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

We analyzed 2,220 dog-collected samples from the Tioga WMU.

We received ODFW original database with no ‘grid 38’ information. However, we received 374 samples (24.G38.C1.08 - 24.G38.C8.79, 24.G38.C9.01-24.G38.C9.43) that have printed labels saying ‘grid 38’ and never received 374 out of 381 samples from ‘grid 32’ according to ODFW original database. Samples we received from ‘grid 38’ have same number of samples per cell as well as same quality scores as those missing samples from ‘grid 32’. We are unsure if the database or the sample labels are where the mistake is, but we kept the original sample names that were printed on the tube and added them to the database. These samples are highlighted in light orange.

*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.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 1.3x10-6 | 3.6x10-3 |
| 6 | 1.5x10-5 | 9.4x10-3 |
| 5 | 1.7x10-4 | 2.4x10-2 |
| 4 | 1.6x10-3 | 5.9x10-2 |
|  |  |  |

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 2,220 samples, 885 samples worked at ≥ 5 loci (40%). There were 779 samples that did not amplify at any loci (35%).

We classified 259 samples as "diarrhea" when processing (12%).

Of the 259 samples classified as "diarrhea": 63 generated genotypes at ≥ 5 loci 24%

Of the 1961 samples not classified as "diarrhea": 822 generated genotypes at ≥ 5 loci 42%

From the 885 samples that worked at ≥ 5 loci, we identified 324 unique deer. One hundred and seventy-six of the 324 unique deer were recaptured 1-14X (Deer #4 was sampled 14X). The remaining 148 of the 324 unique deer were captured once (46%)

Of the 324 unique deer, 186 individuals were female and 138 individuals were male (1.35F:1M).

**Tioga human-collected**

There were 2 human-collected samples analyzed from the Tioga WMU. Only 1 of the 2 samples had any amplification and only amplified at 3 of the 7 neutral markers. No further analysis was completed.

**Locus Information**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |
| C273 | 4 | 142-170 | 0.537 | 0.572 |  |  |
| C89 | 8 | 159-191 | 0.706 | 0.768 |  |  |
| OdhE | 3 | 141-163 | 0.497 | 0.497 |  |  |
| SBTD05 | 9 | 113-145 | 0.540 | 0.738 |  | |
| SBTD06 | 5 | 183-209 | 0.597 | 0.659 |  |  |
| T159s | 9 | 183-223 | 0.469 | 0.735 |  | |
| T7 | 9 | 215-247 | 0.732 | 0.777 |  | |

C89, SBTD05, and T159s were significantly out of HWE due to heterozygote deficiency, which could be due to allelic dropout, null alleles, or population substructuring.