

Plant Genomics

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Analysis of olfactory genes in *Sitobion avenae* by antennal transcriptome

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Olfaction is the essential sense of insect's feeding and mating. It achieves semiochemical and pheromone perception through olfactory pathway which coupled components by expressing series olfactory genes, distributing in antenna. transcriptome of antenna is a good way to understand the complicated olfactory system components. Analysis of chemical sensing system is a crucial basic work for studying the olfactory physiology of aphids and developing biological control technologies. In this study, we sequenced winged and wingless antennae transcriptome of *Sitobion avenae* (Fabricius), one of the most serious pests of cereals using IlluminaHiSeqTM2500/MiseqTM technology and Trinity assembly. A total of 133,331 unigenes were obtained with an average length of 594 bp. To annotate the transcripts, we searched against the Nr, Nt, Pfam, KOG/COG, Swiss-prot, KEGG and GO databases and 100,345 unigenes (75.26%) were annotated in at least one database. There were 1,517 genes (1,107 up-regulated and 410 down-regulated genes) differentially expressed between wingless and winged antennae, respectively. Nine of them are associated with odour binding pathway. 13 OBPs, 5 CSPs genes were identified from *S. avenae*. All of these transcripts have the typical structural features of insect (six conserved cysteines for OBPs and 4 for CSPs). Through multiple comparisons phylogenetic tree constructed of OBPs across several aphids, we can see that there is a high similarity between orthologs within a range of aphid species. Besides, 48 Ors (odorant receptors) were annotated as well and further studies are in progress.

Biography

Julian Chen has completed her PhD at Graduate School & Institute of Plant Protection, Chinese Academy of Agricultural Sciences (IPP-CAAS). She is a Group Leader of Wheat Insect Pest Research Group, IPP-CAAS. She has published more than 110 papers in reputed peer-review journals.

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