

STRONG SUBSTRUCTURE OF GREATER YELLOWSTONE AREA BISON REVEALED BY MITOCHONDRIAL DNA FROM AMPLIFIED FECAL SAMPLES

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Bison (*Bison bison*) in the Greater Yellowstone Area (GYA) congregate in distinct geographic areas during the rut. We hypothesized that fidelity to breeding areas would result in genetic differences among GYA breeding groups. We analyzed fecal samples from 120 bison in five breeding groups during the ruts of 2005 and 2006. Sequencing and restriction fragment length polymorphism analysis of a 470 bp segment of the mtDNA control region revealed significant differentiation between bison in Yellowstone National Park (YNP) and Grand Teton National Park ($F_{ST} = 0.236$, $P < 0.001$). We found even greater differentiation within YNP between the Lamar Valley and Hayden Valley breeding groups ($F_{ST} = 0.505$, $P < 0.001$), which are <50 km apart. This fine-scale genetic differentiation among breeding groups within YNP suggested strong female philopatry to natal ranges. These findings also suggested that these breeding groups should be considered separate management units with respect to conservation of current levels of genetic diversity. However, examination of nuclear loci is necessary to assess male mediated gene flow and better understand population structure of GYA bison. Decision-makers should consider genetic monitoring in the future to determine which breeding group winter migrants have emigrated from when taking actions to resolve brucellosis risk management priorities at park boundaries. The probability of conserving current levels of genetic diversity under various management scenarios should be evaluated as well.