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GENETIC DIFFERENTIATION OF DABBLING DUCKS (Anseriformes: *Anas*) POPULATIONS FROM PALAEARCTIC IN TIME AND SPACE

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The genetic variation among populations of dabbling ducks (563 samples of A. acuta, A. clypeata, A. crecca, A. querquedula, A. falcata, A. penelope, A. platyrhynchos*) in the Palaearctic region (Lithuania, Chukotka, Kamchatka, Lena, Ob and Kara rivers) was investigated between 1980 and 1998. Fifteen loci of blood serum proteins were surveyed for genetic variation using polyacrylamid gel electrophoresis, and eight polymorphic loci were found. The analysis of genetic variation at population and species levels shows that allele frequencies are temporarily variable. The general genetic diversity of dabbling ducks differed among geographically different populations: for Northern Pintail between H_o = 0.264 from Ob river and H_o = 0.331 from Kamchatka; for Eurasian Wigeon between H_o=0.185 from Ob and H_o = 0.263 from Lena river. In Mallard populations mean heterozygosity ranged from H_o = 0.242 (Vente 1998, Lithuania) to H_o = 0.366 (Antanavas 1987, Lithuania). The data obtained from genetic distances revealed that Mallards of Lithuania form no discrete populations and vary temporarily and spatially.*

Key words: *palaearctic, genetic variability,* Anas*, blood plasma proteins.*

INTRODUCTION

In recent years, a diverse array of molecular genetic tools has become available for high-resolution genetic studies of population-level processes in ecosystems. Genetic markers have been employed to characterise patterns of genetic variation within and among populations, and to examine the processes of dispersal and the patterns of mating that influence levels of genetic differentiation in ecosystems (Nevo *et al*., 1984, Parker *et al*., 1998). To achieve these aims in waterfowl species various techniques have been used: protein polymorphism (Kuznetsov *et al.,* 1995, 1998; Rhodes *et al.,* 1996; Sruoga *et al.,* 1998; 2005), microsatellite polymorphism (McCracken *et al.,* 2001; Williams *et al.*, 2002; Slavenaite *et al.*, 2004; Sruoga *et al.,* 2005; Ahmadi *et al.,* 2007), RAPD (Kulikova *et al.,* 2003), mtDNA haplotypes (Scribner *et al.,* 2001; Pearce *et al.,* 2004; Kulikova *et al.,* 2005), genetic maps (Huand *et al.,* 2006), and MHC genes (Xia *et al.,* 2004). These studies have contributed an evolutionary dimension to our understanding of contemporary ecological processes and the role of various organisms in ecosystems. Genetic variability is considered an essential prerequisite for adaptation to changing environmental conditions (Soulé, 1986).

It is important to understand the patterns of migration among wintering and breeding grounds, and survival and reproductively success of dabbling ducks (Doherty *et al.,* 2002; Blums and Clark, 2004; Drever and Clark, 2007). Philopatry is characteristic of several bird species (Evrard 1990; Robertson 1999; Cooke *et al.,* 2000; Iverson *et al.,* 2004). Genetic information helps to understand the extent of philopatry in dabbling ducks and within migratory families and different species. On the basis of ringing recoveries (Scott and Rose 1996), dabbling ducks have been divided into different populations, but no discrete populations are identifiable.

Dabbling ducks are widespread worldwide. Species of the genus *Anas* display long-distance dispersal (Johnson and Sorenson, 1999) and it has been suggested that superior dispersal ability in birds results in different biogeographical patterns compared with those commonly observed for other organisms (Chesser and Zink, 1994). The wide distribution of dabbling ducks shows that dispersal-driven speciation has been common in this group of birds (Chesser and Zink, 1994; Ronquist, 1997). To fully interpret the biogeographical pattern of dabbling ducks, it is important to place species distributions in a phylogenetic context based on genetic research.

New genes appear in populations of dabbling ducks not only by paring between different sub-populations, but also due to hybrids. Williams and colleagues (2004) noted that

Mottled ducks and Mallard populations exhibited hybridisation rates ranging from zero to 24% in different areas of Florida. Compared with other dabbling ducks, Mallards shows the biggest rate of hybridisation with other closely related species (McCracken *et al.,* 2001; Kulikova *et al.,* 2005).

