**2021 ODFW Blacktailed Deer Analysis Summary-Santiam**

We analyzed 986 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.

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| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 1.4x10-6 | 3.9x10-3 |
| 6 | 2.3x10-5 | 1.0x10-2 |
| 5 | 3.0x10-4 | 2.9x10-2 |
| 4 | 3.7x10-3 | 7.5x10-2 |
|  |  |  |

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 986 samples, 400 samples worked at ≥ 5 loci (41%). There were 303 samples that did not amplify at any loci (31%).

From the 400 samples that worked at ≥ 5 loci, we identified 225 unique deer. Eighty-nine of the 225 unique deer were recaptured 1-7X (Deer #68 was sampled 8X). The remaining 136 of the 225 unique deer were captured once (60%)

Of the 225 unique deer, 159 individuals were female and 66 individuals were male (2.40F:1M).

**Locus Information**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |  |
| C273 | 4 | 142-170 | 0.474 | 0.528 |  |  |  |
| C89 | 8 | 155-183 | 0.722 | 0.790 |  |  |  |
| OdhE | 6 | 137-163 | 0.499 | 0.515 |  |  |  |
| SBTD05 | 6 | 113-141 | 0.491 | 0.657 |  | |  |
| SBTD06 | 4 | 183-209 | 0.516 | 0.606 |  |  |  |
| T159s | 10 | 183-227 | 0.532 | 0.812 |  | |  |
| T7 | 7 | 219-243 | 0.668 | 0.778 |  | |  |

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.