WEST SIDE STORY: GENETIC POPULATION STRUCTURE OF ELK GANGS IN THE NORTHERN ROCKY MOUNTAINS^TWS

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Managing and conserving wildlife populations over large spatial areas challenge wildlife and conservation biologists to take new approaches. Large mammals, such as Rocky Mountain elk (*Cervus elaphus nelsoni*), exemplify this challenge because they have seasonal and annual ranges that cover areas the size of watersheds or sub-basins, respectively. To meet

this challenge of managing elk, we performed spatial analysis of populations at the landscape level using the metapopulation concept and a genetic analysis approach. We collected tissue samples of individual elk from across the northern Rocky Mountains and genotyped each individual using microsatellites at multiple loci. We examined genetic population structure with 5 approaches. Individuals were assigned to local populations based on their relative similarity or dissimilarity to each local population using genotypes and geographical location. Our results indicated little genetic differentiation between specific regions. Understanding the genetic population structure of elk from a metapopulation perspective provides both theoretical and practical benefits for managing and sustaining this species.