

Sequence and cis-regulatory evolution of heat shock protein *hsp83*, in social Hymenoptera

Abstract:

Hsp83 is one of many evolutionarily conserved heat shock proteins (HSPs) that functions in diverse pathways such as hormonal signaling, responses to stress, and the regulation of gene expression. Eusociality is associated with fundamental changes in individual developmental flexibility; following the genetic toolkit hypothesis, social insects may have co-opted ancestral molecular pathways for novel social functions. We investigated functional and regulatory evolution associated with eusociality in *hsp83* by phylogenetic reconstruction of *hsp83* amino acid sequences and cis-regulatory elements within the insects. Amino acid sequences and promoter sequences were obtained from published sources for 17 insect species representing 5 insect orders. Amino acid sequences were aligned for maximum phylogeny construction. Whereas, promoter sequences were extracted from predicted transcriptional start sites and locally aligned for the identification of conserved cis-regulatory elements. The amino acid phylogeny reveals a Hymenopteran-specific duplication accompanied by significant sequence and cis-regulatory divergence, suggesting that the gene duplicate acquired a distinct, novel function. The novel homologue may be particularly important for eusocial species, because the ants and bees show independent evolutionary expansions of transcription factor binding sites and high sequence conservation. In contrast, the solitary wasp *Nasonia* shows multiple amino acid changes and a 94 amino acid deletion within the middle domain. The ancestral homologue was secondarily lost in the ants, but both homologues are retained in bees (*Apis* and *Bombus*) and in *Nasonia*. Taken together, the amino acid sequence and cis-regulatory evolution of *hsp83* suggest novel function and differential expression associated with eusociality.