The aim of this study was to examine and evaluate the temporal and spatial genetic variability of different populations of dabbling ducks *Anas* and to determine the level of fragmentation in Lithuanian Mallard species.

MATERIALS AND METHODS

Blood serum of 319 samples of Northern Pintail *Anas acuta,* Northern Shoveler *A. clypeata,* Common Teal *A. crecca,* Garganey *A. querquedula,* Falcated Duck *A. falcata,* Eurasian Wigeon *A. penelope* were collected between 1980 and 1998 in different localities of Siberia (Chukchia, Kamchatka in 1981 (KAM81), 1988 (KAM88), the Lena in 1989 (LENA89), Ob in 1982 (OB82), 1984 (OB84), 1986 (OB86) and Kara in 1985 (KARA85) rivers) and 244 samples of Mallards *A. platyrhynchos* from Lithuania (Antanavas in 1980–1989 (ANT80 to ANT89), Zuvintas in 1984 (ZUV84), Nemunas delta in 1998 (VEN98)) (Table 1). The geographical locations of the studied dabbling ducks are shown in Figure 1.

Blood sampling (about 5 ml of blood) was made by wing vein puncture into test tubes with heparin. After shooting, blood was taken immediately from bird heart. Samples were centrifuged at room temperature for 15 min at 6,000 g. The plasma was separated and stored in a fridge at 20 ^{o}C below zero until use.

In total fifteen loci of enzyme and plasma proteins were separated electrophoretically: lactate dehydrogenase (LDH, 1. 1. 1. 27, *Ldh-1, 2*), malate dehydrogenase (MDH, 1. 1. 1. 37, *Mdh*), alkaline phosphatase (ALP, 3. 1. 3. 1, *Alp*), esterase (EST, 4. 2. 1. 1, *Est-6, 7*), ceruloplasmin (CEP, *Cep-2*), pre-albumin (PRA, *Pra-1, 2*), albumin (ALB, *Alb*), post-albumin (POA, *Poa*), pre-transferrin (PRT, *Prt*), transferrin (TRF, *Trf*), post-transferrin (POT, *Pot*), and macroglobulin (MCG, *Mcg*). Isozymes were detected by non-denaturing vertical gel electrophoresis (PAGE). Samples were loaded into two-layer (2.5/7.5%) polyacrylamide gel blocks. Protein electrophoresis were made in 10% Tris-glycine buffer (0.0495 M Tris, 0.383 M glycine, pH ~ 8.3–8.5). Enzymes and plasma proteins were visualised using the staining system of Show and Prasad (1970) with few modifications as described earlier (Paulauskas and Sruoga, 1993, Sruoga *et al.*, 1999). Allelic variants were resolved by direct side-by-side comparison of migrating allozymes on the same gels. Indistinct polymorphic loci were not included in further analysis.

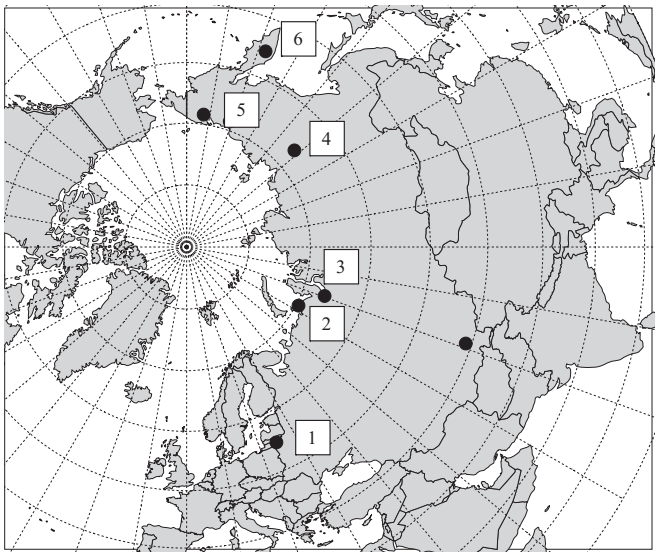

Fig. 1. Geographical location of the studied dabbling ducks: 1, Lithuania; 2, Kara river; 3, Ob delta; 4, Lena and Viluy river confluence; 5, Chukchia; 6, Kamchatka.

