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Molecular phylogenetics of Aspidiotini armored scale insects (Hemiptera: Diaspididae) reveals rampant paraphyly, curious species radiations, and multiple origins of association with *Melissotarsus* ants (Hymenoptera: Formicidae)

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**Molecular phylogenetics of Aspidiotini armored scale insects (Hemiptera: Diaspididae) reveals rampant paraphyly, curious species radiations, and multiple origins of association with *Melissotarsus* ants (Hymenoptera: Formicidae)**

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**Abstract**

The armored scale insect tribe Aspidiotini comprises many pest species that are globally invasive and economically damaging. The taxonomy of scale insects is based almost solely upon morphological characters of adult females, and little prior work has been done to test the classification of aspidiotines against molecular evidence. To address these concerns, we reconstruct a molecular phylogeny for aspidiotine armored scales that expands greatly upon taxonomic and character representations from previous studies. Our dataset includes 127 species (356 terminal taxa) and four gene regions: 28S, EF-1 $\alpha$ , COI-COII, and CAD. Nearly 50% of the species treated are identified as pests and several more may represent emerging pests.

Phylogenetic data were analyzed in a Bayesian framework using MC<sup>3</sup> iterations. The majority of sampled aspidiotine genera are not monophyletic as currently defined. Monophyly constraints for 'worst offenders' were imposed on the phylogeny and stepping-stone MCMC was performed to calculate marginal likelihood scores. Comparisons of marginal likelihoods from runs with constrained vs. informative priors support the interpretation that pest-rich genera are not

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