DNA Microsatellite variation in Captured Elk (Cervus elaphus) in Manitoba

D. P. Rasali[1], G.H. Crow[1] and E. Trout[2]
[1]Department of Animal Science, University of Manitoba, Winnipeg, R3T 2N2
[2]Manitoba Agriculture and Food, 545 University Crescent, Winnipeg, R3T 5S6.

Abstract

Elk are captured from the wild for ranching to produce valuable antler products and meat. About 95 licenced elk farms are currently active in Manitoba. Duck Mountain (DM) and Riding Mountain (RM) are the two main origins of wild elk captured to supply the ranches with breeding stock. To assess the genetic variability in Manitoban elk (Cervus elaphus manitobensis) populations by way of determining the differences in microsatellite allele frequencies in the two elk populations, 532 elk captured from these two origins were investigated. Using the Manitoba Agriculture and Food database of 11 microsatellite markers in 379 elk from DM and 153 from RM, allele frequencies and frequency of heterozygotes were studied.

The numbers of alleles detected in all microsatellites, BL42, BM203, BM4107, BM4208, BM5004, BM888, BMC1009, CAL124, CAL2, ETH152 and VH110 were 11, 11, 13, 8, 6, 7, 13, 13, 9, 8 and 12 respectively, and their allele sizes were in the ranges of 246-260, 225-236, 160-175, 135-157, 133-139, 179-190, 275-293, 88-111, 230-242, 160-198 and 124-142 bp respectively. At most microsatellite loci, the range of allele frequencies was generally larger, and the size of DNA fragment (measured in number of bp) higher in both the populations compared to the corresponding loci reported for cattle and sheep. Chi-square statistics showed that the frequencies of alleles were significantly different ($P<0.05$) between DM and RM elk for all loci. The actual proportion of the elk at DM that were heterozygous at the 11 microsatellite loci ranged from 0.44 at the BM5004 and BM888 loci to 0.66 at the BM203 locus. At RM this proportion ranged from 0.42 at the BM5004 locus to 0.76 at the CAL 124 locus. At most of these loci, therefore, over half of the animals were heterozygous. The expected proportion of heterozygosity was generally higher than the actual level of heterozygosity, possibly due to non-random mating such as inbreeding. The two origins differed significantly ($P<0.05$) for the actual proportion of heterozygotes only for two markers (CAL124 and ETH152). High genetic variability was evident from the high level of polymorphism and heterozygosity of alleles at all 11 loci and this is useful when these marker loci are used for identification and parentage validation.

Key words: *elk, elk ranching, microsatellites, polymorphism, allele frequency, heterozygosity.*

Background

Elk Population Studies

North American elk (*Cervus elaphus)*, also known as wapiti, are recovering from a massive population decline that occurred with European settlement of North America (Bryant and Maser, 1982; Witmer, 1990). Elk are now being captured for ranching to produce valuable velvet antler and meat. The farming of elk has lead the quest for greater knowledge of genetic variation in ranched populations for breeding

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and improvement from their genetic base. Kucera (1991) studied genetic variability in Tule elk (*Cervus elaphus nannodes*) using allozymes, most of which showed no variability. A few studies reported the use of DNA microsatellites to determine parentage (Talbot et. al., 1996; Eggleton, 1991) and phylogenetic status (Polzeihn et. al., 1998) in elk.

Purpose of this study

The purpose of this study is to assess the genetic variability in populations of Manitoba elk (*Cervus elaphus manitobensis)* using DNA microsatellites and to determine if there are differences in gene frequencies in populations of elk from two locations, Duck Mountain and Riding Mountain.

Methodology

About 95 licensed elk farms were active at the time of study in Manitoba, where elk were captured from the wild to supply these ranches with breeding stock. The two main origins of Manitoba elk that were captured from 1996 to 1999 were Duck Mountain (DM), and Riding Mountain (RM). As part of animal identification and parentage testing, elk were genotyped for a number of microsatellite loci by the Saskatchewan Research Council using methods described by Talbot et. al. (1996). The loci chosen by the researchers were meant to be polymorphic because of the use of these loci in parentage verification. At each locus there were a variety of alleles, each differing in the molecular size—as measured by the number of base-pairs (bp). These data were collected and maintained by Manitoba Agriculture and Food Department. There were 379 elk from DM origin and 153 from RM origin.

Polymorphisms of 11 microsatellite loci in a total of 532 animals from the two origins (Table 1) were investigated, with analyses of allele frequency, expected proportion of the population that was heterozygous, (Buchanan and Thue, 1998), and the actual proportion of the population that was heterozygous. In a population size of N animals, with 2N alleles, allele frequencies at each locus represent the proportion of the total alleles of a given kind. The expected proportion of the population that were heterozygous was calculated from allele frequencies on the assumption of random mating in a large population. The actual proportion heterozygous was measured by categorizing each animal as homozygous or heterozygous at each locus and then calculating the proportion that were heterozygous. Differences in expected and actual heterozygosity indicate non-random mating.

Results

The Eleven Microsatellite loci.

Table 1 shows the number of alleles at each microsatellite locus, the most predominant alleles, and the range of allele frequencies detected in the two elk populations. The range of allele frequencies was generally larger, and the number of bp higher for most loci compared to the corresponding loci reported

in the cattle and sheep genome database (http://sol.marc.usda.gov; http://www.ncbi.nlm.nih.gov.80/entrez/...=GenBank).

