**JSOES Genetics SOP**

1. Sample Collection
   1. May Cruise
      1. Provide labeled, ETOH filled vials for onboard sampling of Chinook. Only Chinook are sampled onboard; Other species are sampled at the cutting party after the June cruise
      2. Vials are labeled consecutively beginning with #0001
      3. After sampling data sheets are received, create a sheet to convert between vial labels and Salmon ID numbers. The Salmon ID numbers are how individual fish are identified in the database.
   2. June Cruise
      1. Provide labeled, ETOH filled vials for cutting party which usually occurs in July
      2. This will include non-Chinook from the May cruise, and all species from the June cruise
      3. Vials are labeled with Salmon ID numbers, as provided by Cheryl
2. Genotyping
   1. Genotype all Chinook using at least the Ots299 SNP panel. We genotype for a 334 locus panel that includes the GREB loci, but none of those loci are currently used for JSOES.
   2. Exclude any individuals with more than 20% missing genotypes
   3. Determine genotypic sex from Ots\_Sexy3 locus
3. Analyses
   1. Species ID – Use Rubias with species ID baseline to check for non-Chinook
      1. R code and baseline to run Rubias for species ID: <https://github.com/dvandoornik/Chinook_SpeciesID>
   2. GSI
      1. Baseline files: <https://datadryad.org/stash/dataset/doi:10.5061/dryad.dz08kps5b>
      2. R code to run Ms.GSI: <https://github.com/dvandoornik/Chinook_GSI>
      3. Make assignments to the GAPS reporting groups (see [Van Doornik et al. 2024](https://afspubs.onlinelibrary.wiley.com/doi/10.1002/nafm.11019))
         1. The Mid/Up Columbia sp and Snake sp groups will be combined into an Interior sp group, and Up Columbia su/fa and Snake fa groups will be combined into an Interior fa group by Cheryl for downstream analyses.
         2. Report all assignments, however most downstream analyses will filter out assignments with *P* < 0.80.
   3. PBT
      1. Download appropriate files from [FishGen.net](http://www.fishgen.net)
      2. Make PBT assignments using [SNPPIT](https://github.com/eriqande/snppit) using default parameters
4. Reporting
   1. Individual GSI & PBT assignments (and *P* values), genotypic sex for every fish
   2. Send results to Cheryl for inclusion in project database that includes (see example datasheet):
      1. Individuals with a new species ID
      2. Genotypic sex
      3. Individuals dropped due to insufficient genotypes
      4. GSI assignments (best and 2nd best) with *P* values
      5. PBT assignments with *P* values and associated data from PBT database
      6. Genetic marker set used – GSI or PBT locus sets
5. Currently, we’re only analyzing Chinook, but we have done steelhead and coho in the past