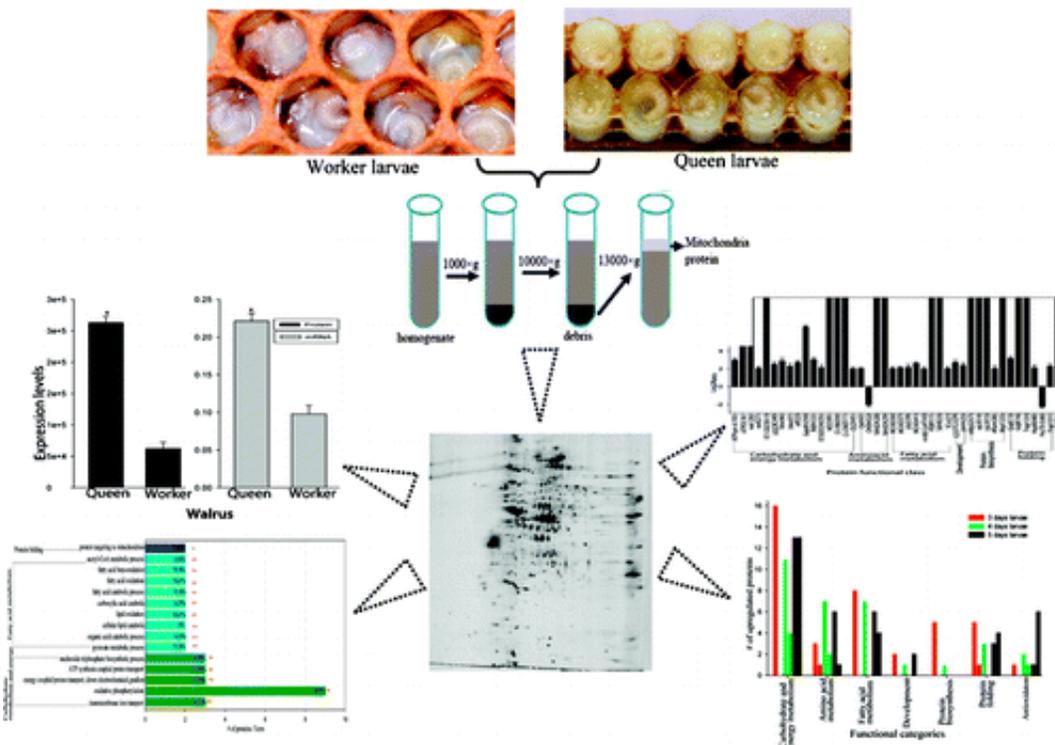


Queen bee or worker bee? New insights into famous honeybee society caste system

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Scientists are reporting deep new insights into whys and hows of the famous caste system that dominates honey bee societies, with a select few bee larvae destined for royalty and the masses for worker status. Their study probing the innermost biological makings of queen bees and worker bees appears in ACS's *Journal of Proteome Research*.

Jianke Li and colleagues (The joint work of scientists from China and Ethiopia) note that despite more than a century of research, mysteries remain about the biochemical factors at the basis of the fascinating caste system in [honeybee colonies](#). Schoolchildren learn that the (usually) one [queen bee](#) in a colony develops from larvae fed royal jelly, a protein-rich secretion from glands on the heads of worker bees. Other larvae develop into female workers or male drones. Although queen and [worker bees](#) share almost identical genes, their destinies could be more different.

"The female queen is large in size and specializes in reproduction," the scientists explain, "whereas workers are small and engage in colony-maintaining activities. Their life spans also vary, with the queen living for 1 to 2 years and the workers living only 6 to 7 weeks. To gain further information, the scientists looked at proteins inside the cells of larvae destined for queen and worker status.

Their findings reveal major differences, during early stages of life, in the activity of proteins in the mitochondria, structures that produce energy for cells. The differences include changes in the amounts of protein produced in cells and the activity of those proteins. In pre-queen larvae, proteins involved in carbohydrate and [energy metabolism](#), for instance, are much more active than in workers. "This suggests proteins with metabolic enhancing activities generally appear to have significant roles in the process of caste determination," the researchers conclude.

More information: Mitochondrial Proteins Differential Expression during Honeybee (*Apis mellifera* L.) Queen and Worker Larvae Caste Determination, *J. Proteome Res.*, 2011, 10 (9), pp 4263–4280. [DOI: 10.1021/pr200473a](#)

Abstract

Despite their similar genetic makeup, honeybee (*A. mellifera*) queens and workers show alternative morphologies driven by nutritional

difference during the larval stage. Although much research has been done to investigate the causes of honeybee caste polymorphism, information at subcellular protein levels is limited. We analyzed queen- and worker-destined larvae mitochondrial proteome at three early developmental stages using combinations of differential centrifugation, two-dimensional electrophoresis, mass spectrometry, bioinformatics, and quantitative real time PCR. In total, 67, 69, and 97 protein spots were reproducibly identified as mitochondrial proteins at 72, 96, and 120 h, respectively. There were significant qualitative and quantitative protein expression differences between the two castes at three developmental stages. In general, the queen-destined larvae up-regulated large proportions of proteins at all of the developmental stages and, in particular, 95% at 72 h. An overwhelming majority of the queen larvae up-regulated proteins were physiometabolic-enriched proteins (metabolism of carbohydrate and energy, amino acid, and fatty acid) and involved in protein folding, and this was further verified by functional enrichment and biological interaction network analyses as a direct link with metabolic rates and cellular responses to hormones. Although wide-ranging mitochondrial proteomes participate to shape the metabolic, physiologic, and anatomic differences between the two castes at 72 h, physiometabolic-enriched proteins were found as the major modulators of the profound marking of this caste differentiation. Owing to nutritional difference, prospective queen larvae showed enhanced growth, and this was manifested through the overexpression of metabolic enzymes. Differently from similar studies targeting the causes of honeybee caste polymorphism, this subcellular level study provides an in-depth insight into mitochondrial proteins-mediated caste polymorphism and greatly improves protein coverage involved during honeybee caste determination. Hence, it is a major step forward in the analysis of the fundamental causes of honeybee caste pathway decision and greatly contributes to the knowledge of honeybee biology. In particular, the consistency between the 22 proteins and mRNA expressions provides us important target genes for the reverse genetic analysis of caste pathway

modulation through RNA interference.

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