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Table 1. General summary of the 11 microsatellite loci and their alleles for the 532 animals from the two locations.

Locus	Number of alleles detected	Allele size range (bp)	Two most predominant alleles (bp)	Frequency range
BL42	11	246-260	256, 246	~ 0 – 0.21
BM203	11	225-236	231, 229	~ 0 – 0.31
BM4107	13	160-175	173, 172	~ 0 – 0.31
BM4208	8	135-157	153, 157	~ 0 – 0.51
BM5004	6	133-139	139, 138	0.02 - 0.36
BM888	7	179-190	188, 180	~ 0 – 0.31
BMC1009	13	275-293	289, 288	~ 0 – 0.32
CAL124	13	88-111	103, 101	0.03 – 0.53
CAL2	9	230-242	237, 141	~ 0 – 0.35
ETH152	8	160-198	197, 195	~ 0 – 0.52
VH110	12	124-142	125, 140	~ 0 – 0.40

Comparison of Allele Frequencies for the Duck Mountain and Riding Mountain Populations.

Chi-Square statistics showed that the frequencies of alleles were significantly different ($P<0.01$) between DM and RM elk for all loci. The frequency distribution of alleles for one of the loci, BL42, for the two elk origins are shown in Figure1as an example of how the allele frequencies differ.

Comparison of the two populations for heterozygosity.

The actual proportion of the elk at the DM location that were heterozygotes at the 11 microsatellite loci ranged from 0.44 at the BM4208 and BM5004 loci to 0.66 at the BM203 locus (Table 2). At the RM location, this proportion ranted from 0.42 at the BM5004 locus to 0.76 at the CAL124 locus. At most loci, therefore, over half of the animals were heterozygous. The two locations differed significantly ($P<0.05$) for the actual proportion of heterozygotes only for two markers (CAL124 and ETH152).

The proportion of elk that were expected to be heterozygous (Table 2) was calculated on the assumption of random mating in a large population with no selection or other forces to change gene frequencies. This expected proportion was generally higher than the actual level of heterozygosity. Non-random mating such as inbreeding may be one explanation for this.

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Figure 1. Frequency of alleles at the BL42 locus in two elk populations.

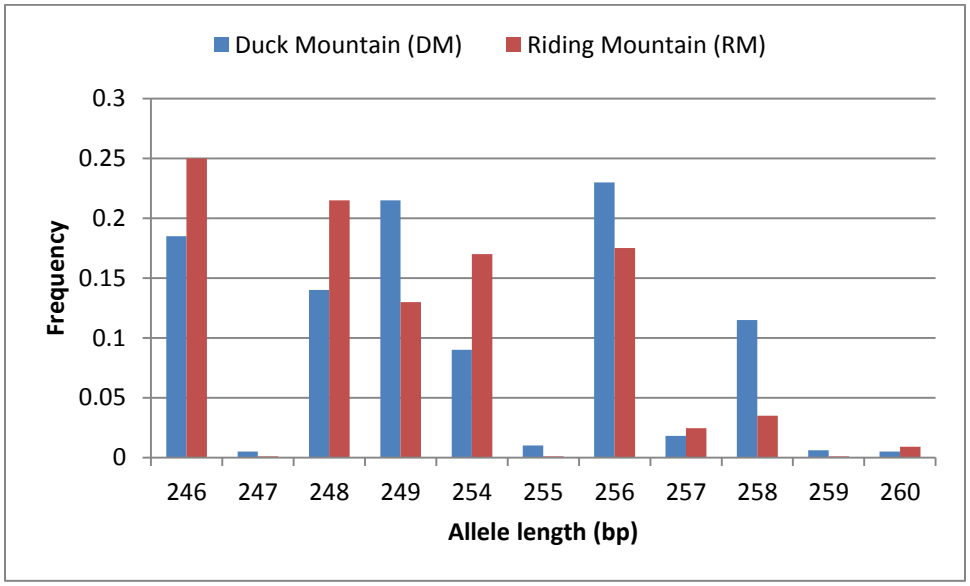

Table 2. Expected and actual heterozygosity for microsatellite loci in elk from Duck Mountain (DM) and Riding Mountain (RM).

Locus	Expected Heterozygosity *		Actual Heterozygosity *	
	DM	RM	DM	RM
BL42	0.83	0.82	0.58	0.51
BM203	0.75	0.75	0.66	0.69
BM4107	0.79	0.85	0.60	0.65
BM4208	0.67	0.53	0.44	0.50
BM5004	0.72	0.73	0.44	0.42
BM888	0.73	0.75	0.50	0.45
BMC1009	0.75	0.80	0.50	0.58
CAL124	0.64	0.80	0.50[a]	0.76[b]
CAL2	0.82	0.68	0.64	0.64
ETH152	0.67	0.59	0.50[a]	0.65[b]
VH110	0.69	0.71	0.52	0.55

* Proportion of the population

[a, b] Actual heterozygosity in the two elk populations was compared using Chi-square. Frequencies in the same row with different letter superscripts differ (P<0.05).

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Conclusions

The microsatellites used in this study had a high level of polymorphism—many alleles with a high degree of heterozygosity—this is useful when these microsatellites are used for identification and parentage validation. The significant differences ($p<0.05$) in allele frequencies for elk captured from the two locations suggest that there is some genetic differentiation between the two populations.

Acknowledgements

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