

A. Genes up-regulated in *D. simulans* ($q \geq 0.95$)

B. Genes down-regulated in *D. simulans* ($q \geq 0.95$)

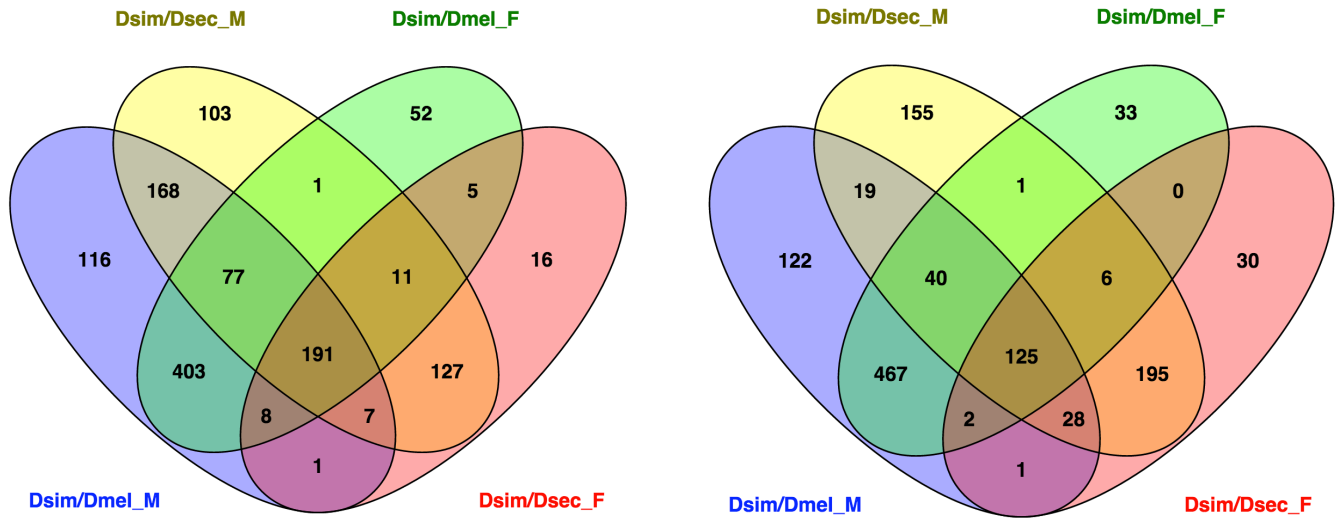
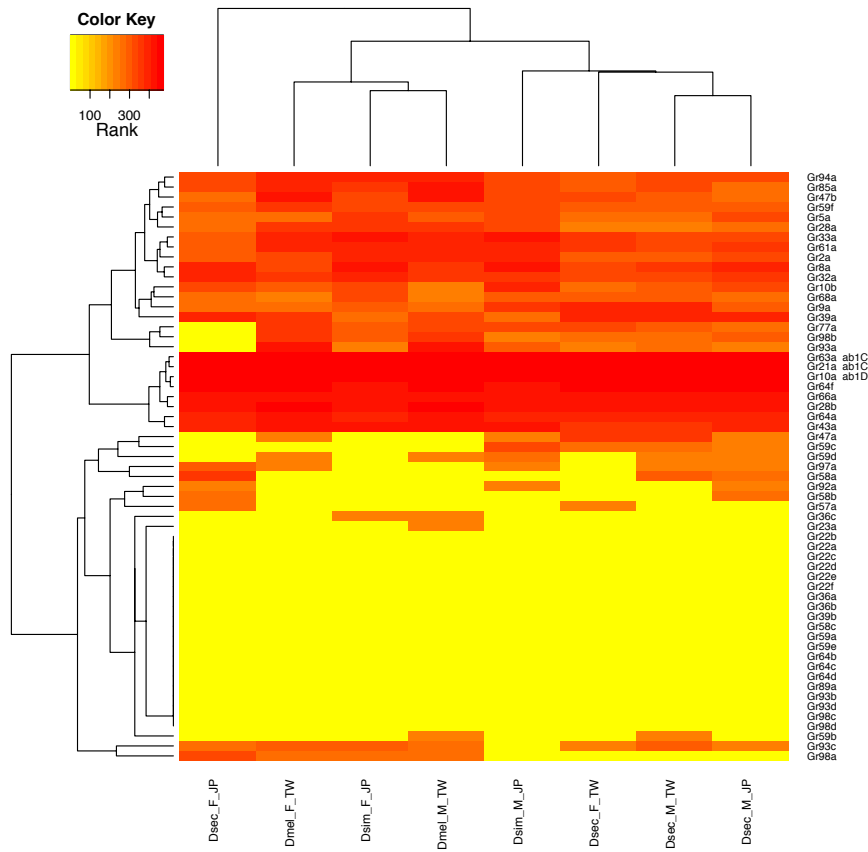


