

# Choose Your Own Adventure in Molecular Ecology Webinar

## Webinar Questions and Answers (June 10, 2021)

#	Question	Answer(s)
1	Is there a published paper on the Mountain Gorilla Mark-Recapture study? Love to read more!	It's a report right now (loads of coauthors), but here's the report. <a href="https://igcp.org/content/uploads/2020/09/Bwindi-Sarambwe-2018-Final-Report-2019_12_16.pdf">https://igcp.org/content/uploads/2020/09/Bwindi-Sarambwe-2018-Final-Report-2019_12_16.pdf</a>
2	What steps would you use or name of the process we can look up in determining WHAT would be an appropriate sample size for population questions	I am not aware of a standard process, but I would consider your question (what parameters are you interested in estimating), the variability of the population, and the type of marker you are planning to use. Your average microsatellite study to assess population structure might need 30 samples per population, whereas you might need fewer samples (10-15 perhaps) for a large suite of SNPs.
3	Could you go into more detail on what allelic drop-out is, and are there ways to decrease the chance of having allelic drop-out?	Allelic dropout (ADO) is when one allele within a heterozygous genotype fails to amplify. This is most common in low-quality samples. To address ADO, we try to sample the freshest samples, or conduct sampling under conditions that will have relatively lower DNA degradation. Finally, we typically analyze samples multiple times, and use variation in the genotypes across replicates to try to develop a consensus genotype that we have greater confidence in.
4	What potential is there to use epigenetic markers to measure connectivity or dispersal?	Great question :) Given epimarks can be environmentally influenced, as well as inherited, you would need a lot of information about epimarks before being able to use it for movement info.
5	Can "domestic" bobwhites be readily distinguished from bobwhites that are "wild" or that may have undergone some introgression?	I think there would be potential for that, but it would depend on how genetically different they are. If there are detectable and reliable differences between domestic and wild bobwhites, then yes, genetic tools would be able to distinguish the. Hybridization and introgression gets increasingly more difficult, because the variation starts to get mixed around and you need more resolution to be able to distinguish between different categories of hybrid. An F1 hybrid would be easier to distinguish than an F2. If you have F3s (if hybridization has been going on a long time), they would be much more difficult to detect. You would need many more markers and more samples.
6	Is it common for eDNA to suffer from allelic dropout? If so, how is this addressed?	So that is going to depend on what method you're doing for sequencing. Metabarcoding wouldn't suffer from allelic dropout because you're sequencing a gene fragment, not something like a msat with bi-allelic genotypes