA.	TCCACATCATACTT
nyraceus	GCCCTI	CACTTTATCO	TTCCATTCAC	CATCATCTCG	GTATCCTCTA	TCCACATCATACTA
nandarinus	GCCCT	CACTTTATCO	TACCATTCAC	TATTATCTCA	ATATCCTCAA	TTATTATTATA

AF471076.1_Daboia_russelii
GQ359441.1_Echis_carinatus_isolate_
MK193094.1_Protobothrops_mucrosquamatus
KX019144.1_Trimeresurus_stejnegeri_
HM567533.1_Protobothrops_jerdonii
LC094069.1_Sinomicrurus_macclellandi_iwasak
FR693730.1_Ophiophagus_hannah
KU527540.1_Naja_kaouthia
GQ225657.1_Naja_naja_naja_
U69859.1_Python_reticulatus
JX401136.1_Python_bivittatus
AY099983.1_Python_molurus
LC105627.1_Enhydris_enhydris
DQ902119.1_Gonyosoma_prasinum_
AF471084.1_Gonyosoma_oxycephalum_
DQ902121.1_Coelognathus_radiatus
AY486921.1_Platyceps_rhodorachis_
DQ902128.1_Coelognathus_flavolineatus
AY486929.1_Ptyas_korros
AY611998.1_Ptyas_mucosus
AF471054.1_Ptyas_mucosa
EF076709.1_Orthriophis_taeniurus
DQ902132.1_Orthriophis_taeniurus
DQ902118.1_Oreophis_porphyraceus
DQ902115.1_Euprepiophis_mandarinus

	530
AF471076.1 Daboia russelii	C
GQ359441.1 Echis carinatus isolate	СТ
MK193094.1 Protobothrops mucrosquamatus	СТ
KX019144.1_Trimeresurus_stejnegeri_	СТ
HM567533.1_Protobothrops_jerdonii	СТ
LC094069.1_Sinomicrurus_macclellandi_iwasakii	тт
FR693730.1_Ophiophagus_hannah	СТ
KU527540.1_Naja_kaouthia	СТ
GQ225657.1_Naja_naja_naja_	СТ
U69859.1_Python_reticulatus	СТ
JX401136.1_Python_bivittatus	СТ
AY099983.1_Python_molurus	СТ
LC105627.1_Enhydris_enhydris	СТ
DQ902119.1_Gonyosoma_prasinum_	СТ
AF471084.1_Gonyosoma_oxycephalum_	СТ
DQ902121.1_Coelognathus_radiatus	СТ
AY486921.1_Platyceps_rhodorachis_	СТ
DQ902128.1_Coelognathus_flavolineatus	СТ
AY486929.1_Ptyas_korros	СТ
AY611998.1_Ptyas_mucosus	СТ
AF471054.1_Ptyas_mucosa	СТ
EF076709.1_Orthriophis_taeniurus	СТ
DQ902132.1_Orthriophis_taeniurus	СТ
DQ902118.1_Oreophis_porphyraceus	СТ
DQ902115.1_Euprepiophis_mandarinus	СТ

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C	CA	CC	A	CG	A		GG	C	T	C	A	A	C	AA	C	C	P	A T	Т	A	G	T	A	C	C 7	A	C I	C	C	G			Т	GZ	C		AA	AI	C	C	A
1 T	CA	CP	A		A	GC	50	c	Ť	c	A	A	т	AA	c	CC	c	C C	Ť	G	G	G	A	C 2	A Z	A	Cl	C	A	GZ	c	A	c	GZ	c	AZ	ÀA	A	c	C	A
Т	CA CA	C A	A'	TG	A A	AC	GC	С т	T T		A	G ∡	C	A A A A	C	C	Г г	C	Т	A A	G	G	A a	C	A 7	A	C 1	C	A A	G Z	T.	A	Т	GZ	Т	A / 2 2	A A	A 1 A 1	C		G
Ā	CA	CZ	A	CA	A	A	GC	ċ	Ť	C	A	G	с	AA	c	c	Z	VC	Ī	Т	G	Τ	A	C	C 2	A	TI	C	A	GZ	Т	A	т	GZ	т	AZ	ÀA	A	c	C	A
C A	CA CA	C A T A	A	CG CG	A A	A Z G C		C C	T T		A	G A	C T	A A A A	T C			C C	Т	A C	G G G	A	A A		A	A A	C1 C1	C C	A A	G Z	C	A A	C C	G Z G Z	C C	A / A /	A A A A	A 1 A 1	C C		A A
A	CA	TA	A	CG	A	G	G	c	Т	C	A	A	Т	AA	C	c	C	C	Т	C	G	C	A	C	7	A	Ċı	C	A	GZ	Т	A	C	GZ	C	A /	AA	A	С	C	A
c	CA	CG	A A	A G	A	A	50	A	T T	C	A	G	c	A A A A	c	CC	Z		Ť	A G	G	A	A		A <mark>A</mark>	A		C	A A	G Z	C	A	c	GP	c	A/ A/	AA AA	AI	c	C	A
C	CA			AG	A A	A	GC	A A	T	C	A	G	c	A A A A	C	C	Z		Т	A T	G	A	A	C	A 7	A		C	A	C Z	C	A	C	GZ	C	A Z	A A	A 1 A 1	C		A
Т	CA	CA	c	AG	A	G	GG	G	Ť	c	A	G	т	AA	c	c	C	T	Ť	Ġ	G	зT	A	c	۸Ż	A	C 1	C	Ġ	GZ	ċ	A	т	GZ	т	Al	A	AI	c	C	A
T T	CA CA	C A C A	C i	A G A G	A A	A (A (A G	T T	C/ C	A	G G	C T	A A A A	C T		A T		T	G A	G(G(A A	A A		4	A A	C1 C1	C C	A A	G Z	C	A A	T T	G A G A	C C	A / A /	AA AA	A 1 A 1	C C		G A
Т	CA	CA	C	AG	A	A	G	G	Т	C	A	G	c	AA	C	c	A		Т	G	G	A	A	C	AZ	A	C 1	C	A	GZ	C	A	Т	GZ	C	A /	AA	A	С	C	с
A T	C A C A		C	AG AG	A A	A (A (A C	T T	C C	A	A G	C T	A A A A	C C	CC		C	Ť	A A	GC	A	A A		4	A A	C 1	C	A T	c/ c/		A A	T T	G P G P	C C	A / A /	AA AA	A'I A J	C C	C	A A
Т	CA	CA	C	AG	A	A	G	A	T	C	A	G	c	A A	C	C	A		Т	A	G	A	A	C	C 7	A	T 1	C	A	G Z	C	A	C	GZ	C	A /	AA	A	Т	C	A
A	CA	CA	c	AG	A	A	50	A	T	Cz	À	G	c	A A	c	C	Z	ΔT	Ì	A	G	A	A	C	۲ A	A	C 1	c	A	GZ	T	A	т	GZ	c	A/	AA	AI	с	C	A
A A	CA CA		C	T G A G	A A	A (30	A C	T T		A	G	C	A A A A	C C		A Z	A T	Т	A A	G	A	A A	C C	A A r A	A	С 1 С 1	C C	G A	G Z	C	A	Т	G Z	C C	A / A /	A A A A	A 1 A 1	С		A
Α	CA	CA	c	AG	A	A	30	G	T	C	A	G	č	AA	c	c	Z	VC	Ī	A	G	A	A	C	2	A	C 1	c	A	GZ	c	A	Ť	GZ	с	AZ	١A	A	Ť	C	A

	590		600		61	0	620	630	640
AF471076.1 Daboia russelii	TTCCA	CCCGTA	TCAT	TCCTZ	CAAA	GACTCC <mark>C</mark> I		ACAATATTAA	
GQ359441.1 Echis carinatus isolate	TTCCA	CCCCTA	CCAC	тсста	CAAA	GATGCCC	ТАТАСТА	ACCACCCTGA	TCACCCTTATT
MK193094.1 Protobothrops mucrosquamatus	TTTCA	CCCCTA	CCAC	тсста	CAAA	GACACCC	CATACTA	ACAACAATAA	TTACCCTACTA
KX019144.1 Trimeresurus stejnegeri	T T C C A	CCCATA	TCAC	TCATA	TAAA	GACACCC	TATATTA	ACAATAATAA	TTACCCTACTA
HM567533.1 Protobothrops jerdonii	TTCCA	CCCCTA	CCAC	тсста	CAAA	GACACCC	TATACTT	ACAATAATAA	TTACCCTACTA
LC094069.1_Sinomicrurus_macclellandi_iwasakii	TTTCA	CCCCTA	CCAC	тсстд	CAAA	GATATACI	AATAACC	ACCTCTATAT	TTACCCTACTA
FR693730.1_Ophiophagus_hannah	TTCCA	CCCATA	CCAC	тсттд	CAAA	GATATACI	AATAATC	ACAACCATAA	TCACCCTACTA
KU527540.1 Naja kaouthia	TTCCA	CCCCTA	CCAC	тсста	CAAA	GATATAC	GATAATC	ACCTCTACGA	TCACCCTACTA
GQ225657.1_Naja_naja_naja_	TTCCA	CCCCTA	CCAC	ТССТА	TAAA	GATATGC	GATAATC	ACCTCTATGA	TTACCCTGTTA
U69859.1_Python_reticulatus	TTCCA	CCCATA	CCAC	тсттд	CAAA	GACTTCC	CTTACTA	ACATTAATAG	TCCTATCTC
JX401136.1_Python_bivittatus	TTCCA	CCCATA	CCAC	TCATA	CAAA	GATCTACI	CTTCCTA	ACCCTGATAA	TCCTATCTATA
AY099983.1_Python_molurus	TTCCA	CCCATA	CCAC	TCAT	CAAA	GACCTAC	CTTCCTG	ACCCTAATAA	TCCTATTATA
LC105627.1_Enhydris_enhydris	TTCCA	CCCCTA	CCAC	TCCC	CAAA	GACATATI	TATACTA	ACTATTATAA	TAACACTAATT
DQ902119.1_Gonyosoma_prasinum_	TTCCA	CCCATA	CCAC	TCTCA	CAAA	GATATCC	AATGCTC	ACTATCATAC	TCACCTCAATT
AF471084.1_Gonyosoma_oxycephalum_	TTCCA	CCCCTA	TCAC	TCTC	CAAA	GATATTT	AATACTT	ACCACCTTAA	TCACCCTAATA
DQ902121.1_Coelognathus_radiatus	TTTCA	CCCATA	TCAC	TCCTA	TAAA	GACACCC	AATACTT	ACTATTATAA	TTACACTTCTA
AY486921.1_Platyceps_rhodorachis_	TTCCA	CCCGTA	CCAC	TCTT	CAAA	GACACTC	AATACTA	ACTATCATAG	TCACCACTATA
DQ902128.1_Coelognathus_flavolineatus	TTCCA	CCCCTA	CCAC	ТСТТА	CAAA	GACACCT	AATACTA	ACCATTATAA	TCACTATCCTA
AY486929.1_Ptyas_korros	TTTCA	CCCATA	CCAC	TCTC	CAAG	GACATTC	CATACTA	ACCGTAATAA	TCACCCTAATA
AY611998.1_Ptyas_mucosus	TTTCA	CCCATA	CCAC	TCTC	CAAA	GATATCC	AATATTA	ACCCTATTAA	TTACTATAATA
AF471054.1_Ptyas_mucosa	TTTCA	CCCATA	CCAC	TCTC	CAAA	GATATCC	AATACTA	ACCTTATTAA	TTACCATAATA
EF076709.1_Orthriophis_taeniurus	TTTCA	TCCATA	CCAC	TCAC	TAAA	GACATATI	AATACTA	ACTATTATAC	TAACTACAATA
DQ902132.1_Orthriophis_taeniurus	TTCCA	TCCATA	CCAC	TCAC	TAAA	GACATACI	AATACTG	ACTATTATAC	TAACCATAATA
DQ902118.1_Oreophis_porphyraceus	TTTCA	CCCATA	CCAC	TCTC	CAAA	GACATAT	AATATTA	ACTATTATAA	TCGTTATACTA
DQ902115.1_Euprepiophis_mandarinus	TTCCA	CCCATA	CCAC	TCTC	CAAA	GACATCC	CATACTA	ACTGTTATAA	TACCACACTA

	650	660	670	680	690	7 O O
AF471076.1_Daboia_russelii	CTTATTAT	CCTATCATTTGA	TCCAAACA	TAATAAACGACC	CAGAAAACT	TCTCTAAAGCT
GQ359441.1_Echis_carinatus_isolate_	TTCCTCAT	CCTCTCATTGA	CCCCAATA	T <mark>aataaac</mark> gacc	CAGAAAACT	TCACAAAAGCC
MK193094.1_Protobothrops_mucrosquamatus	TTCATCAT	CCTTTCATTCTA	CCCCGATA	TCTTAAACGACC	CAGAAAACT	TCTCAAAGGCT
KX019144.1_Trimeresurus_stejnegeri_	TTTATCAT	CATATCATTCTT	CCCTAACA	TCCTAAATGACC	CAGAAAACT	TCTCGAAAGCC
HM567533.1_Protobothrops_jerdonii	TTCATCAC	CCTCTCATTCTA	CCCCGATA	TACTAAACGACC	CAGAAAACT	TCTCAAAAGCC
LC094069.1_Sinomicrurus_macclellandi_iwasakii	TTCCTTAT	CCTATCATTAC	ACCAGATT	TATTCAATGACC	CGGAAAATT	TTTCTAAGGCT
FR693730.1_Ophiophagus_hannah	TTCCTTAT	TATATCATTCT	CACTGACC	TACTTAACGACC	CAGAAAATT	TCTCTAAAGCT
KU527540.1_Naja_kaouthia	CTTCTTAT	CCTATCATTCTT	ACCCAATT	TGCTCAACGACC	CAGAAAATT	TCTCCAAAGCT
GQ225657.1_Naja_naja_naja_	CTTATCAT	CCTATCATTCTC	ACCCAACT	TGCTCAACGACC	CAGAAAATT	TCTCCAAAGCT
U69859.1_Python_reticulatus	TTCATTAT	CGTCTCATTCTT	CCCAGATA	TCTTCAACGACC	CAGACAA T T	TCTCAAAAGCC
JX401136.1_Python_bivittatus	CTCATCAT	CGTCTCATTCTT	CCCTGACA	T T T T C A A C G A C C	CAGACAACT	TTTCAAAAGCC
AY099983.1_Python_molurus	CTCATCAT	CGTCTCATTCTT	CCCTGATA	TCTTCAACGACC	CAGACAACT	TCTCAAAAGCC
LC105627.1_Enhydris_enhydris	TTCCTTAT	CATATCCTTCTC	ACCAG <mark>A</mark> CT	T <mark>ATTTAAC</mark> GACC	CAGAAAACT	TCTCTAAAGCC
DQ902119.1_Gonyosoma_prasinum_	CTAATCAT	TATATCATTTAC	CCCAGACA	T <mark>ATTCAAC</mark> GACC	CAGAAAATT	TCTCAAAAGCT
AF471084.1_Gonyosoma_oxycephalum_	TTTACTAT	TATAACATTCAC	CCCAAACA	T T T T C A A C G A C C	CAGAAAACT	TCTCAAAAGCC
DQ902121.1_Coelognathus_radiatus	TTTATTAT	TATATCATTTC	CCCAAACA	T <mark>a t t t a a t</mark> g a c c	CAGAAAACT	TCTCAAAAGCC
AY486921.1_Platyceps_rhodorachis_	TTTACTAT	CATATCATTCAC	CCCAGACA	TATTCAACGACC	CAGAAAACT	TCTCAAAAGCC
DQ902128.1_Coelognathus_flavolineatus	TTCTCTAT	TATATCATTCAC	CCCAAATG	T <mark>g t t t a a c</mark> g a c c	CAGAAAACT	TCTCAAAAGCT
AY486929.1_Ptyas_korros	TTCGCTAT	CATAACTTTCAC	CCCAAACA	T T T T T A A C G A C C	CAGAAAACT	TCTCAAAAGCA
AY611998.1_Ptyas_mucosus	TTTACTAT	TATAGCATTCAC	CCCAAATA	T <mark>g t t t a a t</mark> g a c c	CAGAAAATT	TCTCAAAAGCC
AF471054.1_Ptyas_mucosa	TTTACTAT	TATAGCATTCAC	CCCAAACA	T <mark>a t t t a a t</mark> g a c c	CAGAAAATT	TCTCAAAAGCT
EF076709.1_Orthriophis_taeniurus	TTCATTAT	TATATCATTCGC	CCCAAACA	TCTTTAATGACC	CCGAAAATT	TCTCAAAAGCC
DQ902132.1_Orthriophis_taeniurus	TTCATTAT	TATATCGTTCAT	CCCAAATA	TCTTTAATGACC	CTGAAAACT	TCTCAAAAGCT
DQ902118.1_Oreophis_porphyraceus	TTCATCAT	CATATCATTAC	CCCAAATA	TCTTTAACGACC	CAGAAAACT	TCTCAAAGGCC
DQ902115.1_Euprepiophis_mandarinus	TTCACAAT	CA <mark>TAACATTC</mark> AC	CCCAAACA	TCTTTAACGACC	CAGAAAACT	TCTCAAAAGCC

27471076 1 Babaia ana anii
AF4/10/6.1_Dabola_russell1
GQ359441.1_Echis_carinatus_isolate_
MK193094.1_Protobothrops_mucrosquamatus
KX019144.1_Trimeresurus_stejnegeri_
HM567533.1_Protobothrops_jerdonii
LC094069.1_Sinomicrurus_macclellandi_iwasakii
FR693730.1_Ophiophagus_hannah
KU527540.1_Naja_kaouthia
GQ225657.1 Naja naja naja
U69859.1_Python_reticulatus
JX401136.1 Python bivittatus
AY099983.1 Python molurus
LC105627.1 Enhydris enhydris
DQ902119.1 Gonyosoma prasinum
AF471084.1 Gonyosoma oxycephalum
DQ902121.1 Coelognathus radiatus
AY486921.1 Platyceps rhodorachis
D0902128.1 Coelognathus flavolineatus
AY486929.1 Ptvas korros
AY611998.1 Ptvas mucosus
AF471054.1 Ptvas mucosa
EF076709.1 Orthriophis taeniurus
D0902132.1 Orthriophis taeniurus
D0902118.1 Oreophis porphyraceus
D0902115 1 Euprepiophis mandarinus
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AA	C	С	CC	Т	AG	т	C	AC	С	cc	A	CA	Α	CA	С	Α'	гТ	A	A	GC	C	A	GA	G	ТG	A	ТА	С	ТΊ	С	С	G	ТΊ	Т	G	C	Ξ	A	G	GA
AA		C	CA	H	AA	C	C	AC	С	cc	C	CA	A	CA	С	Α'	T	A	A	9	C	Т	GA	A	TG	A	ТА	С	ТТ	С	T	А	ТТ	Т	G			A	9	GA
AA		C	AC C A	H	A A	C		AC	A		C		Å		T	A :		A.	A			C	GA	G	тe	G	ТА	Т	T 1	T		A	T 1	T C	G			A		GA A
		C		H.	н н л л	T T	2				2		5		2	А. Л		Ā	A				G A	A C	т с т с	C	TΑ	Ē	1 1 7 7		2	C.	T 1	Ē	G			Ā		
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AA	С	С	сc	Т	AG	т	A	AC	А	СС	A	CA	А	CA	С	Α'	гТ	A	AZ	١C	C	А	GΑ	A	ТС	A	ТΑ	С	т1	С	Ċ	А	т٦	с	G	C 1	т	A	G	GТ
AA	٢C	С	AC	Т	AG	т	т	AC	A	СС	т	CA	А	CA	С	A'	гт	А	AZ	١C	C	Α	GA	A	ТG	А	ТΑ	С	т1	С	С	А	т٦	С	G	C	Ξ	A (CG	GA
AA	۲C	С	AC	Т	AG	т	т	AC	A	СС	С	CA	А	C₽	С	Α'	гт	A	AŻ	١C	CC	A	GA	G	ТС	G	ТА	С	т1	С	С	Α	т٦	С	G	C	Т	A	r G	GG
A A (C	С	AA	Т	AG	T.	A	AC	A	СС	A	CA	А	CA	С	Α'	r C	A	Al	٩C	C	A	GA	A	ТG	A	ТА	т	ті	С	С	А	т٦	т	G	C	Ξ	A	G	GC
A A (С	С	AC	Т	AG	T.	A	AC	Α	CC	С	CA	А	CA	С	Α'	гт	A	AŻ	٩C	C	A	GA	A	ТС	A	ТА	С	тт	т	C	A	тл	С	G	C	Т	A	CG	GA
AA	2	C	AC	Ξ	GA	Т	Т	AC	Α	cc	A	CA	А	CA	Т	A'	ГТ	A	A	A C	C	A	GA	A	ΤG	A	ТА	С	ТТ	С	C	А	ТТ	Т	G	C	Ξ	A	ſG	GA
AA		C	CC	Ë	AG	T	T	AC	C	cc	C		A	CA	T	A'.	1	A	A/	A C	:C	A	GA	A	TG	A	ТА	C	T 1	Т	C	A	T 1	C	G			A	-	GA
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AA	C	С	AC	Т	AG	т	A	AC	А	СС	А	CA	А	CA	С	Α'	гC	A	AZ	١C	C	А	GA	А	ТG	А	ТА	C	тт	с	С	А	тт	c	G	C	Т	A	ГG	GC
AA	С	С	тт	т	GG	т	A	AC	А	сс	A	CA	А	CA	т	Α'	гт	A	A	١C	c	А	GA	А	ТG	А	ТА	С	тт	С	С	Α	т٦	т	G	C	Т	A	CG	GC
A A	C	С	CA	Т	GG	т	A	AC	Α	cc	A	CA	А	CA	С	A'	ГТ	А	A	١C	C	Α	GA	G	ТС	G	ТА	С	тт	С	т	Α	т٦	т	G	C		A	ГG	GA

