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

We analyzed 755 dog-collected samples from the Rogue 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 Rogue WMU using seven microsatellite markers.

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| **# of loci** | **PID** | **PIDsibs** |
| 7 | 2.2x10-7 | 2.3x10-3 |
| 6 | 5.6x10-6 | 7.1x10-3 |
| 5 | 8.2x10-5 | 1.9x10-2 |
| 4 | 3.1x10-3 | 5.1x10-2 |

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

Of the 755 samples, 602 samples worked at ≥ 5 loci (80%). There were 94 samples that did not amplify at any loci (12%).

From the 755 samples that worked at ≥ 5 loci, we identified 324 unique deer. One hundred and thirty-nine deer were recaptured 1-10X (Deer #98 was sampled 11X). The remaining 185 of the 324 unique deer were captured once (57%)

Of the 185 unique deer, 120 individuals were female, and 64 individuals were male (1.87F:1M). There were 5 deer that did not amplify with the sexing markers (Deer #7, Deer #10, Deer #34, Deer #113 and Deer #79) and so we could not determine the sex for these individuals.

**Locus Information**

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| --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 6 | 142-170 | 0.545 | 0.586 |
| C89 | 7 | 159-183 | 0.769 | 0.778 |
| OdhE | 4 | 137-153 | 0.557 | 0.523 |
| SBTD05 | 9 | 113-145 | 0.594 | 0.800 |
| SBTD06 | 5 | 183-199 | 0.695 | 0.728 |
| T159s | 10 | 183-223 | 0.624 | 0.849 |
| T7 | 8 | 219-243 | 0.613 | 0.730 |

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.