**2022 ODFW Blacktailed Deer Analysis Summary-Wilson**

We analyzed 1,309 dog-collected samples from the Wilson 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 Wilson WMU using the original seven microsatellite markers.

|  |  |  |
| --- | --- | --- |
| **# of loci** | **PID** | **PIDsibs** |
| 7 | 2.6x10-6 | 4.1x10-3 |
| 6 | 3.1x10-5 | 1.1x10-2 |
| 5 | 2.7x10-4 | 2.6x10-2 |
| 4 | 2.3x10-3 | 6.2x10-2 |
|  |  |  |

Based on the PID and PIDsibs values, a minimum of five loci per individual sample were needed for the Wilson WMU. Samples that worked at fewer than five loci were excluded from recapture analyses.

Of the 1,309 samples, 590 samples worked at ≥ 5 loci (45%). There were 406 samples that did not amplify at any loci (31%).

From the 590 samples that worked at ≥ 5 loci, we identified 252 unique deer. One hundred thirty-one of the 252 unique deer were recaptured 1-15X (Deer #103 was sampled 16X). The remaining 121 of the 252 unique deer were captured once (48%)

Of the 252 unique deer, 187 individuals were female, and 64 individuals were male (2.92F:1M), one individual did not amplify at any sexing markers (Deer #118).

**Locus Information**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |  |  |  |
| C273 | 3 | 142-170 | 0.602 | 0.601 |  |  |  |
| C89 | 9 | 159-183 | 0.767 | 0.773 |  |  |  |
| OdhE | 3 | 141-153 | 0.528 | 0.501 |  |  |  |
| SBTD05 | 9 | 113-141 | 0.496 | 0.651 |  | |  |
| SBTD06 | 4 | 183-209 | 0.679 | 0.742 |  |  |  |
| T159s | 9 | 183-235 | 0.505 | 0.700 |  | |  |
| T7 | 9 | 219-247 | 0.653 | 0.719 |  | |  |

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