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A supergene controlling social structure in Alpine ants also affects the dispersal ability and fecundity of each sex

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Social organization, dispersal and fecundity coevolve, but whether they are genetically linked remains little known. Supergenes are prime candidates for coupling adaptive traits and mediating sex-specific trade-offs. Here, we test whether a supergene that controls social structure in *Formica selysi* also influences dispersal-related traits and fecundity within each sex. In this ant species, single-queen colonies contain only the ancestral supergene haplotype *M* and produce *MM* queens and *M* males, while multi-queen colonies contain the derived haplotype *P* and produce *MP* queens, *PP* queens and *P* males. By combining multiple experiments, we show that the *M* haplotype induces phenotypes with higher dispersal potential and higher fecundity in both sexes. Specifically, *MM* queens, *MP* queens and *M* males are more aerodynamic and more fecund than *PP* queens and *P* males, respectively. Differences between *MP* and *PP* queens from the same colonies reveal a direct genetic effect of the supergene on dispersal-related traits and fecundity. The derived haplotype *P*, associated with multi-queen colonies, produces queens and males with reduced dispersal abilities and lower fecundity. More broadly, similarities between the *Formica* and *Solenopsis* systems reveal that supergenes play a major role in linking behavioural, morphological and physiological traits associated with intraspecific social polymorphisms.

1. Introduction

Dispersal shapes patterns of genetic relatedness within and between social groups [1,2]. Dispersal therefore coevolves with multiple social traits (reviewed in [3]), including social group living [4], number of breeders per group [5], division of labour [6] and production of public goods [7]. Dispersal also typically covaries with fecundity [8] and sex allocation [9]. If alternative dispersal traits covary with multiple other characters within a species, an immediate question that arises is what prevents maladaptive combinations of traits from occurring?

One possible solution for generating intraspecific polymorphisms that adaptively combine multiple traits is to link co-adapted alleles in supergenes [10]. Supergenes are non-recombining genomic regions that collectively produce discrete multi-trait phenotypes, like sexes, ecotypes and social forms [11–13]. A theoretical model predicted that social polymorphism arises from the coevolution of dispersal and social