Table 1

LOCATION, YEAR OF COLLECTION AND ACRONYM OF 11 GEOGRAPHIC SAMPLES OF 7 DIFFERENT *Anas* SPECIES AND THEIR POPULATIONS

Species	Location		Acronym	The year of sampling	N
A. acuta	Ob River	66^{o}N, 65^{o}E	OB84	1984	41
	Kara River	69^{o}N, 64^{o}E	KAR85	1985	6
	Ob River	66^{o}N, 65^{o}E	OB86	1986	16
	Kamchatka	56^{o}N, 161^{o}E	KAM88	1988	15
A. clypeata	Kamchatka	56^{o}N, 162^{o}E	KAM81	1981	5
	Ob River	66^{o}N, 65^{o}E	OB84	1984	4
	Ob River	66^{o}N, 65^{o}E	OB86	1986	8
A. creca	Ob River	66^{o}N, 65^{o}E	OB86	1986	4
A. falcata	Kamchatka	56^{o}N, 161^{o}E	KAM88	1988	27
A. querqeudula	Ob River	66^{o}N, 65^{o}E	OB84	1984	22
	Ob River	66^{o}N, 65^{o}E	OB86	1986	68
	Kamchatka	56^{o}N, 161^{o}E	KAM88	1988	9
A. penelope	Ob River	67^{o}N, 66^{o}E	OB82	1982	10
	Ob River	66^{o}N, 65^{o}E	OB84	1984	34
	Lena river	64^{o}N, 125^{o}E	LEN89	1989	50
A. plathyrhynchos	Lithuania	55^{o}N, 23^{o}E	ANT80	1980	36
	Lithuania	55^{o}N, 23^{o}E	ANT81	1981	12
	Lithuania	55^{o}N, 23^{o}E	ANT82	1982	11
	Lithuania	55^{o}N, 23^{o}E	ANT83	1983	9
	Lithuania	55^{o}N, 23^{o}E	ANT84	1984	10
	Lithuania	55^{o}N, 23^{o}E	ANT85	1985	18
	Lithuania	55^{o}N, 23^{o}E	ANT86	1986	37
	Lithuania	55^{o}N, 23^{o}E	ANT87	1987	19
	Lithuania	55^{o}N, 23^{o}E	ANT89	1989	8
	Lithuania	54^{o}30'N, 23^{o}40' E	ZUV84	1984	39
	Lithuania	55^{o}20'N, 21^{o}20' E	PAN86	1986	29
	Lithuania	55^{o}40'N, 24^{o}30' E	VEN98	1998	16

N, number of individuals

Temporal and spatial population differences of dabbling ducks have been described in time and space by standard measures using BIOSYS-2 (Swofford *et al.*, 1997). Genetic variability parameters—frequency of allele, of genotype, significance test using exact probabilities for deviation of genotype frequencies from Hardy-Weinberg expectations, the percentage of polymorphic loci (P) (a locus was considered to be polymorphic if the frequency of the most common allele did not exceed 0.95), the mean number of alleles per locus (A) and average heterozygosities (H_o – observed, H_e – expected), were calculated for each geographical sample. Relative genetic distance and similarity between populations and species were quantified according to Roger's modified distance (Wright, 1978).

RESULTS

Of the 15 loci analyzed, seven loci (*Ldh-1, 2, Mdh, Alp, Cep-2, Est-6, 7*) were monomorphic in all species investigated. Eight loci — *Pra-1, 2, Alb, Poa, Prt, Trf, Pot* and *Mcg*, were polymorphic for each dabbling ducks species. The mean value of polymorphic loci in blood plasma proteins for all dabbling ducks examined was similar —53.3%.

Tests of significance using exact probabilities for deviation of genotype frequencies from Hardy-Weinberg expectations showed significant gene frequency differences among populations. Allele Alb^C was found only in one population of Eurasian Wigeon (from Lena, 1989). It must be noted, that the rear Trf^E allele of the polyallelic system of transferrins was detected only in two Siberian populations of dabbling ducks (Garganey from Ob, 1986, and Kamchatka, 1988) and even in six populations of Mallard from Lithuania (from Antanavas 1980, 1983, 1985, 1986, 1987 and from Zuvintas 1984). The alleles Trf^E and Trf^D were not found in all Northern Shoveler and Falcated duck populations (Kama 1981, 1988, and Ob 1984, 1986, Siberia) and one Mallard population (Nemunas delta 1998, Lithuania). The gene frequencies at polymorphic loci in the population of studied dabbling ducks from Siberia and Lithuania are shown in Tables 2 and 3.

