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Molecular evolution of immune genes in the invasive Argentine ant

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Ants are among the most abundant and influential social insects in terrestrial ecosystems. Most ant populations are kin structured meaning that the nestmates are highly related to each other. High relatedness between nestmates assures that natural selection is working efficiently. Some ant species, however, possess an unusual form of social organization called unicoloniality. The nests of unicolonial populations contain many reproducing queens which together with the free movement of individuals between the nests lead to extremely low relatedness between the nestmates creating a potential problem for efficacy of selection on worker traits. The introduced populations of the Argentine ant (*Linepithema humile*) represent one of the most extreme examples of unicoloniality. The species has invaded almost all continents in the world. In the introduced range the relatedness within nests and supercolonies is extremely low. In contrast, nestmates in the native range are more closely related, and local genetic differentiation is evident. Introduced populations may have a competitive advantage over the native arthropod fauna, but at the same time the high population densities combined with exposure to new pathogens and reduced genetic diversity pose a threat to the survival of Argentine ants in its introduced range creating potential novel selection pressures on the immune genes. We will compare evolutionary rates of immune genes in invasive and native *L. humile* populations. To separate the effects of changes in population demography and genetic structure from adaptive evolution specific to immune genes, also control genes are included in the study. Our data will provide quantitative estimates of the rate of adaptive evolution in immune system genes relative to the rest of the genome, associated with invasions and changes in the social colony structure.