

## SEXUAL SELECTION CONTROLS

Sexual selection results from violation of the Hardy–Weinberg assumption that mating is random. EVOLVE allows you to simulate this by entering proportions or probabilities of one genotype ‘choosing’ to mate with each of the other genotypes.

For example, assume in a species like deer or antelope that the *A* & *B* alleles are incompletely dominant and the *B* allele produces large antlers or horns, which are preferred by all females. The phenotypes would then be *AA* = small, *AB* = medium, and *BB* = large. EVOLVE randomly picks ‘females’ who then each choose a ‘male’. The mating preferences might look like the following:

	<b><i>AA</i></b>	<b><i>AB</i></b>	<b><i>BB</i></b>
<b><i>AA</i> Preference for:</b>	.1	.2	.7
<b><i>AB</i> Preference for:</b>	.1	.2	.7
<b><i>BB</i> Preference for:</b>	.1	.2	.7

On average, 10% of the females would choose *AA* mates, 20% would choose *AB* mates and 70% would choose *BB*s. Note that the sum of the preferences in each row must add to 1.0 (100%).

### Known Issue

There may be a bug in this code. Although preferential mating appears to work alone, it appears to have no effect when combined with selection.