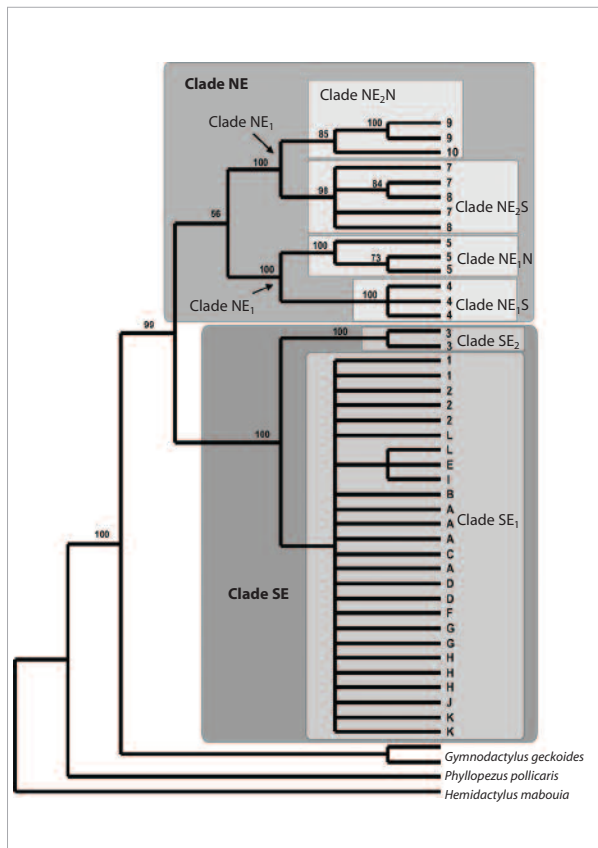


SYSTEMATIC AND EVOLUTION OF NEOTROPICAL HERPETOFAUNA

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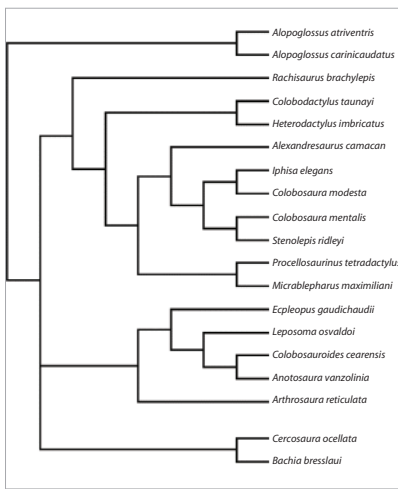


Molecular phylogeny of the *Gymnodactylus darwinii* complex for a region of mtDNA cytochrome *b* recovered by maximum parsimony ($L=699$; $CI=0.72$; $RI=0.88$). Numbers at nodes are bootstrap values (>50%)/posterior probability (Bayesian searches). Numbers and letters at terminals correspond to sampling localities (Pellegrino et al., 2005)

The present proposal aims to continue and expand the ongoing multidisciplinary research on the systematic and evolution of the herpetological fauna from Neotropical areas, as well as the study of historical biogeography of Neotropical reptile, amphibian and small mammal faunas. We intend to: (1) expand the karyological data so far gathered for Brazilian lizards, amphibians and rodents, in order to better understand their chromosomal evolution and detect useful characters for phylogenetic analyses; (2) complete the ongoing studies on taxonomy, karyotypes and DNA sequencing on the herpetological fauna of São Francisco dunes, obtaining intra and interspecific rates of divergences for endemic ratio; (3) study the heterocrony of the genus *Calyptommatus* and the ontogeny of the related *Gymnophthalmi* genera in order to drive future studies on the developmental biology of the group; (4) proceed with the ongoing collection of karyotypes and DNA sequences data on lizards of genus *Leposoma* to better understand its diversity and phylogeny; investigate the origin of parthenogenesis in *L. percarinatum* comparing the process with that of occurring in *Gymnophthalmus underwoodii*; (5) increase the taxonomic and character sampling to the study of the phylogenetic relationships within the *Gymnophthalmidae*, in order to obtain a robust hypothesis based on multiple data sets; (6) increase the sampling for lizards of genera *Gymnodactylus*, *Coleodactylus*, and *Mabuya* to allow phylogenetic and historical biogeography studies using morphological, karyological and molecular data; (7) conduct preliminary comparative studies on selected ratio of herps and small rodents with discontinuous distribution on Amazon and Atlantic forests and on rainforest remnants in the northeastern Caatingas, in order to obtain approximate times of divergence for different groups in these forested areas.

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

We have described the adult skeleton and developmental series for five lizard genera of tribe Gymnophthalmini (*Calyptommatus*, *Notobachia*, *Procellosaurinus*, *Psyllophthalmus*, *Scriptosaura*, and *Vanzosaura*). A series on studies on the genetical mechanisms involved in limb degeneration, and ecological and physiological studies on adaptation to fossoriality in some of the lineages of Gymnophthalmidae are



Phylogenetic tree for gymnophthalmid genera estimated under Bayesian method of the combined morphology and molecular data set and posterior probabilities (above nodes) for clades recovered at the 50% majority rule consensus topology (Rodrigues et al. 2007)

being conducted. A preliminary phylogeny of Gymnophthalmidae was recently published. We are now working on a new molecular based hypothesis for the Gymnophthalminae with 40 terminals (27 genera and 38 species), using as external groups, exemplars of the sub-families Cercosaurinae, Rhachisaurinae and Alopoglossinae. Our studies on the phylogeny of other Neotropical lizard's genus *Cnemidophorus*, *Enyalius*, *Leposoma*, *Coleodactylus*, and *Gymnodactylus* have also been fruitful. Molecular data on the small forest litter lizards genus *Coleodactylus* has shown a high and unexpected diversity, as well as very high species divergence rates, oldest clades dating from Cretaceous. The morphological data shows that there are cryptic species to be described, but the morphology seems to be highly conservative in the large Amazonian group, where molecular data shows high levels of differentiation. The molecular studies on the forest lizards genus *Gymnodactylus* and *Enyalius* has also revealed the existence of undescribed new species and general patterns of differentiation for the Atlantic forest populations. We are now exploring along the role of the Doce River, as a barrier to speciation using selected populations of frogs and lizards obtained from North and South of Doce River.

The results on anuran chromosomal characterization have been published for genera *Chaunus*, *Leptodactylus*, and *Proceratophrys*. The later has been subject of molecular studies considering mitochondrial and nuclear genes revealing different degrees of divergence among populations of southeastern Brazil. We are working also on the construction of new hypothesis of relationships for specific anuran groups using morphological data.

MAIN PUBLICATIONS

Amaro-Ghilardi RC, Silva MJJ, Rodrigues MT, Yonenaga-Yassuda Y. 2008. Chromosomal studies in four species of genus *Chaunus* (Bufonidae, Anura): localization of telomeric and ribosomal sequences after fluorescence in situ hybridization (FISH). *Genetica*. **134**: 159-168.

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