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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 identical to them. The desert plant is also able to back breed with either widespread species to produce more viable offspring.

Homozygotes creating a heterozygote/hybrid zone in the desert that has decreased viability because of mispairing

Better viability when they are back bred each time bc everytime you breed them to contain more and more of that one parent the less mispairings they have an easier time breeding

1b. The reason you have large chunks of annus and petiolaris is because they do not recombine when making anomalus. The chromosome with mutations is unpairable as they no longer line up correctly, prevent new DNA sequences to be 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. The inversion and translocation prevent proper pairing and recombination of the parent chromosomes, which prevents new genes from being created, prevent that and so large chunks of parent DNA would be retained.

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 introduce 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 parasitic and we know they have an effect on gene compatibility of male and female, who is to say it doesn’t exhibit 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.

4.

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. 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. 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.

5d.

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.