Genetic management of a small and recently salvaged herd of wood bison

Greg Wilson[1], John S. Nishi[2] and Keri Zittlau[3]

[1]Department of Integrative Biology, University of California, Berkeley, Berkeley, CA. 94720-3140, < gregwils@uclink.berkeley.edu >, Ph: 510-643 - 6299; Fax: 510-643-6264. [2]Resources, Wildlife and Economic Development, Government of the Northwest Territories, Fort Smith, NT. X0E 0P0. [3]Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9.

Genetic salvage of healthy wood bison *(Bison bison athabascae)* from the Wood Buffalo National Park population, where bovine tuberculosis *(Mycobacterium bovis)* and brucellosis *(Brucella abortus)* are prevalent, has been important for the conservation of this threatened subspecies in Canada. To date, three such attempts have been made. The first occurred in 1963, when 16 animals were taken from northwestern Wood Buffalo National Park and successfully introduced to the Mackenzie Bison Sanctuary. Another followed shortly thereafter, when 21 animals were successfully shipped from northern Wood Buffalo National Park to Elk Island National Park. While both of these populations are now considered free of bovine tuberculosis and brucellosis, they contain significantly less genetic variation than that found in Wood Buffalo National Park. The most recent salvage attempt is the Hook Lake Wood Bison Recovery Project (HLWBRP), which has seen 62 calves captured from the Hook Lake area, located west of WBNP, from 1996 to 1998. From the original calf captures, 57 founders remain in the population along with 75 captive-born progeny. The HLWBRP population is the most variable of all the founded wood bison populations. However as this bison herd is now at the upper capacity of the captive breeding facility, it is critically important to implement management strategies to ensure that the genetic diversity present in this population is not reduced to unacceptable levels through the process of genetic drift and differential reproductive success. In this paper we outline a management strategy for the HLWBRP that includes monitoring reproductive success of individuals within this population to make certain that the greatest possible number of founders are able to contribute their genes to subsequent generations. We compare levels of genetic diversity between the founder and offspring generations to monitor the loss of diversity through time. The genetic importance of all animals can be determined using such measures as mean kinship, and the most genetically redundant animals can subsequently be selected if culling is required. Long-term genetic management strategies for the HLWBRP will reflect how this project may contribute to wood bison conservation through the establishment of additional recovery herds and through genetic augmentation of existing populations.