



Identification of gene co-expression networks linked to differential ageing in insects

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A hallmark of ageing is the trade-off between fecundity and longevity. Particularly intriguing is the reversal of this trade-off within several insect groups with independent evolutionary origins of eusociality. This convergent reversal of the fecundity/longevity trade-off means that the reproductive castes of these lineages (ant, bee, wasp and termite queens, and termite kings) live much longer than their sterile siblings. Within our collaborative research unit, funded by the DFG, comparisons of transcriptomes between old and young, sterile and reproductive individuals within ants, bees and termites have revealed largely species specific lists of differentially expressed genes. However, many of these genes belong to similar pathways, such as IIS, TOR and JH. In order to investigate how these and other pathways have led to the reversal of the fecundity/longevity trade-off across independent origins of eusociality, we are conducting comparative gene co-expression analyses within an ant, a bee, a termite and *Drosophila melanogaster*, as a non-social control. Initial results indicate that similar pathways are consistently involved in the trade-off between fecundity and longevity, both in the fly and the eusocial species. With our ongoing analyses we expect to find that a number of these complex pathways have been rewired several times compared to non-social species. The details and the positions of these “switches” may differ between eusocial species, indicating an innate plasticity of some parts of pathways, thus allowing several independent reversals of the fecundity/longevity trade-off. Future research will be directed towards understanding how this convergent rewiring of pathways involved in fecundity and longevity is linked to eusociality.