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AF471076.1_Daboia_russelii	ATC	TT2	ACGGTCAGT	CC	AAATA	AATT	AGGC	GGAAC	ACTA	GCCC	TAA	TTA	TAT	CAA	TCACT
GQ359441.1_Echis_carinatus_isolate_	АТТ	СТ	CGATCAA T	CC	A										
MK193094.1_Protobothrops_mucrosquamatus	АТТ	СТ	ICGATCAA I	CC	AAACA	AACT	CGGC	GGGG	CCTC	GCCT	TAG	TCC	TAT	CCA	TCACC
KX019144.1_Trimeresurus_stejnegeri_	ATC	СТС	CGATCAAT	CC	AAATA	AACT	CGGT	GGGG	CCTA	GCCT	TAG	ттс	TAT	CTA	TCGCT
HM567533.1_Protobothrops_jerdonii	ATC	СТС	CGATCAAT	CC	AAACA	AGCT	CGGA	GAAC	TTTA	GCCT	TAG	TCC	TGT	CCA	TCGTT
LC094069.1_Sinomicrurus_macclellandi_iwasakii	АТТ	CT	ACGATCTAT	тс	TAATA	AACT	AGGC	GAAC	ACTC	GCCC	ТАТ	ТТА	TAT	CCA	TCATT
FR693730.1_Ophiophagus_hannah	ATC	СТ	ACGATCAAT	TC	AAACA	AACT	AGGA	GCTG	ATTA	GCCC	TAC	ТТА	TAT	CAA	TCGCT
KU527540.1 Naja kaouthia	ATC	СТ	ACGATCAAT	CC	AAACA	ААСТ	AGGAC	GAAC	ACTA	GCAC	TAC	ттт	TAT	CGG	TCATA
GQ225657.1_Naja_naja_naja_	ATC	СТС	GCGATCAA T	CC	AAACA	AACT	AGGA	GAAC	ACTA	GCAT	TAC	ттт	TAT	CGG	TCCTA
U69859.1_Python_reticulatus	АТТ	СТ	ACGATCCAT	CC	CAACC	AACT	TGGA	GAG	ATTA	GCCT	TAG	TAA	TAT	CTA	TATA
JX401136.1 Python_bivittatus	ATC	СТС	GCGATCCAT	тС	AAATA	AACT	AGGT	GCGC	ATTG	GCCC	TAG	TAA	TAT	CAA	TCATA
AY099983.1_Python_molurus	ATC	СТ	ACGATCCAT	CC	AAACA	AACT	AGGT	GGCGC	ATTA	GCCC	TAG	TAA	TAT	CAA	TCATA
LC105627.1_Enhydris_enhydris	АТТ	СТС	CGATCCAT	CC	CAACA	AATT	AGGG	GGAG	TGTA	GCAC	TGA	CAC	TAT	CCA	TCCTT
DQ902119.1_Gonyosoma_prasinum_	АТТ	СТ	ACGATCCAT	тС	CAACA	AACT	CGGA	GGAC	TTTA	GCTC	TTG	TAA	TAT	CCG	TAGCC
AF471084.1_Gonyosoma_oxycephalum_	ATC	СТ	ACGTTCAAT	CC	CAATA	AACT	AGGA	GAAC	TATT	GCCC	TTA	ΤΑ	TAT	CAG	TAGCA
DQ902121.1_Coelognathus_radiatus	ATC	СТ	CGTTCTA T	CC	TAATA	AACT	CGGA	GAAC	CATG	GCTC	TTA	тт	TAT	CTG	TAACC
AY486921.1_Platyceps_rhodorachis_	ATC	СТС	GCGGTCTAT	CC	AAACA	AACT	TGGA	GGAAC	AGTA	GCTC	TAG	TAC	TTT	CAG	TAACC
DQ902128.1_Coelognathus_flavolineatus	АТТ	СТ	CGATCTA	TC	AAATA	AACT	AGGA	GAAC	AATA	GCCC	TCA	TCA	TAT	CTA	TGCC
AY486929.1_Ptyas_korros	ATC	СТ	ACGATCCAT	CC	AAACA	AACT	AGGA	GGAC	CATA	GCTC	TAG	ТАТ	TAT	CCG	TAATA
AY611998.1_Ptyas_mucosus	АТТ	СТ	ACGATCCAT	тС	AAACA	AACT	AGGG	GGAC	CGTA	GCCC	TAG	ΤΑ	TAT	CAG	TAATA
AF471054.1_Ptyas_mucosa	АТТ	TTZ	ACGATCCAT	CC	AAACA	AACT	AGGA	GGAC	CGTA	GCCC	TAG	ΤΑ	TAT	CAG	TAATA
EF076709.1_Orthriophis_taeniurus	ATC	СТ	A <mark>CGATC</mark> AGI	TC	AAATA	AACT	G <mark>GG</mark> G	GAAC	TTTA	GCCC	TAG	TAC	TAT	CCG	ТААСТ
DQ902132.1_Orthriophis_taeniurus	ATC	СТ	ACGATCAAT	тС	AAACA	AGCT	AGGAC	GGAAC	CTTA	GCAC	TAG	TAC	TCT	CCG	ТААСТ
DQ902118.1_Oreophis_porphyraceus	ATC	TTZ	ACGTTCTAT	CC	CAACA	AACT	AGGG	GGAC	CCTA	GCTC	TTG	TAC	TAT	CCG	TAACT
DQ902115.1_Euprepiophis_mandarinus	АТТ	СТС	CGATCCAT	CC	CAACA	AACT	TGGA	GAAC	AATC	GCCC	TTA	TC	TAT	CCG	TAACT

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AF471076.1_Daboia_russelii	ATTCTCC	TAACATC	ACC	TTTC	ACC	CACAC	CTCAA	CCACC	ATCTA	FGA TA	TCCGACCT
GQ359441.1_Echis_carinatus_isolate_											
MK193094.1_Protobothrops_mucrosquamatus	ATCCTAT	TCACAAT	ACC	CTAC	ACC	CACAC	CGCCC	ACACTCO	ATCTA	FGA TA	TTCGACCC
KX019144.1_Trimeresurus_stejnegeri_	ATTCTCI	TCACAAC	CCC	СТТТ	ACC	CACAC	CTCAC	ACATTCO	CTCTA	TAA TA 7	TCCGACCC
HM567533.1_Protobothrops_jerdonii	ATCCTCI	TTACAAT	ACC	СТТТ	ACC	CACAC	CTCTC	ACACTCO	CTCTA	TAA TA 7	TCCGACCC
LC094069.1_Sinomicrurus_macclellandi_iwasakii	ATCCTA	TAACAGC	ACC	TTTC	ACC	CACAC	CTCAT	ACGTGCO	GTCCA	TAACC	TCCGTCCA
FR693730.1_Ophiophagus_hannah	ATTCTAA	TAACAAC	ACC	ATTC	ACC	CACAC	CTCAC	ATACCCC	ATCTA	ГААСТ	TTMGGCCA
KU527540.1_Naja_kaouthia	ATCTTAA	CAACAGC	ACC	ттс	ACC	CACAC	TTCGT	ACACACO	ATCTA	TAA TA 1	TCCGTCCA
GQ225657.1_Naja_naja_naja_	ATCTTA	CAACAGC	ACC	CTTC	ACC	CACAC	TTCGT	ACACACO	ATCTA	TAA TA 1	TCCGCCCA
U69859.1_Python_reticulatus	ATCTTAT	TCACTAT	CCC	ATTC	ACA	CACAC	AGCTA	ATCTTCC	TCCCA	FAA CC	TCCGACCA
JX401136.1_Python_bivittatus	ATCCTAT	TTATTAC	CCC	ATTC	ACA	CATAC	AGCCT	ACTTCCC	CCCAA	ГААСТ	TCCGCCCA
AY099983.1_Python_molurus	ATCCTAT	' <mark>TTA</mark> TTAT	CCC	ATTC	ACA	CATAC	AGCCC	ACTTCC	CCCAA	FAA CT	TCCGCCCA
LC105627.1_Enhydris_enhydris	ATCCTTA	TAACAAC	ACC	АТТТ	тсс	CACAC	CTCCA	CAACCCC	AACCC	FAA CA'	TCCGCCCC
DQ902119.1_Gonyosoma_prasinum_	ATCCTA	TAACAAC	ACC	АТТТ	ACC	CACAC	CTCAT	ACATACO	ACCTA	FAA CC	TTCGCCCA
AF471084.1_Gonyosoma_oxycephalum_	ATCCTA	TAACAAC	CCC	ATTC	ACC	CACAC	CTCAA	GTGTA <mark>C</mark>	ATCCA	FAA CC	TTCGACCA
DQ902121.1_Coelognathus_radiatus	ATCCTAC	TAACAAT	ACC	CTTC	ACC	CATAC	TTCTC	ATACACO	ATCTA	ГААСТ	TCCGCCCA
AY486921.1_Platyceps_rhodorachis_	ATCCTGA	TAACAGC	ACC	ATTC	ACA	CACAC	ATCAC	ACCTTC	ACCAA	ГААСТ	TCCGCCCA
DQ902128.1_Coelognathus_flavolineatus	ATTCTAA	TAACAAC	ACC	АТТТ	ACC	CACAC	TTCAC	ACATACO	ATCTA	TAATT 1	TTCGCCCA
AY486929.1_Ptyas_korros	ATCCTA	TAACAGC	ACC	CTTC	ACA	CATAC	CTCGC	ATGTACO	TTCAA	FAA CC	TCCGCCCA
AY611998.1_Ptyas_mucosus	ATCCTA	TAACAAC	ACC	ATTC	ACA	CACAC	CTCAT	ATGTTCC	ATCCA	FAA CA	TCCGCCCA
AF471054.1_Ptyas_mucosa	ATCCTA	TAACAAC	ACC	ATTC	ACA	CACAC	CTCAT	ATGTTCC	ATCCA	FAA CA	TCCGCCCA
EF076709.1_Orthriophis_taeniurus	ATCCTA	TAACATC	ACC	АТТТ	ACA	CACAC	CTCAC	ACATCC	ATCTA	FAA CA	TCCGTCCT
DQ902132.1_Orthriophis_taeniurus	ATCCTA	TAACAGC	ACC	АТТТ	ACA	CACAC	CTCAC	GCATCC	ATCTA	FAA CA	TCCGTCCC
DQ902118.1_Oreophis_porphyraceus	ATCCTAT	TAACACT	ACC	АТТТ	ACA	CACAC	CTCAC	ACATACO	ACCCA	FAA CC	TTCGCCCA
DQ902115.1_Euprepiophis_mandarinus	ATTCTA	TAACAAT	ACC	ATTC	ACA	CACAC	CTCTC	ACGTAC	ACCTA	TAACC1	TCCGCCCA

AF471076.1_Daboia_russelii	С	ľ
GQ359441.1_Echis_carinatus_isolate_		l
MK193094.1 Protobothrops mucrosquamatus	т	t
KX019144.1_Trimeresurus_stejnegeri_	т	t
HM567533.1_Protobothrops_jerdonii	т	t
LC094069.1_Sinomicrurus_macclellandi_iwasakii	С	t
FR693730.1_Ophiophagus_hannah	т	t
KU527540.1_Naja_kaouthia	С	t
GQ225657.1_Naja_naja_naja_	С	t
U69859.1_Python_reticulatus	С	t
JX401136.1_Python_bivittatus	С	t
AY099983.1_Python_molurus	С	t
LC105627.1_Enhydris_enhydris	т	1
DQ902119.1_Gonyosoma_prasinum_	С	1
AF471084.1_Gonyosoma_oxycephalum_	Α	ł
DQ902121.1_Coelognathus_radiatus	A	1
AY486921.1_Platyceps_rhodorachis_	Α	ł
DQ902128.1_Coelognathus_flavolineatus	С	1
AY486929.1_Ptyas_korros	Α	ł
AY611998.1_Ptyas_mucosus	A	1
AF471054.1_Ptyas_mucosa	Α	ł
EF076709.1_Orthriophis_taeniurus	Α	ł
DQ902132.1_Orthriophis_taeniurus	Α	1
DQ902118.1_Oreophis_porphyraceus	С	ľ
DQ902115.1_Euprepiophis_mandarinus	т	ľ

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	т	т	C.	A	A	С	A	AC	Т	c	'A	C1	١	'т	т	т	G Z	T	C.	r 1	r T	c	А	т	CA	С	С	AC	CA	тı	r c	A	гт	A 1	c.	ΑΊ	C2	AC	т	ГG	G	GC	С	GC	с
	т	т	C.	A	A	С	A I	AC	Т	т	A	C I	١	ЧT	C	T (G Z	A	C	21	r T	т	A	C	ΑA	С	т	AC	CA	T 1	C C	A	r c	A 1	C.	ΑΊ	'T/	AC	С	ГG	βA	GC	С	GC	C
	т	т	C.	A	'G	С	A I	AC	Т	c	A	ΤŻ	١	ЧT	C	T (G Z	T	C	r 1	r T	т	G	C	CA	С	т	AC	CA	С	ΓT	A	r c	A 1	гт	ΑΊ	:C1	AC	С	ГG	JA.	AC	С	GC	C
i	С	т	Α	GQ	A	С	A I	A Z	٩C	c:	A	ТŻ	١	ЧT	C	T (G Z	A	C	ГC	Т	A	A	Т	CA	С	С	AC	C	T I	ΓT	A	r c	AC	С	ΑΊ	:C1	AC	Α'	ГG	JA.	AC	А	GC	C
	т	т	Α.	AC	A	С	A I	A Z	۱T	C	c	T2	Υ	T T	С	T (G I	A	C	A 1	r T	A	A	Т	ΤG	С	т	AC	CA	T 1	C C	Α	гт	AC	С	SV	IT I	A C	Α'	T C	JA.	AC	С	GC	C
	С	т	A	Т	A	С	A I	A Z	۱T	т	C	T2	Υ	T T	С	T (G I	A	C	A 1	r T	A	A	т	CG	С	т	AC	Т	T 1	C C	G	гт	AC	С	ΑΊ	'T/	A C	Α'	T C	JA.	AC	С	GC	C
	С	т	G	Т	A	С	A I	A Z	۱T	т	C	T2	Υ	T T	С	T (G I	A	C	A 1	r T	A	A	Т	ΤG	С	т	AC	Т	T 1	C C	G	гт	AC	С	ΑΊ	'T/	A C	Α'	T C	JA.	AC	т	GC	C
	С	т	С	ΤZ	чт	С	A I	AC	Т	C	A	то	31	T '	С	T (G I	A	C	A C	T	A	G	т	СТ	С	С	AC	т	T I	ΓT	A	гт	AC	т	ΑΊ	:C2	A C	A'	ΓG	βA	GC	С	GC	т
	С	т	Α	ТС	A	С	A I	AC	Т	A	A	то	31	T '	С	T (G I	A	C	A C	T	A	G	Т	ΑT	С	A	AC	CA	TI	C C	Α	гc	AC	т	ΑΊ	:C2	A C	A'	ΓG	βA	GC	С	GC	C
	С	т	Α	ТС	A	С	A I	AC	Т	A	A	то	31	T '	С	T (G I	A	C	A C	Т	A	G	Т	ΑT	С	A	AC	CA	TI	C C	Α	гc	AC	т	ΑΊ	:C2	A C	A'	ΓG	βA	GC	С	GC	C
	т	т	G	ТС	Т	С	A I	AC	T	A	A	тс	ΓI	T T	С	T (G Z	T	C	CC	T	A	A	T	CG	С	т	AC	CA	TI	C C	A	гc	A I	'A	ΓA	:C1	4C	Α.	ΓG	JA.	AC	A	GC	A
	С	т	Α.	A 1	A	С	A I	AC	T	A	A	T2	Υ	T T	С	T (G Z	A	C	CC	T	A	G	Т	AG	С	С	AC	CA	TI	C C	A	гт	AC	A	ΓA	:C1	4C	Α'	ΓG	βA	GC	A	GC	C
	Α	т	A	GC	A	С	A I	AC	Т	A	A	C1	Υ	T T	С	T (GZ	A	C	CC	Т	A	A	C	AG	С	С	AC	CA	TI	ΓT	A	r C	AC	т	ΓA	:C1	4C	Α'	ΓG	βA	GC	A	GC	A
	Α	т	Т.	A	Α	С	A I	AC	T	С	'A	T2	ΥI	T T	т	T	GZ	A	C	GC	Т	'A	G	T	CA	С	Т	AC	CA	TI	C C	A	rc	AC	A	ΓA	:C2	4C	Α'	ΓG	ŞΑ	GC	A	GC	С
	Α	т	Α.	A	A	С	A	A Z	۱T	С	G	T2	ΥI	T 1	C	T (GO	A	C	гс	T	'A	A	Т	ΤG	С	С	AC	CA	TI	r c	A	гт	AC	A	ΑΊ	:C1	4C	A'	ΓG	ŞΑ	GC	A	GC	с
	С	т	A	ТС	A	С	A I	AC	T	A	A	T2	ΥI	T T	C	T	GZ	A	C	r A	ΔT	'A	G	T.	AG	С	С	AC	CA	TI	C C	A	rc	AC	A	ΓA	'T2	4C	Α'	ΓG	G	GC	т	GC	т
	A	Т	C.	A 1	Α	C	A	A Z	۱T	Т	G	T2	Υ	T T	C	T	GZ	A	C	CA	۱T	Α	A	C	AG	С	Т	AC	A	TI	C C	Α	гт	AC	Α	ΑΊ	:C2	4C	A !	ΓG	βA	GC	A	GC	Т
	A	Т	C.	A 1	A	C	A	A Z	۱T	A	G	ΤŻ	Υ	T	C	T	GI	A	C	AZ	ΔT	A	G	T.	AG	С	С	AC	A	TI	r c	Α	гт	AC	A	ΓA	:C1	4C	Α'	ΓĢ	ξA	GC	A	GC	С
	Α	т	C.	A	Α	С	A I	A Z	Υ	A	G	T2	ΥI	T T	C	T	GZ	A	C	AZ	ΔT	'A	G	Т	AG	С	С	AC	CA	TI	C C	A	гт	AC	A	ΓA	:C2	4C	Α'	ΓG	ŞΑ	GC	A	GC	С
	A	Т	Α.	A	A	C	A	AC	C	C:C	A	T 2	Υ	T	C	T	GF	G	C	20	T	A	G	Т	AG	С	С	AC	A	TI	r c	Α	ΓA	A	Т	ΓA	:C2	4C	Α'	го	βA	GC	A	GC	С
	A	Т	Α.	A	A	C	A	AC	T	Т	'A	ΤŻ	Υ	T	C	T	GI	A	C	CC	T	A	G	T.	AG	С	С	AC	A	TI	r c	Α	ΓA	AC	т	ΓA	:C1	4C	G	ΓĢ	ŞΑ	GC	A	GC	Т
	C	т	A	ТC	- A	C	A	A T	ΓT	A	A	Т'2	Υ	: T	C	T	G I	A		A C	T	A	G	Т	GG	C	C.	AC	C	11	ĽC	Α	гт	AC	A	ΑΊ	:01	4C	A '	L C	÷Α	GC	A	GC	C
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	950	960	970	980	990
AF471076.1_Daboia_russelii	ACTAAAC	CAGTGGAAACC	CCATTCAC	AGAA <mark>AT</mark> TA <mark>GCCA</mark>	CTTGCCTCAATT
GQ359441.1_Echis_carinatus_isolate_					
MK193094.1_Protobothrops_mucrosquamatus	ACTAAGC	CAGTAGAACCG	CCATTCAC	AGAA <mark>AT</mark> TG <mark>GACA</mark> (GTT <mark>AGCTTC</mark> AATT
KX019144.1_Trimeresurus_stejnegeri_	ACTAAAC	CAGTTGAGCCC	CCATTCAC	AGAA <mark>AT</mark> CG <mark>GCCA</mark>	CTGGCTTCAATC
HM567533.1 Protobothrops jerdonii	ACTAAAC	CAGTAGAACCA	CCATTCAC	AGAAATTGGTCAA	ACTAGCCTCAGTC
LC094069.1_Sinomicrurus_macclellandi_iwasakii	TCTAAAC	CGATAGAACCC	CCGTTCAT	CATTATCAACCA	GATAACCTCAATC
FR693730.1_Ophiophagus_hannah	ACTAAAC	CAGTAGAATCA	CCATGTAT	CATCATTAGCCA	ATAACTTCAATT
KU527540.1_Naja_kaouthia	TCTAAAC	CAGTAGAACCA	CCATTTAT	TACTATCAGTCA	GACAACGTCAATT
GQ225657.1_Naja_naja_naja_	TCTAAAC	CAGTAGAACCA	CCATTTAT	TACCATCAGTCA	GACAACATCAATT
U69859.1_Python_reticulatus	ACAAAAC	CCGTAGAGCCC	CCTTTTAT	CACTATTAGTCA	GTAACTTCAACA
JX401136.1 Python_bivittatus	ACAAAAC	CAGTAGAACCT	CCATACAT	CATCATTAGCCA	GTAACAGCAACA
AY099983.1_Python_molurus	ACAAAAC	CAGTAGAACCT	CCATATAT	CATCATTAGCCA	GTAACAGCAACA
LC105627.1_Enhydris_enhydris	ACTAAAC	CAGT			
DQ902119.1_Gonyosoma_prasinum_	ACCAAAC	CAGTTGAACCA	CCATTTAC	ATCT <mark>AT</mark> TGGTCA1	ACAACCTCTCTA
AF471084.1_Gonyosoma_oxycephalum_	ACTAAAC	CAGTAGAACCA	CCATTTAC	CCTCATCGGCCA	GTAACCGC TACA
DQ902121.1_Coelognathus_radiatus	ACCAAAC	CAGTAGAGTCC	CCATTTAC	TACTATTGGACA	ACAACTTCTTTC
AY486921.1_Platyceps_rhodorachis_	ACTAAAC	CAGTAGAACCG	CCATTTAC	CCTAATCGGACA/	ATCACCTCTTCA
DQ902128.1_Coelognathus_flavolineatus	ACTAAGC	CAGTAGAACCC	CCCTTTAC	TTTT <mark>AT</mark> TG <mark>GACA</mark>	ACAACTTCCTCT
AY486929.1_Ptyas_korros	ACTAAAC	CGGTAGAACCA	CCATTTAC	CCTTATTGGTCA	TTGACATCCGCA
AY611998.1_Ptyas_mucosus	ACCAAAC	CAGTAGAACCA	CCATTCAC	CATAATTGGACA	TTAACATCAATT
AF471054.1_Ptyas_mucosa	ACCAAAC	CAGTAGAACCA	CCATTCAC	CATAATCGGACA	ATTAACATCAATT
EF076709.1_Orthriophis_taeniurus	ACCAAAC	CAGTAGAACCA	CCATTTAA	CACTATCGGTCA	GTAACCTCAATT
DQ902132.1_Orthriophis_taeniurus	ACTAAAC	CAGTAGAACCA	CCATTTAA	TACTATCGGCCA	GT <mark>AAC</mark> CGCCATT
DQ902118.1_Oreophis_porphyraceus	ACTAAAC	CAGTAGAACCC	CCATTCGT	TCTT <mark>AT</mark> TA <mark>G</mark> CCA	TCAACCTCTACT
DQ902115.1_Euprepiophis_mandarinus	ACTAAAC	CAGTAGAACCC	CCATTCAC	TATA <mark>AT</mark> TA <mark>G</mark> CCA1	ACAACCTCTATT

