**2020 ODFW Blacktailed Deer Analysis Summary-Saddle Mountain**

We analyzed 3,491 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 | 5.4x10-6 | 5.2x10-3 |
| 6 | 6.8x10-5 | 1.3x10-2 |
| 5 | 6.1x10-4 | 3.4x10-2 |
| 4 | 3.9x10-3 | 7.4x10-2 |

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 3,491 samples, 1,872 samples worked at ≥ 5 loci (54%). There were 735 samples that did not amplify at any loci (21%).

From the 1,872 samples that worked at ≥ 5 loci, we identified 706 unique deer. Four hundred and five of the 706 unique deer were recaptured 1-13X (Deer #67 was sampled 14X). The remaining 301 of the 706 unique deer were captured once (43%)

Of the 706 unique deer, 463 individuals were female and 231 individuals were male (2.02F:1M). There were 11 deer that did not amplify with the sexing markers (Deer# 286, Deer# 322, Deer# 404, Deer# 436, Deer# 443, Deer# 476, Deer# 528, Deer# 602, Deer# 639, Deer# 640 and Deer# 660) and so we could not determine the sex for these individuals. Deer# 179 has multiple individuals that matched at least 5 or more loci, but we were unable to determine a sex for these samples. Because they matched at the required number of 5 or more loci to be considered a match, they were grouped together and considered a recapture event.

**Locus Information**

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| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 5 | 142-170 | 0.571 | 0.577 |
| C89 | 10 | 159-191 | 0.773 | 0.780 |
| OdhE | 3 | 141-161 | 0.451 | 0.473 |
| SBTD05 | 6 | 113-141 | 0.468 | 0.624 |
| SBTD06 | 5 | 183-209 | 0.692 | 0.746 |
| T159s | 9 | 183-223 | 0.541 | 0.671 |
| T7 | 8 | 219-247 | 0.618 | 0.645 |

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.