**2023 ODFW Blacktailed Deer Analysis Summary-Dixon**

We analyzed 1,011 dog-collected samples from the Dixon 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 Dixon WMU using seven microsatellite markers.

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| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 7.7x10-7 | 3.3x10-3 |
| 6 | 1.1x10-5 | 8.6x10-3 |
| 5 | 1.3x10-4 | 2.2x10-2 |
| 4 | 1.6x10-3 | 5.8x10-2 |

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

Of the 1,011 samples, 675 samples worked at ≥ 5 loci (67%). There were 118 samples that did not amplify at any loci (12%).

From the 675 samples that worked at ≥ 5 loci, we identified 375 unique deer. One hundred and fifty-three were recaptured 1-12X (Deer #193 was sampled 13X). The remaining 222 of the 675 unique deer were captured once (33%)

Of the 222 unique deer, 116 individuals were female, 105 individuals were male (1.91F:1M) and one individual did not amplify with the sexing markers (Deer #338) so we could not determine a sex. There were 3 additional deer that did not amplify with the sexing markers (Deer #33, Deer #78, and Deer #111) and so we could not determine the sex for these individuals either.

**Locus Information**

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| --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 4 | 142-170 | 0.581 | 0.613 |
| C89 | 9 | 159-191 | 0.758 | 0.775 |
| OdhE | 6 | 125-153 | 0.513 | 0.487 |
| SBTD05 | 8 | 113-145 | 0.563 | 0.786 |
| SBTD06 | 7 | 183-199 | 0.626 | 0.635 |
| T159s | 12 | 183-223 | 0.487 | 0.769 |
| T7 | 7 | 219-243 | 0.547 | 0.734 |

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.