Function and Evolution
of Putative Odorant Carriers
in the Honey Bee (Apis mellifera)

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Sylvain FORÊT July 31, 2006
A mes parents
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Abstract

The remarkable olfactory power of insect species is thought to be generated by a combinatorial action of G-protein-coupled olfactory receptors (ORs) and olfactory carriers. Two such carrier gene families are found in insects: the odorant binding proteins (OBPs) and the chemosensory proteins (CSPs). In olfactory sensilla, OBPs and CSPs are believed to deliver hydrophobic airborne molecules to ORs, but their expression in non-olfactory tissues suggests that they also may function as general carriers in other developmental and physiological processes.

Bioinformatics and experimental approaches were used to characterise the OBP and CSP gene families in a highly social insect, the western honey bee (*Apis mellifera*). Comparison with other insects reveals that the honey bee has the smallest set of these genes, consisting of only 21 OBPs and 6 CSPs. These numbers stand in stark contrast to the 66 OBPs and 7 CSPs in the mosquito *Anopheles gambiae* and the 46 OBPs and 20 CSPs in the beetle *Tribolium castaneum*. The genes belonging to both families are often organised in clusters, and evolve by lineage specific expansions. Positive selection has been found to play a role in generating a greater sequence diversification
in the OBP family in contrast to the CSP gene family that is more conserved, especially in the binding pocket. Expression profiling under a wide range of conditions shows that, in the honey bee only a minority of these genes are antenna-specific. The remaining genes are expressed either ubiquitously, or are tightly regulated in specialized tissues or during development. These findings support the view that OBPs and CSPs are not restricted to olfaction, and are likely to be involved in broader physiological functions.

Finally, the detailed expression study and the functional characterization of a member of the CSP family, \emph{uth (unable-to-hatch)}, is reported. This gene is expressed in a maternal-zygotic fashion, and is restricted to the egg and embryo. Blocking the zygotic expression of \emph{uth} with double-stranded RNA causes abnormalities in all body parts where this gene is highly expressed. The treated embryos are ‘unable-to-hatch’ and cannot progress to the larval stages. Our findings reveal a novel, essential role for this gene family and suggest that \emph{uth} is an ectodermal gene involved in embryonic cuticle formation.
Publications resulting from this project:


Publications partially related to this project:


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