	1	
MW144275.1 Malayopython reticulatus	T	Z
MT215102.1 Python molurus	т	2
LC086062.1 Python bivittatus	T	2
LC075329.1 Python bivittatus	T	2
MZ031479.1 Trimeresurus steinegeri	т	2
MZ031477.1 Protobothrops mucrosquamatus	т	2
KF170929.1 Protobothrops jerdonii		2
MT348390.1 Naja kaouthia	т	2
MT348389.1 Naja kaouthia	т	2
MT348388.1_Naja_kaouthia	т	2
MT348387.1_Naja_kaouthia	т	2
MT215097.1_Naja_naja_	т	2
MT215096.1_Naja_naja	т	2
MT215095.1_Naja_naja_	т	2
MT215094.1_Daboia_russelii_	т	2
LC105604.1_Enhydris_enhydris_	т	Z
LC105603.1_Enhydris_enhydris	т	Z
LC105602.1_Enhydris_enhydris_	т	Z
LC105601.1_Enhydris_enhydris	т	Z
MZ031450.1_Elaphe_taeniura_voucher	т	2
MZ031467.1_Ptyas_korros	т	2
MW144274.1_Ptyas_mucosa_	т	Z
MZ045970.1_Ptyas_mucosa_	т	2
LC105608.1_Ptyas_mucosa	т	2
MZ045947.1_Coelognathus_radiatus_	т	2
MZ045946.1_Coelognathus_radiatus_	т	2
LC105611.1_Coelognathus_radiatus_	т	2
LC105610.1_Coelognathus_radiatus_	т	2
LC105609.1_Coelognathus_radiatus_	т	2
LC105618.1_Rhadinophis_prasinus_	т	2
LC105617.1_Rhadinophis_prasinus_	Т	4
MZ045988.1_Coelognathus_flavolineatus_	Т	4
LC075340.1_Coelognathus_flavolineatus_	Т	4
MZ031453.1_Euprepiophis_mandarinus	Т	4
MT215100.1_Boiga_ochracea_	T	4
MT215099.1_Boiga_ochracea	T	4
MT215098.1_Boiga_ochracea_	T	4
M2031437.1_Oreocryptophis_porphyraceus_	T	4
LC0/5339.1_Gonyosoma_oxycephalum_	T	4
LC075338.1_Gonyosoma_oxycephalum_	т	L

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MT215102.1_Python_molurus_
LC086062.1_Python_bivittatus_
LC075329.1_Python_bivittatus_
MZ031479.1_Trimeresurus_stejnegeri_
MZ031477.1_Protobothrops_mucrosquamatus_
KF170929.1_Protobothrops_jerdonii
MT348390.1_Naja_kaouthia_
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MT215097.1_Naja_naja_
MT215096.1_Naja_naja
MT215095.1_Naja_naja_
MT215094.1_Daboia_russelii_
LC105604.1_Enhydris_enhydris_
LC105603.1_Enhydris_enhydris
LC105602.1_Enhydris_enhydris_
LC105601.1_Enhydris_enhydris
MZ031450.1_Elaphe_taeniura_voucher
MZ031467.1_Ptyas_korros
MW144274.1_Ptyas_mucosa_
MZ045970.1_Ptyas_mucosa_
LC105608.1_Ptyas_mucosa
MZ045947.1_Coelognathus_radiatus_
MZ045946.1_Coelognathus_radiatus_
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MZ031453.1_Euprepiopnis_mandarinus
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ATA	GA	AC	۳.	A	C	CA	A	CC	A	GG	GI	C	AC	1	C		G	GG	C	A	GC	GA	С	CA	AA		벁	ЧΤ	AA	ΤG	-	AC	μA	GΤ	A
ATA	GA	AC	Ľ	A	C	CA	A	CC	A	GG	GI	i Cr	AC		CC	-	т	GG	C	A	G C	GA	С	CA	AA			T.	AA	ТG	Ľ,	AC	ΠA	GT	A
ATA	GA	AC	Н.	A	C	CA	G	CC	C	GG	A'I	iC/	AC		TC	-	A	GG	Т	A	G C	GA	C	CA	AA			Т	AA	ТG	Ľ.	AA	ΠA	GT	т
ATA	GA	AC	Η.	A	C	CA	G		C	GG	A'I	2	AC		TO		A	GG	Т	A	G C	GA	C	CA	AA			Т	AA	TG	H	AA	I A	GT	Т
ATA	GA	AC		A	C	CA	G		2	GG	A	2	AC		тс		A	GG	Т	A	30	GA	C	CA				Т	AA	ТG	H.	AA	ΠA	GT	Т
	GA	AC		A		CA	G		2	GG	A	C A	AC		TO		A		T	A	30	GA	C	CA				Т	AA	ТG		AA	I A	GT	т
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MW144275.1_Malayopython_reticulatus_
MT215102.1_Python_molurus_
LC086062.1_Python_bivittatus_
LC075329.1_Python_bivittatus_
MZ031479.1_Trimeresurus_stejnegeri_
MZ031477.1_Protobothrops_mucrosquamatus_
KF170929.1_Protobothrops_jerdonii
MT348390.1_Naja_kaouthia_
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MT348387.1_Naja_kaouthia
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MT215096.1_Naja_naja
MT215095.1_Naja_naja_
MT215094.1_Daboia_russelii_
LC105604.1_Enhydris_enhydris_
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LC105602.1_Enhydris_enhydris_
LC105601.1_Enhydris_enhydris
MZ031450.1_Elaphe_taeniura_voucher
MZ031467.1_Ptyas_korros
MW144274.1_Ptyas_mucosa_
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LC105608.1_Ptyas_mucosa
MZ045947.1_Coelognathus_radiatus_
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LC105618.1_Rhadinophis_prasinus_
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LC075340.1_Coelognathus_flavolineatus_
MZ031453.1_Euprepiophis_mandarinus
MT215100.1_Boiga_ochracea_
MT215099.1_Boiga_ochracea
MT215098.1_Boiga_ochracea_
MZ031437.1_Oreocryptophis_porphyraceus_
LC075339.1_Gonyosoma_oxycephalum_
LC075338.1 Gonyosoma oxycephalum

130	140	150 160	170	180
ACAGCCCATGCATTC	GTA <mark>ATAAT</mark> CTT(CTTCATAGTTATAC(AATTATAATCGGA	GGCTTC
ACAGCCCACGCATTC	G <mark>TAATAAT</mark> TTT	I <mark>TTTAT</mark> AGT <mark>TATA</mark> C(CTATTATGATCGGA	GGC <mark>TT</mark> C
ACAGCCCACGCATTC	GTAATAATTTT:	TTTTATAGTTATACO	CATTATGATCGGA	GGTTTC
	GTAATAATTTT Amo ama amommu			GGTTTC
ACCCCCCACCCATTC				
ACCGCCCACGCATTC	ATTATAATTTT	TTCATAGTCATAC	CATCATAATCGGG	GGATTT
ACTGCTCACGCATTT	ATCATAATTTT	TTCATGGTAATAC	CATTATAATGGGA	GGCTTC
ACTGCTCACGCATTTA	ATCATAATTTT	I <mark>TTCATGGT</mark> AATAC(C <mark>attataatggga</mark>	GGC <mark>TT</mark> C
ACTGCTCACGCATTT	ATCATAATTTT?	ITTCATGGTAATAC(CATTATAATGGGA	GGCTTC
ACTGCTCACGCATTT	ATCATAATTTT.	ITTCATGGTAATACO	CATTATAATGGGA	GGCTTC
		FTTCATGGTAATGC(CATTATAATGGGA	GGCTTT
ACCCCCCACCCATTT				
ACCGCACACGCCTTC	ATCATAATCTT	TTCATAGTAATAC	AATTATAATCGGC	GGGTTT
ACAGCCCACGCATTC	ATCATAATTTT	TTCATAGTTATACO	CATTATAATCGGA	GGGTTC
ACAGCCCACGCATTC	ATCATAATTTT(CTTCATAGTTATAC(C <mark>attataatcgga</mark>	GGGTTC
ACAGCCCACGCATTC	ATCATAATTTT(CTTCATAGTTATACO	CATTATAATCGGA	GGGTTC
ACAGCCCACGCATTC	ATCATAATTTT(CTTCATAGTTATAC	CATTATAATCGGA	GGGTTC
ACAGCCCACGCATTT				
ACAGCCCACGCATTC	ATCATAATTTT	TTCATAGTCATAC	AATTATAATTGGC	GGATTC
ACAGCCCACGCATTC	ATCATAATTTTC	TTCATAGTCATAC	AATTATAATTGGC	GGATTC
ACAGCTCATGCATTCA	ATTAATTTT(CTTTATAGTTATACO	AATCAT <mark>AAT</mark> TGGC	GGTTT
ACAGCTCATGCATTC	AT <mark>TATAAT</mark> TTA	CTTTATAGTTATACO	C <mark>AATCATA</mark> ATTGGC	GGTTT
ACAGCTCATGCATTC	ATTATAATTTT(CTTTATAGTTATAC(TATCATAATTGGC	GGTTTT
				GGTTTT
ACAGCCCACGCATTC		TTTTATAGTIATACC	TATCATAATTGGC	
ACAGCCCACGCATTC	ATTATAATTTT	TTTATAGTCATAC	CATCATAATTGGC	GGCTTC
ACAGCCCACGCATTT	ATTATAATTTT	TTTATAGTTATAC	CATTATAATTGGG	GGGTTC
ACAGCCCACGCATTT	AT <mark>TAAAT</mark> TTA	CTTTATGGTTATAC(C <mark>at</mark> t <mark>at</mark> aatcggg	GG <mark>GTT</mark> C
ACAGCCCACGCATTT	ATCATAATTTT(CTTCATGGTAATAC(CTATTATAATCGGG	GGGTTC
ACAGCCCATGCATTT	ATCATAATCTT	CTTTATAGTTATAC(CATCATAATTGGG	GGGTTC
			CATCATAATTGGG	GGGTTC
ACAGCCCATGCATTT				GGGTTC
ACAGCCCATGCATTC	ATCATAATTTT	TTTATAGTTATAC	AATCATAATCGGG	GGGTTT
ACAGCCCATGCATTC	ATCATAATTTT	TTTATAGTTATAC(AATCATAATCGGG	GGGTTT

MW144275.1 Malayopython reticulatus
MT215102.1 Python molurus
LC086062.1_Python_bivittatus_
LC075329.1_Python_bivittatus_
MZ031479.1 Trimeresurus stejnegeri
MZ031477.1_Protobothrops_mucrosquamatus
KF170929.1_Protobothrops_jerdonii
MT348390.1_Naja_kaouthia_
MT348389.1_Naja_kaouthia_
MT348388.1_Naja_kaouthia
MT348387.1_Naja_kaouthia
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MT215095.1_Naja_naja_
MT215094.1_Daboia_russelii_
LC105604.1_Enhydris_enhydris_
LC105603.1_Enhydris_enhydris
LC105602.1_Enhydris_enhydris_
LC105601.1_Enhydris_enhydris
MZ031450.1_Elaphe_taeniura_voucher
MZ031467.1_Ptyas_korros
MW144274.1_Ptyas_mucosa_
MZ045970.1_Ptyas_mucosa_
LC105608.1_Ptyas_mucosa
MZ045947.1_Coelognathus_radiatus_
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LC105611.1_Coelognathus_radiatus_
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LC105609.1_Coelognathus_radiatus_
LC105618.1_Rnadinophis_prasinus_
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LC075340.1_Coelognathus_flavolineatus_
MZ031453.1_Euprepiopnis_mandarinus
MT215100.1_Boiga_ochracea_
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MT215098.1_Boiga_ochracea_
MZ031437.1_Oreocryptopnis_porpnyraceus_
LC0/5559.1_Gonyosoma_oxycepnalum_
LCU/5558.1_GONYOSOMA_OXYCEPNALUM_

IGAAACTGACTCATCCCACTAATAATTGGTGCACCACACATAGCAT GGAAACTGACTAATCCCATTAATAATCGGGGGCACCCGACATAGCAT GGAAACTGATTAATCCCATTAATAATCGGGGCACCACGACATAGCAT GGAAACTGATTAATCCCATTAATAATCGGGGGCACCACGACATAGCAT	TTCCACGAATAAAC TCCCACGAATAAAC TCCCGCGAATAAAT TCCCGCGAATAAAT TCCCCCGAATGAAC TCCCCCGAATAAAC
GAAACTGACTAATCCCATTAATAATCGGGGCACCCGACATAGCAT GAAACTGATTAATCCCATTAATAATCGGAGCACCACAGACATAGCAT GAAACTGATTAATCCCATTAATATCGGAGCACCACGACAACATAGCAT	TCCCACGAATAAAC TCCCGCGAATAAAT TCCCGCGAATAAAT TCCCCCGAATGAAC TCCCCCGAATGAAC
CAAACTGATTAATCCCATTAATAATCGGAGCACCAGACATAGCAT CAAACTGATTAATCCCATTAATAATCGGAGCACCAGACATAGCAT	TCCCGCGAATAAAT TCCCGCGAATAAAT TCCCCCGAATGAAC TCCCCCGAATAAAC
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	TCCCCCGAATGAAC TCCCCCCGAATAAAC
GAAACTGACTAATCCCCCTAATAATTGGAACCCCAGACATAGCCT	TCCCCCGAATAAAC
GAAACTGACTAATTCCCCCTAATGCTAGGAACCCCCGACATAGCCT	
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GCAACTGACTTATCCCCTTGATAATTGGGGGCCCCAGATATGGCCT	TCCCACGAATAAAC
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GAAACHGACHAAHCOCACHAAHAAHCIGGAGCACCGGATAHAGOCH	TTCCACGCATAAAT
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	TTCCACCCATAAAT
	TTCCACCCATAAAT
	TCCCCCCTATAAAC
	TTCCACGTATAAAC
	TTCCACGAATAAAC
	TTCCACGAATAAAC
GAAACTGACTAATCCCCTTAATAATCGGGGGCCCCTGACATGGCCT	TTCCGCGAATAAAT
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MW144275.1_Malayopython_reticulatus_
MT215102.1_Python_molurus_
LC086062.1_Python_bivittatus_
LC075329.1_Python_bivittatus_
MZ031479.1_Trimeresurus_stejnegeri_
MZ031477.1 Protobothrops mucrosquamatus
KF170929.1_Protobothrops_jerdonii
MT348390.1_Naja_kaouthia_
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MT348388.1_Naja_kaouthia
MT348387.1_Naja_kaouthia
MT215097.1_Naja_naja_
MT215096.1_Naja_naja
MT215095.1_Naja_naja_
MT215094.1_Daboia_russelii_
LC105604.1_Enhydris_enhydris_
LC105603.1_Enhydris_enhydris
LC105602.1_Enhydris_enhydris_
LC105601.1_Enhydris_enhydris
MZ031450.1_Elaphe_taeniura_voucher
MZ031467.1_Ptyas_korros
MW144274.1_Ptyas_mucosa_
MZ045970.1_Ptyas_mucosa_
LC105608.1_Ptyas_mucosa
MZ045947.1_Coelognathus_radiatus_
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LC105618.1_Rhadinophis_prasinus_
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MZ045988.1_Coelognathus_flavolineatus_
LC075340.1_Coelognathus_flavolineatus_
MZ031453.1_Euprepiophis_mandarinus
MT215100.1_Boiga_ochracea_
MT215099.1_Boiga_ochracea
MT215098.1_Boiga_ochracea_
MZ031437.1_Oreocryptophis_porphyraceus_
LC075339.1_Gonyosoma_oxycephalum_
LC075338.1 Gonyosoma oxycephalum

