Antennal transcriptome of melon fly, *Zeugodacus cucurbitae* (Diptera: Tephritidae): identification of candidate chemosensory genes

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The sense of smell, or olfaction, is essential for driving insect behaviours associated with seeking hosts, mating, oviposition and various other activities. The melon fly, *Zeugodacus cucurbitae* (Coquillett) (Diptera: Tephritidae), poses a significant threat to agriculture, with its distribution spanning across the Asia-Pacific region and certain areas of Africa. Management strategies centered around olfaction, such as employing para-pheromones for population monitoring and bait-and-kill methods for male reduction, have proven effective in managing the populations of *Z. cucurbitae*. However, there has been a dearth of information concerning the molecular underpinnings of olfaction in *Z. cucurbitae*. In the present study, we conducted high-throughput sequencing to sequence and compile the antennal transcriptome of both male and female *Z. cucurbitae* specimens. Our aim was to identify chemoreception gene families associated with odor detection. Through this analysis, we discovered a total of 137 potential chemosensory genes, encompassing 55 odorant binding proteins (OBPs), 18 pheromone binding proteins (PBPs), 54 odorant receptors (ORs) and 10 ionotropic receptors (IRs). This study lays the groundwork for future research focused on the functional characterization of these chemosensory receptors in *Z. cucurbitae* at the molecular level, thereby paving the way for the development of enhanced tools for pest management.

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antennae, housing multiporous hair-like sensilla, where peripheral olfactory signaling events take place. The olfactory receptor neurons (ORNs) and their supporting structures are located at the base of the antennae[6], with the entire olfactory system relying on the receptors expressed in these peripheral ORNs. Olfaction, from the initial detection of chemical cues to the translation of olfactory signals into insect behaviour, necessitates a meticulously organized and sophisticated olfactory system across multiple levels. Various types of olfactory proteins from different chemosensory gene families contribute to the selective recognition of odors. They are odorant receptors (ORs), odorant binding proteins (OBPs), chemosensory proteins (CSPs), gustatory receptors (GRs), ionotropic receptors (IRs), and sensory neuron membrane proteins (SNMPs), all contributing to the intricate process of olfaction in insects[3]. Odorant receptors comprise seven transmembrane domains[7,8], and conventional ORs combine with a conserved co-receptor, orco, to form heteromers, influencing ligand specificity in the olfactory process[9,10]. Orco proteins play a pivotal role in facilitating the localization of conventional ORs on the cellular membrane and are therefore essential for olfactory responses[11–13]. Both OBPs and CSPs are water soluble, small extracellular proteins with a hydrophobic pocket[14–21]. OBPs are strongly expressed in the insect sensillar lymph and they facilitate the transportation of diverse hydrophobic odorant molecules from the environment to the receptors[22,23]. Gustatory receptors display ubiquitous expression within gustatory receptor neurons, playing a role in contact