Transferrin variation and evolution of Canadian barren-ground caribou

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Abstract: Blood samples were obtained from 95 barren-ground caribou (Rangifer tarandus groenlandicus) of the Beverly herd in Northwest Territories, Canada. Polyacrylamid gel electrophoresis was used to score for genetic variation in the locus coding for transferrin. The pattern of allele frequency distribution are compared with previously reported values of Eurasian tundra reindeer (R.t. tarandus), Alaska caribou (R.t. granti), Peary caribou (R.t. pearyi), and Svalbard reindeer (R.t. platyrhynchus). In the Beverly herd a total of 21 different transferrin alleles were detected. The amount of genetic variation was higher in the Canadian barren-ground caribou than what has been detected in other subspecies of reindeer/caribou. Highly genetical differences in the allele frequencies were detected between the Canadian barren-ground caribou and the other subspecies. The genetic identity analyses indicates approximately the same amount of genetic differentiation when the Canadian barren-ground caribou are compared with Alaska caribou as with the Peary caribou. The allele frequency pattern could be explained by a possible origin of the Canadian barren-ground caribou from an ancestral population which was genetical influenced by animals surviving the Weichselian glaciation in refugia both in high Arctic, in Beringia, and south of the ice sheet.

Keywords: Rangifer, reindeer, polymorphism

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Introduction

According to the basic taxonomic study by Banfield (1961), the reindeer/caribou should be divided into two groups: the tundra reindeer (Cyclicornis) and the forest reindeer (Compressicornis). The main distribution of the different subspecies within the tundra reindeer group is given in Fig. 1. Within this group of reindeer it has been reported a major dichotony in the transferrin allele distribution between Alaska caribou (R.t. granti) and Eurasian reindeer (R.t.

tarandus) on the one hand and Peary caribou (R.t pearyi) and Svalbard reindeer (R.t platyrhynchus) on the other (Røed and Whitten, 1986; Røed et al., 1986). The Canadian barrenground caribou (R.t groenlandicus) also belongs to the tundra reindeer group and has its main distribution in the mainland of northern Canada (Fig. 1) We report here the result of an electrophoretic examination of the transferrin locus in Canadian barren-ground caribou sampled from the Beverly herd. The allele fre-

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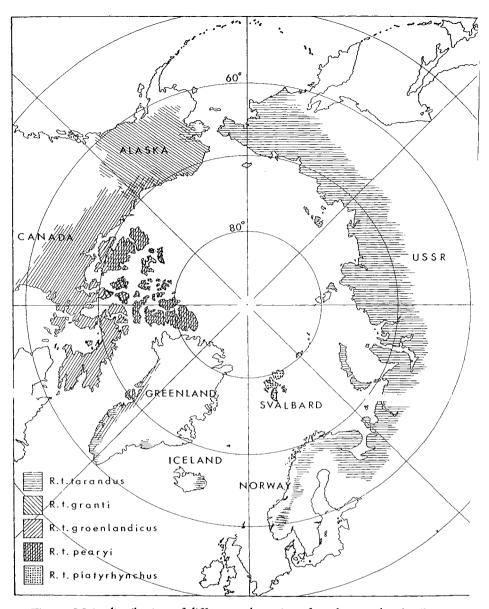


Fig. 1. Main distribution of different subspecies of tundra reindeer/caribou.

quency distribution is compared with those in other subspecies of the tundra reindeer and the results are discussed in relation to the origin of different subspecies of the genus.

Material and methods

Blood samples were obtained from 95 barrenground caribou of the Beverly herd in Northwest Territories, Canada. The blood samples were taken into heparinized test tubes and centrifuged, after which the plasma fraction was removed and stored at -20°C until the electrophoretic analysis was performed. Plasma samples were subjected to vertical slab polyacrylamide gel electrophoresis as previously described by Røed (1985a). The transferrins were made visible by overnight staining with Coomassie Brilliant Blue R250 (Diezel et al., 1972). Relative mobilities of transferrin bands were confirmed by re-running samples of approximately the same mobility side by side on

the same gel. Reference plasma was from continental Norwegian wild and domestic reindeer, R.t. tarandus, (Røed, 1985a), from Svalbard reindeer, R.t. platyrhynchus, (Røed, 1985b), from Peary caribou, R.t pearyi (Røed et al., 1986) and from Alaska caribou, R.t. granti (Røed and Whitten, 1986).

Results

The amount of genetic variation at the transferrin locus was high in the Canadian barrenground caribou. 21 separate alleles could be resolved in the present material. Compared with the reference plasma, three new alleles were detected. These have been designated according to their mobility relative to the reference alleles: two alleles with banding patterns anodal to Tf^a were arbitrarily given the designation Tf^{a-1} and Tf^{a-2} according to their increasing mobility, and one with bands slightly anodal to Tf^{M} (cathodal to Tf^{L}) was labeled Tf^{L2} . Accordingly, Tf^L is here renamed Tf^{L_1} . Table 1 presents the allele frequencies in the sampled R.t. groenlandicus together with previously reported values for R.t. pearyi from the Canadian Arctic islands (Røed et al., 1986), R.t. granti from Alaska (Røed and Whitten, 1986), R.t. tarandus from Norway (Røed, 1985a), and R.t. platyrhynchus from Svalbard (Røed, 1985b). The presence of 21 different alleles in R.t. groenlandicus (95 individuals analysed) compared to 16 alleles in R.t. pearyi (86 individuals analysed), 18 alleles in R.t granti (112 individuals analysed) and 2 alleles in R. t. platyrhynchus (49 individuals analysed) indicated higher amount of genetic variation in the R.t groenlandicus than in the other subspecies of the tundra reindeer tvoe.

