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*Molecular evolution of the honeybee brain transcription regulatory network*

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Honeybees are highly social animals, and worker bees exhibit division of labour by specializing on specific tasks over the course of their life. Shifts in worker behaviuor are coordinated by a complex transcription regulatory network (TRN) that has been recently elucidated in the honeybee *Apis mellifera* (Chandrasekaran et. al. 20122, PNAS 108: 18020-18025). I studied patterns of molecular evolution of the honeybee's brain TRN to understand the degree to which pleiotropy constrains adaptive protein and regulatory sequence evolution. I estimated the coefficient of selection acting on coding and regulatory sequences of transcription factors and their target genes. My results indicate that pleiotropy constraints molecular evolution of transcription factors and their targets via different mechanisms.