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

We analyzed 2,571 dog-collected samples from the Tioga 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 Tioga WMU using the original seven microsatellite markers.

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| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 1.1x10-6 | 3.4x10-3 |
| 6 | 1.4x10-5 | 9.1x10-3 |
| 5 | 1.5x10-4 | 2.3x10-2 |
| 4 | 1.5x10-3 | 5.7x10-2 |
|  |  |  |

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 excluded from recapture analyses.

Of the 2,571 samples, 701 samples worked at ≥ 5 loci (27%). There were 1,179 samples that did not amplify at any loci (46%).

From the 701 samples that worked at ≥ 5 loci, we identified 286 unique deer. One hundred and fifty-nine of the 286 unique deer were recaptured 1-12X (Deer #155 was sampled 13X). The remaining 127 of the 286 unique deer were captured once (43%)

Of the 286 unique deer, 186 individuals were female and 97 individuals were male (1.92F:1M). There were three deer that did not amplify with the sexing markers (Deer# 26 and Deer# 229) and so we could not determine the sex for these individuals. Deer #26 has two individuals that matched at all seven loci but we were unable to determine sex for either sample. Because they matched at all seven loci, they were grouped together and considered a recapture event.

**Tioga human-collected**

There were 5 human-collected samples analyzed from the Tioga WMU. Only one sample amplified at five of the seven loci. No further analysis was completed.

**Locus Information**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |  |
| C273 | 4 | 142-170 | 0.616 | 0.625 |  |  |  |
| C89 | 8 | 159-191 | 0.767 | 0.783 |  |  |  |
| OdhE | 2 | 141-161 | 0.496 | 0.493 |  |  |  |
| SBTD05 | 8 | 113-145 | 0.623 | 0.746 |  | |  |
| SBTD06 | 5 | 183-209 | 0.597 | 0.624 |  |  |  |
| T159s | 9 | 183-223 | 0.516 | 0.747 |  | |  |
| T7 | 9 | 219-247 | 0.678 | 0.759 |  | |  |

SBTD05, and T159s were significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population substructuring.