250	260	270	280	290 30	ò
AACATAAGCTTTG	ATTACTACCACC	AGCATTACTAC	TCCTTCTATC	CTCCTCTTATGT	т
AATATAAGCTTTTG	ACTTCTACCACC	AGCACTACTTC	TTCTCCTATC	TTCCTCATACGT	Α
AATATAAGCTTTTG	ACTTTTACCACC	AGCACTACTTC	TCCTCCTATC	TTCCTCATACGT	Α
AATATAAGCTTTTG	ACTITITACCACC	AGCACHACHTC	TCCTCCTATC	CTCCTCATACGT	A
AACATGAGCTTTTG		AGCACHACHTC			C
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AACATAAGCIIIIG		ATCCCTCCTAC			Ā
AACATAAGCTTCTC	GCTTCTACCCCC	ATCCCTCCTAC		CTCCTCATACGT	Σ
AACATAAGCTTCTG	GCTTCTACCCC	ATCCCTCCTAC	TTCTCTTATC	CTCCTCATACGT	A
AACATAAGCTTCTG	GCTTCTACCCCC	ATCCCTCCTAC	TTCTCTTATC	CTCCTCATACGT	А
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AACATAAGCTTCTG	GCTCCTACCCCC	GTCCCTCCTAC	TTCTCTTGTC	CTCTTCGTACGT	Α
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AACATGAGCTTCTG	ACTICCTTCCACC	AGCACUTCUAC	TTCHGCHARC	ATCCTCCTACGT	Α
AACATGAGCTTCTG	ACHCCTTCCACC				A
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AACATAAGTTTCTG	ATTATTACCACC	AGCATTACTCC	TCTTACTATC	ATCATCTTACGT	Ť.
AACATAAGTTTCTG	ATTATTACCACC	AGCATTACTCC	TCTTACTATO	ATCATCTTACGT	т
AATATAAGCTTTTG	ACTICTICCCCC	AGCATTATTAC	ТССТАСТСТС	CTCTTCCTACGT	т
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AACATAAGTTTTTG	ACTTCTACCACC	AGCACHACHTC		ATCCTCCTATGT	T
AACATAAGTTTCTG				GTCCTCCTATGT	T
AALATAAGCITTTG					Σ Τ
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AACATAAGCTTCTC	GTTACTACCACC	AGGACHACHTC		TTCTTCATACGT	Δ
AATATGAGCTTCTG	GTTACTACCGCC	AGCCTACTAC	TTCTACTATO	CTCCTCCTACGT	c
AATATAAGCTTTTG	GCTACTACCACC	AGCCCTACTTC	TCCTACTATO	CTCTTCTTACGT	č
AATATAAGCTTTG	GCTACTACCACC	AGCCCTACTTC	TCCTACTATO	CTCTTCTTACGT	С

MW144275.1_Malayopython_reticulatus_
MT215102.1_Python_molurus_
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MZ031479.1_Trimeresurus_stejnegeri_
MZ031477.1_Protobothrops_mucrosquamatus
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LC105610.1_Coelognathus_radiatus_
LC105609.1_Coelognathus_radiatus_
LC105618.1_Rhadinophis_prasinus_
LC105617.1_Rhadinophis_prasinus_
MZ045988.1_Coelognathus_flavolineatus_
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MT215099.1_Boiga_ochracea
MT215098.1_Bolga_ochracea_
MZ03143/.1_Oreocryptophis_porphyraceus_
LC0/5339.1_Gonyosoma_oxycephalum_
LCU/5338.1 Gonyosoma oxycephalum

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A	GCI		19			1	10				L.		Ā	GI	2		2				5	1		6		^	- A A			19	11		
AG	GCI	GG	TG		GG	ΞŤ	A C I	GGG	C	те	A	AC	A	GT	2	ΤA	C		G		C	ЦA		G	GG	А	A A	CC	14	76	тт	CA	C
AG	GCI	GG	TG	C	GG	T.	ΑC	CGG	C	TG	A	AC	A	GT	ç	ΤA	C	CC	G		C	ЦA	1	G	GG	А	AA	CC	14	76	тт	CA	C
AA	GCI	GG	TG	C	GG	C	A C (CGG	ΞT	ТС	A	AC	A	GT	C	TA	C	СC	G		C	II A	LT C	G	GG	А	AA	CC	14	۶G	тт	CA	C
AA	GCI	GG	ТG	C	GG	C	4 C	CGG	Γ	ΤG	A/	AC	А	GΤ	С	ΤA	С	СС	G		С	ΠA	T C	G	GG	А	AA	СС	- U Z	٢G	тт	CA	С
AA	GCI	GG	ТG	C	GG	C	AC	CG	GΤ	ΤG	A/	AC	A	GΤ	С	ΤA	С	сс	G		С	цA	T (G	GG	А	AA	СС	<u>11</u> 2	١G	тт	CA	С
AA	GCI	GG	ΤG	CC	GG	C	A C	AGO	A	ΤG	A/	AC	С	GΤ	С	ΤA	С	СС	A	CCZ	٢C	цС	Т	Α	GG	А	AA	тс	- T Z	١G	тт	CP	С
AA	GCA	GG	GG	СТ	GG	C	ΑC	AGO	C	ΤG	A/	AC	С	GΤ	G	ΤA	С	СС	G	CCZ	١C	ΗA	T	А	GG	А	AA	СС	- I I I	١G	CA	CZ	С
AA	GCA	GG	GG	СТ	GG	C	ΑC	AG	С	ТG	A/	AC	С	GΤ	G	ТΑ	С	СС	G	CCZ	١C	ΠA	T	Α	GG	А	AA	СС	. 🗖 Z	١G	CA	CP	С
AA	GCA	GG	GG	СТ	GG	C	ΑC	AGO	С	ТG	A/	AC	С	GΤ	G	ΤA	С	СС	G	CCZ	١C	цA	T	A	GG	А	AA	СС	. <u></u> 7	١G	CA	CP	С
AA	GCA	GG	GG	СТ	GG	C	AC	AGO	C	ТG	A	AC	С	GΤ	G	ТΑ	С	СС	G	CCZ	١C	цA	Т	A	GG	А	AA	СС	. II Z	١G	CA	CA	С
AA	GCI	GG	GG	СС	GG	c	AC	AGO	A	ТG	A	AC	С	GТ	А	ТΑ	С	СС	G	CCZ	١C	цA	Т	G	GG	А	AA	СС	Т Z	١G	ТА	CZ	С
AA	GCC	GG	AG	CC	GG	A	AC	CG	A	ТG	A	AC	т	GΤ	А	ТΑ	С	CC	С	CCG	ЗT	цA	Т	Α	GG	А	ΑA	тΟ	. I I I	١G	ΤA	CA	С
AA	GCA	GG	GG	Ст	GG	т	AC	CG	A	ТG	G	AC	А	GТ	А	ТΑ	С	сс	C	CCZ	١C	ΠА	т	А	GG	Α	AA	тт	ΠZ	١G	ТА	CA	С
AA	GCA	GG	GG	Ст	GC	c	AC	CG	A	ТG	A	AC	А	GТ	А	ТΑ	c	сc	C	ccz	١Ċ	пА	тс	А	GC	А	АА	тт	. П 2	١G	ТА	CA	c
AA	GCA	GG	GG	СТ	GC	C.	AC	CG	A	ТG	A	AC	Α	GТ	А	ТΑ	c	CC	Ĉ	CCZ	١C	лA	тс	A	GC	А	AA	тт	112	AG	ТА	CZ	c
AA	GCT	GG	CG	Т	GC	T	AC	AG	C	тc	A	AC	т	GТ	С	ТΑ	т	CC	A		c	ΠА	тс	G	GC	А	AΑ	СТ	11.7	A G	ТΑ	CZ	c
AZ	GCT	GG	CC	- т	GC	Ψ.			c	тc	Δ	A C	Ŧ	GТ	č	тΔ	Ŧ	CC	Δ		- C	ΠA	T	G	G	Δ	ΔΔ	CT		1 C	TΔ	CZ	ic.
AZ	GCT	CC	CC	Т	GC	÷.			č	ΤG	Δ	AC	÷	ст	č	тΔ	÷	cc	Δ		- C	īλ	Tτ	G	G	Δ	ΔΔ	CT			TΔ	CZ	č
A 2	CCT	CC		1		.			- C	ΨC	Δ		÷	с т	č	TΔ	÷		Z			īΖ	TT C	c	ac	Δ	λλ	CI			ŢΔ	CZ	č
	CCT	GG		.		"			2	- C			÷	с т	2	- A	÷.		7		2		The second			2	<u>א א</u>				т л	C 7	č
						.			2	т с	5		÷.,	с т	2	т л т л	2		2		2		i i i	2		5	<u>Α</u> Α λ λ				T 7		
									2		Ω.		÷.		2	T 7	2							ς,		5	~ ~		H.		T 7		
	GCC					5			A				1		G		2				12		1	A.		A	**						2
AG	GCC	GG	GG		GG	A	A C	AGO	А	те	A	AC	т	GT	2	ΤA	C		A		C	4 A		Т	GG	А	A A	CC	14	76	TA	CA	C
AG	GCC	GG	AG	C	GG	A	A C	AGO	А	TG	A	AC	Т	GT	C	ΤA	т	CC	A		C	ΠA	110	Т	GG	G	AA	CC	14	7G	TA	CA	C
AA	GCA	GG	CG	C	GG	C'	чC	AGO	G	ТG	A/	AC	C	GΤ	T	TA	т	сc	C		C	цΤ	T	А	GG	А	AA	CC	Ľ	٢G	ТА	CA	C
AA	GCA	GG	GG	CA	GG	T	чC	AGO	G	ТG	A/	AC	С	GΊ	С	ΤÀ	С	СĊ	A	CC	С	цA	T (A	GG	А	AA	СС	2	١G	TC	CA	т
AA	GCA	GG	GG	CA	GG	Т	ΑC	AGO	G	ΤG	A/	AC	С	GΤ	С	ΤA	С	CC	A		C	ΗA	T	A	GG	А	AA	СС	2	٢G	TC	CA	т
AA	GCA	GG	GG	CA	GG	T Z	ΑC	AGO	G	ΤG	A/	AC	С	GΤ	С	ΤA	С	CC	A		C	цA	T	A	GG	А	AA	СС	T 7	١G	TC	CA	т
AA	GCI	GG	AG	C	GG	A	٩C	AGO	A	ΤG	A/	ΑC	G	GΤ	С	ТΑ	С	СС	С	CCZ	١C	ιA	T	А	GG	А	AA	СС	- I I	١G	TA	C₽	С
AA	GCI	GG	GG	C	GG	C	ΑC	AGO	A	ТG	A/	AC	т	GΤ	А	ТΑ	С	СС	С	CCC	C	ΠA	Т	Α	GG	А	AA	тс	- E Z	١G	TA	CA	т
1 1 2	CO	CC	CO		CC				1	TT C	λ.		m	C	2	m 7.		20				л х	m c	3 7	CC		7 7	m			m a	C 7	m

MW144275.1 Malayopython reticulatus
MT215102.1_Python_molurus_
LC086062.1 Python bivittatus
LC075329.1_Python_bivittatus_
MZ031479.1_Trimeresurus_stejnegeri_
MZ031477.1_Protobothrops_mucrosquamatus_
KF170929.1_Protobothrops_jerdonii
MT348390.1_Naja_kaouthia_
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MT348387.1_Naja_kaouthia
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MT215094.1_Daboia_russelii_
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MT215099.1_Boiga_ochracea
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LC075339.1_Gonyosoma_oxycephalum_
LC075338.1_Gonyosoma_oxycephalum_

370	380	390 40	0 <u>410</u>	4 2
CA <mark>GGCCCA</mark> TCAGTA	GACTTAGC TAT	TTTTTCCCTCCAT	TTAGCCGGAGCATCC1	'CAA'
CAGGCCCATCAGTA	GATCTGGCAAT	TTTCTCACTACAC	TTAGCCGGCGCCTCT	
CAGGCCCATCAGTA	GATCTAGCAAT	TTTCTCACTACAC	TTAGCTGGCGCCTCT	
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GGGCCCATCAGTA	GACCTAGCCAT	CITCICACICCAC	CTAGGAGGAGGCTGA	CAA
LAGGCCCATCAGTT	GACCTAGCTAT	TITTTCGCTACAT	CTAGGAGGAGGCTGT	CCA.
	GACCTAGCTAT	TITTTCGCTACAT	CHAGGAGGAGGCTGT	CCA
	GACCTAGCTAT	TTTTTCGCTACAT		
	GACCTAGCTAT			
	GATCTTGC TAT			
	CARCTIGCIAI			
	CACCUACCAA			
	GACCTAGCAAT CACCTAGCAAT			
	GACCIAGCAAI			
	CACCTACCAAT			
	GACCIAGCAAI			
	CACCTAGCAAT			
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	CACTTACCCAT	TTTTTCCCTACAT	TTACCACCCCTTCC	
AGGCCCATCAGTT	GACTTAGCCAT	TTTTTCCCTACAT	TTACCACCCCCCCCC	
AGGCCCATCAGTT	GACTTAGCCAT	TTTTTCCCTACAT	TTAGCAGGCGCTTCC	CCA
TGGCCCATCAGTA	GACCTAGCAAT	CTTTTCTCTCCAC	TTAGCAGGCGCCTCT	CTA
TGGCCCATCAGTA	GACCTAGCAAT	CTTTTCTCTCCAC	TTACCAGCCCCTCT	CTA
AGGCCCATCAGTA	GACCTAGCAAT	CTTTTCTCTCCAC	TTAGCAGGCGCCTCT	CTAT
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CAGGCCCATCAGTA	GACTTAGCAAT	TTTCTCCCTACAT	CTAGCAGGCGCCTCC	CCAT
CGGACCATCCGTA	GACCTAGCAAT	CTTCTCTCTCAC	CTAGCAGGCGCCTCC	CCA
CGGCCCATCCGTG	GACCTGGCAAT	TTTCTCCCTACAT	CTAGCAGGCGCCTCG	CCA:
CGGCCCATCCGTG	GACCTGGCAAT	TTTCTCCCTACAT	CTAGCAGGCGCCTCG	CCA
CGGCCCATCCGTG	GACCTGGCAAT	TTTCTCCCTACAT	CTAGCAGGCGCCTCG	CCA
CGGGCCCATCAGTG	GACTTAGCAAT	CTTCTCCCTACAT	CTAGCAGGCGCCTCC	CCA
CGGCCCATCCGTA	GACTTAGCAAT	TTTCTCCCTACAC	CTAGCAGGCGCCTCC	CCA
CGGCCCATCCGTA	GACTTAGC A <mark>AT</mark>	TTTCTCCCTACAC	CTACCACCCCCCCC	CCA

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MT215102.1_Python_molurus_
LC086062.1_Python_bivittatus_
LC075329.1_Python_bivittatus_
MZ031479.1_Trimeresurus_stejnegeri_
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KF170929.1_Protobothrops_jerdonii
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MT215095.1_Naja_naja_
MT215094.1_Daboia_russelii_
LC105604.1_Enhydris_enhydris_
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MZ031467.1_Ptyas_korros
MW144274.1_Ptyas_mucosa_
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LC075339.1_Gonyosoma_oxycephalum_
LC075338.1_Gonyosoma_oxycephalum_

430	440	450 46	50 470 480
CTAGGGGCAATCAACT	TATCACCAC	TGGATCAATATA	
CTAGGGGCAATTAACT	TATCACCACZ	TGCATTAACATA	AAACCTGCATCAATACCTATA
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		ATGCATCAACATA	
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CICCOCCACCAATCAACT			
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CIGGGGGCAATCAATTI	CATHACAAC	ATGCATTAACATA	AAAACCTAAATCCATACCAATA
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MT215102.1 Python molurus			
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LC075329.1_Python_bivittatus_			
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MZ031477.1_Protobothrops_mucrosquamatus_			
KF170929.1_Protobothrops_jerdonii			
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MT215095.1_Naja_naja_			
MT215094.1_Daboia_russelii_			
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MZ031453.1_Euprepiopnis_mandarinus			
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MT215099.1_Boiga_ochracea			
MILLIUVO.I_BOIGA_OCHIACEA_ MZ031437 1 Orocarumtophia porphyrocaru			
1C075220 1 Convergence ouverage balum			
IC075229 1 Convogoma ouvgombalum			
LC0/3556.1_GONYOSOMa_OXYCephalum_			

490	500	510	520	530	540
TTTAACATTCCATTAT	TTGTGTGATC	AGTATTGATCA	ACGGCAATTA	GCTTCTTT	AGCT
TTCAACATCCCTTTAT	T T G T T T G A T C	C <mark>GT</mark> ACT <mark>AAT</mark> T	AC <mark>GGC</mark> AATTA:	TACTCCTCCT?	AGCC
TTCAACATCCCTTTAT	T T G T T T G A T C	CGTACTAATT2	ACAGCAATCA:	ACTCCTCCT	AGCC
TTTAACATCCCTTTAT	TTGTTTGATC	CGTACTAATT2	ACAGCAATCA:	IACTCCTCCT2	AGCC
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	TTGTGTGATC.				AGCC
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TTTAATATTCCTTTAT	TTGTCTGATC	ACTACTAATT	ACCGCCATTA		
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TTTAACATTCCATTAT	TTGTGTGATC	AGTACTAATT	ACTGCCATTA	ACTCCTACT	
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TTCAACATCCCACTAT	TTGTCTGGTC	GGTGCTTATC2	ACTGCCATTA:	ACTACTTCT/	AGCC
TTCAACATCCCCCTAT	TTGTCTGGTC	AGTACTAATC ²	ACCGCTATTA:	ACTCCTCCT	CGCA
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MW144275.1_Malayopython_reticulatus_
MT215102.1_Python_molurus_
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MZ031467.1_Ptyas_korros
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KF170929.1_Protobothrops_jerdonii	т
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MT348389.1_Naja_kaouthia_	т
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MT215094.1_Daboia_russelii_	т
LC105604.1_Enhydris_enhydris_	т
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LC105601.1_Enhydris_enhydris	т
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MZ031467.1_Ptyas_korros	т
MW144274.1_Ptyas_mucosa_	т
MZ045970.1_Ptyas_mucosa_	т
LC105608.1_Ptyas_mucosa	т
MZ045947.1_Coelognathus_radiatus_	т
MZ045946.1_Coelognathus_radiatus_	т
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LC105610.1_Coelognathus_radiatus_	т
LC105609.1_Coelognathus_radiatus_	т
LC105618.1_Rhadinophis_prasinus_	т
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LC075340.1_Coelognathus_flavolineatus_	т
MZ031453.1_Euprepiophis_mandarinus	т
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MZ031437.1_Oreocryptophis_porphyraceus_	т
LC075339.1_Gonyosoma_oxycephalum_	т
LC075338.1_Gonyosoma_oxycephalum_	т
	_

RESULT:-

The evolutionary history was inherited during the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 is taken to represent the evolutionary history of the taxa analyzed.

From this two phylogenetic tree, it can be observed that species of both the gene comes under the same nodes. Like, Naja naja and Naja kaiuthia of cytb comes under the 90 mode i.e. monophyletic group. In the same way, these two species are also monophyletic group in the cox1 phylogenetic tree. Like this many species comes under the common ancestors. Species like, Elaphe taeniura, Ptyas mucosa, Australotaenia bunthangi are also the mono phylatic group in both the cytb and cox1 gene. This shows that these species comes under the same ancestors. So it is observed that in the cox1 there is more divergence than in the cytb. This things is required to study further.

