Exam 3

Jaelynn Parks

3/29/2021

1. (a) These desert sunflowers are a result of hybridization that has taken place between *H. annus* and *H. petiolaris*. Geographically speaking, the red circles show the location of *Helianthus anomalus* within the areas where *Helianthus annuus* and *Helianthus petiolaris* are found. The three species differ in soil preferences, *H. annuus* likes heavy clay soils and *H. petiolaris* tends to live in dry, sandy soils. These habitats are found within close proximity of one another throughout Western and central United States, which creates a variety of hybrid zones. The seeds are dispersed via large mammal dispersal. Aside from helping disperse the seeds, these mammals may also have a role in presenting opportunities for hybridization. Divergence patterns indicate that the three hybrid species arose shortly after the colonization of North America by bison, due to the environmental disturbances these mammals caused. There are 4 possibilities as to why the hybrid *H. anomalis* has been so successful: 1) they exist on an intermediate habitat, 2) hybridization created new combinations of parental phenotypes, 3) extreme phenotypes that are more adaptive spawned, 4) habitat divergence gradually evolved via fixation of mutations (Shwarzback et. Al 2001). Because the traits have been intermediate in the studies I found, as well as stated in the question text, *H. anomalis* is an ideal intermediate of the two parents.

Knowing that the origin of *H. anomalis* is a hybrid of *H. anuus* and *petiolaris*,

we’re left with the question of how speciation happened so fast. (In this case species is defined as a group of organisms capable of reproduction of viable offspring with almost perfect consistency) Rapid karyotypic evolution could be the reason for how quickly speciation took place between the hybrids and their parents. Though the hybrids contain parental DNA in a 50/50 ratio, the combination in chromosomal arrangements is unique in each hybrid. The incompatibility of anomalis with its parent species are due to multiple chromosomal breakages.

(b) Recently evolved hybrid species tend to decrease the size of parental species linkage blocks over time as a result of recombination. If our species has large linkage blocks, then that would indicate that it is either newly evolved or has a powerful genome stabilization mechanism. When the genome is stabilized, reduction by recombination cannot occur, as drift has finished the job, like we saw in the class about reinforcement. Given that we know this is a fairly recently evolved species, I have concluded that the speed of hybridization in these plants has been accelerated by selection for intermediate traits, lowering the number of generations required to achieve genomic stability. Ungerer et. Al found the magic number of generations to be 10-60 for stabilization, meaning the rate of hybridization in this species is relatively quick. The speed of hybridization here also supports my theory from the previous question, that rapid karyotype evolution must play a role in this hybridization event.

(c) Inversions and translocations are used to duplicate specific segments of the parental DNA that are key to hybrid survival. Large blocks of the parental genome are retained and shielded from recombination by these mutations. Inversions are associated with locally favored traits, which aid in adaptation and speciation. If inversion and translocation prevent recombination and retain large chunks of parental DNA, it is easier to determine the origin of the desert sunflower.

Sources:

Dary, D. 1974. The Buffalo Book: The Full Saga of the American Animal. Sage Books,

Chicago.

Griffiths, Anthony JF, William M. Gelbart, Jeffrey H. Miller, and Richard C. Lewontin.

1999. “Chromosomal Rearrangements.” *Modern Genetic Analysis*.

<https://www.ncbi.nlm.nih.gov/books/NBK21367/>.

Huang, Kaichi, and Loren H. Rieseberg. 2020. “Frequency, Origins, and Evolutionary Role

of Chromosomal Inversions in Plants.” *Frontiers in Plant Science* 11 (March).

<https://doi.org/10.3389/fpls.2020.00296>.

Rieseberg, Loren H. “Hybrid Speciation in Wild Sunflowers.” *Annals of the Missouri*

*Botanical Garden*, vol. 93, no. 1, 2006, pp. 34–48. *JSTOR*, [www.jstor.org/stable/40035044. Accessed 29 Mar. 2021](http://www.jstor.org/stable/40035044.%20Accessed%2029%20Mar.%202021).

