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Are social-immunity biofilms of attine ants monocultures or polycultures? **Tabitha Innocent**, Sandra B Andersen, Morten Schiott, Jacobus Boomsma

The association between fungus-growing attine ants and antibiotic-producing cuticular actinobacteria has created some controversy. Are these bacteria really social immunity mutualists? And if so, what pathogens do they suppress? Is it the case that actinobacteria are frequently acquired from the local environment and, consequently, do not co-adapt to their ant hosts? Or does the original idea of strict vertical transmission and substantial coevolution remain largely correct, but with some interesting modifications?

Recent modeling (Scheuring and Yu, 2013) predicted that a single bacterial strain acquired vertically by callow ant workers could maintain a monopoly if the primary function of the antibiotics produced is to suppress competing strains - meaning that the benefits to ant hosts, in terms of controlling fungus garden pests, are indirect. A simultaneous empirical study by Andersen et al. (Molecular Ecology, 2013) showed that *Acromyrmex* workers start their lives with a monoculture of one of only two 'native' *Pseudonocardia symbionts*. Second, results showed that workers only pick up additional strains once they become foragers - i.e. from the point in time when their main role is no longer restricted to tasks within the fungus garden that help suppress *Escovopsis* infections.

We are now extending this empirical approach. We are comparing the biofilms of callow and mature workers in multiple attine genera, using 454 metagenome sequencing; and testing the inhibition efficiency of native and secondarily acquired actinomycete strains against an array of fungus-garden and insect pathogens. We are also initiating collaborative work to test the potency of antibiotics produced by native and secondary strains. Results so far indicate that environmentally acquired secondary strains play little role in *Escovopsis* control, and that native strains are associated with host lineages for sufficient time that at least some co-adaptations have evolved.