Katelyn Skaggs

Evolution Exam 3

1. (1 point) Sunflowers are fascinating plants. They can orient themselves to the sun over the course of the day, live in a wide-variety of habitats, and are incapable of self-fertilization. There are many species of sunflowers in North America, with the two most widespread being Helianthus annus and Helianthus petiolaris. If taken into a lab, less than 1% of crosses between these two sunflowers produce viable seeds, and the hybrids that result tend to have very low viability (around 5%). That is, 1% of the time you cross them you get viable seeds, then only 5% of those viable seeds are capable of growing into a plant that can also produce offspring. In the deserts of the southwest, among the dunes and in the salt flats, you may also find a few other strange sunflowers like Helianthus anomalus. The DNA of these desert sunflowers is about 50% identical to H. annuus and the other 50% of their DNA is identical to H. petiolaris. The genes in the desert sunflowers are found in long blocks (haplotypes) identical to similar chunks from the two widespread species, with many loci identical to one sunflower followed by a long stretch of loci identical to those from the other (think of long alternating bands). However, these desert sunflowers also often have large inversions and translocated genes. Cross-breeding the desert sunflowers to either of the two widespread species typically doesn’t work well, with fewer than 10% of the offspring being viable, although the desert sunflowers breed just fine (≥ 90% seed success, similar to the other species). (a) What is the probable origin of the desert sunflowers? (b) What is the likely explanation for the “large blocks” of widespread sunflower DNA in the desert sunflowers? (c & d) Please briefly (≤ 100 words) explain the importance of the inversions, translocations, and large blocks to understanding the origin of the desert sunflowers.

1. Helianthus anomalus is a hybrid species between the two ancestral sunflowers, Helianthus annus and Helianthus petiolaris. Helianthus annus and Helianthus petiolaris may have been as successful in the dry environment which caused them to adapt and pass down DNA that is fit for other environments along with the new adaptions.
2. The large blocks are parental DNA which did not go through recombination because of the presence of inversions that was passed down to Helianthus anomalus. The large blocks contain the DNA sequence for the ancestral DNA along with the different adaptations that will help the desert sunflower survive, and they were passed down after going to fixation. For instance, how the sunflower can move towards the light and/or the timing of flowering. Adaptations like these are very important for the Helianthus anomalus species because of the intense dryness and sun that they are exposed to in the desert environment.

C and d.) The large blocks, translocation, and inversion of the sunflower is very important because you can track what parent DNA was passed down, where the change in DNA took place, and what adaptations did the species gain or lose due to the changes. These are also used to protect the parent DNA that are passed down in sequences from recombination which would break apart the parental DNA segments. This can really help when trying to determine the origin of the flower because there will be a large amount of parental DNA left in the offspring that can be used to compare to possible parent species.

2. (1 point) Above are data for 244 species of bird color-coded by clade from a 2013 paper by the Daniels Matute & Rabosky. The x-axis shows the estimated speed at which postzygotic barriers form in a specific species (based on rates of geneitc differences between populations, basically think Fst; lower numbers = more genetic differences). The y-axis shows the estimated speciation rates (based on the length of the branches that lead to each species; lower numbers = longer branches; n.b. speciation rate is defined the same way anywhere else you see it in this exam). In the same paper, they found essentially identical results across the many species of Drosophila fruit flies. Further, another study by Dr. Sonal Singhal and colleagues in 2018 found similar results when they compared Fst in Australian lizard populations to speciation rates. Please clearly explain to me how you interpret the meaning of these results in 500 words or fewer.

Looking at this graph, there is no relationship between the postzygotic RI velocity and speciation rate in this data. I noticed that some clades have a wide range of postzygotic RI velocity (specifically, the orange clade, but also includes others), but the speciation rate is constant for these clades. For these species, the postzygotic RI velocity ranges from low to high, in other words, there are some species in the clade that are highly genetically different and some that are not. This proves that there is no relationship between postzygotic RI velocity and speciation in this date set because looking at these clades that have a very prominent genetic variation, but they have a constant speciation rate. Also, if we look at the dark purple clade, we see that they have a high speciation rate, but the postzygotic RI velocity is around 0. These two species have the about same rate of postzygotic RI velocity, but they have a different speciation rates.

