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Blood protein polymorphism in harp seals off eastern Canada.

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INTRODUCTION

Protein polymorphism in harp seal, Pagophilus groenlandicus (Erxleben), have been described and utilized to identify populations (Nævdal 1966). Samples were collected in the breeding and moulting patches east of northeast Newfoundland and Labrador (the Front), in the Jan Mayen area, in the Barents Sea, and in the White Sea, and hemoglobins and serum proteins were analysed by use of gel electrophoresis.

The serum proteins were found to be polymorphic and controlled by three co-dominant autosomal alleles, named Tf^A, Tf^B, and Tf^C,. Statistically significant differences on the 5 per cent (but not on the 2 per cent) level were observed in freqencies of the genes Tf^A and Tf^B between the sample from Newfoundland and the total samples from the northeast Atlantic. No significant differences were found between samples from the northeast Atlantic.

Material had not been collected for a comparision between harp seals breeding in the Gulf of St.Lawrence and harp seals breeding on the Front. Reasons for regarding the Front and Gulf herds as seperate units were summarized by Sergeant (1967). He also reported recaptures on the Front in 1967 of 14 one year old harp seals tagged as pups in the southern Gulf, and this is an indication that the two herds mingle with each other to a certain extent.

In the present paper comparisions are made of serum proteins in harp seals breeding in the Gulf and samples from harp seals breeding on the Front based partly on analyses of new material and partly on the material used before.

MATERIAL AND METHODS

Samples from the Front were collected during sealing seasons by observers from the Institute of Marine Research, Bergen, onboard commercial sealing vessels in 1964 (Nævdal 1966) and 1967. The sample from the Gulf was collected during a helicopter expedition organized by the Artic Biological Station, Fisheries Research Board of Canada, ^ , prior to the sealing season 1968. Only specimens collected in breeding patches have been used for these comparisions, and consequently they have been taken from adult females or pups. In 1968 the blood was drawn from live seals by puncture of a vein in the hind flippers. Otherwise sampling, storage, and analyses by electrophoresis were made as formerly described (Nævdal 1966). The number of specimens in each sample are shown in Table 1.

RESULTS AND DISCUSSION

All specimens showed the normal hemoglobin patterns described before (Nævdal 1966), i.e. one major component (Hb A) moving towards the anode and one minor component (Hb A_2) moving towards the cathode at pH 9.0. Consequently the hemoglobins are not useful characteristics for comparision of samples from the Front and Gulf herds.

Table 1 shows the observed distribution of transferrin groups together with calculated gene frequencies and expected Hardy-Weinberg distributions.

The Front sample from 1967 show a higher value of q_A and a lower value of q_B than the sample from 1964. This observation implies that the significant differences observed before between samples from eastern and western harp seal populations is accidental, and does not represent real differences between the populations, because this difference was based on low values of q_A and high values of q_B in the 1964 Front sample.

The prime purpose of this study : a comparision between samples from the Gulf and the Front seal herds, is summarized in the lower lines of Table 1 , distributions of transferrin groups in the total Front samples and in the Gulf sample. No marked differences can be discovered in the distributions or in the gene frequencies. The differences are clearly not significant, and no statistical tests are needed. Therefore the present study has not revealed any clear difference between Front and Gulf harp seals, and on this basis it can not be deided whether the two herds are separated or not. However, even if isolation is not effective

enough to produce or maintain differences in gene frequencies it is still possible that the herds are isolated to such a degree that for practical management purposes they may be regarded at seperate and selfsustaining units.

The final conclusion to be drawn from this study is that blood proteins as revealed by present metnods do not offer very promising clues for the identification of harp seal population, and accordingly the studies will not be persued.

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Table 1. Transferrin groups in harp seals. Distributions and frequencies. obs = observed distributions, exp = expected Hardy-Weinberg distributions.

Area and year of sampling		No.	Transferrin groups												Gene frequencies		
			Tf AA		Tf AB		Tf BB		Tf AC		Tf BC		Tf CC				
			No.	%	No.	%	No.	%	No.	%	No.	%	No.	%	q_A	q_B	q_C
Front 1964	obs.	78	3	3.8	31	39.7	29	37.2	6	7.7	9	11.5	-	-	0.28	0.63	0.10
	exp.		5.9		27.0		30.8		4.1		9.4		0.7				
Front 1967	obs.	97	13	13.4	37	38.1	26	26.8	9	9.3	12	12.4	-	-	0.37	0.52	0.11
	exp.		13.4		37.5		26.3		7.8		10.9		1.1				
Total Front	obs.	175	16	9.1	68	38.9	55	31.4	15	8.6	21	12.0	-	-	0.33	0.57	0.10
	exp.		18.9		65.5		56.7		11.9		20.1		1.9				
Gulf 1968	obs.	208	21	10.1	72	34.6	69	33.2	19	9.1	24	11.5	3	1.4	0.33	0.55	0.12
	exp.		22.9		76.0		62.9		16.3		27.0		2.9				