**2023 and 2024 ODFW Black-tailed Deer Analysis Summary-North Bank Wildlife Area within Melrose WMU**

***2023 Black-tailed deer***

We analyzed 144 dog-collected samples from the North Bank Wildlife Area in the Melrose 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 North Bank Wildlife area in the Melrose WMU using seven microsatellite markers.

Based on the PID and PIDsibs values, a minimum of five loci per individual sample of the black-tailed deer were needed for the North Bank Wildlife area in the Melrose WMU in 2023. Samples that worked at fewer than five loci were excluded from recapture analyses.

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| **# of loci** | **PID** | **PIDsibs** |
| 7 | 4.8x10-6 | 5.7x10-3 |
| 6 | 3.4x10-5 | 1.3x10-2 |
| 5 | 1.1x10-4 | 2.2x10-2 |
| 4 | 8.2x10-4 | 5.2x10-2 |

Of the 144 samples, we were able to identify 33 Columbian white-tailed deer via sequencing and depending on the alleles seen for locus T159S, the remaining 111 were black-tailed deer.

Out of the 111 black-tailed deer, 67 samples worked at ≥ 5 loci (60%). There were 12 samples that did not amplify at any loci (9%). From the 67 black-tailed deer samples that worked at ≥ 5 loci, we identified 48 unique deer. Thirteen deer were recaptured 1-4X (Deer #5 was sampled 5X). The remaining 35 of the 48 unique deer were captured once (73%).

Of the 48 unique deer, 33 individuals were female, and 13 individuals were male. There were 2 deer that did not amplify with the sexing markers (Deer #19, and Deer #45) and so we could not determine the sex for these individuals.

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| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 4 | 142-170 | 0.596 | 0.577 |
| C89 | 6 | 159-179 | 0.804 | 0.763 |
| OdhE | 2 | 141,149 | 0.383 | 0.503 |
| SBTD05 | 7 | 113-141 | 0.553 | 0.786 |
| SBTD06 | 4 | 183-199 | 0.682 | 0.702 |
| T159s | 5 | 191-219 | 0.410 | 0.507 |
| T7 | 7 | 219-243 | 0.594 | 0.748 |

The loci SBTD05, T159s and T7 showed to be out of Hardy-Weinberg which could be due to null alleles, allelic dropout, or population substructure.

***2024 Black-tailed deer***

We analyzed 187 dog-collected samples from the North Bank Wildlife Area in the Melrose 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 North Bank Wildlife area in the Melrose WMU using seven microsatellite markers.

Based on the PID and PIDsibs values, a minimum of five loci per individual sample of the black-tailed deer were needed for the North Bank Wildlife area in the Melrose WMU in 2024. Samples that worked at fewer than five loci were excluded from recapture analyses

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| **# of loci** | **PID** | **PIDsibs** |
| 7 | 2.4x10-6 | 4.3x10-3 |
| 6 | 2.9x10-5 | 1.1x10-2 |
| 5 | 3.2x10-4 | 2.9x10-2 |
| 4 | 3.4x10-3 | 7.3x10-2 |

Of the 187 samples, we were able to identify 6 Columbian white-tailed deer via sequencing and depending on the alleles seen for locus T159s. The remaining 181 samples were black-tailed deer.

Out of the 181 black-tailed deer, 151 samples worked at ≥ 5 loci (83%). There were 4 samples that did not amplify at any loci (2%). From the 151 black-tailed deer samples that worked at ≥ 5 loci, we identified 93 unique deer. Twenty-nine deer were recaptured 1-6X (Deer #8 was sampled 7X). The remaining 64 of the 93 unique deer were captured once (69%).

Of the 93 unique deer, 60 individuals were female, and 32 individuals were male. There was 1 deer that did not amplify with the sexing markers (Deer #10 ) and so we could not determine the sex for this individual.

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| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 4 | 142-170 | 0.585 | 0.572 |
| C89 | 8 | 159-191 | 0.714 | 0.745 |
| OdhE | 2 | 141,149 | 0.478 | 0.502 |
| SBTD05 | 7 | 113-141 | 0.565 | 0.767 |
| SBTD06 | 4 | 183-199 | 0.703 | 0.699 |
| T159s | 6 | 183-207 | 0.328 | 0.570 |
| T7 | 8 | 219-243 | 0.704 | 0.776 |

The loci SBTD05 and T159s showed to be out of Hardy-Weinberg which could be due to null alleles, allelic dropout or population substructure.