THE USE OF FECAL DNA TO DESCRIBE THE GENETIC POPULATION STRUCTURE OF THE GREATER YELLOWSTONE AREA BISON WITH MTDNA

Florence M. Gardipee, Fish and Wildlife Biology, The University of Montana, 32 Campus Drive, Missoula, MT 59812

Michael P. O'Brien, Wildlife Biology, The University of Montana, 32 Campus Drive, Missoula, MT 59812

Gordon Luikart and Fred Allendorf, Division of Biological Sciences, The University of Montana, 32 Campus Drive, Missoula, MT 59812

Bison (*Bison bison*) populations of Yellowstone National Park (YNP) and Grand Teton National Park (GTNP) are the last remaining representatives of their wild, free ranging ancestors. Knowledge regarding population structure is crucial to their conservation, and may have important implications for understanding their ecology and evolution. Prior microsatellite studies of YNP bison captured outside of the park suggested the possibility of three subpopulations. An expanded assessment of population structure and gene flow between GYA bison populations through non-invasive fecal sampling, and the addition of mtDNA sequencing could provide further insight. Non-invasive fecal sampling has been used, with a high degree of success, in genetic studies of other ungulates. However, DNA amplification from fecal samples can be challenging and result in high genotyping error rates. Variation in fecal DNA quality and quantity, PCR amplification rates, and genotyping error rates from fecal samples has not been assessed in bison. We evaluated the feasibility of fecal DNA sampling for genetic analysis of wild bison populations. Variation in fecal mtDNA quality and quantity, PCR amplification rates, and sequencing error for bison fecal samples was evaluated. Sequencing of the bison mtDNA control region was used to evaluate haplotype diversity, population structure between breeding groups among YNP, and between GTNP and YNP bison populations. We found differentiation among breeding groups and a unique haplotype. Female philopatry may play a significant role in population structure and gene flow in naturally regulated, free ranging wild bison populations. Future studies using microsatellites could provide further insight.