

You are studying a *large* population of *annual, insect-pollinated* plants with an interesting *flower-color polymorphism* that is controlled by two alleles at a conventional diploid genetic locus. **Red-flowered** individuals are homozygous for the **R** allele (**RR**), *pink-flowered* individuals are heterozygotes (**Rr**), and *white-flowered* individuals are homozygous for the **r** allele (**rr**). You examine 1000 randomly selected plants in your population and score their flower colors. The totals are 275 red-flowered, 650 pink-flowered, and 75 white-flowered.

What are the *frequencies* of the two *alleles* (**R** and **r**) in your sample? [5 points]

0.6 and 0.4

These *genotype* frequencies are *not* in Hardy-Weinberg proportions! What are the *observed* proportions of the three genotypes, and the *expected* proportions, assuming no selection, no migration, random mating, and so on? [5 points]

Observed: **RR** 0.275 **Rr** 0.650 **rr** 0.075

Expected: **RR** 0.36 **Rr** 0.48 **rr** 0.16

Note: The puzzle is that we have way too many Rr heterozygotes, for these (or any other) allele frequencies.

Puzzled by your data, you return to the population the following year, carry out a similar survey, and get essentially the same result. In other words, the *offspring* generation has (adult) allele and genotype frequencies indistinguishable from those of the *parental* generation.

How can you potentially *explain* this **disagreement between the observed and expected genotype frequencies** in your population? Please evaluate the plausibility of each of the following evolutionary processes, as a possible explanation for the disagreement. For each one, circle “yes”, “no”, or “maybe” to indicate whether you think it plausibly *could* explain, clearly *could not* explain, or *possibly* (but not with high probability) could explain why the observed genotype frequencies differ from those expected under the assumptions of the Hardy-Weinberg principle. Then in each case *briefly* explain *why* you think “yes”, “no”, or “maybe” is the best choice. Note: You do not need to circle “maybe” even once to get a perfect score; it’s there because some people may find really *creative* ways to use a few of the possibilities. So if you say “maybe”, be sure to explain your reasoning especially clearly! (We’re prepared to give extra credit...) [10 points each]

mutation yes no maybe

NO. Mutation is much too weak and slow to affect the genotype proportions.

drift yes no maybe

NO. We said the population is “large”, and your data show no detectable change of allele frequencies between generations. So drift is also weak and slow here.

directional selection caused by *pollinator preference* for *darker* flowers yes no maybe

NO. This would increase the frequency of RR even more than Rr, and it would cause a change of allele frequencies between generations (increasing the frequency of the R allele), which didn’t happen.

balancing selection caused by *pollinator preference* for *pink* flowers yes no maybe

NO. This could stabilize the allele frequencies, but it could not increase the relative frequency of Rr genotypes (that is, of pink-flowered individuals). Suppose the bees visit *only* pink flowers (so red and white have *no* reproductive success). Then the offspring will be 1:2:1 of RR, Rr, and rr, in perfect Hardy-Weinberg proportions.

balancing selection caused by pollinators tending to fly *alternately* between red and white flowers yes no maybe

YES. If RR and rr trade pollen more often than expected, then there will be an excess of heterozygous offspring, since *all* offspring of RR x rr crosses are Rr.

balancing selection caused by *inferiority of both homozygotes* (recessive deleterious alleles) yes no maybe

YES. This is classic heterozygote advantage. Both homozygotes are less fit than the heterozygote. It's just like the polymorphism for "V" and "L" in *Drosophila melanogaster* (which we discussed in lecture, and which is treated at length in the book), except that both homozygotes are viable (although RR apparently does somewhat better than rr).

migration (*i.e.*, recent or ongoing immigration into your study population) yes no maybe

NO. Migration would change the allele frequencies between generations. And it's hard to see how it could create a large heterozygote excess, unless immigrating males came in with an excess of one allele, while females came in from somewhere else with an excess of the other allele. Pretty far fetched. And anyway, these plants are hermaphrodites, so they do not have separate sexes to (hypothetically) have different allele frequencies!

inbreeding (*e.g.*, self-fertilization or preferential mating between close relatives) yes no maybe

NO. This would create an excess of *homozygotes*, not heterozygotes.

How could you *test* your favorite (most plausible) hypothesis? Describe some observations or experiments that you could perform to *eliminate* or *tentatively confirm* one or more of the hypotheses that cannot easily be dismissed as obviously implausible. [10 points]

I would follow bees around to see if they tend to go from red flowers to white flowers and back again. And I would make controlled crosses between all of the genotypes (flower-color phenotypes) and grow the resulting seeds up in the greenhouse (and/or in experimental plots in the field) to see if homozygotes really do survive less well than heterozygotes. But I'm sure there are other ways to test the "alternating bees" and "sick homozygotes" hypotheses.