It is interesting to note that near 0 on the x-axis was where most of the clades saw the highest speciation rate. This could be linked to mutations like insertions and translocations preserving the DNA.

3. (2 points) Wolbachia is a profoundly strange bacterium. It infects insects, but it does so by actively invading their cells and living in their cytoplasm. When Wolbachia invades the germline cells, it can be passed on by the female to her eggs. That is, baby insects inherit this bacterium from their mother. Further, it has evolved the ability to manipulate gene expression in the insects it infects, which can make the cytoplasm of the sperm from male insects incompatible with the cytoplasm of female eggs if one or the other is uninfected or infected with a different strain. A study published early this year by Sicard et al. examined how different strains of Wolbachia present in mosquitoes of the species Culex pipiens impact the hatching rates of their eggs. They brought males with one of four different Wolbachia strains, and females with one of those same four strains into a lab, cross-bred them, and analyzed the hatching rate of their eggs. The data shown above reveal the success rate by cross. The x-axis shows the strain infecting the female mosquito, the y-axis shows the strain infecting the male, and the size and darkness of the points plotted are proportional to the hatching success (defined as the proportion of crosses with ≥ 78% hatching success). Wolbachia strains vary in frequency by region. How do you expect Wolbachia strain to impact (a) the linkage disequilibrium in Culex mosquitoes? (b) mutation rate in Culex ? (c) gene flow in Culex ? (d) local adaptation in Culex mosquito genes?

1. In general, we know that linkage equilibrium increases a small affected population. So, the linkage equilibrium in Culex mosquitos will increase due to Wolbachia. This bacterium alters the gene expression making the sperm noncompatible with the female egg. This alteration affects the genes that are below on the sequence. The incompatibility would decrease the affected population size over time because only certain individuals are reproducing successfully which limits the amount of genetic variation in the population. It does this as a form of selection through non-random association because the similar infection DNA is going to be passed at a higher frequency than the other DNA strands.
2. The mutation rate is going to decrease because the new alleles are not going to appear as fast as they did prior to in the infection due to the incompatibilities that the bacterium produces. This will decrease genetic variation which in turn decreases mutation rate. DNA that is very similar is being passed down faster than mutations can arise now. There is still some genetic variation taking place through recombination, insertions, translocations, etc, but these new genetic variations are not hatching which means the population is not being exposed so they are not being passed down to offspring. Also, the incompatibilities produce a smaller affected population size. In general, small affected population sizes contribute to a decrease in genetic variation which would decrease the mutations.
3. Gene flow is still going on in these species, but it is going to decrease because the incompatibilities prevent the original gene flow which produced genetic variation to take place. Gene flow does not solely refer to the number of offspring, but also the viability of those offspring. In this case, the genetically different offspring do not survive, and the genetically similar offspring do survive.
4. Overall, gene flow impeded adaptations in a species. In this case, we saw that gene flow in decreased because of the postzygotic barriers that appear. Because of the decrease in gene flow, adaptations are increasing. The mosquitoes that are infected by similar bacteria strands will produce genetically similar offspring that have inherited that adaptative genes that were found in the parent species.

4. (2 points) Sticklebacks are fascinating little fish. They’re small and they live mostly in the oceans of the northern hemisphere. However, they breed in streams, and since the last Ice Age ended about 10,000 years ago, several populations invaded the large lakes that formed from the melting of the glaciers. Some also have taken up permanent residence in streams, giving up the return to the ocean. Once adapted to a freshwater setting, the fish rarely (if ever) return to the Ocean, and so cannot directly immigrate to other freshwater basins. Stickleback ecotypes refer to whether they live in marine or freshwater settings. In these freshwater systems, their primary predators are insect larvae such as dragonfly nymphs, which means that the spikes and bony armor that serve them well in the ocean (where fish eat them) do not work as well in freshwater. So freshwater sticklebacks tend to be smaller, with fewer bony plates and fewer spines than their oceanic relatives. The Ectodysplasin (Eda) gene has a major influence on the degree of armor. Above are data from one of many, many studies on sticklebacks showing their mating preferences in lab studies (left), a pattern of coalescent times for the Eda locus in different populations (multiple samples from some populations), and the pattern of population-level divergence times. (a - c) Provide three distinct but possible explanations for the discord between the population divergence and coalescent times brief (≤ 50 words for each explanation, so ≤ 150 total words). (d) Which of your answers from a-c is most likely? (e) Please describe a clear and specific dataset that could test your answer for part d.

