**2021 ODFW Blacktailed Deer Analysis Summary-Saddle Mountain**

We analyzed 4,079 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 | 6.3x10-6 | 5.3x10-3 |
| 6 | 7.9x10-5 | 1.4x10-2 |
| 5 | 7.1x10-4 | 3.5x10-2 |
| 4 | 4.2x10-3 | 7.6x10-2 |

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 4,079 samples, 2,016 samples worked at ≥ 5 loci (49%). There were 986 samples that did not amplify at any loci (24%).

From the 2,016 samples that worked at ≥ 5 loci, we identified 749 unique deer. Three hundred eighty-two deer were recaptured 1-21X (Deer #16 was sampled 22X). The remaining 367 of the 749 unique deer were captured once (49%)

Of the 749 unique deer, 522 individuals were female and 223 individuals were male (2.34F:1M). There were 4 deer that did not amplify with the sexing markers (Deer #484, Deer #625, Deer #663 and Deer #728) 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 | 4 | 142-170 | 0.583 | 0.582 |
| C89 | 10 | 159-195 | 0.797 | 0.778 |
| OdhE | 5 | 137-163 | 0.443 | 0.478 |
| SBTD05 | 7 | 113-141 | 0.456 | 0.611 |
| SBTD06 | 5 | 183-209 | 0.694 | 0.748 |
| T159s | 9 | 183-227 | 0.512 | 0.659 |
| T7 | 9 | 203-247 | 0.596 | 0.632 |

SBTD05, SBTD06, T159s and T7 were significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population substructuring.