

Molecular adaptations to heat stress in the thermophilic ant genus *Cataglyphis*

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Abstract

Over the last decade, increasing attention has been paid to the molecular adaptations used by organisms to cope with thermal stress. However, to date, few studies have focused on thermophilic species living in hot, arid climates. In this study, we explored molecular adaptations to heat stress in the thermophilic ant genus *Cataglyphis*, one of the world's most thermotolerant animal taxa. We compared heat tolerance and gene expression patterns across six phylogenetically distant species that live in different habitats and experience different thermal regimes. We found that all six species had similar heat tolerance levels and critical thermal maxima. Furthermore, the transcriptome analyses revealed that, although the number of differentially expressed genes varied widely for the 6 species (from 54 to 1,118), many were also shared. Functional annotation of the differentially expressed and co-expressed genes then showed that the biological pathways involved in heat-shock responses were similar among species and were associated with four major processes: the regulation of transcriptional machinery and DNA metabolism; the preservation of proteome stability; the elimination of toxic residues; and the maintenance of cellular integrity. Overall, our results suggest that molecular responses to heat stress have been evolutionarily conserved in the ant genus *Cataglyphis* and that their versatility may help workers withstand temperatures close to their physiological limits.

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