

## POPULATION GENETICS PROBLEM #2

Yoshiko Tobar and Ken-Ichi Kojima (*Genetics* 57:179-188; 1967) studied the evolutionary dynamics of an inversion polymorphism on chromosome 2 of *Drosophila ananassae* in a population cage. Through the standard sort of tricky genetic manipulations that *Drosophila* geneticists do, they derived two lines that were homozygous for each chromosome type. They then started different population cages with differing numbers of flies homozygous for each chromosomal arrangement. Specifically,

Population	Chromosome configuration	
	AA	BB
1	100	900
2	900	100

After one generation of reproduction in the cage they took a sample of adults and obtained the following “genotype” counts:<sup>1</sup>

Population	Genotype		
	AA	AB	BB
1	19	125	156
2	206	87	7

Assume that newly formed zygotes in the generation from which the adult sample was taken are found in Hardy-Weinberg proportions. Using these data answer the following questions:

1. What are the fitnesses of AA and BB relative to AB in each population, and what are the 95% credible limits on those fitnesses? For purposes of this exercise, assume that the counts of homozygous genotypes in the first table are based on a sample from a larger population. Hint: You’ll need to remember how to estimate proportions in a

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<sup>1</sup>Where I’m treating each inversion type as an allele. These counts combine results from two replicate populations.

multinomial.<sup>2</sup> Use a uniform prior on (0,1) to estimate the frequency of A in the initial population.<sup>3</sup> Use the trick used in the notes from 6 September on estimating allele frequencies in the ABO blood system to set a uniform prior on genotype frequencies in the adults of the next generation that are sampled.

```

model {
  # p.z is the frequency of A in zygotes
  # n.z is the number of AA individuals in the parental population
  n.z ~ dbin(p.z, N.z)

  # frequencies of the three genotypes in zygotes (before selection)
  x.z[1] <- p.z*p.z
  x.z[2] <- 2*p.z*(1.0-p.z)
  x.z[3] <- (1.0-p.z)*(1.0-p.z)

  # frequencies of the three genotypes in adults (after selection)
  # n.a[] is the vector of genotype counts in adults
  # x.a[] is the vector of genotype frequencies in adults
  n.a[1:3] ~ dmulti(x.a[], N.a)
  N.a <- sum(n.a[])

  # relative fitnesses
  # w11 = (w11/w12)
  # w22 = (w22/w12)
  w11 <- (x.a[1]/x.a[2])*(x.z[2]/x.z[1])
  w22 <- (x.a[3]/x.a[2])*(x.z[2]/x.z[1])

  # priors
  p.z ~ dunif(0, 1)
  # dummy variables first, then convert to frequencies
  y[1] ~ dexp(1)
  y[2] ~ dexp(1)
  y[3] ~ dexp(1)
  x.a[1] <- y[1]/sum(y[])
  x.a[2] <- y[2]/sum(y[])

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<sup>2</sup>Look back at Problem #1

<sup>3</sup>And remember that since all individuals are homozygous, the frequency of AA is the same as the frequency of A.

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x.a[3] <- y[3]/sum(y[])
}

# data for population 1
list(n.z=100, N.z=1000, n.a=c(19, 125, 156))
# data for population 2
list(n.z=900, N.z=1000, n.a=c(206, 87, 7))

```

Population	Relative fitnesses – mean (95% credible interval)	
	AA	BB
1	2.882 (1.614, 4.613)	0.2815 (0.2023, 0.3782)
2	0.5347 (0.382, 0.7239)	1.666 (0.6704, 3.147)

- Are the relative fitnesses of the genotypes the same or different in the two populations?  
The fitnesses are *very* different. Not only are the means very different (2.882 *versus* 0.5347 for AA; 0.2815 *versus* 1.666 for BB), but the 95% credible intervals don't even overlap.
- Given your answers to (1) & (2) and assuming that those fitnesses are the only evolutionary force acting, what do you predict about the equilibrium composition of *Drosophila ananassae* populations. Will they be polymorphic? monomorphic for A? monomorphic for B? or will the result depend on initial frequencies? Be sure to explain your answer because (a) if you look up the original paper you will see the result and (b) the pattern of selection happening here is different from anything we've discussed in class.<sup>4</sup>

The equilibrium composition will be polymorphic. When AA is rare (population 1), there is directional selection in favor of AA ( $2.882 > 1 > 0.5347$ ). When BB is rare (population 2), there is directional selection in favor of BB ( $0.5347 < 1 < 1.666$ ). Thus, there is a protected polymorphism. If A becomes rare, selection will act to increase its frequency. If B becomes rare selection will act to increase its frequency. This is an example of *frequency-dependent selection*. Note: the 95% credible interval for BB in population 2 even contains fitnesses that are consistent with heterozygote advantage, i.e., values for the fitness of BB that are less than 1, even though the best guess is still that there is directional selection in favor of B when it is rare.

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<sup>4</sup>But you have the tools to be able to figure out the results nonetheless if you think about it.