Contents

Week 3

Populus Simulations

Exercise 1: Stimulating Strong Selection

1. Describe how the frequency of the *A* allele changes due to strong selection.

    ▷ The frequency of the *A* allele increases rapidly due to strong selection.

2. How many generations passed before the *A* allele was fixed or lost?

    ▷ Roughly 65–70 generations.

3. How many generations passed before the *a* allele was fixed or lost.

    ▷ Roughly 40–45 generations.

Exercise 2: Simulating Modereate Selection

4. Describe how the frequency of the *A* allele changes due to slightly weaker selection.

    ▷ Moderate sigmodal increases in frequency.

5. How many generations passed before the *A* allele was fixed or lost?

    ▷ Roughly 125–130 generations.

6. How many generations passed before the *a* allele was fixed or lost?

    ▷ Roughly 80–85 generations.

Exercise 3: Simulating Weak Selection

7. Describe how the frequency of the *A* allele changes due to weak selection.

    ▷ Relatively small increases in frequency until about 400 generations, then the a slightly increasing exponential curve.

8. How many generations passed before the *A* allele was fixed or lost?

    ▷ Was not fixed or lost after 1000 generations.

9. How many generations passed before the *a* allele was fixed or lost?

    ▷ Same, the allele was not fixed or lost.

10. If a generation was equal to 10 years, how many years would it take for the frequency of the *A* allele to double in frequency (from 10% to 20%)

    ▷ 800–975 generations, so approximately 1,750 years.

Week 2

Dog Domestication

▷ Background and Goals

- ○ What hypotheses about dog domestication are examined in this paper?

    – The origin of domestic dogs was the main focus; genetic data suggests East Asia, but other data suggests Europe and Siberia.

- ○ What predictions do these hypotheses make? What would the expected phylogenetic trees look like under each of these hypotheses (i.e. what are the expected topologies)?

    – The most recent common ancestor would indicate origin and genetic data would help confirm time frame.

▷ Methods

- ○ What taxa were sampled for this study?

    – Hypothesis was tested using DNA extracted to trace mitochondrial genomes from 18 prehistoric canids and 20 modern wolves from Eurasian and American origin.

- ○ What gene sequences were used for this study?

    – Wolves, dogs, including divergent breeds, recently published chinese indigenous dogs, and coyotes. (148 mitochondrial genomes)

- ○ What phylogenetic methods were used to reconstruct the phylogenetic tree in Figure 1?

    – Maximum likelyhood, coalescence, and Bayesian.

▷ Results and Discussion

- ○ In Figure 1, which wolf sequence is most closely related to the extant dog clade A, and what geographic region is it from?

    – Wolves: Switzerland 2 14,500.

    – Dogs: Argentina, USA (8,500, 1,000)

- ○ In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?

    – Dog clade A, Russia, 18,000 years ago.

- ○ Based upon Figure 1, how many times does it appear that modern extant dogs could possibly have been domesticated?

        – Figure 1 suggests 4, but the the authors state, "the inferred recent divergence of clade B from wolves now found in Sweden and Ukraine implies that is might represent a mitochondrial genome introgressed from wolves rather than one established by domestication."

    ○ What was the topology of the phylogenetic tree that was recovered, and therefore, which hypothesis was supported?

        – The findings support the conclusion that legacy of dogs derives from wolves of European origin.

        – Analysis of coalescence times support divergence time of >15,000 years ago.

        – Past mitochondrial and Y chromosome analysis suggestesd non-European, but had less supported data than these findings.

▷ Conclusions

    ○ What are the major conclusions of the paper?

        – Three of four modern dog clades are more closely related to sequences from ancient European rather than extant wolves with divergence times >15,000 years ago.

    ○ Was the taxonomic sampling sufficient to rule out alternative hypotheses?

        – Ancient panel did not contain specimens from Middle East or China. No, no ancient dog remains older than 13,000 years are known from those regions.

        – The mtDNA sequence tree is well supported, but represents a single genetic locus. Independent loci could offer more power to resolve phylogenetic relations.

How Farming Reshaped Our Smiles and Our Speech

▷ Gibbons A 2019; doi: 10.1126/science.363.6432.113

1. What is this news article about?

    ▷ How farming may have reshaped our jaws and thus indirectly influencing how we speak.

2. How could diet change the structure of the jaw?

    ▷ Less wear and tear changed how jaws and teeth developped, creating an overbite with the now less worn down teeth.

3. How could jaw structure change speech patterns of humans?

    ▷ Jaw and teeth placement changes how easy it is to make certain sounds, and overbites made "f" and "v" easier to make.

4. Are these changes in jaw structure permanent? Why or why not?

    ▷ Not likely, if you ate diets similar to early humans your teeth would wear down more and impact from wisdom teeth would minimize overbite. Though, there may have been some lasting selection pressure for a natural overbite.

5. Did natural selection shape these changes in jaw structure? Explain.

    ▷ Not likely, mostly likely from behavior change due to mostly diet change.

6. Can natural selection shape speech patterns? Explain.

    ▷ Yes, sexual selection could be a significant. Or if the change in speech pattern could confer a advantage in communication.

7. Can you think of any parallels with other animals where diet influenced feeding structures?

    ▷ Lots of animals, birds (finches!!), dogs, snakes. Huge impact.

How Farming Reshaped Our Smiles and Our Speech