The analysis of genetic variation among species showed that genotype frequency was divergent for different population of dabbling ducks in all species examined. The loci *Alb-1, Mcg-1* and *Trf-1* had the highest frequency of heterozygous genotypes. Individual heterozygous in these loci individuals in Mallard population constituted from 61 to 75%. Heterozygous *Alb-1* locus individuals in the Eurasian Wigeon populations constituted 69 %, in Falcated ducks — 81%.

Genetic variability estimated by mean number of alleles per locus, percentage of loci polymorphic, mean observed and expected heterozygosity, in different *Anas* populations was

Table 2

ALLELE FREQUENCIES OF POLYMORPHIC LOCI OF *A. acuta, A. clypeata, A. crecca, A. querquedula, A. falcate, A. penelope* FROM DIFFERENT POPULATIONS

Locus	Allele	*A. acuta*				*A. clypeata*			*A. crecca*	*A. querquedula*			*A. falcata*	*A. penelope*		
		OB84	KAR85	OB86	KAM88	KAM81	OB84	OB86	OB86	OB84	OB86	KAM88	KAM88	OB82	OB84	LEN89
N		41	6	16	15	5	4	8	4	22	68	9	27	10	34	50
Pra-1	A	0.581	0.583	0.438	0.500	0.400	0.625	0.571	0.500	0.452	0.493	0.722	0.519	0.300	0.500	0.550
	B	0.419	0.417	0.563	0.500	0.600	0.375	0.429	0.500	0.548	0.507	0.278	0.481	0.700	0.500	0.450
Pra-2	A	0.671	0.583	0.500	0.567	0.600	0.750	0.688	0.625	0.675	0.731	0.611	0.537	0.700	0.779	0.380
	B	0.171	0.250	0.219	0.267	0.100	0.125	0.250	0.125	0.100	0.097	0.167	0.463	0.100	0.074	0.620
	C	0.159	0.167	0.281	0.167	0.300	0.125	0.063	0.250	0.225	0.172	0.222	0	0.200	0.147	0
Alb-1	A	0.561	0.583	0.625	0.567	0.400	0.375	0.438	0.500	0.455	0.567	0.500	0.519	0.400	0.603	0.610
	B	0.439	0.417	0.375	0.433	0.600	0.625	0.563	0.500	0.545	0.433	0.500	0.481	0.600	0.397	0.340
	C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.050
Poa-1	A	0.585	0.417	0.719	0.625	0.600	0.500	0.500	0.750	0.357	0.614	0.833	0.574	0.900	0.647	0.530
	B	0.415	0.583	0.281	0.375	0.400	0.500	0.500	0.250	0.643	0.386	0.167	0.426	0.100	0.353	0.470
Prt-1	A	0.641	0.333	0.719	0.633	0.200	0.625	0.250	0.375	0.636	0.432	0.944	0.241	0.450	0.603	0.590
	B	0.359	0.667	0.281	0.367	0.800	0.375	0.750	0.625	0.364	0.568	0.056	0.759	0.550	0.397	0.410
Trf-1	A	0.518	0.500	0.344	0.400	0.400	0.500	0.250	0.500	0.375	0.608	0.455	0.444	0.650	0.603	0.435
	B	0.143	0	0.188	0.133	0.500	0.125	0.625	0.125	0.250	0.042	0.045	0.352	0.150	0.207	0.274
	C	0.071	0.333	0.156	0.033	0.100	0.375	0.125	0.125	0.225	0.008	0.045	0.204	0.050	0.103	0.161
	D	0.268	0.167	0.313	0.433	0	0	0	0.250	0.150	0.233	0.136	0	0.150	0.086	0.129
	E	0	0	0	0	0	0	0	0	0	0.108	0.318	0	0	0	0
Pot-1	A	0.488	0.750	0.625	0.633	0.800	0.625	0.563	0.625	0.432	0.415	0.222	0.574	0.350	0.588	0.420
	B	0.512	0.250	0.375	0.367	0.200	0.375	0.438	0.375	0.568	0.585	0.778	0.426	0.650	0.412	0.580
Mcg-1	A	0.313	0.500	0.344	0.400	0.500	0.375	0.375	0.750	0.238	0.469	0.889	0.500	0.450	0.250	0.410
	B	0.688	0.500	0.656	0.600	0.500	0.625	0.625	0.250	0.762	0.531	0.111	0.500	0.550	0.750	0.590

N, number of individuals. For acronyms see Fig.1 and Table 1.

