Parasitism and gene family evolution: a comparison of slave-maker ants and their hosts

Background: Socially parasitic ants avoid nursing, housekeeping and foraging by exploiting the care behaviour of other ant species. Through destructive raids, parasites capture brood from colonies of their host species that will act as their worker force. These host workers not only supply parasites with food and care but may also provide immunological benefits, because trophallaxis (*i.e.* sharing of food through regurgitation) can boost colony-level immunocompetence. Reliance of the social parasites on the innate immune system of their host may spare them costly investments in their own immune defences, which may lead to the loss of immune gene repertoire in parasites. Hence, we hypothesise that the evolution of a parasitic lifestyle in parasite lineages is accompanied by the loss of immunity genes.

Objectives: In this project, you will use bioinformatic tools to identify immunity genes in several parasite and host genomes, representing independent origins of parasitism. The aim is then to compare immunity gene repertoires across multiple independent origins of parasitism.

Figure 1: Trophallaxis between the slavemaker ant, *Temnothorax americanus* (left) and its slave *T. longispinosus* (right). Credit: Susanne Foitzik.

Requirements:

- Interest in social evolution and the evolution of insect immunity
- Interest in learning how to use bioinformatic tools for comparative genomics

Methods:

- Create a database of known immunity genes in ants
- Identify best matching gene annotations in target species using BLASTp
- Align sequences from all target species and investigate the evolutionary dynamics of immune genes (expansions, contractions)

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Selected literature:

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