Fig. 1. Venn diagrams showing genes expressed differentially in *D. simulans* (Dsim) in comparison with *D. melanogaster* (Dmel) or *D. sechellia* (Dsec). A total of 191 genes were significantly up-regulated (A) including 10 chemosensory genes, and a total of 125 genes were significantly down-regulated (B) including 7 chemosensory genes in *D. sechellia*. M: males; F: females are as indicated.

A.



B.

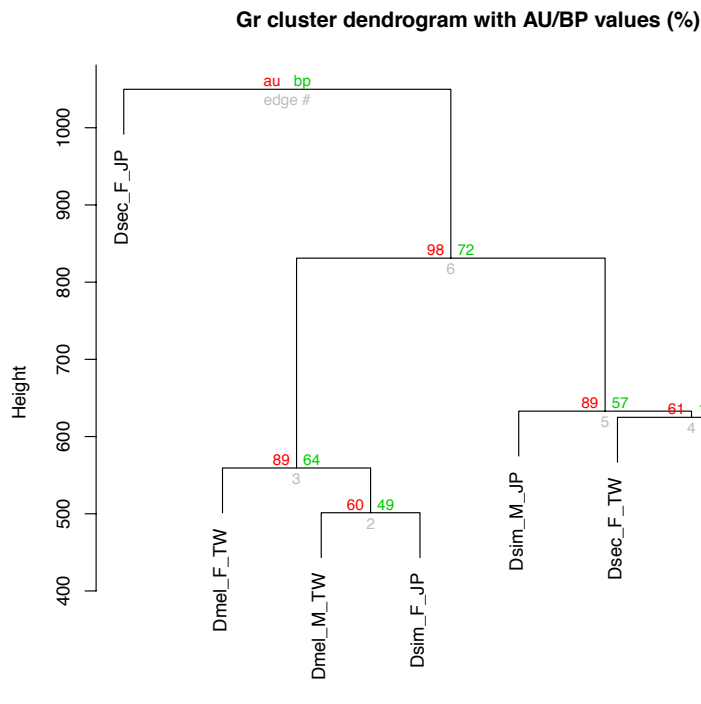
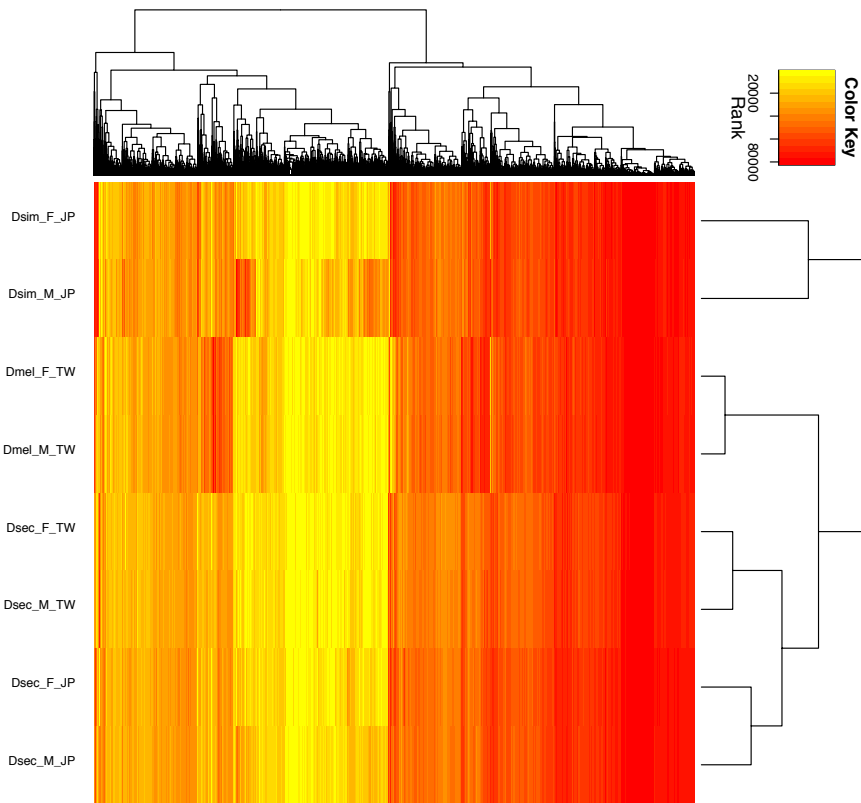


