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Phylogenetics of Acari and their cousins reshuffled by ultraconserved elements (UCE's): can beauty emerge from chaos?*

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Determining the chelicerate tree of life has been the subject of much research, with deep phylogenetic divergences and high evolutionary rates complicating both morphological and molecular approaches (Noah *et al.*, 2020; Ontano *et al.*, 2021; Sharma *et al.*, 2021; Ballesteros *et al.*, 2022). Within Acari, similar challenges exist—even the basic question of whether Acari is mono- or diphyletic remains unresolved (Pepato & Klimov, 2015; Lozano-Fernandez *et al.*, 2019; Van Dam *et al.*, 2019; Ontano *et al.*, 2021). Several recent molecular studies have attempted to resolve these issues using large multi-gene datasets (Pepato *et al.*, 2022; Klimov *et al.*, 2018), mitochondrial genomes (Ban *et al.*, 2022), and transcriptomes (Lozano-Fernandez *et al.*, 2019). Ultraconserved elements (Faircloth *et al.*, 2012) have recently shown great promise for constructing phylogenies for both deeply- and shallowly-diverged taxa (Zhang *et al.*, 2019), including for Chelicerata (Starrett *et al.*, 2017) and for Arrenuridae within Acari (Shoop, 2019), but have not yet been used across the Acari.

Here we present recent UCE data from over 550 taxa, representing all extant arachnid orders (except Schizomida) and over 240 families of mites distributed across all higher acarine taxa. UCEs were targeted using an Acari-specific probe set designed by Van Dam *et al.* (2019). DNA was extracted non-destructively and vouchers were retrieved and identified to the generic or species level. For each specimen, the COI barcode region was sequenced to confirm DNA quality and to check for DNA contamination. DNA libraries were prepared and pooled according to post-amplification concentration, and then were hybridized with the UCE probes using a myBaits Hyb Capture Kit (Arbor Biosciences) and sequenced on the Illumina MiSeq platform. Sequence data were assembled using three different assemblers (Abyss, rnaSPAdes and SPAdes) which have been found to increase the number of recovered targets (Brunke *et al.*, 2021).

Overall, the bait set was highly effective, with 300–1000 loci sequenced for most taxa (an average of 624 loci per taxon). Filtering and trimming of loci were performed within the PHYLUCE package (Faircloth, 2016). Sequences were aligned using MAFFT and preliminary maximum likelihood trees were constructed using IQ-tree, based on loci with a minimum of 50% taxon occupancy.

This analysis is preliminary, as it does not yet take into account the different rates of evolution present in the dataset. However, initial results indicate some support for a monophyletic Acari, though more robust analyses (*e.g.,* improving model fit with sliding-window site characteristics (Tagliacollo & Lansfear, 2018), amino acid phylogenetic reconstruction, rogue taxon analysis) and explicit hypothesis testing for this and other nodes of interest will be conducted to improve our confidence in the results.

Keywords: Ultraconserved elements, phylogeny, phylogenomics, Chelicerata, Arachnida, Acari

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