In the cytb and cox 1 gene, I get the phylogenetic tree with respect to the complete cds and the larger gene length. In that it is observed that there are more diversity in the cox 1 phylogeny than cytb gene. After that when I move for the multiple sequence allignment i.e. Clastal omega I get the conservation region which is shown above. The result shows that species of cox1 have more diversity than cytb gene.

The biological species concept (BSC) implies that a species is an isolated reproductive unity. The molecular data, especially pertaining to mtDNA, show that, on the one hand, natural hybridization between species may lead to introgression of genes from one gene pool to the other one. On the other hand, sequences of individual genes exemplify that the variability of DNA markers increases with the rank of the taxon.

The BSC basic idea that taxon formation necessarily requires the isolation of gene pools followed by their gradual genetic divergence. Within species the differentiation may be reversed, while it is normally irreversible at upper divisions or at taxa levels. Secondly, correlated evidence suggest that the geographic, allopatric, or divergent (D1; Templeton 1981) speciation mode (SM) prevails in nature, implying a common rule of a gradual accumulation of small genetic differences after the separation of gene pools and differences increase in a hierarchy of taxa levels.

The differences in p-distance estimates between the two genes can have the following interpretations. Firstly, the substitution rate may in fact be different in the two genes but hidden somehow. For instance, the data on taxonomic groups from the most representative sources (Johns and Avise 1998; Hebert et al. 2002a,b), which can differ in divergence level.

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INTERLEUKIN-17 ROLE IN IMMUNITY AND INFLAMATION

Name-Subhankar Mahapatra; Roll no. 537

INTRODUCTION: Interleukin 17 family(IL17) said to a member of pro-inflamatory cystine knot cytokines family. Interleukin-17 is a key cytokine that links T cell activation to neutrophil mobilization also activation. They are produced by a group of T helper cell known as T helper 17 cell in response to their stimulation with IL-23. Th17 was identified by Rouvier et al. who isolated IL17A transcript from rodent T-cell hybridoma. The protein encoded by IL-17A is founding member of IL-17 family. IL17A protein exhibits high homology with viral IL-17 like protein encoded in the genome to T-lymphotropic rhadinovirus Herpesvirus saimiri.

OVJECTIVE: The review summarizes the basic biology of IL-17 and discusses its emerging role in Periodontal disease. The current burden of evidence from human and animal model studies suggested that the net effect of IL-17 signaling promotes disease development.

DISCUSSION:

Interleukin-17 and IL-17 producing lymphocytes, innate immunity are emerging as important players in the pathogenesis of periodontitis. Approximately all the IL-17 related research in the field of periodontal disease involves the IL-17A isoform and therefore, will be the focus of this review. Fore understand the IL-17 role in peridontitis, it is instructive to firest understand the basic biology of interleukin and the cell that it produce.

The gene encoding IL-17 was cloned in 1993 from a mouse cytotoxic T lymphocyte hybridoma cDNA library and the role in human IL-17 inflamation. Interleukin17 or IL-17A is founding member of family ot cytokines that also includes IL-17B, IL-17F and IL-17C. The good characterized cytokines in the family are IL-17 and IL-17F which can signaling homodimers or as IL-17A/F heterodimers through same heterodimeric receptor that comprises IL-17RA, IL-17RC subunits. IL-17RA is abundantly expressed in hematopoietic cell compartments. If binding repertoire IL-17RA and IL-17RC includes distinct ligands. In this context IL-17RA oligomerizes also with IL-17RB and the IL-17RA/RB complex binds IL-17E, also knoen to IL-25. IL-17RA additionally pairs with IL-17RD, although the cognate ligand for the IL-17RA/RD complex hasn't been identified. The different tissue distribution of IL-17RA and IL-17RA, and IL-17RC may also serve to allow tissue specific signaling by IL-17A, IL-17F and IL-17A/F, since these ligands have difference binding affinity each of the IL-17RC and IL-17RA subunits.



FIG: INTERLEUKIN-17 RECEPTOR SIGNALING

IL-17 producing CD4+ T helper cells have recently been defined as a unique subset of proinflammatory helper cells whose development depends on signaling initiated by IL-6 and TGF-beta ,autocrine activity of IL-21, activation of SATE3, and induction of the orphan nuclear receptor RORyt. The maintenance, expansion, and further differentiation o the commited Th17 cells dependant on IL-1 beta and IL-23.IL-17 was originnaly found produced by circulating human Cd4RO⁺ memory T cells .A recent study found in human TH-17 memory selectively high levels of CCR6 .In this study, we report that human peripheral blood and lymph tissue contain a significant number of CD4+FOXP3+ T cells that express CCR6 and have the capacity to produce IL-17 upon activating. These cells coexpress FOXP3 and RORyt transcription factors. The CD4+FOXP3+CCR6+ IL-17 producing cells strongly inhibit the proliferation of CD4+ responder Tcells. CD4+CD25^{high} derive T-cell clones express FOXP3, RORyt and IL-17 and maintain their suppressive function via a cell-cell contact mechanism.

ROLE OF INTERLEUKIN-17 IN PERIDONTITIS: The initiation and progression of periodontal disease on complex interactions between periodontal bacteria and cell of immune system. Studies have demonstrate that a number of proinflamatory cytokines are released in response periodontal bacteria. Andrukhov eyal. Suggested that due to differences in the bacterial profile in peridontitis can be associated with different cytokine profiles.

It is generally acknowledged that control of the the Th1/Th2 balance is central to the immunoregulation of periodontal disease. It has been suggested that stable periodontal lesions are mediate by Th1 cells and progression of periodontal reflects a shift towards Th2 cell, and therefore, the pathogenesis of periodontitis is clinically considered as involving Th1/Th2 pattern.

AGP is generally seen in teenagers and young adult. It is the most severe from of periodontitis which can lead to significant periodontal inflammation and premature tooth loss in maximum number of cases at early age. There is abundantly literature suggesting aberrant polymorphonuclear leukocytes function as a key pathogenic mechanism in AGP exhibiting defective in vitro PMN chemotactic response and enhanced oxidative metabolic response. Evidence suggest that the rate of bone destruction is about the three to four times faster than in chronic periodontitis.

II-17 may play a significant role in AGP because of the functional impairment of PMN and because of the association of IL-17 pathway with the recruitment of neutrophils which results in enhanced inflammation and bone resorption.



FIG: Biological function of IL-17 and their role in peridontitis

DIFFERENTIATION AND FUNCTION OF II-17 PRODUCING T CELLS: various hematopoietic and lymphoid progenitors are mobilized from the bone marrow and initiate T cell development in the thymus. During this process, they express an antigen receptor (the T cell receptor, TCR), and most cells differentiate into CD4-positive T cells or CD8-positive T cells. After completion of the maturation process, CD8-positive T cells circulate throughout the body, acquiring cytotoxic functions. They contribute to immunological homeostatis by killing cells that have been infected by viruses as well as cancer cells. On the other hand, CD4-positive T cells are helper T cells. They exhibit an immunological regulatory function. Helper T cells are helper T cells. They exhibit an immunological regulatory function. Helper T cells have previously been divided into mainly two subsets. Th1 cells differentiate under the influence of IL-12 and mainly produce interferon-gama. IFN-gama strongly activates macrophages, promoting the eliminating of intracellular pathogens. In other words, it support cellular immunity in the acquired immune system. On the other hand, Th2 cells differentiate under the influence of IL-4. Th2 cells support B cells through IL-4 production. As a result, the antibodies production by B cells switch their class from IgM to IgG or IgE. By induction the production of IgG or IgE, elimination of extraclellular parasites is promoted. While cellular immunity is performed by Th1 cells, Th2 cells support humoral immunity. Thus, although derived from the same precursor cells, when activated by antigen stimuli, helper T cells differentiate into subsets with different properties due to the surrounding environmental factors. The mechanism of differentiation has been previously analyzed in detail to clarify mutually exclusive properties. Namely, IFN-gama suppresses the differentiation of Th2 cells, while IL-4 inhibits Th1 differentiation. Therefore, the functional imbalance between Th1 and Th2 is at the origin of various immunological diseases. For example, when there is a bias toward Th1, autoimmune diseases such as MS and RA are more likely to occur, while if Th2 is dominant then allergic reactions represented by pollinosis are provoked. However, energetic research in recent years identified subsets other then Th1 and Th2 cells. Among these, the Th17 cell subset, which produces IL-17, contributes to autoimmune diseases accompanied by chronic immune and inflammatory reactions, working together with Th1 cells.

INTERLEUKIN-17 AND INFLAMMATORY INTERACTIONS WITH OTHER CYTOKINES: IL-17 is also responsible to stimulate other pro-inflammatory cytokines such as IL-1 beta, IL-6,IL-8, prostaglandin E₂, and matrix metalloproteinases through the stimulation of epithelial of epithelial , endothelial, and fibroblastic cells. IL-17 appear to be inadequate to mount a potent inflammatory response by itself, but in collaboration and/or synergism with other inflammatory cytokines, it accelerates the inflammatory. IL-17 can induce a potent inflammatory cascade by increasing the expression of target genes. Il-8 release is functionally important for neutrophil recruitment. IL-6 inceases the relese of elastase from human neutrophils in vitro. IL-17 shares transcriptional pathway with IL-1 and tumor necrosis factor alpha. P38 and nuclear factor kB are the key transcriptional factor for Il-17 function. IL-17 induces the production and relese of colony- stimulating factor granulocyte and granulocyte-macrophage CFSs are powerful anti-apoptotic survival factors for neutrophils.

CONCLUSION: Interleukin-17 plays a central role in innate immunity, inflammation, and osteoclastogenesis and links T cell activation to neutrophil mobilization and activation. Although it is likely that IL-17 exerts both protective and destructive effects in periodontitis, the burden of evidence from human and animal model studies suggested that the net effect of IL-17 signaling leades to disease. Systemic anti – IL-17 intervention, as already performed for rheumatoid arthritis, ankylosing spondylitis, and psoriasis, could potentially shed light on the true effects of IL-17 responses in human periodontitis.

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Cytokine Storm in COVED-19

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Introduction:

Outbreaks of coronavirus disease 2019 (COVED -19) have spread rapidly around the world caused by the deadly acute respiratory syndrome coronavirus 2 (SARS-CoV-2).Early symptoms of COVID-19 mainly include fever, cough, mayalgia, fatigue or shortness of breath. In later stages of the disease, dyspnea can occur and gradually lead to acute respiratory problems syndrome (ARDS)or multiple organ failure(MOF).

Cytokine storms not only limit the spread of the virus in the body but also cause damage to secoundary tissues through the secretion of large amount of active mediators and inflammatory factors. It has been determined that cytokine storm of coved-19 is a leading cause of death; so cytokine storm is a major therapeutic target of critical ill patients &for prevention of disease. Although specific mechanism of cytokine storms in COVED-19 have not been fully expounded, hyper activated immune response and dysregulation of ACE(angiotensin converting enzyme 2) expression and its downstream pathways might be provide possibilities.

Objectives:

In the early stage of COVED-19, symptoms of severe acute respiratory infections appear and some patients develop rapid acute respiratory problem syndrome, acute respiratory failure, and other series complications. There is significant evidence of cytokine storms as an important of diseases progression and health, especially who are seriously ill. Early detection and control of cytokine storm can effectively prevent disease progression and reduce mortality. This review will summarize on causes of cytokine storm as well as possible mechanism and control of COVED-19.

Discussion:

Cytokine storm induced viral infections

The virus can stimulate the activation of immune cells (e.g., T cells, B cells, macrophages and dendritic cells) and resident tissue cells ,resulting in the production of large amounts of inflammatory cytokines is produced. Previous studies have shown that serum levels of proinflamatory factors include IFN-g,IL1b, IL-6, IL-12, IL-18, MCP-1 and CCL2 (CC chemokine ligand-2), CXCL-10 and IL-8 positively correlated with lung inflammation and lung tissue injury in SARS patients. Where level of serum proinflamatory cytokines IL-6, IFN-g,

TNF-a, IL-15, IL-17 and chemokines IL-8,CXCL-10 and CCl-5 were significantly increased in MARS patients.^[2]

Clinical and pathological manifestation in COVED-19

The incubation of COVED-19 patients is 1 to 14 days and mostly 3 to 7 days. Common symptoms early in the illness were fever, dry cough, myalgia, dyspnea and anorexia; however, few patients present initially with symptoms, such as diarrhea and nausea. Most patients had good results and treatment ,while the elderly patients and those with chorionic disease usually had bad health. Although most patients with COVED-19 dad mid and moderate symptoms, severe critically ill patients progressed rapidly to acute respiratory failure, ARDS, metabolic acidosis, coagulopathy, septic shock and MOF.^{[2][3]}

Possible Mechanisms Of Cytokine Storm In COVED-19

1) Hyperactivated innate immune responses

During the process of antiviral immune responses, innate and adaptive immune responses interact with each other and produced to immune protection. Innate immune responses occer immediately and the adaptive immune response usually get take 4-7 days after infection for fully in virus clearance. For virus clearance innate immunity is relatively weak that's why adaptive immunity is the key factor in complete elimination of the virus. If the body does not produce the antiviral immune response for that time of virus clearance, the innate immune system is will be strong, which can't fully illuminate the virus and ultimately leads to systematic inflammation response with which uncontrolled release of inflammatory cytokine. For elderly patients and people with chorionic disease, it takes a long time to produce effective adaptive immunity due to deterioration of immune function. This patients really depend in the innate antiviral immune responses in the early stages of infection, which increases the risk of cytokine storm , severe illness and a higher mortality rate.^[2]

2) Dysregulation of ACE2 and its downstream pathway

Angiotensin converting enzyme 2 (ACE2)primarily catalyzes the breakdown of angotensin II to maintain homeostasis of the ranin-angiotension-aldosteron system (RASS).recent studies have also revealed potential role in ACE2 in regulating immune responses rather than merely viral-binding receptor in COVED-19.

Cellular entry of SARS-CoV-2 depend on the binding of S proteins covering the surface of the virion to cellular ACE2 receptor and on S protein priming by TMPRSS2, a host membrane serine protease. Particularly, SARS-CoV-2 can rapidly active pathogenic Th1 cells to secrete pro inflammatory cytokines, such as Granulocyte- macrophage- colony- stimulating factor (GM-CSF) and interlukin-6. GM-CSF farther activates CD14⁺ and CD16⁺ inflammatory monocytes to produce large quantities of IL-6, Tumor necrosis factor –a (TNF-a)and other cytokines.

Membrane bound immune receptor (e.g; toll like receptor) may contribute to an imbalanced inflammatory responses, and and week IFN-g indication may be important amplifier to cytokine production. The cytokine storm of COVED-19 is characterized by high expression of IL-6 and TNF-a.

Hirano et al. proposed a potential mechanism of the cytokine storm caused by the angiotensin II pathway. SARS-CoV-2 activates NF-kB, via pattern recognition receptors (PPRs). It occupies ACE2 on the cell surface, resulting In a reduction in a ACE2 expression followed by an increases in angiotensin II. In addition to activating NF-kB the angiotensin II – angiotensin receptor type 1(AngII-AT1R)axis can also induces TNF-a and the soluble from of IL-6Ra(sIL-6Ra)via disintegrin matalloprotease 17 . IL-6 binds to sIL-6R through gp130to from the IL-6-sIL-6R complex, which can active STAT3 in ion immune cells. Both NF-kB and STAT3 are capable of activating the IL-6amplifier to induce virus pro inflammatory cytokine and chemokines, including Vascular endothelial growth factor (VEGF) and monocyte chemoattractant protein-1 (MCP-1), IL-8 and IL-63.^{[4][3]}

Controlling Cytokine Storm In COVED-19

Inhibition of cytokines

1) Blocking of IL-6/IL-6R

The cytokine storm may be the cause of SARS and COVID-19 infections. T lymphocyte are hyper activated , and huge amount of pro-inflammatory cytokines including IL-6 and IL-1, which contribute to vascular permeability, plasma leakage, thereby causing pulmonary damage and ARDS, as well as Multi organ failure(MOF).

Similar problems are also observed after the chimeric antigen receptor T cell(CAR-T) treatment. TCZ is a humanized anti IL-6 receptor antibody, inhibiting IL-6. TCZ is used not only for therapy of RA, temporal arteritis, and and many other autoimmune rheumatic disease but also for the treatment of the cytokine storm, which may be induced by CAR-T treatment.^{[1][2]}

2) Blocking of IL-1 Family

As mentioned above, IL-1 is another pro-inflammatory cytokine playing a dominant role in cytokine storm , and SARSCoV-2 may cause pyroptosis by IL-1B. Anakrina is a recombinant IL-1R antagonist and the first IL-1 blocking biologic agent. Anakinra blocks the binding of both IL-1a and IL-1B to IL-1R, thereby inhibit the pro-inflammatory effect of IL-1. Anakinra was found to be beneficial in patients with severe sepsis without significant adverse effect best upon the data of phase 3 randomized clinical trial. The recommended SC adult dose of Anakinra ranges from 100-200 mg daily to 100 mg three times weekly; the pediatric is 1 mg/kg daily. The bioavailability SC injections 95% with a half-life of 4-6 hours. ^[1]

3) TNF-a inhibitors

TNF-a and IFN-g are also key inflammatory cytokines and attractive targets in the control of cytokines storms, and clinical trials are ongoing to test these blockers in COVED-19^[5]

Conclusion:

Huang et al. observed that patients in intensive care unit (ICU) shows higher level of plasma inflammatory cytokines IL-2, IL-7, IL-10, GM-CSF, IFN-g, MCP and TNF-a then non ICU patients, indicating the positive correlation between cytokine storm and severity of illness. After being infected with the SARS-CoV-2 CD4⁺ cell were activated and differentiated into Th1 cells to secrete pro-inflammatory cytokines such as IL-6, IFN-g, and GM-CSF. GM-CSF can active immune cells for further release of IL-6 and other pro–inflammatory cytokine leading to the generation of cytokine storms . There for IL-6 and GM-CSF released by T lymphocyte and mononuclear cell may be the key link of cytokine storms in COVED-19.

Reference :

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Flower visitors observation on Ocimum tenuiflorum

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Introduction:- *Ocimum tenuiflorum* is commonly known as holy basil Or tulsi. It is an erect, many-branched subshrub, with hairy stems. Leaves are green or purple; they are simple, petioled, with an ovate blade up to 5 cm (2 in) long, which usually has a slightly toothed margin. It is strongly scented. Tulsi is mainly cultivated for religious and traditional medicine purposes, and also for its essential oil. It is widely used as a herbal tea, commonly used in Ayurveda.

Objective of the study:- *Ocimum tenuiflorum* (Tulsi) is a very common plant and having interesting pollination strategies. Through this study we can know about the pollination strategies of tulsi, also about the plant animal interaction between tulsi and its flower visitors, about when around the day the flower visitors come, how they get rewarded by the flower, is they carrying pollen or not, and their activities related with the atmosphere etc.

Study site:- The study site is at 2no. Nutan Fulia Mathapara, Fulia, Nadia, 741402.

- **Habitat:-** The plants are at my house. The plants have grown on the moist soil. At a side there is a building and other side there is a tuboile.
- Long and Lat:- The longitude of the place is 23.236532 and the latitude of the place is 88.489092.

Description of the plant:-

Plant name:- *Ocimum tenuiflorum* Flower:-

Colour	Shape	Size	Odour	Hight from ground level	Position of the nectarie	Position of the ovary
Violet	Bilabiate	4mm	Strong aromatic	Approxima tely 4ft	Besides the ovary	Hypogynou s





Collection methodology:- for this observation work I have made time slots of 2 hour's, like 6-8am, 8-10am, 10-12pm, 12-2pm, 2-4pm, 4-6pm . Everyday at different time slot I have observed the flowers.

