

The evolution of between-sex genetic correlations under directional selection

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Introduction

Selection is often different for males and females^{1,2}, and in these cases the response to selection will depend not only on the mean phenotype and additive genetic variance, but also on the between-sex genetic correlation, r_{mf} ¹ (see **Key**), and understanding whether and how r_{mf} itself evolves becomes important to understanding microevolution. Previous work has focused on the role of nonlinear selection^{3,4,5}).

McGlothlin and Brodie⁶ found that the evolution of r_{mf} is controlled by the ratio of the strength of directional selection in the sexes, and the current value of r_{mf} . In particular, when r_{mf} is high and selection is stronger in one sex, concordant selection will decrease r_{mf} and antagonistic selection will increase r_{mf} .

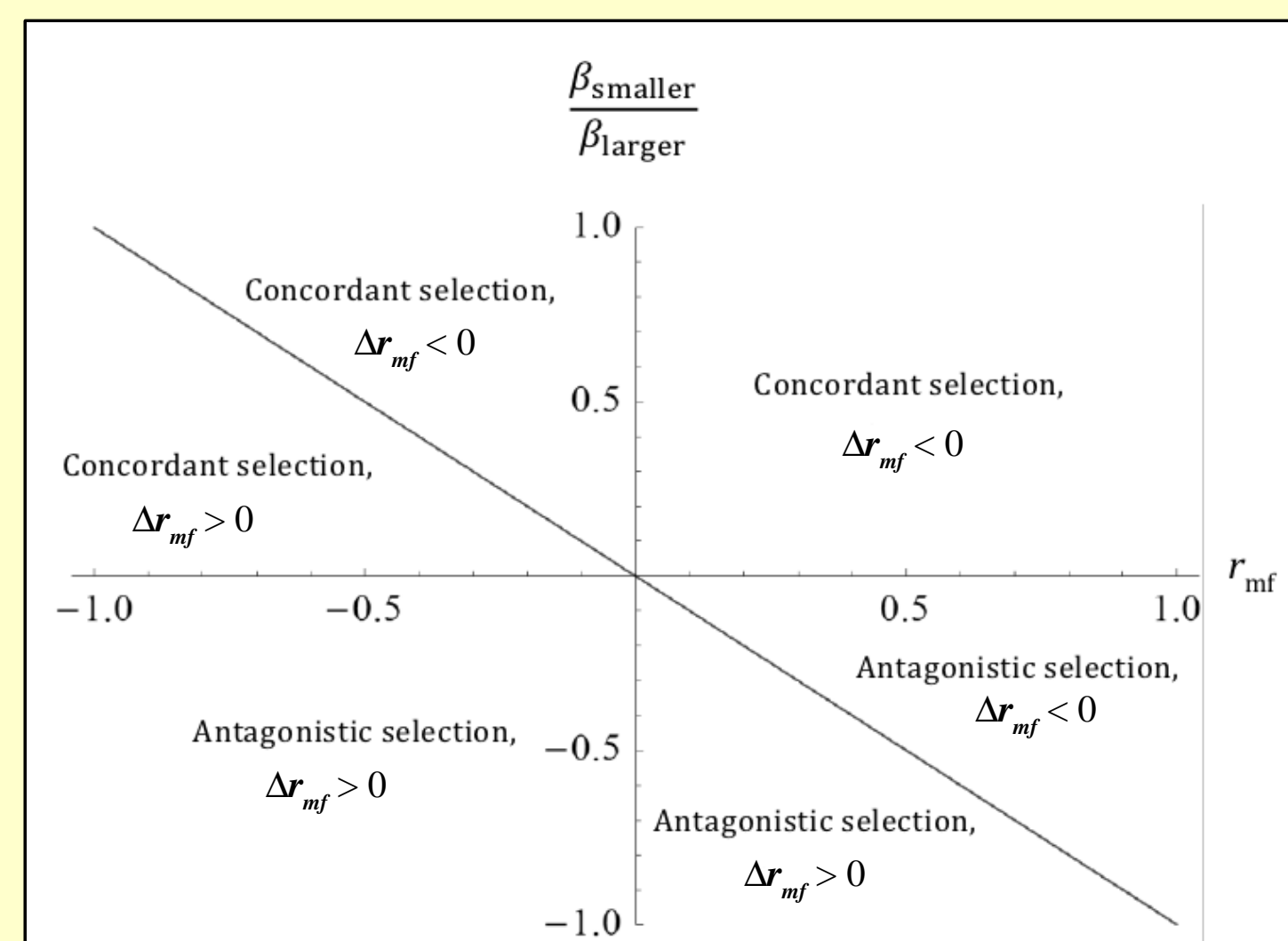


Figure 1. Analytic predictions for the evolution of r_{mf} . Modified from 7.

Methods

- Agent-based model, 2000 sexually-reproducing diploid individuals.
- Single trait expressed differently in males in females.
- Breeding value calculated by adding the effects of 50 loci.
- Two quantitative values stored in each locus: contribution to the breeding value in males and the contribution in females.
- Breeding value calculated for male (a_m) and female values of the trait (a_f), normally-distributed environmental noise added to appropriate breeding value to get the phenotypic value (z).
- Mutations rate of $\mu=0.001$ per locus per generation, mutation effects drawn from a bivariate normal distribution with correlation r_μ and added to the current values.
- One parent of each sex was randomly drawn according to fitness⁷ to create offspring (see **Key** for definitions):
 - $w = \exp\{-0.5(z - \theta_m)^2 W_m^{-1}\}$ for males.
 - $w = \exp\{-0.5(z - \theta_f)^2 W_f^{-1}\}$ for females.
- First 1000 generations: weak stabilizing selection ($\theta_m = \theta_f = 0$, $W_m = W_f = 150000$).
- Next 1000 generations: strong directional selection ($\theta_m = 1000$, $W_m = 75000$) on males. For females, either selection absent ($W_f = 0$), weak ($W_f = 150000$), or strong ($W_f = 75000$), and either antagonistic to ($\theta_f = -1000$) or concordant with ($\theta_f = 1000$) selection on males.

Results

The breeding values of each individual in the population were output every 10 generations and used to calculate the mean male and female breeding values of the trait.

