Exam 2 Evolution

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1. R File
2. In 100 words or fewer, explain why the proportions of mutation types differ between A/B/C as clearly and precisely as you can.

The main takeaway is that there is a tradeoff involved with every mutation. The source for this graph is an article proposing that mutations only occur when and how they are needed, given the risk associated with them. A is not very fit, thus not well adapted, so that is why it has a higher amount of beneficial mutations. C is closest to peak fitness, so beneficial mutations are not possible, as it cannot become more fit. B is higher than A, so it naturally needs a smaller proportion of beneficial mutations. Selection for mutation types correlates with fitness level.

* 1. The regression line, though the slope is not super steep, indicates a positive correlation between heterozygosity and fitness of trees. Heterozygosity increases size and fitness.
  2. Inbreeding reduces the number of heterozygotes in a given population, enhancing the effects of drift and lowering the rate of beneficial mutations. Inbreeding decreases the effective population size, decreasing the amount of gene flow, thus directly reducing heterozygosity. According to the graph from this data, fitness and growth will be lower if heterozygosity is lower. In conclusion, inbreeding will lower the expected tree ring width.
  3. In reference to the lecture that included geometric mean, we discussed that more fluctuation will lower fitness. This is because as changes and instability occur within a population, it increases drift and the likelihood of which it will hit zero. As interference with recombination occurs, selection moves faster and as selection moves faster, variation decreases. As fixation increases, the population is less capable of recombination. All of the above forces are linked in a way that when fluctuation occurs, heterozygosity is lower. Under the assumption that ring width increases with heterozygosity, I would expect that the stable population would have larger tree trunks.

Aside from these relationships, size fluctuations could lead to disruptive selection, favoring the two extremes, eliminating the intermediate phenotype. This would also promote the presence of homozygotes, thus decreasing trunk size.

* 1. Heterozygosity is selected for as trees with larger trunks live longer due to their ability to cover more surface area, outcompeting the other trees for resources and reproduction.

1. Describe effect of different genetics on trichome number in wild arugula.

Selection is strictly about phenotype, and in this example, trichomes. Like the Illinois corn example, additive genetic variation occurred in response to environmental conditions. Initially, gene flow was introduced between two populations that wouldn’t normally cross and when exposed to the jasmonic acid, plants developed an increasing number of trichomes as an adaptive response. Gene flow is evident as the two responded in the exact same way, and differentiation is evident because there was an obvious increase in trichome number when compared to the control.

* 1. The F statistic is a measure of heterozygosity due to genetic exchange between two populations, therefore to get speciation, the closer an Fst is to one, the closer the two are to speciation. When Fst = 1, there’s no overlap between two populations, meaning the two are entirely different. Homozygosity will be high within the subpopulations, that is why Fst is so tricky. It is a measure of difference between two populations to an extent that those two populations are so similar within themselves that they are opposites of one another. The graphs from this article show on the y axis the F statistic (raised to the power of 0.275 for better visualization I assume). To choose the right mix of factors, I would expect those that will produce the highest Fst will be best for speciation conditions. Mating systems and growth forms are pretty obvious outliers, as mixed-mating and non-woody growth have high relative Fsts. I would expect that this is because mixed-mating is going to prevent gene flow between two populations, as it has a component of self-fertilization, thus limiting migration of genes from other populations. Non-woody plants are going to have a hard time reaching large areas for exchange of genetic material, as they are smaller, and closer to the ground. Pollinators are probably the main reason why they aren’t closer to 1.

In terms of pollination mode and seed dispersal, small insects increase the Fst the most, and this is most likely because they are pretty particular and localized in where they pollinate. Gravity is the worst at seed dispersal when compared to wind and animal travel, for reasons that are fairly obvious. If the wind isn’t blowing the seeds around and the animals aren’t pooping them out, then they’re just landing where they fall, localized. This would encourage speciation as they are definitely at very low chance of exchanging genetic material by relocation.

In conclusion, a higher Fst indicates higher similarity within a subpopulation to an extent that makes it totally different from the total population. A good example to describe this question would be if these plants were on close-together islands. Mixed mating, non-woody, small insect pollinated, gravity dispersal plants are not going to have much success in sending their genetic material over to the neighbor, when all of these factors encourage localization. Limiting gene flow and promoting homozygosity within a subpopulation will increase the differentiation between two species. Given that Fst is a measure of differentiation between two populations, we want factors that promote high Fst.

