



Are supergenes required for intra-specific variation of social organisation?

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Ants exhibit tremendous diversity, but we know relatively little about how this diversity evolves. Here we focus on the convergent evolution of a fundamental social trait, the number of reproductive queens in a colony. While ants ancestrally have a single queen per colony, some ant species include two distinct colony types: single-queen colonies and multiple-queen colonies. This is the case in distantly related lineages, including fire ants and wood ants. Although the social polymorphism evolved independently in these two lineages, a large “supergene” region of suppressed recombination carried by a pair ‘social chromosomes’ determines in each lineage whether a colony contains a single queen or multiple queens. Here, we test in a third, unrelated lineage where social dimorphism convergently evolved whether supergene architecture is also involved in determining social form. For this, we created a reference genome using long-read sequencing and performed genome-wide comparisons between >50 single and >50 multiple-queen colonies. Our results shed light on the molecular constraints underlying convergent evolution of major social phenotypes.