

Red Deer versus Elk Genetics

Mitochondrial DNA testing has supported that red deer and elk are in fact two distinct species for almost 20 years.

Elk and red deer can have fertile offspring, often a strong indicator that two animals belong to the same species. There are also many differences between the two. Pregnant elk cows carry their calves for 20 days longer than red deer hinds, while bull elk carry their antlers for 35 days longer than red deer stags. An average bull elk weighs 720 pounds, while a red deer stag averages just 400. And of course, the bugle of an elk is a very different experience from the roar of a red deer.

The ability of the two species to produce fertile offspring has helped spawn controversy about red deer game farms. Along with the ethical issues involving the commercialization of wildlife, and concerns over disease, game farms can also compromise the genetic integrity of wild elk herds. If animals egress or ingress into a captive facility, as is sometimes the case, they can mate with wild elk creating a hybrid offspring that can threaten the purity of wild elk herds.

There are two types of DNA testing; mitochondrial speciation and Single Tandem repeat or Single Nucleotide Polymorphisms (STR/SNP).

Mitochondrial DNA speciation would need to have a 96% or higher similarity or sequence homology to Rocky Mtn. Elk (*Cervus Canadensis*) to be considered pure.

STR/SNP speciation would have to have defined alleles that we only see with that species. You would need to have no presence of the Red Deer specific alleles present to call an animal pure or not a hybrid red deer/elk.

Both tests need to be designed based on standard "pure" individuals. The STR/SNP analyses need to encompass a large enough populations to ensure that the loci or alleles being assessed are truly species specific.

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A phylogenetic comparison of red deer and wapiti using mitochondrial DNA

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Abstract

A phylogeny was constructed for red deer/wapiti (*Cervus elaphus*) subspecies using sequence data from the control region of mitochondrial DNA (mtDNA). The tree was rooted using *Cervus nippon* (sika deer), *Cervus albirostris* (Thorold's white-lipped deer), and several *Odocoileinae* species. A division between the mtDNA haplotypes of red deer (European) and wapiti (Asian/North American) corresponds to subspecies found on opposite sides of the Himalayan Mountains and Gobi, which suggests wapiti should be reconsidered for the status of *C. canadensis*. Using parsimony and distance analysis, red deer and wapiti are derived from a single recent common ancestor, which is consistent with current taxonomy that recognizes the subspecies of *Cervus elaphus* as monophyletic group. However, maximum-likelihood analysis using weighted transitional substitutions caused red deer to form a sister group to sika deer (*Cervus nippon*) and wapiti. A phenetic comparison revealed wapiti also share more nucleotide similarities with sika deer, although approximately 5% sequence divergence separates wapiti, sika, and red deer. Phylogenetic evidence from the cytochrome b sequences corroborated observations from the control region. Observations from this study suggest that the species status of wapiti should be reinstated.

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