Evaluating non-traditional approaches to monitor a small and remote Rocky Mountain bighorn sheep *(Ovis canadensis canadensis)* population

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ABSTRACT: Monitoring demographics of small wildlife populations is often challenging but is especially important given that relatively small declines in abundance can greatly increase small populations' risk of extirpation. Advances in statistics and molecular tools have expanded the suite of techniques that wildlife managers can use to monitor populations. Teton Range bighorn sheep are low in abundance and challenging to monitor using traditional approaches, in large part due to their diffuse, year-round occupation of the range's higher elevations. We are evaluating the utility of using a non-invasive genetics approach to monitoring by systematically collecting fecal samples at mineral licks and high-use areas during the summer, identifying individuals from DNA on samples, and fitting the resulting data into a capture-recapture framework to estimate abundance, survival, and recruitment. We used GPS-collar data from 28 adult female bighorn sheep monitored 2008-2010 to select a set of previously identified mineral licks that all 28 animals visited at least once during summer months (June-September). We collected fecal samples from these sites at approximately two-week intervals or opportunistically each summer 2019-2022, with five site visits 2019-2021 and six site visits in 2022. We measured pellet length and width and subjectively assessed pellet condition. We dried samples after collection and stored them in breathable envelopes before extracting and genotyping DNA at the Epps Population and Conservation Genetics Laboratory at Oregon State University. We did not attempt to genotype samples judged to be from young of the year. We used a nine loci microsatellite panel, plus a sex marking loci, to initially identify unique individuals from the DNA extracted from samples and extended the microsatellite panel to 16 loci (excluding sex) for one sample from each uniquely identified animal. We collected a total of 2166 fecal samples across the four seasons (527 in 2019, 517 in 2020, 579 in 2021, 531 in 2022) and attempted to genotype 1558 samples (316 in 2019, 393 in 2020, 403 in 2021, 467 in 2022). Genotyping success declined over time (88% in 2019, 78% in 2020, 62% in 2021, 62% in 2022). Using the 9-loci microsatellite panel, we identified 97 individuals (58 females, 33 males, 6 unsexed) in 2019, 127 (67 females, 51 males, 9 unsexed) in 2020, 104 (55 females, 44 males, 5 unsexed) in 2021, and 123 (53 females, 43 males, 18 unsexed) in 2022. Extension of genotypes to 16 loci for 139 samples collected 2019-2021 elucidated that genotyping errors related to sample quality (allelic dropout) created Type I errors in animal identification, where multiple samples from one animal were incorrectly determined to be from different animals. After we corrected for known instances of this error, the number of individuals identified was reduced to 89 in 2019, 107 in 2020 and 98 in 2021. These counts were similar to winter helicopter total counts corresponding to the same years, which were 81, 100, and 90. To ensure that individuals are accurately identified, we are extending genotypes of all individuals identified with the nine loci panel to 16 loci. We will subsequently fit the resulting dataset into a capture-

recapture framework to estimate abundance, survival, and reproduction. Although preliminary findings have revealed challenges of using fecal genetics to monitor bighorn sheep in the Teton Range, we anticipate this non-invasive approach to monitoring will yield demographic estimates of comparable accuracy and precision to approaches that require capturing and tagging individuals.

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