



The role of gene expression and regulation in altering social cue responsiveness and division of labor in *Temnothorax* ants

Author(s): Susanne Foitzik, Philip Kohlmeier , Barbara Feldmeyer

Institution(s): Institute of Organismic and Molecular Evolution, Johannes Gutenberg University Mainz ; Institute of Organismic and Molecular Evolution, Johannes Gutenberg University Mainz ; Institute of Organismic and Molecular Evolution, Johannes Gutenberg University Mainz

The ecological success of social insects is based on division of labour, not only between queens and workers, but also among workers. Whether a worker tends the brood or forages is strongly influenced by age, fertility and nutritional status, with brood carers being younger, more fecund and corpulent. We experimentally disentangled behaviour from age and fertility in *Temnothorax longispinosus* ant workers and analysed how these parameters are linked to whole-body gene expression. Our transcriptome analysis reveals four times more genes associated with behaviour than with age and only few fertility-associated genes. Brood carers exhibited an upregulation of genes involved in lipid biosynthesis, whereas foragers invested in metabolism. A *Vitellogenin-like gene*, *Vg-like-A*, was the most overexpressed gene in brood carers and a functional analysis revealed that it takes over a key function by controlling responsiveness to task-related cues: When down-regulated in the fat body, young workers reduce brood care and increase nestmate care, a behavior normally exhibited by older workers. This task switch is based on *Vg-like-A*-dependent shifts in responsiveness from brood to worker cues, demonstrating that a single gene can regulate division of labor via changes in social cue responsiveness. Finally, when studying experimentally the role of *histone acetyltransferase (HAT)* in division of labor, we show that the inhibitor C646 impedes the switch of foragers back to brood care, but promotes the reversed change from brood care to foraging. *HAT* inhibition did not affect workers continuing to execute the same tasks, pointing to the role of histone acetyltransferase in altering gene expression. *HAT* activity keeps young workers in a brood caring mode, possibly to prevent them from leaving the nest prematurely. We are now using ChipSeq analyses to identify genes associated with de-acetylated histones due to the experimental inhibition and study associated changes in gene expression.