

POPULATION GENETICS PROBLEM #3

Peter Buri studied the dynamics of genetic drift in experimental populations of *Drosophila melanogaster* (*Evolution* 10:367–402; 1956). He established a set of 107 experimental populations with eight males and eight females. Every individual in the initial populations was heterozygous bw^{75}/bw at the brown locus. After placing adults in vials, he allowed them to mate freely. Twelve days after mating (or two days after emergence of the first adults), he collected all adult flies, anesthetized them, sexed them, and selected eight males and eight females to be parents of the next generation. He continued this experiment through 19 generations.

bw^{75} homozygotes (bw^{75}/bw^{75}) have a bright red-orange eye color when raised at 25degC, as they were in this experiment. bw^{75} heterozygotes (bw^{75}/bw) have light orange eye, and bw homozygotes (bw/bw) have white eyes. Thus, Buri was able to count the number of bw^{75} (and bw) alleles in the parents used to produce every experimental population during every generation of the experiment. Not surprisingly, given the small number of adults allowed to reproduce in every generation, quite a few of the populations were fixed either for bw^{75} or for bw by after 19 generations. Specifically, 58 of the 107 populations were fixed for one of the two alleles, 30 for bw and 28 for bw^{75} .

In addition, Buri kept track of the number of populations with a given number of bw^{75} alleles in every generation. After the first generation, this is the distribution he found:

# of bw^{75}	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
# of pops	1	0	0	0	2	5	8	10	13	22	9	14	14	7	1	1

Using these data answer the following questions.

1. What is the inbreeding effective size of the populations that Buri studied?

If we thought of f as a measure of departure from Hardy-Weinberg, we'd set $f_0 = -1$.¹ Since inbreeding effective size is defined in terms of identity by descent, we take $f_0 = 0$. $f_{19} = 58/107 \approx 0.542$. So

$$1 - 0.542 = \left(1 - \frac{1}{2N_e^{(f)}}\right)^{19} (1 - 0)$$

¹Test your understanding. Why?

$$\begin{aligned}
0.458 &= \left(1 - \frac{1}{2N_e^{(f)}}\right)^{19} \\
(0.458)^{1/19} &= 1 - \frac{1}{2N_e^{(f)}} \\
\frac{1}{2N_e^{(f)}} &= 1 - (0.458)^{1/19} \\
N_e^{(f)} &= \frac{1}{2(1 - (0.458)^{1/19})} \\
&= 12.4
\end{aligned}$$

2. What is the variance effective size of the populations that Buri studied?

The variance in allele frequency after one generation is 0.00641. So the variance effective size is:

$$\begin{aligned}
0.00641 &= \frac{p(1-p)}{2N_e^{(v)}} \\
N_e^{(v)} &= \frac{0.25}{2(0.00641)} \\
&= 19.5
\end{aligned}$$

We use 0.5 for p rather than 0.506, because it's the allele frequency in the parents that matters, and we know that it's exactly 0.5.

3. Using what you know about coalescent theory, how many generations do you think Buri would have to continue his experiment, on average, before all populations are fixed for one allele or the other?

First, we know it's the inbreeding effective size that matters for the coalescent, so we're going to use $N_e^{(f)} = 12.4$ in our calculation. Second, we pull a sleight of hand. The coalescent looks backward, and it takes $4N_e^{(f)}$ generations, on average, for all alleles in a sample to have a single common ancestor. So now ignore the fact that I told you that for the coalescent to work the size of the sample has to be "small" relative to the population, and think about this. If we treat all alleles currently present in the population as distinct, i.e., $f_0 = 0$, how long will it be, on average, before a future population has all alleles descended from one of those currently present? Answer: $4N_e^{(f)}$ generations, because that's how far we'd have to go back from the present to find the common ancestor of all current alleles. That's a long way of getting to the answer

$$4(12.4) = 49.6 \approx 50 \text{ generations}$$

Note: You're welcome to try WinBUGS² your calculations, if you're so inclined. It's the only way that you'll be able to provide credible intervals on any of the answers you give. But using WinBUGS is optional for this problem.²

Note on the estimating the inbreeding effective populations size

In a set of ideal populations evolving according to genetic drift, the proportion that will be fixed for one allele or the other after t generations can be calculated from the inbreeding analogy with drift. Specifically, if f_t is the fraction of populations fixed for one allele or the other

$$1 - f_t = \left(1 - \frac{1}{2N}\right)^t (1 - f_0) \quad ,$$

where N is the number of diploid individuals in our ideal population.

²And I predict that few, if any, of you will decide to use it.