Fig. 2. Heat maps of expression profiles of *Gr* genes. (A) Heat maps of ranked expression levels of *Gr* genes. Red color indicates the highest expression level, while yellow color indicates a low expression level. Clustering results of genes are shown on the left of the figure, and the gene names and expressed sensilla (*Gr* genes) are shown on the right. Clustering of species is shown at the top of each figure and the information of each sample is shown at the bottom of the figure. Dmel: *D. melanogaster*, Dsim: *D. simulans*, Dsec: *D. sechellia*, M: males, F: females, TW: Taiwan, JP: Japan. (B) Statistical significance of clustering results among three species. The approximately unbiased (*au*) *p*-value (% , in red) and bootstrap probability (*bp*) value (% , in green) are shown on each branch.

A.



B.

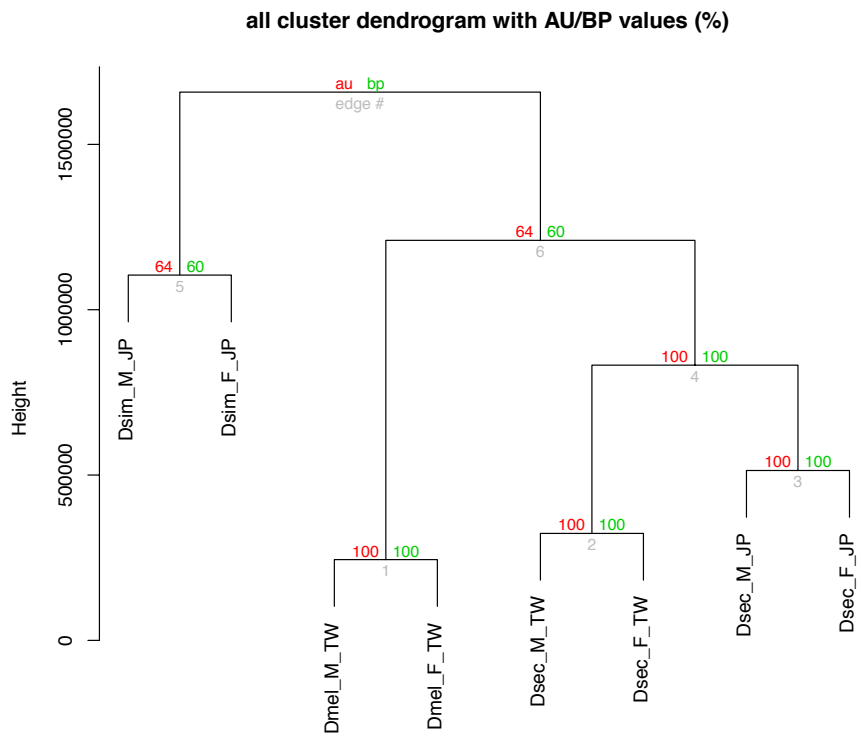


Fig. 3. Heat maps of expression profiles of whole antennal transcriptome. (A) Heat maps of ranked expression levels of genes in the whole transcriptome and (B) statistical significance of clustering results among three species. Color patterns and sample names are as described in Figure 1.