**2018 ODFW Blacktailed Deer Analysis Summary-Applegate**

There were 2,244 total dog-collected samples analyzed from the Applegate WMU.

Of the original 2,311 samples given to us, there were 67 samples (2%) that were considered to be contaminated due to the presence of three or more alleles. To determine whether the contamination was present in the sample itself or due to an error during the PCR amplification, these samples were rerun. All 67 samples still showed signs of contamination and were removed from additional analyses.

*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 dog-collected samples from the Applegate WMU using the original seven microsatellite markers.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 3.8x10-7 | 2.6x10-3 |
| 6 | 7.1x10-6 | 7.4x10-3 |
| 5 | 9.5x10-5 | 2.0x10-2 |
| 4 | 1.0x10-3 | 5.0x10-2 |
| 3 | 1.0x10-2 | 1.2x10-1 |

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

1,528 samples worked at ≥5 loci (68%). There were 383 samples that did not amplify at any loci (17%).

From the 1,528 samples that worked at ≥ 5 loci, we identified 506 unique deer. Of the 506 unique deer, 218 were recaptured 1-14X (Deer #139, 147 and 174 were sampled 14X). The remaining 288 unique deer were captured once (57%).

Of the 506 unique deer, 321 individuals were female and 185 individuals were male (1.74F:1M).

**Applegate human-collected**

There were 12 total human-collected samples analyzed from the Applegate WMU.

All 12 of these samples worked at ≥ 5 loci (100%).

Since all 12 samples worked at ≥ 5 loci, all were included in the identification analysis. Each of the 12 deer were found to be unique deer and were captured once.

Of the 12 unique deer, 10 individuals were female and 2 individuals were male.

No samples matched between the two collection types (dog versus human), suggesting 2018 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 | 4 | 142-170 | | 0.575 | | 0.607 | |  | |  | |  | |
| C89 | 8 | 159-187 | | 0.737 | | 0.759 | |  | |  | |  | |
| OdhE | 3 | 141-157 | | 0.476 | | 0.515 | |  | |  | |  | |
| SBTD05 | 9 | 113-145 | | 0.529 | | 0.787 | |  | | | | | |
| SBTD06 | 5 | 183-203 | | 0.703 | | 0.716 | |  | |  | |  | |
| T159s | 9 | 183-219 | | 0.606 | | 0.823 | |  | | | | | |
| T7 | 8 | 219-243 | | 0.641 | | 0.748 | |  | | | | | |
|  |  |  |  | |  | |  | |  | |  | |
|  |  |  |  | |  | |  | |  | |  | |

C89, 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.