1. Selection because coalescence is affected by selection due to the environment of the species. The environment of the sticklebacks will cause them to gain adaptations to survive and then diverge into another species.
2. Reproductive isolation because the groups would be coalescing to find mates. In the limited reproducing populations, the migration rate may increase if they are unsuccessful which could increase divergence.
3. Gene flow because the alleles are passed through the population, and then altered through coalescence for the specific environment. Once the adaptions are fixated, then the species may diverge.
4. Reproductive isolation is the most likely when it comes to the conflict between population level divergence and coalescent times. The initial migration is what influences the genetic changes and can produce reproduction isolation.
5. I would use coalesced alleles data. Then using the data, I would want to make a simulation to test how the species react in a reproductive isolated population. Then I would record the divergence measurements and compare them to the coalescence data.

5. (2 points) The rate at which reproductive incompatibilities accumulate between populations without gene flow has been a contentious topic for decades. As mutations accumulate within a lineage, some of them will be incompatible with alleles at other loci, resulting in epistatic incompatibilities. Yet the way this must work is that different alleles at different loci that interact epistatically have to go to fixation in the two populations. A recent study modeled this in a demographic framework, and the data shown above compare geographic range size to speciation rate for birds (left) and mammals (right). (a) What fitness effects do most mutations have? (b) Why might you expect the likelihood of a fitness effects for potentially-incompatible mutations to be different from the average mutation? (c) What force(s) have the strongest impact on the probability these incompatibilities go to fixation? (d) Please explain how the graphs reflects the relative importance of the force(s) described in part (c).

1. The effect that mutations have on fitness strongly depends on the type of mutation and location of the mutation. Mutations can increase the fitness if it adds or enhances the more fit alleles to help the species to adapt to their environment. Most commonly though, mutations decrease fitness because the allele no longer functions effectively. Mutations like insertions and deletions are usually more harmful than substitutions because they shift the frame which causes the whole amino acid sequence to change. This would decrease the fitness because it could lead to low viability and non-successful reproduction along with other problems that could affect the functioning of the organisms.
2. The potentially-incompatible mutations will affect the fitness differently because you have to take into consideration the environment, the other loci’s in the organism, and phenotype of the organism. Fitness is based on multiple locus in these cases. The mutations that are causing the incompatibility are passed down which limits the reproducing population size. Speciation would then be increased, and the fitness would be decreased.
3. Genetic drift has a strong force on these mutations going to fixation because of the random changes that could reduce the beneficial alleles. This is increased due to the isolated population size. The small affected population size due to the incompatibilities influence the shift in the allele frequencies which makes the inheritance of the mutated gene more likely in the population because it limits the genetic variation and mating selection.
4. There is a negative slope in both graphs. This shows that as range size decreases, speciation increases. As the population decreases, genetic drift increases because of the limited gene variation which in turn increases the rate at which new species arise.

6. (2 points) Shultz and Burns (2017) used spectrophotometry to measure the precise wavelengths of color coming from major feather patches from a 355 species of tanagers (Thraupidae). They used principal components analysis to reorient their data so they could analyze the axis of maximal color variation. More recently, Dr. Rosalyn Price-Waldman collaborated with them and used phylogenetic methods similar to what you did in your R assigment to calculate the speciation rates for the tanagers, and compared those rates to the plumage coloration (top row) and to the rate of change in plumage coloration (bottom row). Basically, for each species, they (1) measured the actual color of the bird, then used an evolutionary tree to estimate (2) the probability it would speciate soon, and (3) the probability it’s colors would change soon. The top set of figures shows speciation rate against color, while the bottom plot shows speciation rate against the rate of color evolution. Based on these data, please give a concise (≤ 100 words) explanation of how color effects speciation rate in tanagers.

Looking at the graph, there is a positive slop and the rho value is equal to or above 0.50. The speciation rate increases as the evolution rate of plumage color increases and becomes more complex; and this is seen in both male and female according to the graphs. This could be due to the new colorations changing the mating signals which influences the groups of birds that reproduce with one another. For instance, a choosy female may not choose to mate with a male with a certain plumage color. This would cause reproduction isolation which increases the speciation rate.