Table 3

ALLELE FREQUENCIES OF POLYMORPHIC LOCI OF *Anas platyrhynchos* FROM DIFFERENT POPULATIONS

Locus	Allele	*A. platyrhynchos*											
		ANT80	ANT81	ANT82	ANT83	ANT84	ANT85	ANT86	ANT87	ANT89	ZUV84	PAN86	VEN98
N		36	12	11	9	10	18	37	19	8	39	29	16
Pra-1	A	0.475	0.792	0.455	0.778	0.600	0.750	0.405	0.553	0.750	0.707	0.621	0.875
	B	0.528	0.208	0.545	0.222	0.400	0.250	0.595	0.447	0.250	0.293	0.379	0.125
Pra-2	A	0.792	0.500	1.000	0.833	0.700	0.800	0.730	0.500	0.500	0.923	0.643	0.813
	B	0.194	0.500	0	0.111	0.250	0.050	0.162	0.237	0.313	0.064	0.071	0.125
	C	0.014	0	0	0.056	0.050	0.150	0.108	0.263	0.188	0.013	0.286	0.063
Alb-1	A	0.556	0.500	0.545	0.444	0.300	0.611	0.486	0.447	0.063	0.066	0.431	0.250
	B	0.444	0.375	0.455	0.556	0.700	0.389	0.514	0.553	0.938	0.934	0.569	0.750
	C	0	0.125	0	0	0	0	0	0	0	0	0	0
Poa-1	A	0.764	0.542	0.591	0.556	0.750	0.611	0.514	0.395	0.688	0.487	0.534	0.625
	B	0.236	0.458	0.409	0.444	0.250	0.389	0.486	0.605	0.313	0.513	0.466	0.375
Prt-1	A	0.556	0.542	0.455	0.444	0.450	0.722	0.473	0.632	0.438	0.439	0.690	0.625
	B	0.444	0.458	0.545	0.556	0.550	0.278	0.527	0.368	0.563	0.561	0.310	0.375
Trf-1	A	0.556	0.273	0.545	0.056	0.357	0.188	0.519	0.184	0.125	0.167	0.345	0.625
	B	0.019	0.318	0.182	0.444	0.214	0.313	0.037	0.263	0.188	0.303	0.155	0.250
	C	0.037	0.091	0.182	0.111	0.214	0.188	0.204	0.053	0.188	0.030	0.103	0.125
	D	0.278	0.318	0.091	0.278	0.214	0.250	0.167	0.395	0.500	0.121	0.397	0
	E	0.111	0	0	0.111	0	0.063	0.074	0.105	0	0.379	0	0
Pot-1	A	0.529	0.375	0.682	0.333	0.550	0.375	0.568	0.526	0.750	0.438	0.379	0.375
	B	0.471	0.625	0.318	0.667	0.450	0.625	0.432	0.474	0.250	0.563	0.621	0.625
Mcg-1	A	0.431	0.333	0.682	0.889	0.400	0.563	0.459	0.500	0.750	0.618	0.552	0.375
	B	0.569	0.667	0.318	0.111	0.600	0.438	0.541	0.500	0.250	0.382	0.448	0.625

N, number of individuals. For acronyms see Fig.1 and Table 1.

calculated from the allele frequencies of 15 characterised gene loci (Table 4). The mean of values positively correlates with the level of genetic variability. The genetic diversity for dabbling ducks examined fluctuated among geographically different populations: for Northern Pintail fluctuated between H_o = 0.264 from Ob river and H_o = 0.331 from Kamchatka; for Eurasian Wigeon — between H_o = 0.185 from Ob and H_o = 0.263 from Lena river. In Mallard populations mean heterozygosity ranged from H_o = 0.242 (Vente 1998, Lithuania) to H_o = 0.366 (Antanavas 1987, Lithuania). Author's analysis was conducted using a modified Rogers genetic distance (Wright, 1978) to show the genetic relationship among the Mallard populations studied in Lithuania (Figure 2).