The pattern of allele frequency distribution at the transferrin locus indicated considerable genetic heterogeneity among the different subspecies within the tundra reindeer group. The contingency chi-square test for homogeneity among subspecies was highly significant (p < 0.001). Highly significant differences (p < 0.001) in the transferrin locus were also detected when R.t. groenlandicus was compared one by one with the other subspecies. This is illustrated, among others, by the frequence of the $T_f^{E:1}$ allele which was the most common allele both in R.t. granti (p=0.30) and in R.t. tarandus (p=0.31). In R.t. groenlandicus, however, this allele was present with a frequence of only 0.11. Furthermore, $T_f^{G:2}$ was definitely the most common allele both in R.t. pearyi (p=0.30) and in R.t. platyrhynchus (p=0.75), while the frequence of this allele was considerable less in R.t. groenlandicus (p=0.12).

Coefficient of genetic identity, I (Nei, 1972), was calculated from the allele frequencies in Table 1. Table 2 gives the genetic identity between the different subspecies of the tundra reindeer type and illustrates that the genetic identity between subspecies was highly variable, ranging from 0.886 between R.t. tarandus and R.t. granti, to 0.000 between R.t. platyrhynchus and R.t. tarandus. The genetic identity between R.t. groenlandicus and the other subspecies shows that this subspecies is most genetic similar to R.t. pearyi and to R.t. granti, with approximately the same amount of genetic similarity to both subspecies.

Discussion

The results of the present study indicate that *R.t. groenlandicus* contains a high amount of genetic variation, and that considerable genetic divergence has occurred in comparison with other subspecies of the tundra reindeer group. The early evolution of reindeer and caribou is largely unknown. The genus has been traced back to about 440 000 B.C. in central Germany, and its existence in North America may well be equally long (Banfield 1961). The present finding of several more transferrin alleles in subspecies in North America than in the Eurasian reindeer could be of importance in this context. As much as sixteen transferrin alleles

Table 1. Transferrin allele frequencies of different subspecies of tundra reindeer/caribou

Allele	R.t. groen- landicus	R.t. peary ^{a)}	R.t. granti ^{b)}	R.t. tarandus ^{e)}	R.t. platyr- hynchus ^{d)}
A-2	.005				
A-1	.005				
A	.032	.041	.027	.016	
В		.006	.013		
C1	.063	.058	.085	.270	
C2	.068	.099	.036	.038	
C3		.006			
D				-e)	
El	.111	.023	.304	.307	
E2			.036	.006	
G1	.047		.054	.046	
G2	.116	.297	.049		.745
G3					.255
G4			.004		
H1	.011	.023	.013	.036	
Hlb			.009		
H2	.153	.180	.147	.090	
I	.121	.163	.134	.130	
J	.037	.006	.013		
K1	.032		.013	.034	
K2	.016				
L1	.053	.041	.018		
L2	.011				
M	.042	.017	.040	.028	
N	.005	.006			
O1	.026	.023			
O2	.032		.004		
O3	.016				
P		.017			

a) From Røed et al. 1986

Table 2. Paired combinations of genetic identity between subspecies of tundra reindeer/caribou

Subspecies	1	2	3	4	5
1 R.t. groenlandicus	****				
2 R.t. pearyi	.838	****			
3 R.t. granti	.818	.512	****		
4 R.t. tarandus	.671	.360	.886	****	
5 R.t. platyrhynchus	.374	.688	.120	.000	****

d) From Røed 1985b

b) From Røed and Whitten, 1986

e) Frequency < 0.001

c) From Røed 1985a

were detected in subspecies in North America which were not detected in the Eurasian supspecies, while only two alleles present in the Eurasian reindeer were not detected in North American caribou. Such a pattern could indicate a larger evolutionary time of North American caribou and an origin of present Eurasian mainland reindeer from ancestral populations in North America (Røed and Whitten, 1986).

Concerning the origin of the different subspecies of reindeer and caribou, it has been hypothezised that continental tundra forms evolved in the Beringia refugium in Alaska-Yukon during the Wisconsin glaciation, the woodland caribou south of the ice sheet, and the Peary caribou in a refugium in the Canadian Arctic Archipelago or in northern Greenland (Banfield, 1961). A common genetic origin of Svalbard reindeer and Peary caribou has also been suggested from the similarity in the transferrin locus (Røed, 1985b, Røed et al., 1986). As indicated by Roed and Whitten (1986), the genetic similarity between Alaska caribou and the Eurasian reindeer could be explained by a common ancestor of these subspecies in the Beringia refugium during the late Weichselian, and as the ice barriers retreated, this population may thus have colonized the Eurasian tundra region.

The present populations of the Canadian barren-ground caribou could have evolved from the same population in the Beringia area and moved east as the ice retreated. The relatively great genetic difference detected between the Canadian barren-ground caribou and the Alaska caribou, indicate however, either a longer time of isolation between the Canadian barren-ground caribou and the Alaska caribou, or genetic influence form other populations with a different genetic pool. There are indications that an unglaciated corridor form Alberta to the Mackenzie Delta was opened at a late period and possibly was occupied by the woodland caribou before the tundra caribou from the Beringia refuge could reach the eastern tundra (Banfield, 1961). As the ice-barriers retreated, the Alaska caribou in the west, the woodland caribou in the north, could hav re-met in the areas of Mackenzie Delta at an relatively early date. The high amount of gentic variation in the Canadian barren-ground caribou, together with considerable genetic difference with both the Alaska caribou and the Peary caribou, could therefore reflect an origin of the Canadian barren-ground caribou from ancestral population which was genetical influenced by all the three main series of North American subspecies of reindeer and caribou.

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