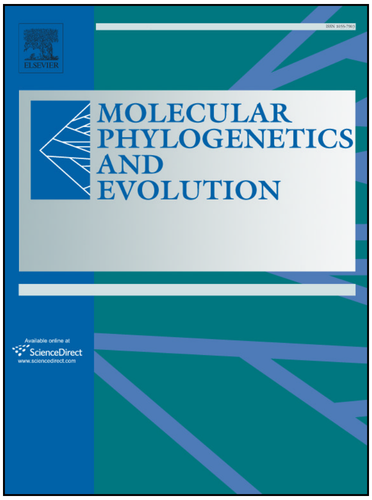

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PII: S1055-7903(18)30014-9
DOI: https://doi.org/10.1016/j.ympev.2018.04.007
Reference: YMPEV 6117

To appear in: *Molecular Phylogenetics and Evolution*

Received Date: 8 January 2018
Revised Date: 5 March 2018
Accepted Date: 6 April 2018

Please cite this article as: Kallal, R.J., Fernández, R., Giribet, G., Hormiga, G., A phylotranscriptomic backbone of the orb-weaving spider family Araneidae (Arachnida, Araneae) supported by multiple methodological approaches, *Molecular Phylogenetics and Evolution* (2018), doi: https://doi.org/10.1016/j.ympev.2018.04.007

# A phylotranscriptomic backbone of the orb-weaving spider family Araneidae (Arachnida, Araneae) supported by multiple methodological approaches

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## Abstract

The orb-weaving spider family Araneidae is extremely diverse (> 3,100 spp.) and its members can be charismatic terrestrial arthropods, many of them recognizable by their iconic orbicular snare web, such as the common garden spiders. Despite considerable effort to better understand their backbone relationships based on multiple sources of data (morphological, behavioral and molecular), pervasive low support remains in recent studies. In addition, no overarching phylogeny of araneids is available to date, hampering further comparative work. In this study, we analyze the transcriptomes of 33 taxa, including 19 araneids – 12 of them new to this study – representing most of the core family lineages, to examine the relationships within the family using genomic-scale datasets resulting from various methodological treatments, namely ortholog selection and gene occupancy as a measure of matrix completion. Six matrices were constructed to assess these effects by varying orthology inference method and gene occupancy threshold. Orthology methods used are the benchmarking tool BUSCO and the tree-based