* 1. Because of the dramatic changes in seasons and temperature between temperate and tropic climates, it makes sense that plants living where climate is unchanging would not experience as much genetic variation. When the climate is the same all year round, it gives the plants and animals highly differentiated and specific niches. It is simply a known fact that there are more species of things in tropical areas. To test this hypothesis, I would want to look at the average temperature in a 6 month period with an emphasis on the standard deviation. Another possible approach is to evaluate the fluctuation in precipitation over a longer time period over the course of 10 years. I would couple one of these with heterozygosity or species richness to demonstrate that genetic exhange is lower in places where climate is relatively stable, as it isn’t entirely necessary.
  2. Pollination mode would have a larger impact on Fst because it directly effects recombination of genetic material whereas seed dispersal is random and there is a chance that the seed won’t germinate. Pollination allows for nuclear genes to be randomized and exchanged and dispersal is just random chance distribution of genetic material with no guarantee of mixing genetic material. I would expect a low Fst in mitochondrial/chloroplast DNA as it is only inherited from one parent and thus retains homozygosity and low genetic variation to an extent that nuclear genes do not.
  3. The negative correlation shown in figure A is a result of selection driving mutation rate in organisms with a smaller genome. Drake’s rule describes this phenomenon in that it states that mutation rate and genome size are inversely proportional. Mutations are how infectious pathogens compete and survive, therefore, the larger the capability for mutation, the more fit the organism is. Figure A kind of goes along with the figure from number two. In the most fit organisms, beneficial mutations were not needed. It is almost the same scenario here, as genome size increases, the need for a high rate of mutation decreases. Selection favors mutants in those with a small genome, thus indirectly selecting for organisms with higher mutation rates. Recombination relaxes this selection and those who evolve to reduce mutation rates suffer physiological cost, driving the genome size toward a neutral middle ground. In conclusion, too much mutation can be deleterious and is limited by recombination and down-regulating is costly to the individual. Therefore, genome size and mutation rate show an inverse relationship as selection for equilibrium exists.
  4. Most of the COVID strains on the graph in Figure B resemble drift as they start out, peak, then fall to zero. It is difficult to choose between selection and drift because selection is a factor that speeds up drift, and this example is a rapidly occurring process, taking less than 6 months to drift to zero. Viral strains that are best suited for infection of a host are selected for while the alleles that existed in previous strains are selected against. As a result, the alleles belonging to the old strains drift to zero. In conclusion, the graph shows drift, but selection can’t be entirely eliminated as it is a force at work speeding up drift.
  5. The more hosts that become available to a virus, the more genomes it has to play with, allowing it to mutate faster. SARS-CoV-2 is especially successful because of its mutation within the spike protein, and the B.1.1.7 strain was reported to have 8 mutations from the original Wuhan strain in the spike protein alone. (Lee 2021) The mutations within the spike protein allow for changes in receptor binding, allowing it to latch on to host receptors (ACE2 in this case) tighter than ever before. This variant has a mutation that changes the amino acid in the binding domain of the spike protein from asparagine to tyrosine. (Lee 2021) This mutation increases the success of viral entry into host cells. As this results in increased transmissibility between hosts, this is classic definition of selection: anything that makes more of you makes there be more of you. With repeated success in competition for host cell attachment, and increased transmissibility, B.1.1.7 frequency grows. Transmissibility is also going to oppose extinction of these super successful mutations, as population number increases exponentially, according to the graph. Additionally, these successful alleles will likely go to fixation very soon, given the exponential growth. The remaining strains of the virus have a higher chance of going to zero, and these are rapidly approaching 1. In conclusion selection and drift are at work here, working together in this case to increase the fixation of this successful mutation. Migration and gene flow are also in action here because as people travel in from other areas as social distancing restrictions are being lifted, there will be gene flow between populations, thus increasing the opportunity for mutations such as this one.
  6. New cases will impact the probability of new strains evolving because as the virus finds new hosts, and we vaccinate, the strains that are most successful in transmission, and those that are capable of evading vaccines and other preventative measures are going to be selected for, and their mutations will go to fixation. The number of new strains is directly proportional with the number of new cases. Survival of pathogens is based primarily on successful mutations. The newer cases we have, the more opportunities there are for mutation, as viruses integrate themselves into the host genome.

1. LD relates to genetic drift in that as it spreads out over time, selection sweeps away surrounding genetic diversity and variation. Selection increases LD which decreases genetic diversity thus making drift too slow for recombination. LD is defined as the correlation between nearby variants in that polymorphisms are linked more often than they would be if they were unlinked. This speeds up genetic drift because diversity is inversely proportional to LD.

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