**2019 ODFW Blacktailed Deer Analysis Summary-Applegate**

We analyzed 3,642 dog-collected samples from the Applegate 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 Applegate WMU using seven microsatellite markers.

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| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 2.7x10-7 | 2.3x10-3 |
| 6 | 4.8x10-6 | 6.6x10-3 |
| 5 | 7.6x10-5 | 1.8x10-2 |
| 4 | 8.4x10-4 | 4.7x10-2 |

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

Of the 3,642 samples, 2,683 samples worked at ≥ 4 loci (74%). There were 493 samples that did not amplify at any loci (13%).

From the 2,683 samples that worked at ≥ 4 loci, we identified 885 unique deer. Five hundred and thirty seven of the 885 unique deer were recaptured 1-16X (Deer #5 was sampled 17X). The remaining 348 of the 885 unique deer were captured once (39%)

Of the 885 unique deer, 555 individuals were female and 328 individuals were male (1.69F:1M). There were two deer where we could not identify sex for these individuals (Deer #564 and Deer #807).

**Applegate human-collected**

There were 22 total human- collected samples analyzed from the Applegate WMU.

Of the 22 samples, 8 samples worked at ≥ 5 loci (36%). There were 10 samples that did not amplify at any loci (45%).

Of the 8 samples that worked at ≥ 5 loci, we identified 7 unique deer. One of the 7 unique deer was recaptured 1X (Deer #1 was sampled 2X). The remaining 6 unique deer were captured once (75%).

Of the 7 unique deer, 3 individuals were female and 4 individuals were male.

No samples matched between the two collection types, suggesting 2019 Applegate human-collected and dog-collected feces sampled different deer.

**Locus Information**

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| --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 6 | 142-170 | 0.648 | 0.654 |
| C89 | 8 | 159-191 | 0.760 | 0.764 |
| OdhE | 4 | 131-161 | 0.506 | 0.524 |
| SBTD05 | 9 | 113-145 | 0.507 | 0.804 |
| SBTD06 | 6 | 183-207 | 0.674 | 0.721 |
| T159s | 11 | 183-231 | 0.587 | 0.820 |
| T7 | 9 | 183-243 | 0.616 | 0.729 |

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.