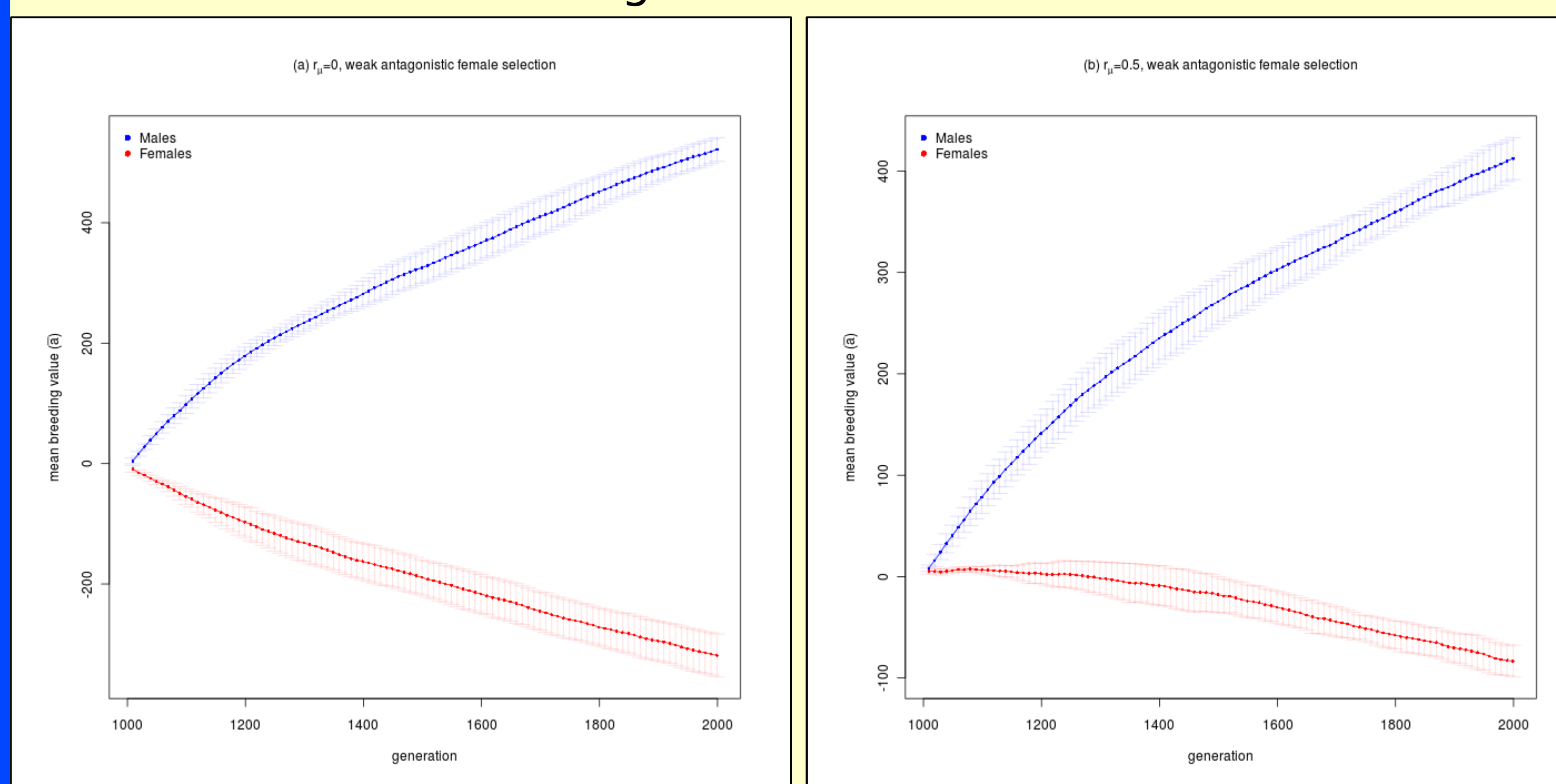


Figure 2. Evolution of the mean breeding value under strong selection on males and weaker antagonistic selection on females (see **Methods**). Mutations were either (a) uncorrelated or (b) positively correlated. Points are the result of averaging over three replicates. Results for other parameter sets not shown here.

The correlation between male and female breeding values (r_{mf}) for the trait was also calculated.

