

# HIGHLIGHTS

## URLs

### CAH1

<http://flybase.bio.indiana.edu/.bin/fbidq.html?FBgn0027844>

### Tps1

[http://flybase.bio.indiana.edu/.bin/fbidq.html?FBgn0027560&resulist=fbgn6073.data\[0\]](http://flybase.bio.indiana.edu/.bin/fbidq.html?FBgn0027560&resulist=fbgn6073.data[0])

### GlyP

<http://flybase.bio.indiana.edu/.bin/fbidq.html?FBgn0004507>

### Eip71CD

<http://flybase.bio.indiana.edu/.bin/fbidq.html?FBgn0000565>

## BEHAVIOURAL GENETICS

### Oh bee-have!

The relationship between genes and behaviour is complex and can be controversial, such as claims of a genetic basis for addiction and criminality. Now, in *Science*, Whitfield and colleagues from the University of Illinois provide clear-cut evidence that mRNA profiles in the brains of eusocial honey bees (*Apis mellifera*) correspond to molecular 'signatures' that can be used to identify the behaviour of individuals.

Honey bee colonies have a well-organized workforce, with a system of age-related socially-regulated division of labour: young worker bees act as 'nurses' caring for the brood, whereas older workers forage for food away from the hive. The exact timing of the behavioural transition from working in the hive to foraging differs between individuals. But to what extent are changes in gene expression involved?

To answer this question, the authors measured genome-wide gene expression in the brains of both types of worker, using a total of 72 microarrays generated from a bee brain expressed sequence tag project. The cDNAs analysed represented ~5,500 different genes, corresponding to ~40% of the total number in the honey bee genome.

Looking first at group tendencies and then focusing on individual profiles, the authors found significant differences between nurses and foragers in the expression of the microarray cDNAs. However, foragers tend to be older than nurses, so to uncouple the effects of age and

behaviour the authors also analysed workers from 'single-cohort' colonies in which all individuals were the same age. Visual inspection of the gene-expression profiles readily distinguished most individuals as nurses or foragers, regardless of age or colony type. In fact, the behaviour of ~95% of the bees studied was correctly predicted on the basis of brain mRNA profiles.

These results were confirmed statistically using class prediction and principal component analysis. The former also identified a set of predictor genes that could discriminate between the two behaviours, 17 of which had strong sequence matches to *Drosophila melanogaster* genes with roles in neural and behavioural plasticity. For example, foragers had elevated expression of a carbonic anhydrase gene (similar to *CAH1* in *D. melanogaster*) that is associated with spatial learning and memory. Also, foragers had altered expression of genes that are similar to trehalose-6-phosphate synthase 1 (*Tps1*), glyco-

gen phosphorylase (*GlyP*) and ecdysone-induced protein 28/29 kD (*Eip71CD*), which are all involved in brain metabolism and might influence cognitive function.

This work conclusively shows that gene-expression profiles can predict behaviour in a natural context. Furthermore, the authors establish that focusing on individuals is more informative than studying group trends alone. The newly uncovered robust relationship between brain gene expression and behavioural plasticity in the honey bee raises a whole new set of questions, not least of which is how the genes involved respond to environmental cues that are known regulators of these behaviours.

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### References and links

**ORIGINAL RESEARCH PAPER** Whitfield, C. W., Cziko, A.-M. & Robinson, G. E. Gene expression profiles in the brain predict behavior in individual honeybees. *Science* **302**, 296–299 (2003)

### WEBSITE

The Robinson Laboratory:  
<http://www.life.uiuc.edu/robinson>



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