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Exploring queen longevity by RNA-Seq

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It is generally assumed that aging is genetically controlled. Experiments with short-lived organisms (flies, worms, mice) have revealed the involvement of different candidate genetic pathways. However, many of these studies have disregarded the enormous intraspecific variation in longevity among and within species. In social insects, males and the different female castes (queens, workers) differ in many life history traits, including different aging rates. Ant queens are famous for their exceptionally long life spans compared to workers and males, making them a good model for the study of aging. The myrmicine tramp ant *Cardiocondyla obscurior* lacks the 'reproductive senescence' that characterizes most other organisms (Heinze & Schrempf 2012). In addition, queen-male co-evolution affects the life span of the queen (Schrempf et al. 2005, Schrempf & Heinze 2008, Schrempf et al. 2011). Similar to mated queens, sham-mated queens, which mated with a sterilized male, live considerably longer and start laying eggs earlier than virgin queens. In order to gain insights into the regulation of queen longevity, we conducted RNA-Seq of eighteen-week old queens that were subjected to different mating regimes. By comparing the transcriptomes of mated, sham-mated and virgin queens it is possible to disentangle the effects of mating and reproduction on gene expression patterns. We could identify several genes presumably involved in the variation of longevity.