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**PROGRAM,  
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## Biodiversity 3D: Exploring the History of Chameleons

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Biogeographic patterns are often explained by spatial shifts that match changing environmental conditions to which species are adapted. Biogeographic patterns however, can also be explained through the adaptation of organisms *in situ* to changing environments over time, rather than purely through shifting distributions as a response to those changes. Combining dated phylogenies with information on habitat and morphology suggest that most chameleon genera radiated in the Oligocene, resulting in a phylogeny dominated by paleo-endemic lineages which correlate to the reduction of the Pan African forest and concomitant increase in fine structured habitats (grassy savannah, grassland, heathlands) since the Oligocene. Recent Plio-Pleistocene radiations are scarce, and occur in lineages that occur in fine structure habitats. The combination of morphological and performance data (bite force, gripping, sprinting) suggest that adaptation to these fine-structure habitats has resulted in the evolution of small body size, limb lengthening, hand/feet reduction, and ornamentation reduction. In contrast, paleo-endemic lineages have not radiated substantially since the Oligocene-Miocene, and these lineages retain morphological features that are adaptive in habitats that lack fine-structure vegetation (i.e. bushes/trees, or leaf litter). This work suggests that biogeographic patterns of chameleons can be explained primarily by lineage loss that corresponds with forest habitat reduction since the Oligocene, but that certain lineages in this family have adaptively radiated to new habitats since the Pliocene.

## Cryptic diversity of *Synchaeta* spp. (Rotifera, Monogononta) in mountain lakes: relationships with environmental parameters

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Cryptic species (i.e. distinct species that are morphologically similar) may have different ecological requirements and their merging into one species can bias the assessment of the main ecological drivers of biodiversity. We investigated the environmental parameters influencing the occurrence of *Synchaeta* species (*S. pectinata*, *S. grandis*, *S. lakowitziana*, *S. tremula/oblonga* - monogonont rotifers) in 17 waterbodies of the Trentino-South Tyrol region in the Eastern Alps. To improve taxonomic resolution in phylogenetic analysis, a marine *Synchaeta* (i.e. *S. cf. cecilia*) from the United Kingdom was also sampled and sequences from GenBank were downloaded. While *Synchaeta* species were morphologically identified based on trophi structure, cryptic species were identified based on the generalised mixed Yule coalescent (GMYC) model. We performed multivariate ordination both for morphospecies (i.e. unresolved complexes of cryptic species), a common practice in limnological studies based on morphological taxonomy, and for putative cryptic species, made possible by DNA taxonomy. We expected that resolving complexes of cryptic species could provide more information than using morphospecies. Out of the overall phylogenetic tree with 48 haplotypes from 203 individuals, the GMYC model indicated the presence of 14 GMYC entities, 11 from lakes in the Eastern Alps, 2 from Canada, and one from the U.K. *Synchaeta pectinata* showed five GMYC entities and *S. tremula* showed two; all individuals, for which the identification to *S. tremula* or *S. oblonga* was not possible, clustered in one monophyletic clade, here called *S. tremula/oblonga*, that showed additional evidence of three GMYC entities. Environmental-based multivariate ordination on cryptic species explained a significantly higher proportion of variance than that based on morphospecies. Occurrence of putative cryptic species was mainly related to total phosphorus. Moreover, different cryptic species within the same morphospecies showed different, and even opposite, preferences for total phosphorus. In addition, the same GMYC entity of *S. tremula/oblonga* found in Trentino-South Tyrol was also present in Canada and the same haplotype of *S. pectinata* found in Trentino-South Tyrol was also found in the U.K. This wide geographical distribution of haplotypes and cryptic species indicated the absence of dispersal barriers in *Synchaeta*.