

Equilibrium and Extinction in a Trisexual Diploid Mating System: An Investigation

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In order to study the dynamics of a three-sex (trisexual) mating system, we have chosen to extend the heterogametic sex-determining mechanism, used in many species, to include three sexes: XX, XY and YY. In this model, non-like types may mate, but like-types may not mate. Yeasts and fungi are known to have multiple mating types (sometimes numbering in the thousands), but the mechanics of these sex-determining systems are markedly different from the heterogametic system we are interested in studying [5]. Our motivation for using this scheme stems from the knowledge that in some species, such as most fish, XX is female, and XY is male [1]. Under certain conditions, a YY individual may be produced, and in the case of fish, this usually develops into a male. Our goal is to discover the emergent behavior of a hypothetical “diploid trisexual mating system” (DTMS) where the YY type is its own distinct “mating type”, in order to shed light on why such a system is not observed in nature today.

We first constructed a stochastic computer model to simulate a DTMS under Hardy-Weinberg conditions, and found that the mating-type frequencies F_{xx} , F_{xy} and F_{yy} , tend to hover near a Hardy-Weinberg-like equilibrium point. However, the system inevitably converged to a two-sex system containing either $\frac{1}{2}$ XX and $\frac{1}{2}$ XY or $\frac{1}{2}$ YY and $\frac{1}{2}$ XY.

We derived the formulas describing the theoretical equilibrium points for the mating type frequencies, which agree very well with our simulation results. These formulas were then used to compute the starting points for subsequent simulations, to measure frequency changes from one generation to the next.

To give credence to the possibility that a DTMS may exist in nature, we explored the idea of mating efficiency. Because we are assuming random mating, any individual has an equal probability of attempting to mate with any other individual in the population. Therefore, in a two-sex system, 50% of pairings are viable, but in the proposed DTMS, ~57.7% of pairings are viable (assuming the system is balanced at the central equilibrium point, previously derived). As the system falls away from the central equilibrium point, it approaches a two-sex system, and the pairing efficiency approaches 50%. This hints at an advantage for a species to maintain a three-sex mating system.

Next, we carried out an "equilibrium point sweep" on the simulation, in order to uncover evidence for a bias against the less-frequent homozygote. Beginning with an F_{xx} of 0, we computed the corresponding F_{xy} and F_{yy} , and then ran the simulation from this starting point enough times to reliably compute the average frequency change of F_{xx} in the subsequent generation. We incremented F_{xx} slightly, and repeated the process until $F_{xx} = 1/2$. This analysis showed no evidence of any bias for or against the less-frequent homozygote.

Finally, we used the "equilibrium point sweep" technique to measure the variance of the next-generation frequency change, and found that this variance is linearly proportional to the frequency its self. The decreased next-generation frequency change variance results in a lesser ability to recover a frequency loss in the subsequent generation, and inevitably, one of the homozygotes eventually goes extinct. We also found that this tends to occur in roughly $1/2N$ generations (N being the population size).

We approximated the next-generation frequency change distributions using the binomial distribution, constructed a simulation which used the binomial distribution to model the next-generation frequency change, and found its behavior to be nearly identical to that of our original DTMS simulation model. We therefore conclude that this linearly proportional relationship between frequency and next-generation frequency change variance is the root cause of the inevitable two-sex convergence.

Future work is needed to derive the average time to two-sex convergence, and to derive the actual statistical distributions of the next-generation mating-type frequency changes.

References

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