**2020 ODFW Blacktailed Deer Analysis Summary-Santiam**

We analyzed 1,794 dog-collected samples from the Santaim WMU.

*Individual matching analyses:*  
The probability of identity is the probability that two unrelated individuals will have the same genotype (and thus be genetically indistinguishable) using these markers, while the probability of identity for siblings is the probability that two related individuals, whether a parent-offspring pair or siblings, will have the same genotype. As per study goals, we set a threshold of probability of identity (PID) <0.001 and probability of identity for siblings (PIDsibs) <0.05. We calculated these values for the Santaim WMU using the original seven microsatellite markers.

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| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 8.1x10-7 | 3.1x10-3 |
| 6 | 1.1x10-5 | 8.3x10-3 |
| 5 | 1.5x10-4 | 2.2x10-2 |
| 4 | 1.8x10-3 | 5.8x10-2 |
|  |  |  |

Based on the PID and PIDsibs values, a minimum of five loci per individual sample were needed for the Santiam WMU. Samples that worked at fewer than five loci were excluded from recapture analyses.

Of the 1,794 samples, 674 samples worked at ≥ 5 loci (38%). There were 549 samples that did not amplify at any loci (31%).

From the 674 samples that worked at ≥ 5 loci, we identified 274 unique deer. One hundred and forty-nine of the 274 unique deer were recaptured 1-14X (Deer #32 was sampled 15X). The remaining 125 of the 274 unique deer were captured once (46%)

Of the 274 unique deer, 143 individuals were female and 124 individuals were male (1.15F:1M). There were 5 deer that did not amplify with the sexing markers (Deer# 48 and Deer# 91, Deer# 228, Deer# 243 and Deer# 245) and so we could not determine the sex for these individuals. Deer #28 and Deer# 39 all have multiple individuals that matched at least 5 or more loci, but we were unable to determine a sex for these samples. Because they matched at the required number of 5 or more loci to be considered a match, they were grouped together and considered a recapture event.

**Locus Information**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |  |
| C273 | 5 | 142-170 | 0.576 | 0.612 |  |  |  |
| C89 | 8 | 155-183 | 0.715 | 0.791 |  |  |  |
| OdhE | 5 | 141-157 | 0.522 | 0.520 |  |  |  |
| SBTD05 | 7 | 113-141 | 0.345 | 0.697 |  | |  |
| SBTD06 | 4 | 183-199 | 0.627 | 0.663 |  |  |  |
| T159s | 9 | 183-223 | 0.516 | 0.789 |  | |  |
| T7 | 7 | 219-243 | 0.677 | 0.781 |  | |  |

SBTD05, T159s and T7 were significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population substructuring.