Blacktailed Deer Report for South Slough-Wasson Creek and Control sites

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**2024 Blacktailed Deer Analysis Summary-South Slough**

This is a brief summary of results from the fecal samples collected at two South Slough research sites: Wasson Creek and a control site in January and February of 2024. DNA was extracted from each sample and then analyzed using 7 microsatellite markers and one sexing marker to determine individual ID. Each sample was amplified three times, and a final consensus genotype was made using the information from the three amplicons and collapsing the three genotypes into one final call. Alleles at each locus had to match at least 2 out 3 times if they were heterozygous in order to be considered real and any homozygous call that was only seen 2 out of 3 times was highlighted in yellow to indicate a potential case of allelic dropout.

We analyzed 61 dog-collected samples from two research sites within the South Slough (control site and Wasson site).

To be able to tell the samples collected from the different research sites apart from one another, we relabeled the samples either with the suffix “SoS” for Wasson site collected samples and “SoS-ref” for control site collected samples.

*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 two research sites within the South Slough using seven microsatellite markers.

Based on the PID and PIDsibs values, a minimum of six loci per individual sample were needed for the samples collected at both research sites. Samples that worked at fewer than six loci were excluded from recapture analyses.

Of the 61 samples, 35 samples worked at ≥ 6 loci (57%). There were 9 samples that did not amplify at any loci (15%).

From the 35 samples that worked at ≥ 6 loci, we identified 14 unique deer. Nine deer were recaptured 1-5X (Deer #6 was sampled 6X). The remaining 5 of the 35 unique deer were captured once (14%)

Of the 35 unique deer, 8 individuals were female, and 6 individuals were male.