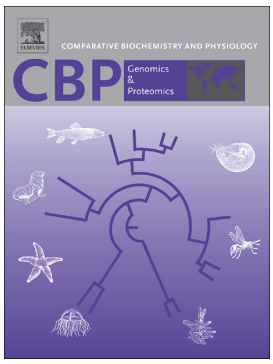

A whole-body transcriptome analysis and expression profiling of odorant binding protein genes in Oedaleus infernalis

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A whole-body transcriptome analysis and expression profiling of odorant binding protein genes in *Oedaleus infernalis*

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Running title: Transcript and OBPs in *Oedaleus infernalis*

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Abstract
To investigate the olfactory mechanisms in *Oedaleus infernalis*, one of important pests of cereals and pasture in the northern China, the whole-body transcriptome was constructed by RNA-Seq in this study. By *de novo* assembly, a total of 92476 unigenes were generated in the adult sample, and 32693 unigenes (35.35%) were successfully annotated by Blastx. Eighteen putative odorant binding proteins (OBPs) were identified, and phylogenetic analysis indicated the closest genetic relationship of eight OBPs in *O. infernalis* with those in its sibling species, *Oedaleus asaiticus*, while five OBPs in *O. infernalis* with those in *Locusta migratoria*. qRT-PCR analysis of the expression patterns of all 18 *OinfOBPs* in different tissues indicated that most *OinfOBP*s, especially *OinfOBP7* and *OinfOBP12*, had higher expression levels in the antennae meanwhile no or faint expression in other body parts, including heads (without antennae), thoraxes, abdomens, legs, and wings, suggesting that these OBPs may play important roles in olfaction. *OinfOBP2* was highly expressed only in male heads. Interestingly, only *OinfOBP13* displayed high expressions in nearly all tested tissues. These two OBPs may have different physiological functions in *O. infernalis*. The remaining *OBP*s were not or weakly detected in all tested tissues. Our results provide important molecular information for further studies on chemosensory mechanisms in this pest.

Keywords: *Oedaleus infernalis*, transcriptome, odorant-binding proteins, expression profile, RNA-Seq

1. Introduction

In insects, a sophisticated and sensitive sensory system was indispensable for a number of behaviors, such as seeking food, looking for mates, and avoiding predators (Asahina et al., 2008; Field et al., 2009). In insect sensory systems, olfactory organs mainly include antennae, maxillary palps and/or labial palps. Diverse proteins are involved in olfactory sensation, including odorant binding proteins (OBPs), chemosensory proteins (CSPs), membrane-bound olfactory receptors (ORs), ionotropic receptors (IRs), gustatory receptors (GRs) and sensory neuron membrane proteins (SNMPs) (Leal, 2013; Pelosi et al., 2014). OBPs are believed to bind and transport external odorant molecules to ORs across the sensillum lymph, and thus OBPs play important roles in olfaction (Vogt et al., 2002; Pelosi et al., 2006). According to the numbers of conserved cysteine residues, OBPs were divided into four subclasses: Classic OBPs with six conserved cysteine residues, Minus-C OBPs with four, Plus-C OBPs with eight, and Atypical OBPs with more than eight (Zhou et al., 2004). Therefore, the conserved motifs in OBPs were essential elements of functional domains (Xue et al., 2016).

The identification and functional analyses of candidate chemosensory genes are key initial steps