**Replicating Andrew’s Results**

**April 24, 2020**

Sandra Bohn replicated Andrew Black’s analysis from the 2015 North Santiam report, which assigned the 2015 NOR returns (n = 613) to HOR outplants and carcass samples from 2010 (n = 2109), 2011 (n = 351), and 2012 (n = 342). Total lifetime fitness and cohort replacement rates were calculated for the 2010 cohort.

*Parentage assignments*

The Colony and Cervus outputs were identical, so there were no software issues with the parentage analysis. However, there were some disagreements interpreting the results of the outputs:

* NS\_15\_C\_AD\_M\_039 – I assigned a mother that had <7 loci compared
* NS\_15\_C\_BD\_M\_064 – Andrew assigned a mother that had 3 mismatches, I assigned a father that was a better match
* NS\_15\_C\_BD\_M\_065 – I overlooked a year mismatch in the trio assigned by Cervus
* NS\_15\_OP\_AD\_F\_110 – Andrew assigned a trio with 4 mismatches, I assigned only the mother
* NS\_15\_OP\_AD\_F\_156 – Andrew assigned a mother with 2 mismatches, mismatches did not appear to be scoring error
* NS\_15\_OP\_AD\_F\_435 – I assigned the parent with higher LOD, Andrew assigned the 2011 parent over the 2010 parent because age-4 returns are more common
* NS\_15\_OP\_AD\_F\_586 – Cervus assigned two parents that were not a trio, I picked higher LOD, Andrew did not, both parents released in 2010
* NS\_15\_OP\_AD\_M\_248 – Andrew assigned a father that had <7 loci matched
* NS\_15\_OP\_AD\_M\_298 – I assigned a father that Andrew did not, father met all criteria
* NS\_15\_OP\_AD\_M\_383 – I assigned a trio, Andrew only assigned mother, parents were outplanted at same location 2 months apart
* NS\_15\_OP\_AD\_M\_394 – Cervus assigned two parents that were not a trio, I picked higher LOD, Andrew did not, both parents released in 2010
* NS\_15\_OP\_AD\_M\_406 – I assigned a trio, Andrew only assigned father, parents outplanted at different locations
* NS\_15\_OP\_AD\_M\_597 – I assigned a mother that matched at more loci, Andrew assigned a father that was released in 2011 instead of 2010, making progeny age-4, a more likely outcome
* NS\_15\_OP\_AD\_M\_638 – I assigned a mother that met all criteria, Andrew did not
* NS\_15\_OP\_AD\_M\_657 – Andrew assigned a father that had <7 loci matched
* NS\_15\_OP\_BD\_F\_026 – Cervus assigned two trios with the same mother, I selected the trio with significant LOD, Andrew selected the trio that agreed with Colony
* NS\_15\_OP\_BD\_F\_144 – I overlooked a year mismatch in the trio assigned by Cervus
* NS\_15\_OP\_BD\_M\_025 – Andrew assigned a mother that had <7 loci matched
* NS\_15\_OP\_BD\_M\_037 – I assigned a mother that met loci matching criteria but had low confidence, Andrew did not
* NS\_15\_OP\_BD\_M\_046 – I assigned father with higher LOD, Andrew assigned father released in 2011 instead of 2010, making progeny age-4, a more likely outcome
* NS\_15\_OP\_BD\_M\_644 – Andrew assigned a father that had <7 loci matched

Out of 613 progeny we had 21 disagreements. The number of disagreements will be reduced by clarifying Andrew’s criteria, and this opportunity to practice will prevent me from overlooking year and location mismatches.

*Fitness estimates and age structure*

I moved forward with Andrew’s data, and our fitness estimates and age structure for the 2015 cohort matched exactly.

*Cohort replacement rate (CRR)*

The CRR spreadsheet breaks down male and female progeny of 2010 adults for each age-class. While replicating this sheet from the spreadsheet used to calculate fitness estimates for the 2010 cohort, I discovered that the IDs for the 2013 progeny were incorrect on that sheet. It looked to be a sorting error before the progeny were copied onto the sheet, and resulted in different numbers of males and females for the age-3 progeny.

Once I fixed that issue my calculations matched Andrew’s except for the number of male and female 2015 progeny.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Total | Offspring of males | Offspring of females | Male progeny (of females) | Female progeny (of females) | | Male Progeny (of Males) |
| 2013 progeny | | 72 | 58 | 43 | 31 | 12 | 42 | |
| 2014 progeny | | 376 | 330 | 317 | 212 | 105 | 213 | |
| 2015 progeny | | 167 | 115 | 121 | 54 | 69 | 56 | |
| Total |  | 615 | 503 | 481 | 297 | 186 | 311 | |

Andrew’s numbers that disagreed with mine are highlighted in red, and I think they are mistakes because if you add the male and female progeny of females you get 123, which is the number that I got. None of the numbers in red were used in the report.

*Effective number of breeders*

When I used the same p-critical value as Andrew (0.02), I obtained the same estimate of Nb. I also ran it with a p-critical value of 0.001, which is what I would usually use after calculating 1/2N, and that yielded an estimate of Nb that was about 50% higher. I think that moving forward we will want to keep using 0.02 to keep our estimates consistent.

*Predictors of fitness*

My GLM results were very close to Andrew’s, although the X2 estimates were off by a little (e.g. 44.9 vs. 45.5). Overall the results would be interpreted the same way and the small discrepancies may have been from using the newest version of JMP.

*Table 3*

When I calculated this table I noticed that the male and female columns were swapped. Otherwise the numbers were identical.