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

There were 2,660 total dog-collected samples analyzed from the Applegate WMU.

Twelve samples (28.G32.C8.68 - 28.G32.C8.79) appeared to have the Easting and Northing coordinates swapped in the ODFW database.

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 Applegate WMU using the original seven microsatellite markers.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 4.3x10-7 | 2.6x10-3 |
| 6 | 7.5x10-6 | 7.4x10-3 |
| 5 | 9.2x10-4 | 1.9x10-2 |
| 4 | 1.0x10-4 | 4.9x10-2 |
| 3 | 9.3x10-3 | 1.2x10-1 |

Based on the PID and PIDsibs values, a minimum number of 4 loci needed for the Applegate WMU. Samples that worked at fewer than four loci were not included in recapture analyses.

Of those 2,660 samples, 2,057 samples worked at >/= 4 loci (77%). There were 315 samples that did not amplify at any loci (12%).

Of the 2,057 samples that worked at >/= 4 loci, we found 638 unique deer. 399 of the 638 unique deer were recaptured 1-18X (Deer #78 was sampled 19X). 239 of the 638 unique deer were captured once.

Of the 638 unique deer, 395 individuals were female and 243 individuals were male (1.63F:1M). All samples that worked at >/= 4 loci produced a sex.

**Locus Information**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | | **Hobs** | | **Hexp** | |  | |  | |  | |
| C273 | 6 | 142-174 | | 0.613 | | 0.625 | |  | |  | |  | |
| C89 | 9 | 159-191 | | 0.752 | | 0.77 | |  | |  | |  | |
| OdhE | 4 | 131-163 | | 0.537 | | 0.516 | |  | |  | |  | |
| SBTD05 | 9 | 113-145 | | 0.584 | | 0.776 | |  | | | | | |
| SBTD06 | 6 | 183-209 | | 0.667 | | 0.719 | |  | |  | |  | |
| T159s | 10 | 183-223 | | 0.645 | | 0.822 | |  | | | | | |
| T7 | 9 | 215-243 | | 0.595 | | 0.738 | |  | | | | | |
|  |  |  |  | |  | |  | |  | |  | |
|  |  |  |  | |  | |  | |  | |  | |

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.