

OR006*Genetic diversity in a honeybee colony influences the behavioral performance*

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Honeybees can detect and remove diseased brood from their nest. This so-called hygienic behavior plays a major role in the colony's overall resistance against pathogens. Here we describe the molecular differences associated with the hygienic performance of honeybee workers which stem from backcrosses with high (xH) or low (xL) hygienic drones. We showed that xH worker bees were more often recruited to engage in hygienic tasks than xL worker bees ($P < 0.01$). We analyzed the genome-wide transcription level differences of 496 hygienic and non-hygienic worker bee brains in a combined loop/replicate design on a total of 82 whole-genome oligonucleotide microarrays. We detected a list of 1408 candidate genes which were associated with the performance of hygienic behavior in xH and xL worker bees ($P < 0.01$). 501 out of 1408 candidate genes differ in transcription level due to the behavior effect attributed to xH backcrosses, 342 out of 1408 candidate genes relate to xL backcrosses; the overlap between hygienic behavior associated genes relating to xH and xL backcrosses is minor (21 genes). GO analysis of the assigned orthologs in *Drosophila melanogaster* revealed that an annotation cluster including the GO terms 'olfactory receptor activity', 'sensory perception of smell', and the Interpro domain 'olfactory receptor', is significantly enriched in the xH candidate gene set when compared to the total set of *Drosophila* orthologs represented on the microarray (enrichment score: 2.8, $P < 0.01$). In the xL candidate gene set, an annotation cluster including the GO terms 'negative regulation of signal transduction', 'negative regulation of cell communication', and 'negative regulation of protein kinase cascade' is enriched (enrichment score 2.0, $P > 0.05$). Combined, these findings suggest that the distribution of hygienic alleles in a colony strongly influences the behavioral performance of the worker bees and the gene transcription associated with it.