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**“IDENTIFICATION OF FORENSICALLY INFORMATIVE  
MARKERS AND PHYLOGENY IN SOME THREATENED SPECIES  
OF SNAKES AND LIZARDS IN INDIA”**

**ABSTRACT**

Global trade in snakes and their products is extensive, involving millions of individuals and their products annually. Approximately 6.2 million live snakes scheduled under Convention on International Trade in Endangered Species (CITES) were traded between the years 1975 to 2018. During the same period, 34-million snake skin were traded. Despite the increase in captive breeding, the majority of the snakes that are traded are from the wild sourced accounting for 60% of the trade. These figures highlight the significant scale of snake and trade of its products emphasizing the importance of monitoring, regulating the conservation of snake population.

Apart from snakes, one other important reptile that is traded as pets and for its products are lizards. Skin of monitor lizards is the most traded for the fashion industry. Among the reptile species scheduled on the IUCN red list, 21% of those involved as vulnerable while 5% is deemed as a high-risk category.

A key basis for wildlife investigations is definitely advancements in forensic technology. Combating the illegal trade of snake and lizard byproducts, which compromises biodiversity and endangers species, molecular identification using DNA has been a vital weapon in hand. For processed or fragmented materials, traditional morphological identification is usually ineffective; thus, DNA analysis is the most precise technique for species identification. With their great sensitivity and specificity, DNA-based methods let one differentiate closely related species. DNA barcoding is one of the molecular techniques used in identification since it sequences homogeneous nucleotide areas and match them to databases. Next-

generation sequencing (NGS) technologies have revolutionized molecular biology and made high-throughput sequencing, incredibly accurate and efficient feasible. NGS has become a valuable technique in wildlife forensics for species identification, especially for reptiles like snakes and lizards since it can precisely identify species from biological samples such blood, scales and tissue. This is critical for both law enforcement and conservation activities.

This thesis explores the whole genome of *Chrysopelea ornata*, commonly known as the ornate flying snake, one of the rarest species in the snake family, renowned for its unique gliding ability between trees. It examines whole genome, microsatellites, proteins, and gene annotation, along with the sequencing of its first complete mitogenome and phylogenetic analysis. Furthermore, the study investigates forensically informative nucleotide sequences (FINS) of *Chrysopelea ornata* and *Varanus bengalensis*, essential for species identification. The Bengal monitor (*Varanus bengalensis*) is categorized under Near Threatened (NT) on the Red List of International Union for Conservation of Nature (IUCN) as of 2018, therefore underlining the possible risk of endangerment should ineffective conservation actions be taken. Declared in Appendix I of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), the species is under the greatest degree of protection since international trade is forbidden except in very rare cases. In India, it is safeguarded under Schedule I, Part II of the Wildlife Protection Act of 1972, ensuring stringent legal protection. It also explores the oral microbiota of the varanus lizards and the findings of harmful bacteria and fungi. The molecular genetic data presented in this study hold significant forensic value, aiding in the accurate identification of these species and contributing to conservation and wildlife protection efforts. Thesis has been divided into chapters explaining experiments.

  
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(Signature of the supervisor date with official seal)

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