Ungerer, Mark C., Stuart J. E. Baird, Jean Pan, and Loren H. Rieseberg. 1998. “Rapid

Hybrid Speciation in Wild Sunflowers.” *Proceedings of the National Academy of*

*Sciences of the United States of America* 95 (20): 11757–62.

Schwarzbach, Andrea E., Lisa A. Donovan, and Loren H. Rieseberg. 2001. “Transgressive

Character Expression in a Hybrid Sunflower Species.” *American Journal of Botany*

88 (2): 270–77. <https://doi.org/10.2307/2657018>.

1. Without looking at the data, reading only the paragraph, I would expect to see a trend where there are low levels of Fst, speciation rate would be quicker. This graph shows that there is no clear correlation between speciation rate and low numbers of Fst. This could be because species are all different and geographic distance may not be the best predictor for speciation in certain species. Another discrepancy in analysis of populations using Fst and geographic distance is that the two tell us nothing about the changes that have occurred in these populations over time. Those in late stages of differentiation are going to show different speciation rates than those in early stages. Lastly, the capability of a population to overcome isolation could determine the rate of speciation as well, and Fst isn’t the best predictor of this. Other parts of the test support that isolation by distance isn’t the best way to analyze rates of speciation because sexual selection and linked traits could drive populations toward speciation with attached incompatibility mutations that don’t change their fitness levels.

Based on the fact that other studies in different species have found a weak or absent correlation indicates that population differentiation may not be the determining factor in formation of species. This study shows that rate of reproductive isolation isn’t the reason for speciation in birds, so it could be the resilience against isolation that limits rates of speciation. In conclusion, Fst isn’t the best representation of what occurs at the genetic level in terms of rate of speciation. Birds are migratory and it was mentioned in lecture that the life stage at which migration occurs can change what happens on a genetic level. It seems that migration in and of itself would eliminate genetic differences between organisms because who is to say that there is more or less gene flow between populations further away due to their patterns of migration?

1. (a) Linkage disequilibrium will increase in a population with a small effective population size, like what we see here. The bacterial infection lowers the number of those capable of reproducing, and as only certain individuals are reproducing, pieces of DNA will be inherited at either higher or lower frequencies with one another than before. The bacteria is acting like selection of mates here, inducing non-random association of alleles. Based on the information given, I would expect strain 1 in females to produce offspring with high relative hatching success with strain 1, strain 2 with strain 2, etc. However, the data shows this isn’t always the case, for example, 3 and 3 have a low hatching success rate, and any male with strain 2 has successful offspring regardless of female strain. This indicates a high LD, as compatibility between organisms is so limited, allowing for only certain alleles to interact, becoming either more or less linked based on whether or not they are within compatible parents.

(b) Mutation rate is likely to decrease in these mosquitos as genetic variation will decrease and new alleles will no longer be introduced at the same rate of which they previously were. Recombination will occur, but because the offspring never hatch, the new genetic variations are not being introduced to the population.

(c) Like mutation rate, gene flow is hindered as mosquitos that would’ve originally exchanged genetic material, increasing variation and diversity no longer matter because their offspring do not survive. Gene flow is not only about reproductive rate, but survivability and viability of the offspring. Gene flow is occurring but cut out by postzygotic barriers, thus never surfacing in the population. This cut off in gene flow could even induce speciation as a long-term effect.

(d) As gene flow decreases, local adaptation will increase, as gene flow hinders local adaptation. Those infected by compatible strains of bacteria, producing viable offspring will produce and distribute adaptive mutations in their genome.

Sources:

Castellano, David, Adam Eyre-Walker, and Kasper Munch. 2020. “Impact of Mutation

Rate and Selection at Linked Sites on DNA Variation across the Genomes of

Humans and Other Homininae.” *Genome Biology and Evolution* 12 (1): 3550–61.

<https://doi.org/10.1093/gbe/evz215>.