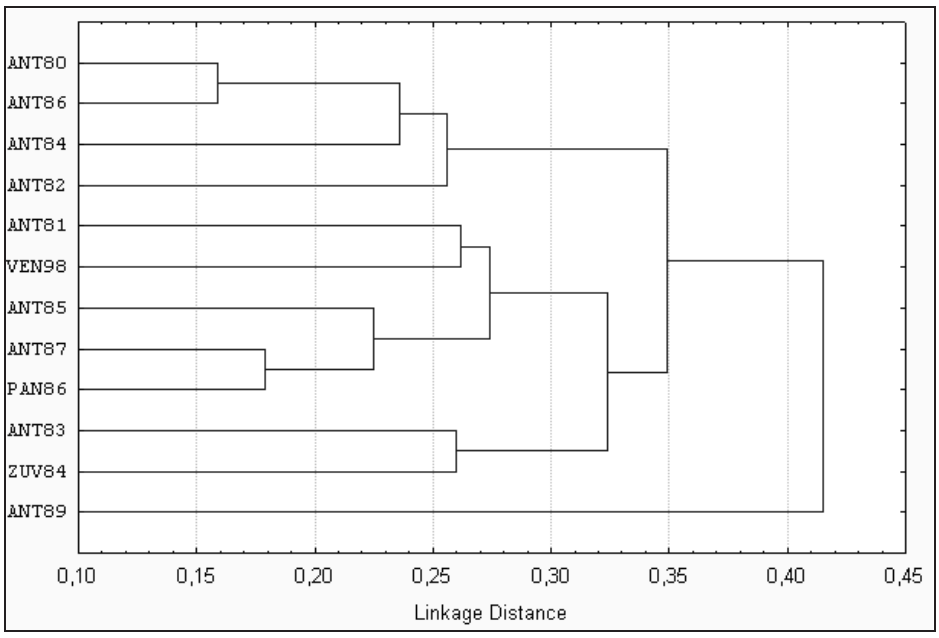

Fig. 2. Distance-based cluster analysis of Lithuanian Mallard populations from different localities. Modified Roger's distance were used. For acronyms see Table 1.

Table 4

GENETIC VARIABILITY OF 15 LOCI IN DIFFERENT *Anas* POPULATIONS (STANDARD ERRORS IN PARENTHESES)

Species	n	A	P*	Mean heterozygosity	
				H_o	H_e**
A .acuta					
OB84	40.0 (0.9)	1.7 (0.2)	53.3	0.264 (0.087)	0.269 (0.068)
KAR85	6.0 (0.0)	1.7 (0.2)	53.3	0.278 (0.097)	0.288 (0.073)
OB86	16.0 (0.0)	1.7 (0.2)	53.3	0.304 (0.100)	0.278 (0.073)
KAM88	14.5 (0.5)	1.7 (0.2)	53.3	0.331 (0.096)	0.283 (0.072)
A.clypeata					
KAM81	5.0 (0.0)	1.7 (0.2)	53.3	0.213 (0.084)	0.274 (0.071)
OB84	4.0 (0.0)	1.7 (0.2)	53.3	0.317 (0.093)	0.293 (0.074)
OB86	7.9 (0.1)	1.7 (0.2)	53.3	0.277 (0.082)	0.271 (0.068)
A. creca					
OB86	4.0 (0.0)	1.7 (0.2)	53.3	0.267 (0.096)	0.295 (0.076)
A .falcata					
KAM88	27.0 (0.0)	1.6 (0.2)	53.3	0.262 (0.087)	0.270 (0.069)
A. querqeudula					
OB84	21.5 (0.2)	1.7 (0.2)	53.3	0.271 (0.087)	0.271 (0.070)
OB86	66.7(0.6)	1.8 (0.3)	53.3	0.213 (0.069)	0.264 (0.066)
KAM88	9.9 (0.9)	1.8 (0.3)	53.3	0.222 (0.098)	0.213 (0.064)
A. penelope					
OB82	9.7 (0.3)	1.7 (0.2)	53.3	0.220 (0.078)	0.247 (0.065)
OB84	33.7 (0.3)	1.7 (0.2)	53.3	0.185 (0.066)	0.251 (0.064)
LEN89	48.7 (1.3)	1.7 (0.2)	53.3	0.263 (0.082)	0.278 (0.071)
A. plathyrhynchos					
ANT80	35.4 (0.6)	1.8 (0.3)	53.3	0.255 (0.076)	0.254 (0.065)
ANT81	11.3 (0.6)	1.7 (0.2)	53.3	0.255 (0.086)	0.287 (0.075)
ANT82	10.3 (0.7)	1.6 (0.2)	53.3	0.224 (0.076)	0.242 (0.070)
ANT83	9.0 (0.0)	1.9 (0.3)	53.3	0.259 (0.099)	0.271 (0.072)
ANT84	9.8 (0.2)	1.7 (0.2)	53.3	0.300 (0.083)	0.277 (0.072)
ANT85	17.1 (0.1)	1.8 (0.3)	53.3	0.266 (0.085)	0.273 (0.074)
ANT86	36.3 (0.7)	1.8 (0.3)	53.3	0.297 (0.088)	0.274 (0.070)
ANT87	17.2 (0.6)	1.8 (0.3)	53.3	0.366 (0.107)	0.293 (0.075)
ANT89	8.0 (0.0)	1.7 (0.2)	53.3	0.275 (0.095)	0.245 (0.070)
ZUV84	36.9 (0.8)	1.8 (0.3)	53.3	0.290 (0.094)	0.227 (0.068)
PAN86	28.5 (0.5)	1.7 (0.2)	53.3	0.303 (0.098)	0.274 (0.070)
VEN98	16.0 (0.0)	1.7 (0.2)	53.3	0.242 (0.065)	0.254 (0.062)