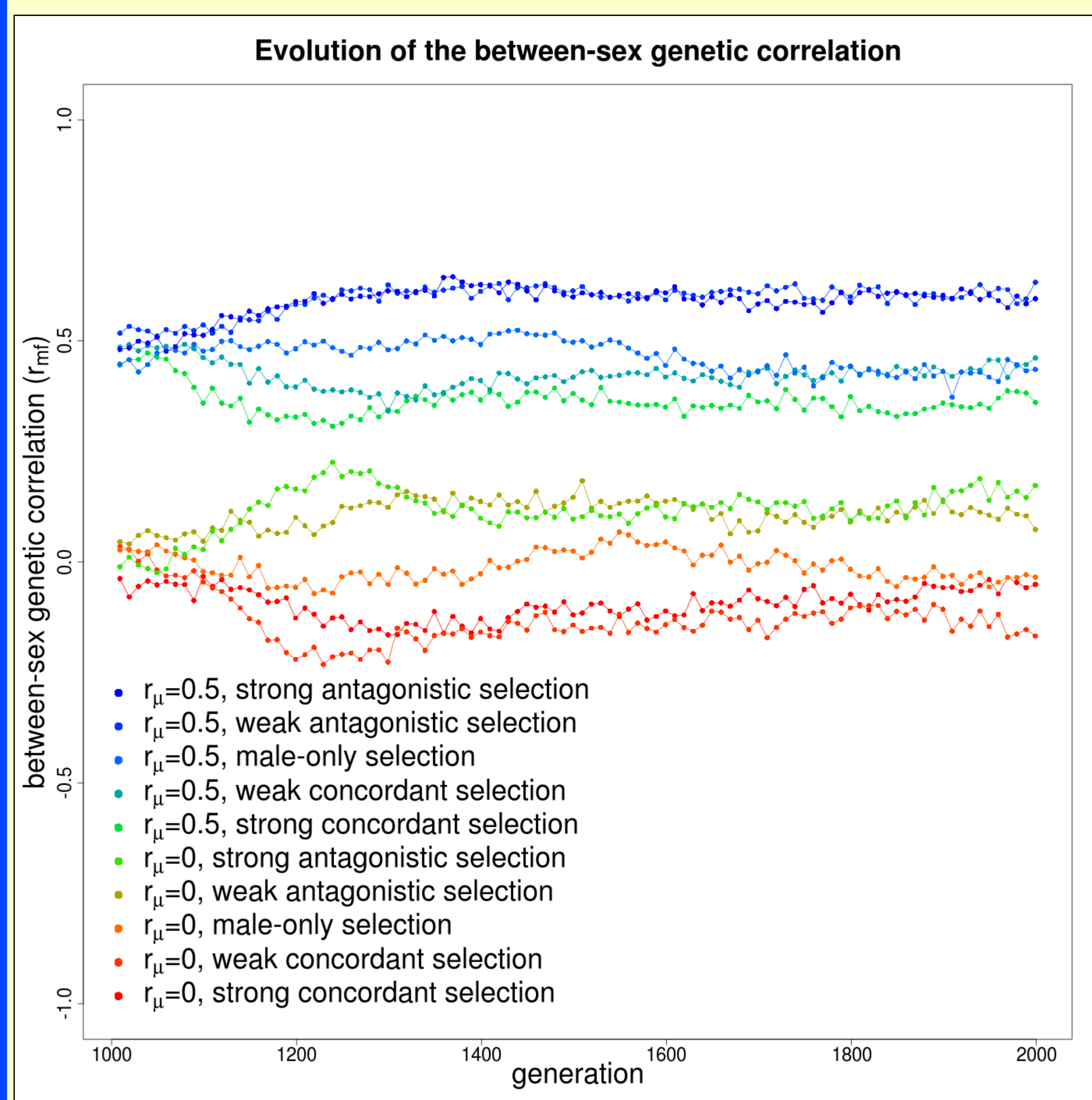


Figure 3. Evolution of the between-sex correlation (r_{mf}). See **Methods** for parameter details. Regardless of mutation effect correlation (r_μ), antagonistic selection increased r_{mf} and concordant selection decreased r_{mf} .

Discussion

- Results generally match predictions presented in **Figure 1**.
- Antagonistic selection in males and females led to more similar breeding values for male and female trait in an individual
- Concordant selection led to divergent breeding values for male and female trait in an individual.
- More investigation necessary to establish the precise mechanism.
- In contrast with predictions, the evolution of r_{mf} reaches an intermediate equilibrium value, though selection and genetic variance are both still high (values not shown here).
- Early work suggests that these patterns may break down as the distribution of mutational effects becomes more leptokurtic⁸.

Acknowledgements

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Literature cited

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Key

- a : breeding value (here equal to genotypic value), the expected phenotype for an individual based on their allele values
- r_{mf} : between-sex genetic correlation, how similar male and female breeding values are, ranges from 1 (similar) to -1 (different)
- r_μ : mutation effect correlation, how similar male and female values at a locus are after mutation
- w : individual fitness
- W : selection matrix, high values yield weak selection
- z : phenotypic value
- θ : optimum (peak) phenotype, maximizes individual fitness
- μ : mutation rate (per-locus, per-generation)