**2017 ODFW Blacktailed Deer Analysis Summary-Applegate**

There were 2,157 total dog-collected samples analyzed from the Applegate WMU.

The probability of identity is the probability that two unrelated individuals will have matching genotypes (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 the original seven microsatellite markers.

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| **# of loci** | **PID** | **PIDsibs** |
| 7 | 2.5x10-7 | 2.3x10-3 |
| 6 | 4.2x10-6 | 6.5x10-3 |
| 5 | 6.8x10-5 | 1.8x10-2 |
| 4 | 8.6x10-4 | 4.7x10-2 |
| 3 | 7.8x10-3 | 1.1x10-1 |

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 those 2,157 samples, 1,444 samples worked at ≥4 loci (67%). There were 391 samples that did not amplify at any loci (18%).

We classified 76 samples as "diarrhea" when processing (4%).

Of the 76 samples classified as "diarrhea": 33 generated genotypes at ≥ 4 loci 43%

Of the 2,081 samples not classified as "diarrhea": 1,411 generated genotypes at ≥ 4 loci 68%

From the 1,444 samples that worked at ≥ 4 loci, we identified 573 unique deer. Three hundred and thirty-three of the 573 unique deer were recaptured 1-10X (Deer #163 was sampled 11X). The remaining 240 of the 573 unique deer were captured once (42%).

Of the 573 unique deer, 366 individuals were female and 207 individuals were male (1.77F:1M).

**Applegate human-collected**

There were 68 total human-collected samples analyzed from the Applegate WMU.

Of those 68 samples, 37 samples worked at ≥ 4 loci (54%). There were 18 samples that did not amplify at any loci (26%).

We classified 12 samples as "diarrhea" when processing (18%).

Of the 12 samples classified as "diarrhea": 5 generated genotypes at ≥ 4 loci 42%

Of the 56 samples not classified as "diarrhea": 32 generated genotypes at ≥ 4 loci 57%

From the 37 samples that worked at ≥ 4 loci, we identified 32 unique deer. Five of the 32 unique deer were recaptured 1X (Deer #1-5 were sampled 2X). The remaining 27 of the 32 unique deer were captured once (84%).

Of the 32 unique deer, 19 individuals were female and 13 individuals were male (1.46F:1M).

No samples matched between the two collection types, suggesting 2017 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 | 5 | 142-170 | | 0.622 | | 0.646 | |  | |  | |  | |
| C89 | 8 | 159-187 | | 0.724 | | 0.779 | |  | |  | |  | |
| OdhE | 4 | 131-153 | | 0.511 | | 0.513 | |  | |  | |  | |
| SBTD05 | 9 | 113-145 | | 0.502 | | 0.811 | |  | | | | | |
| SBTD06 | 5 | 183-199 | | 0.692 | | 0.729 | |  | |  | |  | |
| T159s | 10 | 183-223 | | 0.581 | | 0.809 | |  | | | | | |
| T7 | 8 | 219-243 | | 0.589 | | 0.732 | |  | | | | | |
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SBTD05, T159s, and T7 are significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population substructuring.