EVALUATING REPRODUCTIVE SUCCESS AND CHANGES IN GENETIC DIVERSITY OF GRIZZLY BEARS IN NORTHWESTERN MONTANA

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Current range expansions of large terrestrial carnivores are occurring following anthropogenically-induced range contraction. Contractions are often incomplete, leaving small remnant groups in refugia throughout the former range. We know little about underlying eco-evolutionary processes that influence how remnant groups are affected during range expansion. We used data from a spatially-explicit, long-term genetic sampling effort of grizzly bears (*Ursus arctos*) in the Northern Continental Divide Ecosystem (NCDE) to identify the processes underlying spatial patterns of genetic diversity. We conducted parentage analysis to evaluate how reproductive success and migration contribute to spatio-temporal patterns of genetic diversity in remnant groups of grizzly bears existing in the southwestern (SW), southeastern (SE), and east-central (EC) regions of the NCDE. Highly skewed reproductive success and local inbreeding caused distinct signatures in remnants that eroded rapidly (~1 generation) during population expansion and migration into the regions. Our results highlight that individual-level genetic and reproductive dynamics play critical roles during genetic assimilation, and show that patterns of genetic distinctiveness on the leading edge of an expansion may result from historical demographic patterns that are highly ephemeral.