**Estimating genotyping error rates**

**for the North Santiam genetic pedigree project**

**January 22, 2020**

Objective was to compare Dave and Sandra’s genotype calls to estimate an error rate.

Sandra ran four plates of N Santiam samples from 2013.

Dave and Sandra compared the genotypes and the overall error rate for the panel was 1.37%.

Error rates for each locus:

**Locus Error rate**

211 0.60%

409 1.62%

215 0.86%

515 2.79%

201 1.99%

Ogo2 0.28%

Ssa408 0.56%

249 3.16%

212 0.29%

OtsG474 0.58%

Ogo4 0.29%

311 3.58%

409, 515, 201, 249, and 311 all had allele dropout. While the allele dropout is troubling, I think that we can account for it in the parentage analysis as we discussed. We can visually compare the genotypes of near-assignments in the parentage analysis and determine if locus mismatches are likely the result of allele dropout. For example, locus *311* has a large size range of alleles, and we know that alleles over ~350 bp in size were often not visible in Dave’s electropherograms. When I see that an offspring has a *311* allele of 398 that is not present in an assigned parent, but that parent is homozygous for a smaller allele at *311*, then I can reasonably suppose that the mismatch is due to allele dropout.

515 had a few sizing issues with alleles 199 and 201. I think the 199 allele pulls up in the size standard and messes up the sizing. It’s difficult to be sure, though, because you just end up with a slightly taller 200 peak in the size standard, and the 515 peak is sized right at 200, which falls into the 201 bin. I can look for peaks that fall in the questionable range (size of peak is within 199.5-200.5 bp range). I don’t have that data for Dave’s genotypes because I just have allele calls and not the actual allele sizes, but I know that the 201 allele can be confused with the 199 allele and when I’m visually comparing genotypes I can take known sizing errors into account. Knowing what to look for during the parentage analysis will allow us to account for the problem. We are in good shape to be able to recognize and deal with these challenges during the parentage analysis.