**Clock Foundation Sample Options**

**Option 1: All aged bats**

**Count =** 387

**Price =** 387 x $160 =$61,920

**Pros:** Would be able to compare estimates of dentition aging and epi clock aging (and thus if building a clock from dentition data is viable) – could be a paper. Would get a lot of information to use for identifying PCR candidate sites.

**Cons:** Most expensive, might be overkill (especially for PCR).

**Option 2: Subset of all aged bats**

**Count** **=** < 387

**Price =** < $61,920

**Pros:** Can reduce cost to include only the number of samples we’d need to identify key sites that may be targetable by PCR, then can do PCR on the rest. All in all the cheapest broad-range option. If we don’t have enough statistical power, we can always send in more.

**Cons:** We need to figure out how many samples to send to get enough statistical power in identifying important sites. If there aren’t few enough high-impact sites to make PCR viable, will likely need to send in more samples to the clock foundation, delaying time to data.

**Option 3: Pteropus only (all)**

**Count =** 141

**Price =** 141 x $160 = $22,560

**Pros:** A cheaper way to compare dentition vs epigenetic aging. Possibly most immediately important for Sophia’s thesis (paired with Pteropus metapopulation telemetry data). Allows us to test our idea on one species before moving to the next.

**Cons:** Insights may not be translatable to Eidolon.

**Option 4: Pteropus only (subset)**

**Count =** < 141

**Price =** < $22,560

**Pros:** The cheapest way to start trying to identify sites targetable by PCR.

**Cons:** Insights may not be translatable to Eidolon. If there aren’t few enough high-impact sites to make PCR viable, will likely need to send in more samples to the clock foundation, delaying time to data.

**Option 5: Eidolon only (all)**

**Count =** 226

**Price =** 226 x $160 = $36,160

**Pros:** A cheaper way to compare dentition vs epigenetic aging.

**Cons:** Insights might not be translatable to Pteropus.

**Option 6: Eidolon only (subset)**

**Count =** < 226

**Price =** < $36,160

**Pros:** The cheapest way to start identifying sites targetable by PCR.

**Cons:** Insights may not be translatable to Pteropus. If there aren’t few enough high-impact sites to make PCR viable, will likely need to send in more samples to the clock foundation, delaying time to data.

**Additional Option A: Juveniles (all)**

**Eidolon:** 148

**Cost =** 148 x $160 = $23,680

**Pteropus:** 166

**Cost =** 166 x $160 = $26,560

**Total =** $50,240

**Additional Option B: Juveniles (subset)**

**Eidolon:** <148

**Cost =** < $23,680

**Pteropus:** <166

**Cost =** < $26,560

**Total =** < $50,240

**TLDR;**

**If money is not limiting, and we have an interest in the dentition vs epi clock aging paper… Option 1**

**If money is limiting, or we do not have an interest in the dentition vs epi clock aging paper… Option 2 > Option 3 > Option 5 > Option 4 > Option 6**

**Sophia’s Thoughts:**

Based on my experiences in the bat working group meetings, I think that our position to pilot a ‘PCR-based epigenetic aging’ project is very cool. Having experienced the relative complexity of other lab-based methods (which aren’t fully developed yet, as we know), if we are able to identify a simpler, overall cheaper method that works I think it would be quite high impact within the bat community and would allow non-wet lab scientists to have a go at aging their bats.

If we can afford it, Option 1 would give us the most data, and thus many angles to work with in a paper (A) dentition vs epigenetic aging, B) how many samples are needed to identify reliable age-correlated sites (via some LOO algorithms), how do results for A and B differ between species w/in the same family). It would open the door for others to try out our methods on different bat taxa.

If Option 1 is too expensive, Option 2 still allows us to address many of these questions. We can set the # of samples based on the amount we can afford to process or based on some power analysis of sorts. Soojin may be very helpful here.

We can also target Option 1 via Option 2. This is probably the most practical option, balancing time and cost. If the turnaround time really is 6 weeks (which is questionable), then we can send in one round of samples next week (our best guess of how many we’d need to get some good insight), analyze the data when I’m back from Madagascar, then potentially send out more samples soon after. We could have two rounds of data then theoretically by late November/early December. A benefit of this is that I may have time to apply for small grants to help offset the costs of the clock foundation.

**Meeting with Soojin**

1. Present options and thoughts above. What does she think?
2. Does she have any insight on how many samples we should send as a first pass if we go with option 2?
3. Does she have any insight on how different the sites/top sites may be for *Pteropus* vs *Eidolon*? (different species, same family)
   1. This can help us decide if focusing on one species only may help us be able to reduce sampling needed for the other species (i.e. start with Pteropus all, then possibly move to Eidolon subset)
4. Is she aware of any grants related to epigenetic aging, or mammalian aging, that Cara or I could apply for to offset some clock foundation costs?