- Now after reaching at the observatory place, I waits for the flower visitors.
- Then when I found the flower visitors, I observed them on the flower and their activities.
- Then I take the data all I need and note it.
- Next I take the pictures of the particular flower visitor.
- Now after this until the flower visitors leave the place I waits or walk around there. After they leave I note their total time spent in the field and leave the place.

The pictures are captured from Poco X3 phone on 64mp camera lense.

<u>Results:</u> Throughout the observation I have found 6 species of flower visitors from 26th September to 2nd November. Some of them are regular some are not. There are the summary of my observational data on behalf of the species given below-

Species-1:- It is a hymanoptera. It sits on the flower head, takes nectar. At a stretch it also touches other flowers of a same species. The pollen carrying parts of it are their body, legs, head and in their crop. The observation table of the species-1 is given below-

Date	Weather	Foraging activities	Sitting on the flower (Time count in seconds)	Flower touching per minute	Total time spent in the field (minutes)
26/9/2021	Cloudy	10am-12pm	5	10	45
30/9/2021	Partly cloudy	12pm-2pm	4	12	45
1/10/2021	Clear sky, sunny	8am-10am	7	6	45
5/10/2021	Partly cloudy	8am-10am	5	9	35
7/10/2021	Partly cloudy	10am-12pm	5	9	40
8/10/2021	Clear sky, sunny	12pm-2pm	4-5	10	35
9/10/2021	Clear sky, sunny	8am-10am	4	12	25
21/10/2021	Partly cloudy	6am-8am	4	11	30
22/10/2021	Clear sky,	6am-8am	6	7	40

	sunny				
23/10/2021	Clear sky, sunny	10am-12pm	4-5	10	30
24/10/2021	Clear sky, sunny	8am-10am	4	9	35
25/10/2021	Clear sky, sunny	12pm-2pm	4	10	35
26/10/2021	Partly cloudy	2pm-4pm	3-4	12	35
28/10/2021	Clear sky, sunny	12pm-2pm	4	12	35
29/10/2021	Clear sky	2pm-4pm	5	10	30
2/11/2021	Cloudy	10am-12pm	6	9	30

So in result it can be said that the species-1 is almost regular as a flower visitor. Which a having a average flower sitting time of 5seconds and approximately 10 flower touching per minute. Which spends an average of 40-35 minutes in the field.

Species-2:- The species-2 is also a Hymanoptera. It sits on the flower head. And at a stretch it also touches the other flower of the same species. The pollen carring parts of it are their hairy body, legs, head, pollen baskets. The observation table of species-2 is given below-

Date	Weather	Foraging activities	Sitting on the flower (Time count in seconds)	Flower touching per minute	Total time spent in the field (minutes)
26/9/2021	Cloudy	10am-12pm	8	6	35
1/10/2021	Clear sky, sunny	8am-10am	5	9	30
27/10/2021	Clear sky, sunny	6am-8am	8	6	25

In result we can say that the species-2 having a flower sitting time of average 5 seconds. In a minute it touches approximately 10 flowers. And spends an avarage of 30 minutes in the field.

Species-3:- The species-3 is also a hymanoptea. At a stretch it also touches other flowers of a same species. It a sits on the flower head. The pollen carrying part of it areThe pollen carring parts of it are their hairy body, legs, head, pollen baskets. The observation table of species-3 is given below-

Date	Weather	Foraging activities	Sitting on the flower (Time count in seconds)	Flower touching per minute	Total time spent in the field (minutes)
3/10/2021	Partly cloudy	12pm-2pm	2-3	10	25
4/10/2021	Clear sky, sunny	10am-12am	3-4	8	30
8/10/2021	Clear sky, sunny	12pm-2pm	3	9	40
9/10/2021	Clear sky, sunny	8am-10am	3	10	40
20/10/2021	Clear sky, sunny	12pm-2pm	2-3	13	40
21/10/2021	Partly cloudy	6am-8am	3	13	35
25/10/2021	Clear sky, sunny	12pm-2pm	2-3	14	40
30/10/2021	Partly cloudy	8am-10am	7	7	30

In result we can say that the species-3 having an avarage flower sitting time of 3 seconds. In a minute it touches approximately 10-11 flowers. And spends an avarage of 35-40 minutes in the field.

Species-4:- Species 4 is regular to the plant but not as a flower visitor. They just moving all around the plant. But in my this span time of observation I have seen them some days on the flower. They are also hymanoptea. They have been seen on the plant all day long. The observation table for species-4 is given below-

activitiesthe flowertouching perspent in(Time countminutefieldin seconds)(minute)

26/9/2021	Cloudy	They have been seen there all day long	They are not sitting they are just moving around	10	They have been seen there all day long
1/10/2021	Clear sky, sunny			15	
3/10/2021	Partly cloudy			18	

In result we can say that the species-4 touches an avarage of 14 flowers in a minute.

Species-5:- Its is a hymanoptea. This one is found for very short period of time and on of a particular plant. But like the previous one it also been seen there all day long. Observation table is given below-

Date	Weather	Foraging activities	Sitting on the flower (Time count in seconds)	Flower touching per minute	Total time spent in the field (minutes)
6/10/2021	Clear sky, sunny	They have been seen there all day long	20-23	2	They have been seen there all day long
7/10/2021	Partly cloudy		25	2	
8/10/2021	Clear sky, sunny		25	2	

It having a avarage flower sitting time of 25 seconds. And touches approximately 2 flowers in a minute.

Species-6:- It is a Diptera. It sits on the flower head. And at a stretch it touches the other flowers of a same species. The observation table is given below-

Date	Weather	Foraging activities	Sitting on the flower (Time count in seconds)	Flower touching per minute	Total time spent in the field (minutes)
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6/10/2021	Clear sky, sunny	2pm-4pm	6	8	40
8/10/2021	Clear sky, sunny	12pm-2pm	7	6	35
27/10/2021	Clear sky, sunny	6am-8am	7	7	45

In a result it can be said that the species-6 having an avarage flower sitting time of 7 seconds and it approximately touches 7 flowers in a minute. And it spends an avarage of 40 minutes in the field.

Discussion:- In the observation I have seen that the flower visitor that comes almost regularly is the **Species-1**. In almost every kind of weather except rain I observed the species-1's foraging activities. But in sunny weather it spent much time than the cloudy weather as the observation shows. It refers that the temperature is fact that stimulate the foraging activities of insects. It works also for **Species-2**, **Species-3** and **Species-6**. In bright weather they spent much more time in the field than in cloudy weather.

In rainy day of 27th, 28th, 29th of september I had not found any flower visitor. It may for that the rainy day is not suitable for their foraging. Although heavy rain also washes, and degrades the pollen and dilutes the nectar. So the rain reduces the foraging activities.

It is seen that while taking nectar the species took more time than taking the pollen. Sitting on a flower for very short time, visiting more flower than normal level or spending less time in a field it referres that the place is lack of food supply. It occurs when a species comes regularly in a same place for foraging. So some insects visits the same place not regularly.

In case of **Species-4** and **Species-5** they some different jobs unlike other species. They took nectar reward from the flower (The species-5 took nectar from the flower that it take almost 25 seconds for a single flower) or shelter from the plant. In return they give the plant protection form other insects/animals that can harm the plant or flower. That's why they are seen to there all day long.

This observation gives a beautiful example of plant-insect interaction.



Species-1



Species-2



Species-3



Species-4



Species-5



Species-6



Species-1



Species-2



Species-3



Species-4



Species-6

Pollination Strategy of Lantana camara

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4 Introduction: -

Pollination is a biological process of plant to create offspring for the next generation via transferring the pollen grains from anther to the stigma.

Lantana camara, a species of flowering plant within the 'Verbenaceae' family, usually found in subtropical and tropical America but a few taxa are indigenous to tropical Asia and Africa. *Lantana camara,* is a diurnal flower and the pollination of *L. camara* is occurring by some of the insect; to be more precise, some types of butterflies. So, *L. camara* is an entomophilous flower.

4 Objective of the study: -

Pollination of *Lantana camara* is one of the interesting and advance topics for study and discussion, that depicts about the pollination strategy of *L. camara* and about the insect pollinators as well. It also deals with the common practice of the flower to attract their pollinators including the insect activity. The project summarizes the overall pollination process of *L. camara* and expressing about the role of pollinators in the pollination.

4 Study site: -

The study site was conducted at Bhakunda, Chandannagare in Hooghly district of West Bengal. The insect species of Lantana camara during blooming phase was recorded from 15th September, 2021 to 4th November, 2021. The study was carried out for 10 days/ 1 week and 3 days. The overall observation was recorded by four sessions; 7:00am to 8:00am. 8:00am to 9:00am, 9:00am to 10:00am and 4:30pm to 5:30pm.

4 Longitude and Latitude: -

According to the GPS co-ordinates, the latitude is 22°51′28.44″ N and the longitude of the study site, Bhakunda, is 88°21′26.244″ E.

4 Habitat: -

The study site is a garden and situated at **Bhakunda, Chandannagare** in **Hooghly** district.



Description of Lantana camara: -

- Colour: Lantana come in many different colours such as red, yellow, white, pink and orange, which differ depending on the location, inflorescence, age and maturity. The flower that was observed, was white and pink in colour.
- Shape: Lantana has small tubular shaped flowers and have four petals and arranged in cluster in terminal area of stem.
- Size: Average height of Lantana is 3ft to 4ft.
- $ightarrow ext{Idor:}$ Lantana has a distinct odor in between fermenting citrus and gasoline.
- Height from Ground Level: The height of the observed flower from ground is approximately 3.2ft.
- Position of the Nectaries: Below the overy.
- Position of the ovaries: It contains superior ovary.

Collection Methodology: -

I had observed the flower for 10 days and each day the observation period was at around one to one and a half hours. I also taken few pictures of pollinators of the flower Lantana with the help of my mobile phone's camera. Thus, I have collected same information about this topic.

🕂 Results: -

Lantana camara is a diurnal flower and it shows different variety of flower colours such as red, yellow, white, pink and orange to attract their pollinators. The flowers that I observed was white and pink. Lantana camara is an entomophilous flower; that means the pollination of Lantana is carried out by insects. During the observation period I had observed total four types of insects pollinators

Species	Common Name	Phylum	Order
Dalias eucharis	Common Jezebel	Arthropoda	Lepidoptera
Graphium agamemnon	Tailed Jay	Arthropoda	Lepidoptera
Hesperiidae sp.	Skippers	Arthropoda	Lepidoptera
Polistes versicolor	Paper Wasp	Arthropoda	Hymenoptera

which are discussed below -

They are usually found in sunny days and according to my observation they are found around 29°C to 34°C temperature. They sat on the flower head and suck the nectar with the help of their long proboscis. During ingestion of nectar, the sticky pollen grains are stucked with their legs and proboscis as well. When they sat on the anther flower, they actually carry the pollen grains and helps in pollination. Thus, they serve them as a pollinator of *Lantana camara*.



According to the observation all the insect pollinations are usually found at around 29°C to 34°C. They can not tolerate much temperature than 34°C and less temperature than 29°C. They are not available in rainy days. There was also a *Antigonon leptopus*. Plant found but all of these above pollinators never towards the *Antigonon leptopus* plant to avoid the competition with the wasp named *Vespa tropica* (common name Greater banded hornet). <u>Picture: - *Polistes versicolor* (Paper Wasp)</u>



Picture: - Dalias eucharis (Common Jezebel)







Picture; - *Hesperiidae sp.* (Skipper)


Picture: - The photo was taken during my observation and studying of Pollination behavior of Insects

✤ Species 1: Dalias eucharis (Common jezebel)

Dalias eucharis belong to the phylum Arthropoda and order Lepidoptera. It sat on the flower head and ingested nectar. The pollen carrying parts are their legs and proboscis.

DATE	WEATHER	OBSERVATION TIME	IF I FOUND THE INSECT	IF SITTING, HOW MUCH TIME (APPROX) (SECONDS)	FLOWER TOUCHING PER MINUTE	TOTAL TIME SPENT IN THE FIELD (MINUTES)
15/09/2021	SUNNY	3:30PM-4:30PM	YES	7-8	6	60
03/10/2021	SUNNY	8:00AM-9:00AM	YES	10	5	60
04/10/2021	SUNNY	8:00AM-8:50AM	YES	9	5-6	50
05/10/2021	SUNNY	8:30AM-9:30AM	YES	8	6	60
08/10/2021	SUNNY	7:30AM-8:15AM	NO	-	-	45
10/10/2021	SUNNY	8:15AM-9:30AM	NO	-	-	75
26/10/2021	CLOUDY	7:00AM-8:00AM	NO	-	-	60
31/10/2021	SUNNY	9:30AM-10:20AM	YES	8	5-6	50
03/11/2021	SUNNY	4:00PM-4:30PM	NO	-	-	30
04/11/2021	SUNNY	9:20AM-10:00AM	NO	-	-	40

✤ Species 2: Graphium agamemnon (Tailed Jay)

Graphium agamemnon, commonly known as Tailed Jay, belong to the phylum Arthropoda and order Lepidoptera. It sat on the flower head and took Nectar. The pollen carrying parts are their legs and proboscis.

DATE	WEATHER	OBSERVATION TIME	IF I FOUND THE INSECT	IF SITTING THEN HOW MUCH TIME (APPROX) (SECONDS)	FLOWER TOUCHING PER MINUTES	TOTAL TIME SPENT IN THE FIELD (MINUTES)
15/09/2021	SUNNY	3:30PM-4:30PM	NO	-	-	60
03/10/2021	SUNNY	8:00AM-9:00AM	NO	-	-	60
04/10/2021	SUNNY	8:00AM-8:50AM	YES	4-5	12-14	50
05/10/2021	SUNNY	8:30AM-9:30AM	NO	-	-	60
08/10/2021	SUNNY	7:30AM-8:15AM	YES	4	14	45
10/10/2021	SUNNY	8:15AM-9:30AM	NO	-	-	75
26/10/2021	CLOUDY	7:00AM-8:00AM	NO	-	-	60
31/10/2021	SUNNY	9:30AM-10:20AM	YES	5	12	50
03/11/2021	SUNNY	4:00PM-4:30PM	NO	-	-	30
04/11/2021	SUNNY	9:20AM-10:00AM	YES	3-4	12-13	40

✤ Species 3: Hesperiidae sp. (Skipper)

,	51 5	,				
DATE	WEATHER	OBSERVATION TIME	IF I FOUND THE INSECT	IF SITTING THEN HOW MUCH TIME (APPROX) (SECONDS)	FLOWER TOUCHING PER MINUTES	TOTAL TIME SPENT ON THE FIELD (MINUTES)
15/09/2021	SUNNY	3:30PM-4:30PM	YES	10	3-4	60
03/10/2021	SUNNY	8:00AM-9:00AM	YES	12-13	3	60
04/10/2021	SUNNY	8:00AM-8:50AM	YES	12	4	50
O5/10/2021	SUNNY	8:30AM-9:30AM	YES	10	3	60
08/10/2021	SUNNY	7:30AM-8:15AM	YES	15	2	45
10/10/2021	SUNNY	8:15AM-9:30AM	YES	7-8	4	75
26/10/2021	CLOUDY	7:00AM-8:00AM	YES	12	2	60
31/10/2021	SUNNY	9:30AM-10:20AM	YES	10	3	50
03/11/2021	SUNNY	4:00PM-4:30PM	NO	-	-	30

NO

-

40

-

Hesperiidae sp., commonly known as Skipper, sat on the flower head and took Nectar. Their pollen carrying parts are legs and proboscis.

Species 4: Polistes versicolor (Paper Wasp)

9:20AM-10:00AM

SUNNY

04/11/2021

Polistes versicolor commonly known as Paper Wasp, sat on the flower head and took nectar. Their pollen carrying parts are head, legs and suctorial proboscis.

DATE	WEATHER	OBSERVATION TIME	IF I FOUND THE INSECT	IF SITTING THN HOW MUCH TIME (APPROX) (SECONDS)	FLOWER Touching Per Minutes	TOTAL TIME SPENT ON THE FIELD (MINUTES)
15/09/2021	SUNNY	3:30PM-4:30PM	NO	-	-	60
03/10/2021	SUNNY	8:00AM-9:00AM	YES	15	2	60
04/10/2021	SUNNY	8:00AM-8:50AM	NO	-	-	50
05/10/2021	SUNNY	8:30AM-9:30AM	NO	-	-	60
08/10/2021	SUNNY	7:30AM-8:15AM	NO	-	-	45
10/10/2021	SUNNY	8:15AM-9:30AM	NO	-	-	75
26/10/2021	CLOUDY	7:00AM-8:00AM	NO	-	-	60
31/10/2021	SUNNY	9:30AM-10:20AM	NO	-	-	50
03/11/2021	SUNNY	4:00PM-4:30PM	NO	-	-	30
04/11/2021	SUNNY	9:20AM-10:00AM	NO	-	-	40



The observation study gives us a brief idea about the pollination strategy of Lantana camara and also the importance of insects in pollination process. By this study we got many unknown facts about pollination process and the study surely enriched our knowledge.

* <u>Review work on insect visitors and pollinators of</u> <u>*Tabernaemontana divaricata* (Togor):-</u>

- **Study Site** The study was conducted at village Ala, Dhaniakhali in Hooghly district of West Bengal. The insect species on the flower *Tabernaemontana divaricata* during its blooming phase was recorded from September 27, 2021 to
- Latitude & Longitude 22.97 & 88.08
- **Objective of the study** To study about various insect visitors and pollinators of *Tabernaemontana divaricate* (Togor).
- **Habitat** The study site was a mini garden which is located at the top of our house. The flower pollinators and visitors were observed for an interval of each 3 minutes for approximate 1 hour per day.



Date:-26/9/21, Time:-1.10pm

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
White	Hypocleteriform,Pinwheel shaped	Centimeter in diameter	No	3.7 ft	Base of ovary	Hypogynous ovary

• <u>Description of the Plant (Flower)</u>

4 <u>DAY 1 – 27/09/21:</u> Time – 1.15pm to 2.15pm

 $\circ~$ Temp - 30°C , Humidity - 88% , Wind - 8.4km/h , Partly cloudy weather with a possible thunderstorm.

• Insect visitor : Diurnal/Nocturnal						
Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts		
Hymenopterans	Formicidae					

Insect visitor : Diurnal/Nocturnal



Date:-27/9/21, Time:- 1.25pm

4 <u>DAY 2 – 28/09/21:</u> Time – 1.15pm to 2.15pm

 $\circ \quad Temp-29^{\circ}C$, Humidity – 92% , Wind – 6.8km/h , Partly cloudy weather.

• Insect visitor : Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Hymenopterans	Formicidae			

Date:-28/9/21, Time:- 1.35pm-



↓ <u>DAY 3 – 29/09/21:</u> Time – 1.20pm to 2.20pm

 $\circ~$ Temp – 27°C , Humidity – 85% , Wind – 4.2km/h , Partly cloudy weather.

• Insect visitor : Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Hymenopterans	Formicidae			



Date:-29/9/21, Time:-1.45pm

LAY 4 – 30/09/21: Time – 4.15pm to 5.15.pm

 $\circ \quad Temp-25^{\circ}C$, Humidity - 81% , Wind - 3.2km/h , Clean weather.

• Insect visitor : Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Hymenopterans	Formicidae			



Date:-30/9/21, Time:- 4.42pm

↓ <u>DAY 5– 1/10/21:</u> Time – 3.45pm to 4.45.pm

 $\circ \quad Temp-26^{\circ}C$, Humidity - 83% , Wind - 3.8km/h , Clean weather.

• Insect visitor : Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Hymenopterans	Formicidae			

Date:-1/10/21, Time:-4.30pm



↓ <u>DAY 6– 3/10/21:</u> Time – 1.45pm to 2.45.pm

 $\circ~$ Temp $-\,28^\circ C$, Humidity $-\,85\%$, Wind $-\,4.3 km/h$, Partly cloudy weather.

• Insect visitor : Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Hymenopterans	Formicidae			



Date:-3/10/21, Time :-2.10pm

LAY 7– 5/10/21: Time – 1.10pm to 2.10pm

 $\circ~$ Temp – 29°C , Humidity – 78% , Wind – 3.7km/h , Clean weather.

