Madison Bowles

Evolution Exam 2

1a. There is a chance anomalus came from a crossing of annus and petiolaris, it’s small but there. Although inversion and translocation may cause loss or gain of function, they cannot explain why anomalus has 50% of its DNA from the widespread species, or the large chunks of genes that are identical to them. The desert plant is also able to back breed with either widespread species to produce more viable offspring.

1b. The reason you have large chunks of annus and petiolaris is because they do not recombine when making anomalus due to the inversions and translocations that cause genome stabilization. The chromosome with mutations is unpairable as they no longer line up correctly, prevent new DNA sequences from being created, and allow for large chunks of parent DNA/haplotype to be retained in the offspring.

1c&d. When the original parents (annus and petiolaris) mated, both gametes went through meiosis beforehand, which possibly resulted in an inversion and translocation event in the chromosomes. These mutations and the retention of large chunks of parent DNA that allow for survival can be used to create a distinct lineage map for anomalus.

2. This question can be answered in two parts. First, we explain that the results are not what was expected and second is trying to answer why. We created what we believe to be an observable graph comparing speciation versus postzygotic barriers to show the results do not support speciation rates effect on postzygotic barrier formation. When we look at RI values as Fst then we can use it as a measure of how distinct a subpopulation is when compared to the total population. When the Fst, is high there is more genetic difference, or more distinction between the subpopulation compared to the total population, which would lead to a higher barrier to gene flow, and thus under normal assumption, infer that the speciation rates would be higher driving the populations apart (speciation). Then when Fst is lower, there would be less distinction or less genetic difference between the subpopulation and total population, and less of a barrier to gene flow which would mean a lower speciation rate. To sum that up, when you have gene flow between two populations, they are more likely to be similar to each other genetically and less likely to become isolated from each other and speciate.  So, postzygotic barriers do not affect diversification like we expected.

Why do the results not match what was expected? There must be another factor at play here. Speciation seems to be its own limiting factor. Since this study looks at speciation in macroevolutionary time, the long run, there is a chance that incipient species end up persisting over time while a majority of new species or lots of short branches do not. Basically, it seems as though speciation does not have a large impact on the frame of macroevolution timescale because ultimately newer species often do not last long evolutionarily.

3a. When we look at linkage disequilibrium, we know that it’s the non-random association of alleles or genes between loci, which there are two kinds of tightly linked genes found on the Y chromosome and in mitochondria. If we look at the cytoplasm in female mosquitos with a certain Wolbachia strain like mitochondria, then we can assume they do not recombine when the egg comes together with the sperm and a majority are inherited from the female.

3b. In A we mentioned that the LD is increased in eggs since it is a non-random association via the female like mitochondria, but higher mutation is known to lower LD since recombination is a random event and has the chance of separating those particular linked alleles or loci. A lower mutation rate would increase the LD rate by decreasing the chance the alleles or loci get randomly separated and increase the chance they are inherited together.

3c. Here the Wolbachia introduces a prezygotic barrier by manipulating the genome of its host to impact the compatibility of a sperm and egg. Some eggs that come from two different populations, from different regions, carrying different strains have a lower hatching success rate than others, which ultimately slows down gene flow within Culex.

3d. If we think of Wolbachia as being parasitic and we know they have an effect on gene compatibility of a male and female, there is a chance it exhibits a level of control or a change when introduced, on other genes within Culex that allows for better adaptation to the region it is in or a decreased chance of success in certain regions.

4a. Migration: The population divergence graph shows that the populations of marine and freshwater are closely related over time. Whereas the Eda graph tells a different story. Fish from the ocean have gotten stuck after migrating to a freshwater environment and are no longer able to coalesce.

4b. Drift: Population divergence shows the freshwater and marine populations as not being so different from the total population. But as they have been separated drift acts faster on the smaller populations causing the difference between the marine and freshwater populations.

4c. Ancestral Polymorphism: what the freshwater and marine fish have inherited are the two forms of alleles for the Eda locus. This would alter the population divergence and the phylogenetics for the populations as they go through differential inheritance.

4d. Migration is the most likely hypothesis. Without it, you do not create smaller subpopulations which then do not allow for the other forces to have such a big impact. Like if the populations stayed together, it would be larger, and drift wouldn’t be as substantial as it is in the sub populations.

4e. To go about this I imagine a smaller version of what is going on in the question. A population of oceanic sticklebacks (ocean simulated) that have their genome sequenced for different alleles within the population and to compare plasticity before and after migration events. As a control I would want a generalized genome for the actual oceanic and freshwater for later comparison. The sticklebacks would start in the oceanic “ecosystem”, then be able to migrate to a freshwater “ecosystem”, when they similar obstacles would prevent them from migration back to the ocean. The migration rate could be determined and the allele frequencies  and the final genome sequences within each of the populations could be compared for changes in coalescence and divergence created because of migration only. Gene flow from sub populations other than the original experimental sticklebacks would not be included to prevent further mixing of other genomes.

5a. Normally, mutations are neutral meaning they have no effect on fitness. They are events that happen by themselves and can often still code for the same proteins, genes, or contain the same function.

5b. So, as mentioned normally mutations have no effect on fitness, but epistatic genes need multiple genes working together to affect the expression of another. So, they basically need each other to work properly. But, when you introduce a mutation that creates some sort of incompatibility between these epistatic genes, then most likely fitness will be affected since the alleles at the other loci will no longer be able to interact or go to fixation together.

5c. I would have to say that drift is the strongest force here. The isolated populations are what allow drift to be the strongest driver for change and would have the power to force even “bad” genes to go to fixation because it is random.

5d. Here range is used to as the effective population size, and speciation rate as DMI. The study showed that range is a surrogate for Ne and speciation is a surrogate for DMI and that they are inversely proportional to each other. This can be seen in the graphs. It also described DMI as incompatibilities over time. So, based off the question and this information we know we want to look at a small Ne to increase the number of incompatibilities (DMI), then with an increase in incompatibilities and a small effective population the chances increase that drift, the main force at work in small populations, would be able to drive them to fixation.

6. Here we see that plumage/color variation are increasing over time. The males would be evolving different plumages, which females are less likely to mate with because of the variation in color. This allows for less gene flow, as the female finds less males like herself and drives a prezygotic wedge between them, hastening the speciation rates and isolating different males.