Phylogenies – M1 Genomes and Phenotypes
Correction

1. Introduction

1.1. Exercise from " Biologie Evolutive ", Thomas-Lefèvre-Raymond, p. 193.
Eight trees among the 9 have the same topology, which can be written as follows:
(((((A,B),C),(D,(E,(F,G)))),H),(I,J)). Tree number 3 has a different topology at the relative branching of leaves D and E:
(((((A,B),C),(E,(D,(F,G)))),H),(I,J)).

1.2. If the tree is not rooted, nothing can be concluded about the order of events for the appearance of the red color and the flower shape.

2. Kungas

From Bennett, E. A., Weber, J., Bendhafer, W., Champlot, S., Peters, J., Schwartz, G. M., ... & Geigl, E. M. (2022). The genetic identity of the earliest human-made hybrid animals, the kungas of Syro-Mesopotamia. Science advances, 8(2), eabm0218.

2.1. The mitochondrial sequences of both samples are very similar to the mitochondrial sequences of domestic donkeys. Both samples are probably domestic donkeys. They are not horses or hemiones based on the mitochondrial sequence studied.

2.2. Y chromosomes are passed from father to son and mark the paternal lineage while mitochondria are passed from mother to daughter and mark the maternal lineage. The Y chromosome sequences of both samples are very close to the hemione sequences.
These data suggest that the Umm el-Marra equids are first generation F1 hybrids from a domestic donkey and a male hemione.

2.3. Half of the sequences correspond exactly to the sequences of the domestic donkey, and the other half to the sequences of the hemione. This fits well with our hypothesis that the animal is an F1 hybrid between a domestic donkey and a hemione. Rather than domesticating the wild horses that populated the region, the Sumerians produced and used hybrids that combined the qualities of both parents (stronger and faster than donkeys - and even faster than horses -, more controllable than hemiones).

2.4. To obtain kungas, it was probably necessary to capture male hemiones, then keep them in pens temporarily with domestic donkeys while they interbred.

2.5. These kungas were supplanted by the arrival of the domestic horse, when it was imported into the region from the Pontic steppe, probably because horses were easier to breed.

3. Amylase and starch digestion

From P*ajic, P., Pavlidis, P., Dean, K., Neznanova, L., Romano, R. A., Garneau, D., ... & Gokcumen, O. (2019). Independent amylase gene copy number bursts correlate with dietary preferences in mammals. Elife, 8, e44628.*
https://elifesciences.org/articles/44628

Inchley, C. E., Larbey, C. D., Shwan, N. A., Pagani, L., Saag, L., Antão, T., ... & Kivisild, T. (2016). Selective sweep on human amylase genes postdates the split with Neanderthals. Scientific reports, 6(1), 1-10.
https://www.nature.com/articles/srep37198

3.1. one copy.
3.2. a duplication.
3.3. a deletion.
3.4. An increase in the number of copies of the amylase gene should increase the amount of amylase enzyme produced, and thus increase the ability to digest starch.

3.5. The five copies of the dog amylase gene come from very recent duplications in the dog ancestor. The six copies of the pig amylase gene are from very recent duplications in the pig ancestor. The most recent common ancestor of dogs and pigs probably had only one gene copy.

3.6. The rat and mouse ancestor had one AMY1 copy, which diverged between mouse and rat at the same time as their divergence, and another copy which evolved differently in the rat branch and the mouse branch.
In the rat branch: two duplications resulting in the three AMY2b copies AMY (4) and AMY (3).
In the branch that gave the mice: duplication of the AMY2b copy into a copy that then duplicated four times, and of which one of the duplicates (AMY2a1) evolved very rapidly.

3.7. The largest proportion of individuals carrying the AMY2A deletion is detected in Siberia. Perhaps because their population is smaller than the other regions tested, and thus the effect of genetic drift is higher: the fluctuation of allele frequency may therefore be higher there than in the other regions (and the frequency could very well have been lower). An alternative explanation is that the loss of this gene is advantageous and is under positive selection. Perhaps there is a cost to producing too much amylase. In Siberia, the diet is less starchy, so this allele with a deletion of AMY2A may be advantageous there.

4. Evolution of the lice
From Kittler, R., Kayser, M., & Stoneking, M. (2003). Molecular evolution of Pediculus humanus and the origin of clothing. Current Biology, 13(16), 1414-1417.

4.1. The molecular clock is assumed to be constant. Let T0 be the time elapsed since the most recent common ancestor of man and chimpanzee. The mutations observed between man and chimpanzee have accumulated during 2T0. Similarly, mutations between body lice and head lice accumulated over 2T1, with T1 the time since the most recent common ancestor of body lice and head lice.
2T1 = 2T0 x 0.36 / 30
The body louse and the head louse therefore diverged about: 5.5.106 x 0.36 / 30 = 66,000 years ago. If we assume that these two species began to diverge when the first clothing was worn, then clothing appeared about 66,000 years ago.

4.2. The nucleotide diversity of lice follows that of humans. There was a bottleneck when some of the humans left Africa and began to colonize Europe and then Asia and America.

4.3. Crabs originate from lice that were present in the gorilla's ancestors and that changed host and went to the ancestors of humans. By adapting to this new host, speciation occurred between *Pthirus*

gorillae and *Pthirus pubis*. Note: we cannot say that the louse *Pthirus gorillae* evolved into *Pthirus pubis*: it is an ancestor line of *Pthirus gorillae* which evolved into *Pthirus pubis*.

5. Reconstruction of infectious transmission chains

From Transmission of SARS-CoV-2 (Variant Delta) from Pet Hamsters to Humans and Onward Human Propagation of the Adapted Strain: A Case Study. Preprint. 2022. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4017393

5.1. A priori, this is not a human-to-human transmission from patient 1 to patient 2 because there are 5 mutations between the sequences and the virus accumulates at most 2 mutations per month. If there were sequencing errors, then yes it is possible that there was human-to-human transmission from patient 1 to patient 2. The time between infection and onset of symptoms can vary from 2 to 9 days depending on the individual.

5.2 There was independent contamination of patients 1 and 2, via different hamsters. As there are 5 mutations between the virus infecting patient 1 and the virus infecting patient 2, a horizontal distance of about 1 mm on the tree corresponds to one mutation. Patient 1's virus has one difference mutation from the SARS-CoV-2 virus present in two hamsters in the store (HK sample 1 and HK sample 10). It is therefore very likely that she was infected by a hamster from the store. Same reasoning for patient 2 and HK sample 7: just 3 mutations difference.
The sequence of hamster_sample_1_warehouse has accumulated more than five additional mutations compared to the sequence of patient 2. This suggests that the virus has spread within the hamster population in the warehouse.

5.3. The hamsters are infected with the delta variant. They were probably not infected in Hong Kong because this variant was not circulating in the region. The hamsters were infected either in the Netherlands or during transport between the Netherlands and Hong Kong.
They are all infected with virus strains that are very close to each other, suggesting a common origin, with an ancestor virus that has spread in the hamster population.

5.4. The viral sequences of patients 2 and 3 are identical. Patient 3 was directly infected by patient 2.