• Insect Visitor: Diurnal/Nocturnal

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts
Lepidoptera	Lycaenidae	Neopithecops		



Date:-5/10/21, Time:-1.50pm

Collection methodology:- Data collection regarding the flower *Tabernaemontana* divaricate(*Togor*) pollinators and visitors was done carefully through day by day observation. Each day about 1 hour, I spent my time near our garden. I tried to find the visitors and pollinators everyday but at that time due to the weather was rainy so only find some of the visitors and did not find any specific pollinators species, after got any of them(visitors) I tried to capture their pictures by my mobile. All the data was also recorded in rough notebook for careful and detailed analysis.

Results:- The observation was conducted from mid September 2021 to late early October.Though the observation was done in a regularly pattern on daily basis but still did not find any specific pollinators except once I got a Quaker(*Neopithecops zalmora*)butterfly. I didnot think that it was came as a pollinator cause it was very movable and somehow I captured one photo of that butterfly species. It was seen on the flower buds those were not bloomed and on the leaf sometimes,maybe it came just to take the nectar from the flower. There were many visitors there like different species of ants(Order- Hymenoptera, Family-Formicidae)and some dipterans including house fly. Those ants were seen on the flower buds which were not bloomed. Those various ant species are solely depends on that natural food source for them. They came to take their reward as in form of sweet nectar. From the late of September due to the rainy weather I did not find any specific pollinators but from early October when the rain stops I find some species of butterflies and dragonflies. Most of the time they were not sitting on any flower but one day I got one and I captured that moment of a Quaker sitting on a not fully bloomed Togor flower bud and in other times they just keep flying above the plant about 2-3 times and went off ,so I did not clicked pictures.

Discussion:- From the above results I did not found any specific pollinator to be involved in pollination of this flower Togor though I got some of the flower visitors. These flower visitors are ants, they use that place as their habitat or sometimes they try to protect the flower and plant. Due to the rainy weather high humidity and moisture might be the the reason for not finding any other insect visitors rather then ants. These ants only visits the flower to collects their natural sweet reward which is Nectar or sweet sap.

Pollinator observation on Hibiscus

Name- Avijit Ghosh Roll- 545

Objective:

To know about the various pollinators and their interaction with hibiscus plant in my locality.

Study Site:

The study was conducted Bajarpara, Balurghat, D.Dinajpur, West Bengal. The insect species on Hibiscus rosa sinensis during its blooming phase was recorded from october 21, 2021 to November 3, 2021.

Latitude & Longitude:

22.237284 and 88.753858



Habitat –

The study site was on my rooftop. The flower visitors were observed for an interval of each 2 minutes for approximately 1 hour per day.

Description of the Plant (Flower)

Color	Shape	Size	Odour	Height from GL	Position of the nectaries	Position of the ovaries
Red	Trumpet Shaped	6 - 10 cm In dm	Aren't any,	7ft- 8ft	Inside the calyx	Bottom of the flowers

Collection methodology-

Collection of flower visitors was made by live observing the flower and clicking some pictures by mobile. Flower visitors were observed for 1 hour per day.

What we observed from day by day is listed down below -

Order	Family	Genus/ Species	Posture of sitting	Pollen carrying parts	Sitting time on flower
Hymenopter a	Apidae	Apis indica	The stamen	Wings, Legs	10 seconds
-	-	-	-	-	-

Hymenopter a	Apidae	Apis indica	The stamen	Wings, Legs	20 seconds approx
Odonata	Dipterocarpa ceae	Anisoptera sp	Flying around the flower	-	5 seconds
-	-	-	-	-	-
Odonata		Anisoptera sp	Upper bud	legs	1 minute
Hymenopter a	Apidae	Apis indica	Around the petal	-	5 seconds
Passeriform es	Nectariniidae	Nectariniidae sp.	Around the petal	beak	Stays for 10 second and comes back again
-	-	-	-	-	-
Passeriform es	Nectariniidae	Nectariniidae sp.	On the calyx	beak	3 seconds

 During the observations temperature stayed between 26-31°C, Humidity was around 50-60%, Partly sunny weather stayed all throughout the days with some exceptions.

Conclusion: I am not sure about that all the insects are pollinators, some bees were flying towards the flowers.but some ants were roaming around the roots.

Observation of flower visiting insect on Lantana camara

Ronit Das (546)

Department of zoology ; Ramkrishna Mission Vivekananda Centenary College

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Introduction

Lantana camara is one of the world's most pervasive exotic and inhabits over 60 Regions globally. It relies heavily on pollination services for its reproductive success and flowers Undergo a sequential color change from nectar and pollen rewarding yellow to orange then pink. Four insects are observed to pollinate *Lantana camara* and those are Common Jezebel,, Common Mormon,, Lime Butterfly and Domestic honeybee. *Lantana camara* is one of the world's most pervasive exotic and inhabits over 60 regions globally. It relies heavily on pollination services for its reproductive success and flowers undergo a sequential color change from nectar and pollen rewarding yellow to orange then pink.

Objective

Pollinators like bees and butterflies are important for plant reproduction. One way to keep these pollinators happy is to attract and feed them. Lantana is a sun-loving, warm weather plant that's great for attracting these pollinators . In these plants, the thrips live inside flower buds and lay eggs in the petal tissues. The females pollinate the flowers by flying from flower to flower looking for the comparatively rare, wingless males. In Lantana however, thrips are associated with the flowers only when the stigma is receptive .

Study site

This study was conducted at Majhipara Palashi which is a village area in Kanchrapara in the city of Kolkata.

This observation on Lantana camara took place in 22nd September 2021 and continued till October 5th. The overall observation was recorded by 5 seasons i.e, 6:00-9:00 am ; 11:00am - 12:30pm ; 2:00-3:00pm ; 5:00 – 6:00pm and 9:30-10:15pm each day continuing for 13 days.

Latitude and Longitude of area

22.9 degree and 88.4 degree

<u>Habitat</u>

This study site was a roadside of our house where this flower was bloomed.



Description of flower

Colour	Shape	Size	Odour	Height from the ground level	Position of nectaries	Position of ovaries
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Yellow to Orange to pink	l 2-6 cm	Smell like gasoline	2-3 m		
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Collection methodology

Most of the insects are basically butterflies and bees. Butterfly has a high foraging speed so they used to on the flowers for only few seconds. I took the pictures as much as possible and also videos by my mobile phone . I continue this process in different time intervals to observe their actual foraging behaviour and to witness the pollination by different pollinators. Then I put those information down on a notebook. I note down the the presence of pollinators of different species in different time intervals. And also in which genus, species and order they belong. I also put down the duration of pollination, position of sitting and how many flowers they touch within a minute of same/different flowers.

Result and discussion

Only two types of insects are seen to pollinate the flowers. One is the butterfly and the other one is the honeybee.

Insect 1



Common Jezebel (<u>Delias eucharis</u>)

Order	Family	Genus/Species
Lepidoptera	Nymphalidae	Heliconius

Foraging speed

Position of sitting	Duration	Flowers touching per minute
On the head of the flower	5-6 sec	Approximately 5

Insect 2



Common Mormon (<u>Papilio polytes</u>)

Order	Family	Genus
Lepidoptera	Papilionidae	Papilio

Foraging speed

Position of sitting	Duration	Flowers touching per minute
Head of the flower	Approximately 8 Sec	5-6

Insect 3



Lime Butterfly (<u>Papilio</u> <u>demoleus</u>)

Order	Family	Genus / Species
Lepidoptera	Papilionidae	Papilio demoleus

• Swallowtail Butterfly

Foraging speed

Position of sitting	Duration	Flowers touching	
Position of sitting	Duration	per minute	
Head of the flower	8 sec	6 approximately	



Domestic honeybee (<u>Apis mellifera</u>)

Order	Family	Genus/Species
Hymenoptera	Apidae	Apis mellifera

Foraging speed

Position of sitting	Duration	Flowers touching per minute
On top of flower	7-8 sec	8-9

Discussion

All of these insects were shown to pollinate in the day light from the dawn to afternoon. None of these insects pollinate in the night time. No other pollinators were shown to pollinate probably due to the cloudy weather & rain. Much of the time the butterflies pollinated the flowers. Butterflies of the same species and of the other species both pollinate these flowers. They are attracted to flowers in the broad day light because of the flower or scent. This flowers blooms beautifully in the day time specially in morning which is right time for this pollinates for foraging. Butterfly of different species are attracted at different times. They didn't pollinate in cloudy weather probably because of the absence of sufficient light. Except that honey bees also pollinate at different times more than once in a day. But only domestic honeybees are shown in these observation. Bees were also attracted to this flowers but they also didn't come at night maybe because of the low light. All pollinators in this observation were active in day time but as it was getting dark their pollination activity were seen to be quite in the observation.

Report I

Species	Date	Seasons Am/pm	Total staying time
	23 sep	8:12-8:21	9 min
	24 sep	10:05-10:15	10 min
Dolias oucharis	25 sep	8:42-8:55	13 min
Denus eucharis	29 sep	1:02-1:08p	6 min
	30 sep	9:53-10:02	9 min
	2 Oct	2:11-2:25P	14 min
	23 sep	7:03-7:11	8 min
	24 sep	12:55-1:09p	14 min
	25 sep	11:22-11:37	15 min
	26 sep	2:42-2:55p	13 min
Papilio polytes	28 sep	2:57-3:04p	7 min
	29 sep	5:01-5:09p	8 min
	30 sep	6:52-7:13	21 min
	1 Oct	10:32-10:44	12 min

	22 sep	4:05-4:17p	12 min
	26 sep	6:58-7:11	14 min
Papilio demoleus	27 sep	2:00-2:12p	12 min
	28 sep	10:00-10:08	8 min
	2 Oct	10:26-10:40	14 min
	22 sep	7:55-8:06	11 min
	23 sep	9:22-9:39	17 min
	24 sep	6:00-6:18	18 min
	25 sep	12:59-1:11p	12 min
Apis mellifera	26 sep	3:04-3:18p	14 min
	27 sep	4:07-4:13p	6 min
	29 sep	1:09-1:20p	11 min
	1 Oct	7:00-7:10	10 min
	2 Oct	3:09-3:18p	9 min

Immediate Hypersensitivity to Wheat Consumption: A Brief Review

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Introduction:

The Immune system includes a complex network of cells, tissues, organs and Substances makes body to fight against any foreign body. Immune systems are always on alert and react very quickly to something ongoing, a particular persistent adverse reaction over a certain food item(includes egg, peanut, soyabean, milk and others). Ingredients causing these adverse effects are called **allergen**, which may lead to serious symptoms like breathing difficulty, vomiting, diarrhoea and even cause anaphylactic shock. This phenomenon of food allergy happens when the body's immune system reacts unusually to a specific food item.

Normal ingestion includes interference by the gut microbes (also contributes in strengthening of gut barrier); and normal absorption in intestine. Dendritic cells form the first line of defence in the gut barrier, molecules absorbed by the gut are being treated from the gut microbes generally do not excite the dendritic cells. In absence of gut microbes the leaky barriers of gut continuously encounter the food molecules activating dendritic cells. Activation of dendritic cells stimulates T-cells and leads to IgE antibody production from B cells. Releasing of IgE antibodies activates mast cells (*Sensitization*), second time encounter of the same molecules results in detonation of mast cells in various organs locations including the circulatory systems causing various symptoms and may lead to an anaphylactic shock.

Objective:

Wheat allergy, especially gluten intolerance, is associated with three major conditions: Celiac disease, Wheat Sensitivity and Non-Celiac Gluten Sensitivity.

Retrospective study from the United States reported the median age of resolution is 79 months, and approximately 35% of patients, wheat allergy persisted into adolescence. Another study over Thai childrens of similar median age of resolution of 76 months, and there were only a few reported wheat allergy in adults. A larger study conducted in Italy and Denmark over 37 adults, all having a history of wheat allergy, only 48% Of the cases reported positive for oral food challenge(didn't mention any age of wheat allergy onset).{Source: Pacharn & Vichyanond, 2017}

A proper care over restrictions in food causing allergies is a strict avoidance nowadays. However, Wheat avoidance cannot be strictly implemented in our lifestyle as wheat is being widely consumed and used as a constituent of various food products including cakes, biscuits and other items. Because of difficulty in complete avoidance of this products severe reactions and alternative symptoms are observed, in case need of alternative treatment procedures; among some of this includes oral immunotherapy(OIT)

Discussion:

Gluten includes a family of seed storage proteins (with high proline & glutamine content) found mostly in cereal grains [barley(hordeins), rye(secalins), oats(avenins)] including maze and rice and are considered as most commonly consumed grains worldwide. Broadly, it contains two types of proteins glutenins and gliadins(α/β , $\gamma \& \Omega$) which are resistant to proteolytic enzymes of the gastrointestinal tract (particularly crossing the epithelial barrier and activating immune responses).

Cereal food consumption is a major trigger to gluten-related disorders (gluten intolerance) which could be classified under three categories: Celiac disease(Autoimmune Disease), Non-Celiac gluten sensitivity(gluten sensitivity) and Wheat allergy (Type I & IV hypersensitivity by IgE immunoglobulin) demonstrating symptoms like bloating, abdominal discomfort, diarrhea and flatulence.



Gluten Related Disorders:

Gluten having high glutamine content are resistant to proteolytic enzymes of gastrointestinal tract, while some of them cross the intestinal barrier and activate the immune system and trigger wheat allergy causing incomplete digestion leading to several intestinal symptoms.

Gliadin and other gluten proteins are found to stimulate T cells (IgE immunoglobulins); while the constituents of other wheat proteins like agglutinin-carbohydrate binding protein(ACBP) and exorphins also influence the immune system and damage intestinal epithelium. Amylase trypsin inhibitors (ATIs, albumin proteins) forming 4% of wheat grain are highly resistant to intestinal proteases causes activation of monocytes, macrophages and dendritic cells releasing pro-inflammatory cytokines in celiac disease & non-celiac gluten disease patients.

Compounds like fructo-oligosaccharides, galactooligosaccharides, lactose, fructose, sorbitol, mannitol and polyols are some of prevalent forms of fermentable oligo-, di- & monosaccharides and polyols(FODMAPs) are short chain (less than 10 carbon atoms) molecules. These FODMAPs are neither digested nor absorbed by the gastrointestinal tract and have high cosmetic effect and could undergo rapid fermentation resulting in intestinal liquefaction, gas production, pain while causing certain bowel diseases(irritable bowel syndrome) whereas sometimes patients develops ulcerative colitis, Crohn's disease. Compounds like galactooligosaccharides, fructo-oligosaccharides present in FODMAPs limits the proliferation of certain bacteria like *Bacteroides spp.*, *Clostridium spp.*, and *E.coli* hence affecting intestinal lining(promoting activation of dendritic cells).

Wheat Sensitivity:

Wheat(*Triticum aestivum*) is a food largely consumed throughout the world. Wheat related allergic disorders, especially in IgE mediated allergy, patients suffer severe anaphylactic disorders. On the basis of solubility wheat proteins can be categorised into 4 categories including albumin, globulin, gliadin & glutenin.

Water and dilute salt soluble fraction of wheat corresponds 15% to 20% of the total protein i.e, albumin and globulin. However most of the proteins consist of ethanol & dilute acid soluble fraction (gliadins and glutenins). Gliadins are grouped into α/β , $\gamma \& \omega$ gliadins (recently reported Baker's asthma). Among them, gliadin containing omega5 shows high specificity on IgE mediated disorder diagnosis(especially in children). Also wheat allergy in children shows positive IgE response due to glutamines, $\alpha/\beta \& \gamma$ gliadins and α -amylase inhibitors, thus major type of wheat allergy are associated with IgE responses which could be further categorised into several subtypes of population.

An experiment conducted under Battais *et al.* reveals 27(14 adult & 14 children) patients with wheat allergy, reports percentage of patients with IgE response to α -gliadin is 7%, to β & γ gliadin is 20% and ω -gliadin is 20% in immunoblotting studies. The result demonstrates the importance of gliadin family proteins as allergen for children causing wheat allergy. These Studies also

exposed the importance of the glycan portion of gliadin of where binding of IgE shows greater symptomatic response, signifying the glycan portion of galaidin(7N linked Glycosylation sites were identified).

Conclusion:

New Strategies of oral immunotherapy (OIT) include modification of innate and as well as adaptive immune mechanisms OIT protocols are classified into 3 phases:

The first phase(i.e, escalation phase) includes the initial phase also known as rush phase, where food is given 6-8 doses per day, starting from small quantities of doses and then increasing it rapidly(phase generally conducted in the hospital due to its high risk). At the end of this phase the same starting dose limit was followed for home as earlier. This phase follows by up build up phase, during which the amount of food is increased in 1 to 2 weeks (generally 20% to 30% increase) until the patient reaches a proper maintenance dose(a level of dose which is maintained for several years).

Efficiency of this treatment was measured in terms of desensitization & tolerance, desensitization denotes the limit upto where patient can persist the maintenance dose for several years during which no interruption in dose quantity was observed(sustained on progressiveness); ability of the patient to tolerate dose also determines the patients health after when the treatment discontinues (generally shift in 1 to 3 years of OIT).

Immunological changes that were observed in patients undergone OIT includes decrease in mast cell and basophil release of mediators of inflammation, initial increase in food specific IgG but later decrease in food-specific IgE levels and expansion & affinity maturation of specific memory B-cell. In this regulatory T cell stimulation, release of IL-10 and IFN- γ plays a central role.

Whole gliadin can be considered an important allergen for children undergoing wheat allergy, where the entire range of gliadins are glycosylated whereas the deglycosylation of gliadin reduces the allergenicity of gliadin. The N-glycan moiety of gliadin exhibits allergenicity and acts as a carbohydrate epitope in wheat allergy in children.

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Observation of a Flower Visiting Insect on Ixora coccinea

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Introduction-

Ixora coccinea (also known as Jungle geranium, flame of the woods or Jungle flame or Penduli) is a species of flowering plant in the family Rubiaceae. It is a common flowering shrub native to Southern India, Bangladesh and Sri Lanka. It has become one of the most popular flowering shrubs in South Florida gardens and Landscapes. The flowers ,leaves, roots and the stem are used to treat various ailments in the Indian traditional system of medicine, the Ayurveda and in various folk medicines, in traditional Indian medicine the fusion of juice leaves and the fruit of *Ixora coccinea* is used to care for dysentery, Ulcers and gonorrhea .

Objective-

Pollination acts as a transferring of the pollen grains from the male anther flower to the female stigma to create offspring for the next generation. One of the ways that plants can produce offspring is by making seeds. The pollinator may become particular for food or their behaviors or they are attracted by the flower. This review will summarize insect behavior, insect foreignness and the particular pollinator of the flower.

Study Site-

The study was conducted at Gidhagram, Katwa in Purba Bardhaman district of West Bengal. The insect species on *Ixora coccinea* during the blooming phase was recorded from 25 .10.2021 to 10.11.2021 the study was carried out for 15 days of the flowering season .

Latitude & Longitude-

23°29'44.8"N 88°04'19 .8"E 23.495772, 88.072169

Habitat-

This study site is a garden and is located behind my house. There is the ability of full Sun and light to moderate shade and it is covered with some shrubs and surrounded by other small trees.

Collection Methodology-

The diversity of insect visitors was recorded and the individuals collected by a hand net. Data collection regarding the flower visitors was done by careful observation and clicking the pictures by mobile. Data was also recorded in a rough workbook for careful analysis. The averages of the observations were calculated.

Date	Time	Temp. (°C)	Weather	Wind (Km/h)	Humidity (%)	Barometer (mbar)	Sitting Time (Average)
01/11/20 21	06.00am- 07.00am	24	Partly Sunny	No	80	1015	45 sec
02/11/20 21	07.00am- 8.00am	22	Scattered Clouds	No	86	1016	-
03/11/20 21	4.15pm- 5.15pm	25	Clean	No	78	1011	35 sec
04/11/20 21	04.30pm- 5.30pm	23	Clean	No	75	1010	33 sec
05/11/20 21	06.30am- 07.30am	20	Sunny	2	84	1014	42 sec
06/11/20 21	05.30am- 06.30am	18	Sunny	No	86	1011	No
07/11/20 21	11.30am- 12.30p.	26	Sunny	No	53	1011	15 sec

Results-

Ixora coccinea is a dense ,multi-branched, evergreen shrub ,commonly 4-6 ft (1.2-1.8 m) in height. It has a rounded form ,with a spread that may exceed its height. The glossy, leathery, oblong leaves are about 4 in (10 cm) long ,with entire margins ,and are carried in opposite pairs on the stems .

