**2016 ODFW Blacktailed Deer Analysis Summary-Tioga**

There were 2,129 total dog collected samples analyzed from the Tioga WMU.

Fifteen samples (24.G5.C1.01 - 24.G5.C1.15) appeared to have the Easting and Northing coordinates swapped.

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 Tioga WMU using the original seven microsatellite markers.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 1.4x10-6 | 3.8x10-3 |
| 6 | 1.8x10-5 | 1.0x10-2 |
| 5 | 2.2x10-4 | 2.6x10-2 |
| 4 | 2.1x10-3 | 6.4x10-2 |
|  |  |  |

Based on the PID and PIDsibs values, a minimum of five loci per individual sample were needed for the Tioga WMU. Samples that worked at fewer than five loci were not included in recapture analyses.

Of the 2,129 samples, 936 samples worked at >/= 5 loci (44%). There were 707 samples that did not amplify at any loci (33%).

Of the 936 samples that worked at >/= 5 loci, we found 309 unique deer. 174 of the 309 unique deer were recaptured 1-15X (Deer #18 was sampled 16X). 135 of the 309 unique deer were captured once.

Of the 309 unique deer, 187 individuals were female and 122 individuals were male (1.53F:1M). All samples that worked at >/= 5 loci produced a sex.

Based on the processing notes, there were 500 samples that we classified as "diarrhea" when processing.

Of the 500 samples classified as "diarrhea": 160 generated genotypes at >/= 5 loci 32%

Of the 1629 samples not classified as "diarrhea": 776 generated genotypes at >/= 5 loci 48%

**Locus Information**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |
| C273 | 4 | 142-174 | 0.602 | 0.578 |  |  |
| C89 | 7 | 159-191 | 0.758 | 0.785 |  |  |
| OdhE | 3 | 131-163 | 0.506 | 0.497 |  |  |
| SBTD05 | 8 | 113-145 | 0.57 | 0.742 |  | |
| SBTD06 | 5 | 183-209 | 0.655 | 0.672 |  |  |
| T159s | 9 | 183-223 | 0.404 | 0.668 |  | |
| T7 | 9 | 215-243 | 0.667 | 0.771 |  | |

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.

**Tioga Human Collected Samples**

There were 10 total human collected samples analyzed from the WMU Tioga. Additional analysis was run to identify potential recaptures between dog collected and human collected samples from the WMU Tioga.

No samples matched between the two collection types, suggesting all human collected Tioga deer fecal samples are unique deer and only captured once.

Out of the 10 samples analyzed, 3 failed and the remaining 7 worked at >/= 5 loci. Of those 7 unique deer, 5 were males and 2 were females.