TAGC/PopGroup53 abstract

Intralocus sexually antagonistic variation arises when different alleles are most fit in males and females. However, the fate of this genetic variation in the presence of biases in the operational sex ratio has not been studied. Here we use forward time population genetic models to investigate whether biases in the number of mating females and males in finite populations can produce instances where selection acts primarily on one sex***,*** while genetic drift acts primarily on the other sex. We explore a range of genetic architectures, strengths of selection, and sex determining systems. We show that under certain population sizes and levels of operational sex ratio bias the fate of autosomal sexually antagonistic variation can be determined largely by the sex that is more common. Our results also illustrate that the genetic architecture at the sexually antagonistic locus can have important impacts on the course of evolution at these loci. Taken together these results indicate that operational sex ratio bias may lead to a feminization or masculinization of the genome of some natural populations that have consistent strong bias in the number of males and females that reproduce. Furthermore, our results illustrate a method of breeding that could be applied in the lab to reveal the sexually antagonistic variation present across the genome.