Gene Flow and Mutation. 15 Aug. 2020, <https://chem.libretexts.org/@go/page/13484>.

Sprouffske, Kathleen, José Aguilar-Rodríguez, Paul Sniegowski, and Andreas Wagner.

2018. “High Mutation Rates Limit Evolutionary Adaptation in Escherichia Coli.”

*PLoS Genetics* 14 (4). <https://doi.org/10.1371/journal.pgen.1007324>.

1. (a) Reproductive Isolation: The differences in population divergence times between marine and freshwater fish is secondary to reproductive isolation. They would speciate because the females only mate within their ecotype. This explains why you see different ecotypes in the same area diverging in the population divergence graph.

(b) Genetic drift: As the populations migrate, the alleles best fit to the environment in which they end up go to fixation quickly. The rapid rate at which this occurs could be because subpopulations have such a small effective population size, and on top of that sexual selection enhances this effect.

(c) Selection-Migration: Population divergence graph shows closely related species that on the coalescence graph are not closely related. To be from the same area, and further apart via genetics, would have to be due to migration patterns. Fish migrated out upon population divergence, and then genetically adapted to wherever they ended up.

(d) Selection-Migration is going to play the largest role in discord between population divergence and coalescence because it is the basis underlying all other mechanisms. Drift in the ancestral population, followed by migration is going to allow for several different species to evolve from the same area with the same characteristics, like we see in the coalescent graph. Gene flow is never completely cut off because the fish are constantly migrating, so the same adaptations will be selected for in different areas at different times. Differentiation at the locus is inhibited by the success of alleles in the ancestral population. These super successful alleles drift to fixation in ancestors, and then the subsequent populations end up with the same ones, and speciate by reproductive isolation mechanisms.

(e) The best place to start would be analysis of the interactions between hybrids, as they show the overlap of divergent populations. The most ideal dataset would be able to assess hybrid zones and determine their range relative to the parent populations. Narrow hybrid zones indicate a balance between migration and selection. Adaptive divergence also contributes to the maintenance of hybrid zones, as selection for adaptation promotes reproductive isolation across a genome. Analysis of the relative range of hybrid zones compared to their parent populations should indicate migration-selection and adaptive divergence.

1. (a) Most mutations have no effect on fitness, as they are typically neutral.

(b) I would expect that the fitness effects of incompatible mutations are no different than that of a random mutation. If the mutation is incompatible, it will be suppressed and not affect the fitness of the individual. If the mutation is compatible, it will most likely be a neutral mutation (similar to the average mutation) and also have no effect on the fitness of the individual.

(c) These silent mutations of incompatibility are likely linked to the adaptive traits that confer survival of species in particular environments. Increased recombination creates adaptations as gene flow occurs between the populations, and the silent mutations that are linked to said adaptations will follow. Given that the silent mutations do not inhibit fitness, they will lead to speciation via incompatibility. Therefore, selection for adaptive traits that are genetically linked to incompatible alleles is the strongest force impacting fixation of incompatibilities. This is the definition of epistasis.

(d) The graphs reflect the importance of epistasis because that is the only way we would see increased speciation rate in populations that are geographically close together. We previously found in this class that speciation rate is more likely to occur when populations are further apart, due to lower Fst and more genetic differences. In this example, speciation occurs in populations that are closer together because as they migrate into the same areas, adaptation will occur to fit to the environment. As genetic material is exchanged, and traits that are selected for are integrated with incompatibilities due to epistatic interaction, speciation rate will increase. Those further apart are not going to exchange the special alleles linked to incompatibility as often.

1. Color itself shows little to no correlation with speciation rate, but the rate at which color is changing does. Given that increasing genetic variation lowers gene flow in this graph, resulting in speciation, is evidence of sexual selection. Tanagers are selecting for colors similar to themselves, and as the rate of change in color increases, this prezygotic barrier is more prominent as they stop mating at their full capacity. Sexual selection also lowers the effective population size, thus enhancing the effect of drift, causing alleles to go to fixation and speciation to occur.