SUMMARY

Dispersal events have largely shaped the contemporary distribution of biota from the Indian subcontinent following the late Cretaceous volcanism rather than Gondwanan vicariance. These colonization events, during the Indian subcontinent's northward drift and post-Asia collision likely occurred during favourable climatic periods, leading to in-situ radiations and several endemic lineages. Ancient lizards such as the family Scincidae (skinks) serve as excellent models for studying such evolutionary processes (such as dispersal and vicariance).

Our research focused on the evolutionary trajectories of three endemic genera of Lygosomine skinks: *Ristella* and *Kaestlea*, endemic to the Western Ghats, and *Lankascincus*, endemic to Sri Lanka. We aimed to elucidate their biogeographic patterns within the Indian subcontinent. Initially, by using a multi-locus dataset including mitochondrial and nuclear markers, we examined the evolutionary relationships among these genera, hypothesizing that they might be sister lineages because they are distributed within the same bioregion. Our findings revealed that *Ristella* and *Lankascincus* are phylogenetic sisters, affiliated to the Eugongyline group of skinks while *Kaestlea* is related to the *Sphenomorphus* group. Our molecular dating and ancestral range evolution analyses suggested that the ancestors for *Ristella* + *Lankascincus* originated in Southeast Asia and dispersed to India during the late Paleocene, while that of *Kaestlea* originated in the Sino-Japanese region and moved to India during the early Eocene. These results show that the presence of these three Indo-Sri Lankan skinks in the Indian subcontinent results from two ancient independent dispersal events from Asia.

We further investigated the biogeography and molecular systematics of the Western Ghats endemic skinks *Ristella* and *Kaestlea* using an integrative approach that included phylogenetics, molecular species delimitation techniques, haplotype networks, and species distribution modeling. Our results indicate cryptic diversity within both genera, driven by historical and current geo-climatic factors and ancient biogeographic barriers like the Palghat and Shencottah Gaps. Specifically, within the sky island group *Kaestlea*, we noticed a Pliocene-Pleistocene accumulation of lineages. However, unlike conventional ideas, we found suitable grounds for dispersal rather than isolation during glacial periods such as in the Pleistocene. Within *Ristella*, we found a case of geo-climatic separation between two distinct morphotypes that were also separated phylogenetically. Our ancestral range evolution and ancestral state reconstruction analyses show that *Ristella* started diversifying in the climatically stable southern WG during the early Miocene. Lineage accumulation in these strictly forest-dwelling skinks was majorly during the Late Miocene-Early Pliocene indicating a case of aridity-induced vicariance.

Additionally, we identified a population of *Lankascincus fallax*, previously thought to be endemic to Sri Lanka, on the southwestern coast of India. Paleoclimatic data did not support the existence of a suitable dispersal corridor between southern India and Sri Lanka. Further, since most distribution points were on the coasts around operative ports, we posit that their presence resulted from one or multiple human-mediated dispersal events.