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Natural selection is a relentless force which drives beneficial alleles to fixation and eliminates deleterious ones. With the dynamism natural selection imposes, explaining the maintenance of genetic variation for fitness is an ongoing challenge in evolutionary biology [1]. Mutation-selection balance provides a partial explanation for this phenomenon, however it does not describe the extent to which genetic variation is produced [1]. Strong evidence demonstrates that balancing selection can maintain stable polymorphisms through sexually antagonistic selection, where separate sexes endure opposite fitness effects from the same alleles [2, 3]. Accordingly, opposite sex individuals are in a tug-of-war over optimal traits, allowing separate alleles to be maintained in the population, preventing fixation [3]. Recently it has been proposed that the ability of sexually antagonistic selection to maintain genetic variance in fitness is augmented by the presence of sex-specific dominance reversal (SSDR), where alleles which promote fitness in one sex, are dominant in that sex [4, 8]. On sexually antagonistic loci, it has been theoretically demonstrated that unequal dominance between the sexes causes a concavity in fitness functions near the optima, as the fitness of a heterozygote in each sex is closer in fitness to the more fit homozygote of that sex [5]. Consequently, the allele that is favoured in a sex is dominant in that sex, thereby maintaining alternative alleles for selection to act upon [5]. This theoretical data has recently allowed for the application on animal models.

Sex-specific dominance of sexually antagonistic alleles is predicted to ameliorate the fitness effects of intralocus sexual conflict, therefore dominance reversal likely plays a significant role aiding species displaying higher levels of sexual conflict [6]. The first empirical example of SSDR was investigated at a single major-effect locus controlling age at maturity of salmon. At this locus, sex-dependent dominance was found to reduce sexual conflict and maintain genetic variation [7]. In a more comprehensive study, Grieshop and Arnqvist [8] used a quantitative genetic approach, where a full diallel cross among isogenic strains of seed beetles was used to account for the polygenic nature of fitness. The study revealed genome-wide SSDR for sexually antagonistic loci affecting fitness, and presented an exciting opportunity to reproduce their experiment using an organism of higher complexity. *Drosophila melanogaster* has been found to exhibit ample sexually antagonistic variation, making ita respectable candidate to measure SSDR in maintaining genetic variance for fitness [5]. We hypothesize that SSDR is occurring on sexually antagonistic loci of *D. melanogaster* , and contributes in the maintenance of genetic variance for fitness. This is an important area of research and empirical data is limited, making it essential that dominance reversal for fitness is studied for the first time in *D. melanogaster* . In addition to answering an enduring enigma, this study may uncover a novel phenomenon of masking intralocus sexual conflicts in *D. melanogaster* [6].

The best way to test this idea is to perform a full diallel cross, following the approach taken by Grieshop and Arnqvist [8]. This technique is ideal as it probes the maintenance of genetic variance in fitness by subdividing

phenotypic variance into additive genetic effects, parental effects, dominance, and epistasis [8]. Additionally, by using the full diallel cross and testing for SSDR, sexually antagonistic balancing selection can be distinguished from other forms of balancing selection [8]. To generate inbred lines, we will follow the experimental protocol outlined by Mallet and Chippindale, and use a ‘ clone generator’ system of markers and chromosome translocations [9]. Using *D. melanogaster* from an outbred stock population maintained on a specific selection regime for roughly 30 years, hemiclone lines will be produced using ‘ C’ males of an unknown genotype crossed with virgin clone generator (CG) females. A single male progeny is selected to be crossed again to a virgin CG female thus fixing a genomic paternal haplotype, which will be maintained by crossing hemiclone males to CG females. To generate inbred lines, a hemiclone male is crossed with a virgin wildtype C female with an unknown genotype. Virgin daughters produced will be crossed to hemiclone males, and the procedure is repeated 6 times to generate inbred lines for the given haplotype. Each successive cross increases the quantity of genes identical to the original haplotype by 50%, allowing isogenic strains by 6 generations [9].

The surviving inbred strains will be subject to a full diallel cross, where F_1 offspring will be analyzed for sex specific competitive lifetime reproductive success (fitness) [8]. F_1 male and female fitness will be assayed separately using same sex competitors with a specific visible marker. As a precaution, the experiment will be initiated using 100 lines to account for the loss of strains over multiple generations of inbreeding. It is anticipated that the fitness variance of the inbred lines of *D. melanogaster* is largely determined

by polymorphisms under sexually antagonistic selection opposed to mutation selection balance [8]. Predictions also entail a negative correlation for dominant alleles for fitness amongst male and female flies.

If executed, this study has the potential to produce novel data indicating that SSDR contributes in maintaining genetic variance for fitness in *D. melanogaster* . This analysis may bring knowledge on balancing selection one step closer to resolving the enigma of outstanding genetic variance. Furthermore, if the hypothesis is upheld, it will provide a basis for further tests of SSDR in more complex organisms, and give evolutionary biologists a better understanding of how genetic variance for fitness is maintained.

Citations

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