Flowers are borne at branch-ends, in dense corymb-like cymes, flower-cluster-stalk very short or absent; bracts about 8 mm long. Flowers are stalkless, bright scarlet, hypanthium 1-1.5 mm long, becoming hairless, teeth about 0.5 mm long. The blooms with bright , hot pink flowers are small, tubular, 4 petaled, and are borne in clusters which are 4 to 6 inches across.

Flower-tube is prominently long, 2.5-4.0 cm long, 1.5 mm wide, hairless, petals 8-10 x 4-5 mm, twisted in bud, throat hairless. Stamens are 4, inserted on the throat of the flower-tube, filaments very short. Style protruding; stigma 1.5 mm long.

Discussion-

From the above results, I can find some flower visiting insects and some pollinators of *Ixora coccinea*. Pollinators provide key services to both natural and agricultural ecosystems. Agricultural productivity depends, in part on pollinator populations from adjacent semi-natural habitats. Insect pollinators play a crucial role in improving the productivity of cross pollinated crops. The availability of a sufficient number of suitable pollinators during flowering time is essential for achieving optimum pollination. Pollination, an essential ecosystem service provided by insect pollinators , causes it to produce a huge number of varieties of that plant.High humidity and moisture might be the reason for not finding any other insect visitors other than ants. And the ants only visit the flower only for nectars or sweet sap.

Photo Plate-





Order	Family	Species
Lepidoptera	Papilionidae	<i>Papilio polymnestor</i> (Blue mormon)

• Date:- 02/11/2021



Order	Family	Species
No	No	No

• Date:-03/11/2021



Order	Family	Species
Lepidoptera	Papilionidae	Papilio polytes (Indian Common mormon)

• Date:-04/11/2021



Order	Family	Species
Lepidoptera	Papilionidae	Papilio polytes

• Date:-05/11/2021



Order	Family	Species
Lepidoptera	Papilionidae	Papilio polytes

• Date:-06/11/2021



Order	Family	Species
-	-	-

• Date:-07/11/2021



Order	Family	Species
Lepidoptera	Papilionidae	Papilio polytes
Flower visitors observation on Hibiscus rosa-sinensis

Name:- Pritam Lahiri, B. Sc, Sem-V, Roll-555, Department of Zoology

Introduction:-*Hibiscus rosa-sinensis* also known as china rose or Joba Hibiscus is a genus of flowering plants in the mallow family, Malvaceae. The genus is quite large, comprising several hundred species that are native to warm temperate, subtropical and tropical regions throughout the world. The leaves are alternate, ovate to lanceolate, often with a toothed or lobed margin. The flowers are large, conspicuous, trumpet-shaped, with five or more petals, colour from white to pink, red, blue, orange, peach yellow or purple and from 4–18 cm broad.Flower colour in certain species, such as *H. mutabilis* and *H. tiliaceus*, changes with age. The fruit is a dry five-lobed capsule, containing several seeds in each lobe, which are released when the capsule dehisces (splits open) at maturity. It is of red and white colours. It is an example of complete flowers.

Objective of the study:-*Hibiscus rosa-sinensis*(Joba) is a common plant with very effective pollination strategy through self and cross pollination. The cross pollination happens through various Insects. Through this study we can know about the pollination strategy of joba and the interaction between plant & the pollinators. About when around the flower visitors come, how the rewarded by the plant and is they carry pollen with them or not etc.

Study site:- The study site is 8/2 Masjid Ghat Road, Naihati, North 24 parganas, 743165

Habitat:-The plant is at my garden.the plant is grown on moist soil. East, north and south side sourrounded with houses & west side is the river Ganga.

Description of the plant:-

Plant name:- Hibiscus rosa-sinensis

Flower:-

Colour	Shape	Size	Odour	Hight form the ground	Position of nectarie	Position of ovary
Red	Disc shape	10 cm (4 in) in diameter	No scent	3 miter	Located just inside the calyx and under the ovary at the base of the flower	At the bottom of the blossom

Collection methodology:-For this observation work I have made time 2 hour's time slots. Everyday at different time slot I have observed flowers. Now after the reaching the observatory place and wait for the flower visitors, when it comes I take the data&capture the flower visitors activity. Then capture it with my mobile phone(realme 3i).

Results:-Through out the study I found 2 types of flower visitors from 29/09/2021 to 12/11/2021. 1 type is regular and other is occasional. There are the summery of my data collection given below:-

Species -1:- it is a hymanoptera. It sits on the inside of the calyx or outside of the petal. It also touches other flowers of a same species. The pollen carrying parts of it their body, legs and head. The observation table given below

Date	Weather	Time	Sitting on the flower position	Total time spent in the field(min)
29/09/2021	Sunny	10am-12pm	Calyx	95
02/10/2021	Sunny	1pm-3pm	Walk in the stamen	20
05/10/2021	Cloudy	9am-10am	In the ovary	110
07/10/2021	Sunny	12pm-2pm	Petal	22
08/10/2021	Cloudy	3pm-4pm	Calyx	30
21/10/2021	Sunny	10am-12pm	Petal	15
23/10/2021	Sunny	3pm-4pm	In stamen	5
24/10/2021	Cloudy	9am-11am	Petal	22
25/10/2021	Sunny	10am-12pm	Calyx	30
26/10/2021	Sunny	11am-1pm	Ovary	40
28/10/2021	Sunny	1pm-3pm	Petal	10

30/10/2021	Cloudy	10am-12pm	Calyx	40
01/11/2021	Sunny	3pm -4pm	Petal	15
02/11/2021	Sunny	10am-12pm	Petal	10
08/11/2021	Sunny	10am-12pm	Petal	20
09/11/2021	cloudy	12pm-2pm	Calyx	30
10/11/2021	Sunny	9am-11am	Calyx	40
11/11/2021	Sunny	11am -1pm	Calyx	60
12/11/2021	Sunny	2pm-4pm	Petal	12

So in result we can say the species 1 is a regular flower visitor. It's avarage time of spent inflower 20-40 min.

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	pecies	- 1	10 0	100 0	~ . j	mono	piera.	IU IL	, DICC		un u	10 0	lanten		- <u> </u>	5 0 1 01	une	110 11 0		resur	~~ E	,1,011.

Date	Weather	Time	Sitting on flower's position	Time spent(min)
29/09/2021	Sunny	10am-12am	Flying on the top	2-3
02/10/2021	Sunny	1pm-3pm	Flying over the flower	2
23/10/2021	Sunny	3pm-4pm	Sitting on stamen	5
25/10/2021	Sunny	10am-12pm	Flying over the flower	2
02/11/2021	Sunny	10am-12pm	Sitting on petal	1

10/11/2021 S	Sunny	9am-11am	Flying over the flower	1
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So in result we can say species 2 is a often visit than species 1 and time spent average is 2-3 min

Discussion:- In the observation I see that the species 1 is a regularly visits thr flowering plant.the sitting place of the species is calyx, ovary and petal. It's body touched so many times in the pollen and visited many flowers as much as it can. The average time of the is species 1 is 10am-2 pm.the weather must be sunny. The avarage time spent of the species 1 is 20-40 min. It collected the nector but in this case the pollen struck in legs and the body..

In case of species 2 it visit occationaly.and spent 2-3 min in flying over the flower.

So from this observation I can tell that the cross pollination happens in the joba and main pollinator which works in the pollination is species 1 which is ant. It comes everyday except the rainy weather.

Conclusion:-through is I concluded that china rose main pollinator is ant which visits every da & helps in the pollination. And the flower rewarded the ant with it's nector.

Picture :-

Site:-



Observation pictures:-





















Observation of Geotaetic

Study of geotaxis behavior in earth

W INTERS & FOR AN A

An earthworm is a terrestrial invertibule that belongs to the Phylum Annelida, They exhibit a tube with in - a - tube body plan, are externally Segmenter with corresponding internal segmentation. The objective of thics experiment is to objective of thics experiment earth worm.

So, In this experiment a worm jer is made and observed the movement of the earthworms. Materials: 1 col interest in 200 1) A large transparent glass of jar with lid. 1 damini and 2) Soil. 3) Sand.

> 4) nail ; hanmar. 5) earthworms. 6) Black paper.

Procedure -

1) the Some contribution is collected form wet bond side.

2) when the A jornwith its tid is taken, the state A jornwith its tid is taken, the state of few holes are poked with nail and hammer in the tid for proper

yend ventilation.

and there are don't the of 1 3

3) collect for a amount of soil form the same location from where the carth worm to is taken. wet it up with water.

(4) some amount of sol band in added with the boil and 2/3 added with the boil and 2/3 of the given in fulled.

5) Then the worms are released on the offer,

6) some voel Slices of vægetables pours on the top at day 3 and worthing the jan 2 day internal.

7) The worm jar is kept in a dark place @ wrapped by a dark paper. 2) Adam - Other A Sometrich is in a week (2) Observation:-5 il - I wash in bar. Day O:-\$ 6 conth & worm is poured on the word for ofter some time the contruscen start digging the goid and go down. Day 1-2:-The vagetable slices are untouched, NO worm in pren on the surface. some small hale are seen on the surface. Day 3-4 ._ The vage-table Spices on Untouched, The

Suces are starting not. True Aug to the JANE. Day 5-6:-Some parties of vagetables are portion of A set of a set of a set eater., one worm in Seen on the Surface from its that. AT TERMINIONS THE ALL AS BURGER A and hearing and Davy 7-8:milling to the back back worms a started earter the Stiefed Magetables. Some cannels under the soil is visible from the transport Davy 9-12:-1 worth leat vogetables, their faces are phown on total Surface, some new caninels are farmed. Their movement On the sain clearly shown. Dong 13-16:their movement o in the boil

clearly visible. They also

Interpretation !-

After some few hours they start dissing the soil. It indicates that at the new enviorment they First try to know the new enviorment.

the children as noil)

First 3-4 day they donot show any movement as they are acclimatized the new enviornment. I After days the start eat vagetable. The

Their movement is towards the gravity. Which depiets the geotoxing movement. But when they a need food.

came aparties the jon which is to artigeotaxis movement. But their manenet is very so ploth on a itig

winter season.

a wint be for an in the and

an south

Project on Different kind of Behaviour of Animal

SOUMIK RAY Reg NO, A01-1112-115-093-2019 CJG ROMNO, 557 Paper: DSE 2A Zoology (HONS)



DATE FAGE NO 01 28/08/21 EXPT. NO. 01 Aggresive behavior of Seolopendra and Mantis. Introduction: Mantis: Mantises belong to an Order of flying insects that contains over 2400 Species in about 400 genera. They are distributed worldwide in temperate and tropical habitats. Their necks are plexible and body clorgated. Their forelegs are greatly enlarged and adopted for Catching ad gripping prey. Scolopendra: Sedopendra is a Species -rich genus of lays tropical Confipedes of the family Scolopendidae. They are usually found in toropical and warmer temperate areas. Sestopendra can deliver painful bite, in Porsecting venom through their foreignles, modified logs on the first bady segment. Observation: From the given video we can observe the battle blue Mantis & Sedopendra held in a glass box. In the first sound the Sedopen - dra was small in dize, that the Mantis captured the sectopendra Casily with the help of filia, coxa and forelegs then killed Fib. But in the second found we can see the sectopendra was big in scize and this time of was hard for the Mantis & to escape the venomous bite of Scolopendra. This time Scolopendra killed the Mantis then eat upon of from the abdomenial point. Interpratation: After 2 round of battle we came to know that the Montis & Scolopendra both were voy aggresive in nature but fire was PICHEER abig factor in the 1st round . Finally Sealopendra won the battle over the mantis. Size was a big factor in this battle blo Manti & Scolopartra.

PAGE NO 03 1411 04/09/21 02 Adult aggresive interactions and lawal Scrambling for resources. Adult body size could be considered as a potential predictor of the success of the invader fly. 124 PIONEER

FAGE NO. 04 dt. ?

Black Swan Parents teaching their cygnets Swimming Introduction: Black Swan, the large water-bird usually found In Australia. Black Swans are mostly black-feathered birds with white flight feather. The bill is bright red, legs and feets greyish-black. Males are Slighty larger than females. Cygnets an greyish-brown. Their necks is long and 'S' Shaped Observation: Here in the video we can observe three things about the water-bird. First the parent Swan teaching & their cygnets how to Swim. Second parent and their new-borst body color and third their feeding habit. Parents quarding the ducklings and moves toroands the Storety flowing Stream and jumped in the water withe their new borns. then guiding them to Swim. The parents are fully black in Color and new borns are greyish whete . Then parents Starts Jeeding by dipping its head and neck under the water ad their body remains horizontal. Interpretation: From the given video we came to know about the ponental care of black Swan and their feeding habit also using the neck and bills. Black Swans is Vegetarian and for consist of algae and weeds, which the binds obtains by plunging 37s long neck into water upto Imeter deep. They MOREER are chemsy walkers as accasionally grate on land.

DATE

20/09/21

EXPT. NO 03

DATE 17:4 11: 0.5 23/10/21 di ? EXPT. NO 04 Green Heron; the tool using bind h. fishing Introduction : Coreen heron may found in any aquatic habitat but most common around small bodies of I great water. Lakes, ponds, mashes, Swamps, Streamsides, the use plant species as nest, i.e., Pires, Oaks, willows. mangrooves. (over water alt 30.5+). -Observation: From the given video be can observe that -the green heron bird is fishing in a river. Green Heron is one of the tod-using birds, commonly drops bait onto the Surface of the water and grabs the small fish that are attracted to the bait in the couly Slowing River. Here it was a crust of bread, if drops the bread on the water again and again, when the fish attracted to the bread, that moment it catches the fish. After catching the fish the heron took it the surface and -tuen negurgitated alive with the help of it's bill. Interpretation: We can that if is a amazing bind ad how early it fishes by using tools like a crust of bread That's how we observed the bird is so intelligent ad thew developed about fishing. de 29/2021

DATE 15/12/21 PAGE NO 06 ndt. EXPT. NO. Baby Lamb surviving through Rapid Stream Introduction: The mountain shap is usually white with a white face with no wool on forehead and legs. Females are polled but Rams usually have curved horns althrough some are not normally docked. Breeders give a high priority to hardiness, milling ability, nothing mothering quality and land servival . It is sure footed able to pick its way over nock and find Shelter in stormy weather and find Sufficient food in all condition. Observation: From the video clip of approx 2 min we Can observe the parental behavior and training of an mountain hamp to their baby to cross the stopid Stream. The male lamb to their baby to cross the stops Stream but the baby fears. After so many tries the baby fails to Jump to stream, But sometime the baby jumped into the Stream and very handly cross the hill Stoream. The parent Ahen helped the pales to gripthe store in the river Side. Interpretation: Mountain Sheep's body & Leg Structure is Very much helpful for Serviving through the Stormy on rapid Streams , Here the lamp and baby's river crossing Shows the ponental care & training of Swimming to the FIGHEER baby lamb.

29/126 2021

Title 1: Aggressive behaviour in Tephritidae frouit fly. Title 2: Parcental and Swimming behaviour of Black Swan.

> Name - Ashikesh Mondal Roll - 559

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Tephritidae, also known as 'true fruit flies' have 4000 species, many of which constitute encornous threats to fruits and vegetables production throughout the woold, causing both quantitative and qualitative loses. Many species of tephritidae are highly polyphogony and attack to the economically impositant fruit and vegetable like mango, apple, guava, tomato, pepper.

Anumber of torsing reputitidae are leaving Species, forming aggregations in which males fight to defend a small territory where they court females and mate. Male-male contests also occur in non-leaving species characterized by resource defense polygyny. Tephritidae temales display agonistic behaviour to maintain Single oviposition sites and reduce Larval competition for food.

- male-male fighting behaviour held while mating with temales. The aggressive behaviour between males are is characterized by reciprocal wing waving.
- Female-female fighting behaviour held similar to male-male fight.
- Aggoression can also occur between different Tephritidae Species by sharing the same habitat which is called interspecies contest.

Introduction: The black swan is a large waterbind,

a species of swan which breeds (+) flying birds. mainly in the southeast and southwest region of Australia. Within Australia, the black swan is nomadic, with ematic migration patterny dependent on climatic conti conditions. It is a large toised with black plumage & a red bill.

Obgenvation:

In the video, we saw there is a group of blackswar is swimming in a water. In the group there are two parents and Some ducklings. The parcents are totally black-feathered and the to ducklings are light-grey feathered. The porcents jumped into the water and following them the duckling also jumped exe except one. one of at the duckling were was in fear to jump into water. The parcents were eatching food to feed the ducklings and teaching them how to catch foods.

Interpretation:

At last we can say the ducklings learned to swimming and catching tood with their bill. Review

Study site

Pollination Observation on Moringa Oleifera

Manojit Nandi Roll:- 1566 Sub:- pollination Biology



Locality: The study was conducted at Atrajole, Kotulpur in Bankura district of West Bengal.

Habitat: The locality is a garden in front of my house. This tree is surrounded by many small plant and flower plants.

Data & Time: The insect species on <u>Moringa oleifera</u> is during its blooming phase was recorded from September 26, 2021 to 29th November 2021.

Longitude & latitude:

Description of the plant:

Colour	Shape	Size	Odour	Height from GL .	Position of the Nectarines	Position of the .ovaries
Whitish Gray	Oval to Obovate or Hear drop Shaped	1.0-1.5 cm Long & 2.0 cm broad	Miniscent Of roasted Nuts	9-10 meters	Inside the Calyx	Bottom of the flower.

INSECT VISITORS : DIURNAL

DAY 1 : 26 September, 2021. 11:00am - 12:00pm

Temp: 31° c; Humidity: 60% ; Wind : 9.8 km/h ; sunny weather

Order	Family	Species	Posture of sitting	Pollen carrying



Foraging activities: Collection of the flower visitors was made by live observing the flower and clicking some pictures by mobile. Flower visitors were observed for one hour per day.

Foraging speed:

Sitting on flower head/ else	If sitting then how much time	Flower touching (per minute)	At a stretch visiting the flowers of same plant species	Time of spent in the field
The insect sitting on flower head	1.0-1.5 minutes Approximately	50-55 second	Yes	4 mins

DAY 2: 27 th September2021. 08:00am to 09:00 am

Temp : 34°c ; Humidity: 40%.; Wind: 6.7 km/h ; sunny weather

Order	Family	Genus/species	Posture of sitting	Pollen carrying parts



Foraging activities: Collections of the flower visitors was made by live observing and clicking some pictures by mobile.

Insect Visitors: DIURNAL

Sitting on flower head/ else	If sitting, then how much time	Flower touching	At a stretch visiting the flowers of same plant	Time of spent in the field
Sitting on flower head	01 – 1.5 mins	60 – 78 second	Yes	10 minutes

DAY 3: 28th September2021. 12:00 pm to 01:00 pm

Temp: 30°c ; Humidity:71% ; Wind : 17km /h; Party cloudy weather

Order	Family	Genus/ species	Posture of sitting	Pollen carrying parts
-	-	-	-	-

Foraging activities: Not a single visitors observed for cloudy weather.

DAY 4 : 29th September2021. 03:00 pm to 04:00 pm
Temp: 29°c ; Humidity: 92% ; Wind: 11.2 km/h ; Light rainy weather

Order	Family	Genus/species	Posture of sitting	Pollen carrying parts
-	-	-	-	-

FORAGING ACTIVITIES: Not a single visitors observed

DAY 5 : 1st October 2021 ; 02:00 – 03:00 pm

Temp: $25^{\circ}c$; Humidity: 95%; Wind: 15.2 km / h; Rainy day

Order	Family	Genus/ species	Posture of sitting	Pollen carrying parts

FORAGING ACTIVITIES: No results