

Regular Poster Session II (Thursday, October 10, 2019, 4:15 - 6:15 PM)
WHAT DO OSSIFICATION SEQUENCES TELL US ABOUT THE ORIGIN OF EXTANT AMPHIBIANS?

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The controversial origin of the extant amphibian clades has been studied using several sources of data and methods, including phylogenetic analyses of morphological data, molecular dating, stratigraphic data, and comparisons of ossification sequences. A consensus has failed to emerge, perhaps in part because the diversity of methods used hampers comparisons. We have compiled two datasets of ossification sequences of 101 extant and extinct terminal taxa and seven cranial bones, or 102 terminal taxa and six cranial bones. These data allow us to assess the relative support for six currently or recently competing hypotheses about the origin(s) of the most inclusive uncontroversial extant amphibian clades: a monophyletic origin among temnospondyls, a monophyletic origin among lepospondyls, a diphyletic origin among both temnospondyls and lepospondyls, a diphyletic origin among temnospondyls alone, and two variants of a triphyletic origin, in which anurans and urodeles come from different temnospondyl taxa while caecilians come from lepospondyls and are either closer to temnospondyls (including anurans and urodeles) or to amniotes. The data were analyzed through maximum likelihood, and the AICc (corrected Akaike Information Criterion) weights of the six hypotheses allow us to assess their relative support. By an unexpectedly large margin, our analyses of both datasets support a monophyletic origin among lepospondyls; a monophyletic origin among temnospondyls, the current near-consensus, is a distant second. All other hypotheses are exceedingly unlikely according to our data. Because we find a strong phylogenetic signal in the data, we are cautiously optimistic about future uses of ossification sequence data as characters in phylogenetic analyses.

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