IDENTIFYING LINKAGE ZONES FOR GRIZZLY BEARS ACROSS A SECTION OF HIGHWAY 3 IN SOUTHEAST BRITISH COLUMBIA

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As part of recovery efforts for a small, fragmented, and threatened brown bear (*Ursus arctos*) population in North America shared by Canada and the USA, we used DNA and radio telemetry based methods to identify linkage zones in a fragmented habitat. A human settlement and transportation corridor fragments the international south Purcell-Yaak population (population ~ 50 animals) and consequently threatens its long-term persistence. Because bears are relatively sparse in this population, and sample sizes consequently low, we used two complementary methods -- ecological modeling from hair-snag DNA surveys and Geographic Positioning System (GPS) radio telemetry—to identify "linkage zones" to facilitate improving natural inter-population exchange of animals with adjacent populations, a requirement for recovery. We genetically sampled wild brown bears at 170 hair-snag sites on both sides of the human corridor in 2004 and 2005. Hair follicles were used as a source of DNA to develop microsatellite genotypes that identified 65 different bears at 54 sites totaling 124 capture events. We then characterized the landscape for 24 ecological and human variables (terrain ruggedness, riparian, forest cover, roads, settlement, etc). We correlated these variables to bear presence and absence in a multiple logistic regression and used Geographic Information Systems (GIS) to develop a spatially-explicit "resource selection function" model to predict bear occurrence across our 9500-km^2 study area. We used the model to predict areas of high use (core habitat) and linkage habitat that connects core areas. We also put GPS radio collars on eight brown bears that were captured adjacent to the human corridor. The radio collars acquired hourly locations throughout the non-denning seasons. These data revealed the presence of areas where bears crossed the human corridor and corroborated our predictive model. It is challenging to obtain reliable and objective results in a system with few bears, but we reached our goal of identifying linkage and core habitat

because we used both DNA-based ecological modeling and GPS radio telemetry method. Neither method on its own was sufficient, but each contributed significant information to the ecological solution and provided independent validation of our conclusions. These methods may be of use for other sparse bear populations around the world where conservation solutions are required but low bear numbers make research challenging.