

**(22) POPULATION BOUNDARIES AND THE SUBSPECIFIC DIVIDE IN SOUTHEASTERN ALASKAN MOOSE**KEVIN COLSON<sup>1\*</sup>, KEVIN S. WHITE<sup>2</sup>, AND KRIS HUNDERTMARK<sup>1</sup><sup>1</sup> *University of Alaska, Institute of Arctic Biology, PO Box 757000, Fairbanks, AK 99775-7000, USA*<sup>2</sup> *Alaska Department of Fish and Game, Division of Wildlife Conservation, PO Box 110024, Juneau, AK 99811-0024, USA*

*Abstract:* Moose (*Alces alces*) are a recent arrival to southeastern Alaska, having only colonized this topographically complex region in the last 100 years. While previous studies in Alaska have found little to no population genetic structure across the northern regions of the state, the southeastern region of Alaska has not previously been examined using intensive sampling and nuclear DNA markers. Here, we sample moose from Alaska and British Columbia to examine regionwide population structure, examine what factors may lead to its formation, and attempt to identify any subspecific divides in the area. We find that the area has extensive genetic structuring, with all of our sampled locations being differentiated from each other. Analyses reveal few effective migrants between population pairs, and an assignment test only found 2 potential migrants among the identified populations. We also find large or serial founder effects may account for creating initial genetic differentiation between populations, where after very low levels of dispersal prevent homogenization. Finally, we identify moose in the northernmost part of southeastern Alaska as belonging to *A. a. andersoni*, and not *A. a. gigas* as previously indicated, suggesting the subspecific boundary is further north than previously thought.





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