The evolution of immunity gene repertoire in slavemaker ants and their hosts

Background: Slavemaker ants avoid nursing, housekeeping and foraging by exploiting the care behaviour of other ant species. Through regular, destructive raids, they capture brood that will develop into their slaves. These slaves not only supply slavemakers with food and care but may also provide immunological benefits, because trophallaxis (i.e. food sharing through regurgitation) can boost colony-level immunocompetence. Reliance of slavemaker ants on the innate immune system of their host may spare them costly investments into their own immune defences, which may lead to the loss of immune gene repertoire in slavemakers. Hence, we hypothesize that the evolution of a parasitic lifestyle in slavemaker lineages is accompanied by the loss of immunity genes.

Objectives: In this project, you will develop bioinformatics tools to identify immunity genes in several slavemaker and host genomes, representing independent origins of slavery. Because immunity genes quickly evolve in response to the various immunological challenges ants face, identifying immunity genes across even closely related species can be challenging. Hidden Markov Models have been very successful at identifying divergent immunity gene families in a wide range of taxa. The goal of this project is to construct such HMMs, identify immunity genes in slavemakers and hosts and compare immunity gene repertoires across multiple independent origins of slavery.

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:

- Compile an ant immunity gene database and determine orthology
- Perform multiple sequence alignments for each orthologous cluster
- Build HMMs to identify divergent immunity genes across the genomes

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Selected literature:

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R. Libbrecht, P. R. Oxley, D. J. Kronauer, and L. Keller. Ant genomics sheds light on the molecular regulation of social organization. *Genome biology*, 14(7):212, 2013.

T. B. Sackton, B. P. Lazzaro, and A. G. Clark. Rapid expansion of immune-related gene families in the house fly, musca domestica. *Molecular biology and evolution*, 34(4):857–872, 2017.