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

There were 2,265 total dog-collected samples analyzed from the Tioga WMU.

One hundred and six samples (24.G15.C2.01 - 24.G15.C2.34, 24.G39.C1.01 - 24.G39.C1.60, and 24.G39.C1.62 - 24.G39.C1.73) appeared to have the Easting and Northing coordinates swapped on the ODFW spreadsheet.

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 | 1.8x10-6 | 4.0x10-3 |
| 6 | 2.0x10-5 | 1.0x10-2 |
| 5 | 1.9x10-4 | 2.5x10-2 |
| 4 | 1.7x10-3 | 6.1x10-2 |
|  |  |  |

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 2,265 samples, 834 samples worked at ≥ 5 loci (37%). There were 932 samples that did not amplify at any loci (41%).

We classified 304 samples as "diarrhea" when processing (13%).

Of the 304 samples classified as "diarrhea": 99 generated genotypes at ≥ 5 loci 33%

Of the 1961 samples not classified as "diarrhea": 735 generated genotypes at ≥ 5 loci 37%

In addition, this year we seemed to have a large number of samples that were classified as “pellets crumbled, inner material”. This means the pellets broke apart while scraping, exposing the inner fibrous material of the pellet instead of keeping intact in pellet form, which allows us to scrape the outer portion of the pellet where the epithelial cells are found. There were 87 samples classified as this type (4%).

Of the 87 samples classified as "pellets broke, inner material": 8 generated genotypes at ≥ 5 loci 9%

From the 834 samples that worked at ≥ 5 loci, we identified 312 unique deer. One hundred and ninety of the 312 unique deer were recaptured 1-10X (Deer #62 was sampled 11X). The remaining 122 of the 312 unique deer were captured once (39%)

Of the 312 unique deer, 207 individuals were female and 105 individuals were male (1.97F:1M).

**Tioga human-collected**

There were 36 total human- collected samples analyzed from the Tioga WMU.

All 36 samples arrived with no original ODFW database and therefore Northing and Easting coordinates are not available.

Of the 36 samples, 11 samples worked at ≥ 5 loci (31%). There were 16 samples that did not amplify at any loci (44%).

We classified 29 samples as "diarrhea" when processing (81%).

Of the 29 samples classified as "diarrhea": 8 generated genotypes at ≥ 5 loci 28%

Of the 7 samples not classified as "diarrhea": 3 generated genotypes at ≥ 5 loci 43%

Of the 11 samples that worked at ≥ 5 loci, we identified 8 unique deer. Two of the 8 unique deer were recaptured 1-2X (Deer #2 was sampled 3X). The remaining 6 of the 8 unique deer were captured once (75%).

Of the 8 unique deer, 4 individuals were female and 4 individuals were male.

No samples matched between the two collection types, suggesting 2017 Tioga human-collected and dog-collected feces sampled different deer.

**Locus Information**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |
| C273 | 4 | 142-170 | 0.546 | 0.590 |  |  |
| C89 | 8 | 159-191 | 0.737 | 0.731 |  |  |
| OdhE | 2 | 141-149 | 0.438 | 0.484 |  |  |
| SBTD05 | 8 | 113-145 | 0.624 | 0.763 |  | |
| SBTD06 | 5 | 183-207 | 0.632 | 0.654 |  |  |
| T159s | 9 | 183-223 | 0.636 | 0.739 |  | |
| T7 | 9 | 219-247 | 0.511 | 0.703 |  | |

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.