**2024 ODFW Black-tailed Deer Analysis Summary-Dixon**

We analyzed 1,082 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 | 4.2x10-6 | 4.8x10-3 |
| 6 | 6.1x10-5 | 1.3x10-2 |
| 5 | 5.4x10-4 | 3.2x10-2 |
| 4 | 3.5x10-3 | 7.0x10-2 |

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 1,082 samples, 830 samples worked at ≥ 5 loci (77%). There were 153 samples that did not amplify at any loci (14%).

From the 830 samples that worked at ≥ 5 loci, we identified 349 unique deer. One hundred and sixty-six deer were recaptured 24X (Deer #47 was sampled 25X). The remaining 183 of the 349 unique deer were captured once (53%)

Of the 349 unique deer, 191 individuals were female, and 151 individuals were male. There were 7 deer that did not amplify with the sexing markers and so we could not determine the sex for these individuals.

**Locus Information**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Locus** |  | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 |  | 4 | 142-170 | 0.587 | 0.624 |
| C89 |  | 9 | 159-191 | 0.804 | 0.774 |
| OdhE |  | 4 | 133-153 | 0.479 | 0.489 |
| SBTD05 |  | 9 | 113-145 | 0.482 | 0.743 |
| SBTD06 |  | 4 | 183-199 | 0.597 | 0.633 |
| T159s |  | 10 | 183-223 | 0.524 | 0.780 |
| T7 |  | 9 | 219-247 | 0.631 | 0.711 |

SBTD05, SBTD06, and T159s were significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population sub-structuring.