**2022 ODFW Blacktailed Deer Analysis Summary-Santiam**

We analyzed 1,215 dog-collected samples from the Santiam 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 Santiam WMU using the original seven microsatellite markers.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 8.8x10-7 | 3.3x10-3 |
| 6 | 1.7x10-5 | 9.6x10-3 |
| 5 | 2.3x10-4 | 2.5x10-2 |
| 4 | 3.1x10-3 | 6.8x10-2 |
|  |  |  |

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 1,215 samples, 683 samples worked at ≥ 5 loci (56%). There were 284 samples that did not amplify at any loci (23%).

From the 683 samples that worked at ≥ 5 loci, we identified 238 unique deer. One hundred thirty-one of the 238 unique deer were recaptured 1-14X (Deer #82 was sampled 15X). The remaining 107 of the 238 unique deer were captured once (45%)

Of the 238 unique deer, 143 individuals were female, and 94 individuals were male (1.52F:1M), one individual did not amplify at any sexing markers (Deer #201).

**Locus Information**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |  |
| C273 | 4 | 142-170 | 0.543 | 0.577 |  |  |  |
| C89 | 8 | 155-183 | 0.753 | 0.791 |  |  |  |
| OdhE | 6 | 137-161 | 0.549 | 0.530 |  |  |  |
| SBTD05 | 8 | 113-141 | 0.543 | 0.668 |  | |  |
| SBTD06 | 4 | 183-205 | 0.627 | 0.610 |  |  |  |
| T159s | 9 | 183-223 | 0.565 | 0.831 |  | |  |
| T7 | 8 | 203-243 | 0.668 | 0.787 |  | |  |

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