



Supergenes, supergenomes, and complex social traits

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In a new paper expanding the links between supergenes and complex social traits, Lagunas-Robles et al. (1) describe a supergene implicated in the control of reproductive sex allocation for two species of the ant genus *Formica*. The study identifies a supergene connected to the queen strategy of laying highly skewed or “split” sex ratios, in which colonies produce either almost all male or primarily female reproductive offspring. In doing so, the study offers a genomic insight into one of the most intriguing examples of parent–offspring conflict. Who—queens or workers—has primary control over colony allocation to reproductive sex ratios?

Sex Allocation and Supergenes

In their study, Lagunas-Robles et al. (1) used population genomics analyses to compare the genomes of workers from colonies of *Formica glacialis* (68 colonies) and *Formica podzolica* (12 colonies) that produced predominantly males or predominantly females using a genome-wide association study (GWAS) approach. They identify an ~5-Mb nonrecombining genomic region (supergene) in *F. glacialis* that is highly correlated with sex allocation (GWAS) and is also strongly differentiated between workers of colonies that have male vs. female biased sex allocation (F_{ST}). Those colonies headed by queens with a heterozygote supergene genotype (Sm_A/Sm_D) showed a female biased sex allocation, while colonies headed by queens with the homozygous genotype (Sm_A/Sm_A) produced a heavily male biased sex allocation. They found the same association with the homologous genomic region in the sister species *F. podzolica* with a much smaller sample size, supporting the assertion that there is a strong genotypic effect of the sex allocation supergene in this clade. Intriguingly, this supergene is located adjacent to a second ancestral *Formica* supergene that influences another facet of social organization: the number of queens present within a colony (monogyny vs. polygyny) (2).

With this paper, we count two supergene-associated social organizational strategies in ants with indirect fitness impact: skewed allocation in reproductive sex ratios (1) and monogyny vs. polygynous queen numbers (2–4). Supergenes are described as large nonrecombining genomic regions inherited as a unit and encompassing multiple loci potentially relevant to a complex trait (5). The term supergene has been around for at least 70 y, and the idea that physically linked genes form the genetic basis of complex traits is much older (6, 7). Indeed, sex chromosomes can be considered supergenes because they have no or large nonrecombining regions (8). However, consideration of supergenes as drivers of social organizational traits (and especially those associated with conflict in inclusive fitness strategies) is relatively new.

Females of diverse taxa, both invertebrate and vertebrate, show context-dependent variation in their relative production of male and female offspring (sex allocation). This can occur in association with multiple environmental factors, from local mate competition to other resource, temporal, or climatic influences on potential offspring success (e.g., refs. 9 and 10). In some ant species, however, queens take control of sex allocation by strongly biasing production of reproductively destined eggs toward one sex (1, 11), with the common outcome being a bimodal distribution of males and female reproductives to the extreme of individual colonies consistently producing reproductives of only one sex.

Due to their haplodiploid sex determination mechanism, hymenopteran females have become excellent model systems to test predictions of sex allocation theory in relation to inclusive fitness (12, 13). Haplodiploidy sets the stage for differential inclusive fitness benefits for the queens that produce reproductively destined eggs (primary sex ratios) and the workers that rear them to adulthood (secondary sex ratios) (13). In monogynous colonies with singly mated queens, workers should preferentially rear female reproductives, with female bias decreasing with increasing genotypic

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diversity. Queens, however, share equal relatedness with their male and female offspring and should produce sex ratios that align with population-level conditions. This queen–worker conflict has been shown to function as an important driver of colony sex allocation across a diversity of studies in ants and bees (13–15), although it is not the only driver (e.g., ref. 16).

The finding of supergenes both for sex allocation and for polygyny in *Formica* opens the question of whether sex allocation and queen number may be genomically linked. Because queen number influences the inclusive fitness differential of sex allocation for queens and workers, it would be useful to assess whether these are two discrete genomic regions or whether they in fact represent a larger supergenomic area, an issue not directly addressed in the paper. However, there is evidence that supergene control of queen number may be functionally linked to sex allocation in another species, *Formica selysi* (2, 4, 17). Although, no molecular mechanism has been demonstrated so far, Fontcuberta et al. (17) report a relationship between queen number and split sex ratios in *F. selysi*, with monogyne colonies producing most of the females within mating swarms.

Supergenes, Supergenomes, and the Evolution of Complex Social Traits

If the concept of cosegregation of nonrecombining genomic regions with complex traits is expanded further, starting with supergenes and sex chromosomes and ending with whole nonrecombining genomes (i.e., supergenomes), our list of social polymorphisms mediated by nonrecombining genomes would also include genetic caste determination (18, 19), bringing the number of major social polymorphisms mediated by nonrecombining regions to three. Genetic caste determination in harvester ants, *Pogonomyrmex*, involves two dependent lineages that show no recombination but can only survive together because intralinear matings produce queens and interlineage matings workers only. As with sex allocation, the rearing of diploid brood into reproductives or workers is under worker control, but genotype is the major factor that determines reproductive destiny in these systems. In all three of these examples, some aspect of social and reproductive control and associated inclusive fitness becomes mediated at the

genomic level, helping reshape our understanding of the genomic bases and evolutionary dynamics of social polymorphisms.

In a new paper expanding the links between supergenes and complex social traits, Lagunas-Robles et al. describe a supergene implicated in the control of reproductive sex allocation for two species of the ant genus *Formica*.

We offer the cautionary note that for none of these supergenes have the actual underlying molecular mechanisms or candidate genes been identified. Also, as noted by Lagunas-Robles et al. (1), a majority of cases of social polymorphisms, including queen number and sex allocation, offer no evidence as of yet of genomic control. It is also worth noting that the advantage of keeping coadapted gene pools together via strong genetic regulation has advantages but also comes with a price-reduced plasticity and genetic load. For example, genetic caste determination in *Pogonomyrmex barbatus* leads to a proportion of mated queens that cannot produce any workers, which is essentially lethal (19). In the case of supergene control of polygyny in *F. selysi*, half of the offspring from the heterozygous (polygynous) mothers fail to hatch, generating a large potential genetic load (20).

A genetic regulation of sex allocation would solve the open question of how split sex ratios are determined in some species. In doing so, it also makes us reexamine the theoretical models of queen–worker conflict in sex allocation, which often rely on assumptions of phenotypic plasticity, in which queens and workers vary sex allocation across levels of relatedness and with environmental change. If sex allocation is mostly genetically determined (and these findings produce strong evidence that it is for some species), there are many situations where split sex ratios do not match the social environment and relatedness asymmetry of a population or specific colony. Hence, the predictive power of split sex ratio theory, based on population-wide variations of intracolony relatedness asymmetries, would be severely reduced. We look forward to the puzzles and solutions that these findings will produce.

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