Appendix S1: Supplemental methods.

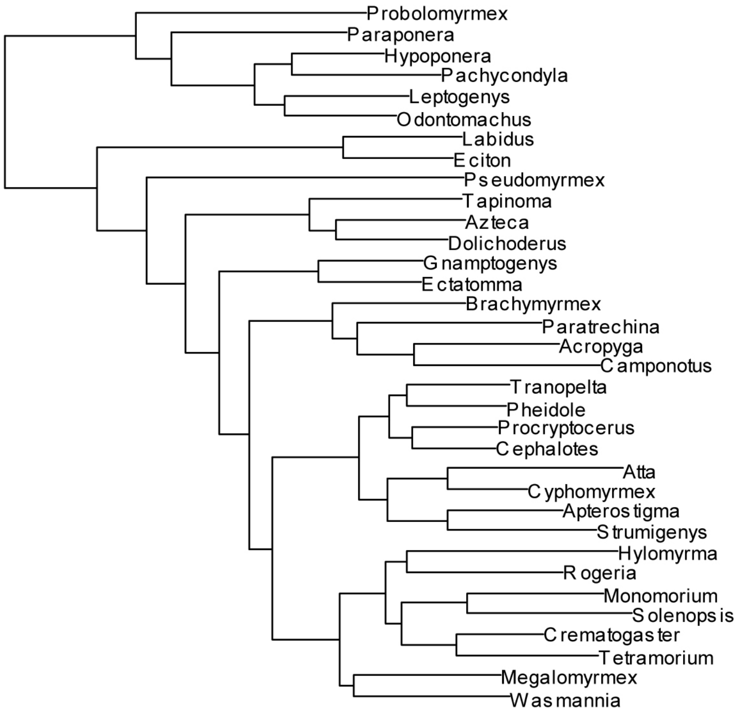

Fig. S1: Genus-level phylogeny used for generating phylogenetically independent contrasts of thermal tolerance in a Neotropical ant community. The tree was constructed using the APE package (Paradis et al. 2004) in R (R Development Core Team 2010) and phylogenetically independent contrasts were calculated using the *pic* function. Data for the topology and branch lengths are from Moreau et al. (2006), with supplemental data for the placement of 2 genera (*Hylomyrma* and *Paratrechina*) from Jansen and Savoleinen (2010) and LaPolla et al. (2010) respectively. Tip data are genus means. For those genera not included in the Moreau et al. (2006) phylogeny, we reviewed the literature to estimate the closest sister genus available in the Moreau et al. phylogeny (Table 1), and used the branch position of the available genus to place our data.

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