**2022 ODFW Blacktailed Deer Analysis Summary-Saddle Mountain**

We analyzed 2,347 dog-collected samples from the Saddle Mountain 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 Saddle Mountain 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 Saddle Mountain WMU. Samples that worked at fewer than five loci were excluded from recapture analyses.

Of the 2,347 samples, 902 samples worked at ≥ 5 loci (38%). There were 764 samples that did not amplify at any loci (32%).

From the 902 samples that worked at ≥ 5 loci, we identified 386 unique deer. Two hundred and five deer were recaptured 1-9X (Deer #193 was sampled 10X). The remaining 181 of the 386 unique deer were captured once (47%)

Of the 386 unique deer, 268 individuals were female, and 115 individuals were male (2.33F:1M). There were 3 deer that did not amplify with the sexing markers (Deer #12, Deer #29, 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 | 5 | 142-170 | 0.613 | 0.586 |
| C89 | 9 | 155-191 | 0.768 | 0.793 |
| OdhE | 5 | 137-161 | 0.492 | 0.477 |
| SBTD05 | 6 | 113-149 | 0.409 | 0.618 |
| SBTD06 | 5 | 183-203 | 0.664 | 0.743 |
| T159s | 8 | 183-223 | 0.522 | 0.683 |
| T7 | 8 | 219-247 | 0.628 | 0.673 |

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