

Colonization of North America by Moose: A Phylogeographic Perspective

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We assessed nucleotide variation within the mitochondrial control region of North American moose (*Alces alces*) to test predictions concerning the mode of colonization of the continent, and to determine if phylogeographic patterns are consistent with the recognition of 4 subspecies. Haplotypes formed a star phylogeny indicative of a recent population expansion. Nucleotide and haplotype diversity were low continent-wide, but were greatest in the central part of the continent and least among peripheral populations. Despite low mitochondrial diversity, moose exhibited a high degree of differentiation regionally, which was not explained by isolation by distance. Our data indicate a pattern of colonization consistent with a large central population that supplied founders to peripheral populations other than Alaska, perhaps through rare, long-distance dispersal events (leptokurtic dispersal) rather than mass dispersal via a stepping-stone model. Our colonization scenario does not account for the low haplotype diversity we observed in Alaskan moose, which may derive from a post-colonization bottleneck associated with a climatic reversal. Establishment of peripheral populations through leptokurtic dispersal, combined with selection, may have been sufficient for development of morphological differentiation among extant subspecies.



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