Exam 3

Jaelynn Parks

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A picture containing diagram

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Photo: [https://www-jstor-org.wvu.idm.oclc.org/](https://www-jstor-org.wvu.idm.oclc.org/stable/pdf/40035044.pdf?refreqid=excelsior%3Afd5a2bb94d0973dfb0a3ff0c466c2e5e)

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 speices differ in soil preferences, *H. annuus* likes heavy clay soils and *H. petiolaris* tends to live in dry, sandy soils (Reiseberg 2006). These habitats are found within close proximity of one another throughout Western and central United States, which creates a variety of hybrid zones. (Reiseberg 2006). The seeds are dispersed via large mammal dispersal (Reisberg 2006). 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 (Dary, 1974). 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 found to be intermediate in the studies I found, as well as stated in the question text, *H. anomalis* is an ideal intermediate of the two parents. Schwarzbach found the ecological selection to be towards *H. petiolaris* with the fertility selection favoring genetic material from *H. annuus*.

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 (Schwarzbach et. Al 2001).

(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:

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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. The graph shows that the species with high ranges of velocity tend to have around the same speciation rate, and those with clustered levels of postzygotic RI velocity can be on either end of the spectrum, with a high or low speciation rate. The dark purple cluster at the very top has a high speciation rate, and the clusters closer to the bottom have low speciation rates. The species toward the middle of the graph with larger ranges of velocities tend to stay in the lower area, between 0.2 and 0.3. Red has an intermediate range, but is still pretty spread out, thus close to the intermediate speciation rate, yet still leaning more towards the lower end. This could mean that as there are variations in speed of velocity of postzygotic barriers, the pattern in speciation rate becomes more linear. As the velocity of the formation of postzygotic barriers slows, the speciation rate starts to vary. The two are inversely proportional in this sense.

As the postzygotic RI velocity approaches zero, the values vary more in terms of speciation rate. They even look like they distinctly demonstrate the negative correlation that we expected to see in values closer to zero.

1. (a) Linkage disequilibrium will increase in a population with a small effective population size, like what we see here. The bacteria lowers the number of those capable of reproducing, and with certain individuals 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. For example, chunks of DNA in those with the same strain of bacteria are going to be inherited in higher frequencies than those with differing strains, such as 1 and 4.

(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 brought to an abrupt hault 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 it is known that gene flow hinders local adaptation. Those infected by similar strains of bacteria, producing viable offspring will produce and distribute adaptative mutations in their genome.

Sources:

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

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1. (a) High Migration Rate - plays a factor in the evidence that Eda coalescent times are before population divergence times because divergence needs a complete or lengthy separation of gene flow. If fish are constantly migrating between subpopulations, this will delay the population divergence time, regardless of coalescence time.

(b) Reproductive Isolation – initiates differences in coalescence and divergence of population times because populations would diverge sooner. If the two are living amongst one another, for example, a limnetic female won’t mate with a benthic female, drift will encourage divergence, even if they share a recent common ancestor and share a habitat.

(c) Genetic drift in ancestral population due to effective population size – different alleles go to fixation in different ancestral populations, and through time and gene expression, subsequent populations will end up different from one another based on their common ancestor.

(d) Genetic drift in ancestral populations is the most likely cause for the phenomena in question 3, as it also includes effects from b. As an ancestral population suffers reproductive isolation, gene flow is limited, drift is faster, Fst is lower. As certain alleles go to fixation in isolated ancestral populations, this mechanism trickles down to the subsequent populations, making them all different from one another.

(e)