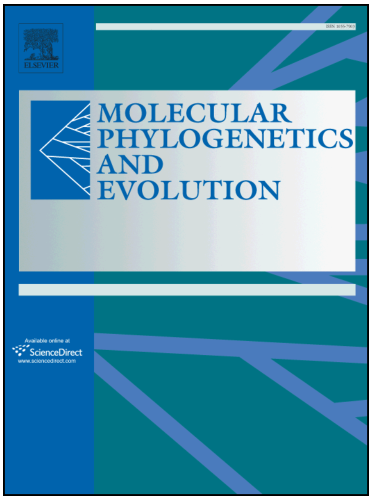

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Phylogenomic analysis of yellowjackets and hornets (Hymenoptera: Vespidae, Vespinae)

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Abstract

The phylogenetic relationships among genera of the subfamily Vespinae (yellowjackets and hornets) remain unclear. Yellowjackets and hornets constitute one of the only two lineages of highly eusocial wasps, and the distribution of key behavioral traits correlates closely with the current classification of the group. The potential of the Vespinae to elucidate the evolution of social life, however, remains limited due to ambiguous genus-level relationships. Here, we address the relationships among genera within the Vespinae using transcriptomic (RNA-seq) data. We sequenced the transcriptomes of six vespid wasps, including three of the four genera recognized in the Vespinae, combined our data with publicly available transcriptomes, and assembled two matrices comprising 1,507 and 3,356 putative single-copy genes. The results of our phylogenomic analyses recover *Dolichovespula* as more closely related to *Vespa* than to *Vespula*, therefore challenging the prevailing hypothesis of yellowjacket (*Dolichovespula* + *Vespula*) monophyly. This suggests that traits such as large colony size and high paternity arose in the genus *Vespula* following its early divergence from the remaining vespine genera.

Keywords
Phylogenomics, RNA-seq, transcriptomics, evolution, sociality, Vespinae

1. Introduction

Eusocial groups consist of overlapping generations of workers collectively caring for the offspring of the queen caste. Among wasps, eusociality is thought