* A locus is considered polymorphic if the frequency of the most common allele does not exceed 0.95;

** Unbiased estimate (see Nei, 1978)

DISCUSSION

There is a great range in geographical regions and habitats used by different biogeographical populations of the ducks. The concept of "geographical population" was elaborated for migratory populations of birds by Isakov (1967) and modified by Atkinson-Wiles *et al.* (1982) as a "biogeographical population", which comprises a discrete population unit with a specific flyway, linking the breeding, moulting and wintering grounds. Such a distributing range of populations spatially and temporally may be the outcome of alteration in wetland ecosystems.

Very different environmental conditions are characteristic for the biogeographical populations of dabbling ducks in the Palaearctic. The distribution range of the Northwest Europe population generally coincides with a maritime climate on vast plains usually located not far from the coast of Atlantic and Arctic Oceans, in European tundra, boreal and temperate zones. The Eastern-Central Europe/Mediterranean region population is mainly located within a continental climate in the temperate and Mediterranean zones of Europe and in the sub-tropical zone of North-West Africa. The distribution range of the SE Europe/SW Asia/East Africa population generally coincides with the steppe zone of Europe/SW Asia and savannah region in East Africa. Thus, the genetic differentiation between the biographical populations can be caused by the ecological and geographical isolation. Natural selection can be an important factor, as different populations of dabbling ducks breed, migrate and winter in very different habitats.

Similar observations have been reported for other waterbird species population. For example, the NW Europe, East Europe/Mediterranean and West Siberian/Caspian/East Africa populations have been delineated for common European duck species (Mallard, Common Teal, Northern Pintail, Eurasian Wigeon and Garganey) by Shevareva (1970) based on nearly 11,000 ring recoveries. Later the population range limits were slightly modified by Atkinson-Wiles *et al.* (1982) and recently by Scott and Rose (1996).

Our data shows that the dabbling duck species examined form no discrete populations, as dabbling ducks show low philopatric compared with other waterbirds (Robertson and Gregory, 1999), and due to large local migration in the breeding grounds (Doherty *et al.,* 2002). The genetic variability of dabbling ducks is also raised by yearly change of breeding pairs (Lossito and Baltassarre, 1996).

The data obtained for Lithuanian Mallards confirmed genetic differences among the populations studied (Fig. 2). Cluster analysis showed that individuals sampled from the same place (Antanavas) for nine years did not form a discrete population, and furthermore mixed with Mallards from more distant Lithuania sites (Panevezys, Nemunas delta, Zuvintas). The gene frequency data confirms differences among Antanavas breeding populations studied annually from 1980 to 1989: allele $Alb\text{-}1^{C}$ was detected only in the ANT81 population, $Pra\text{-}2^{B}$ not found only in ANT82, $Pra\text{-}2^{C}$ — not founded in ANT81 and ANT82 populations, $Trf\text{-}1^{E}$ — not founded in ANT81, ANT82, ANT84, and ANT89 populations (Table 3). The results strongly support the hypothesis that dabbling ducks are not philopatric, exhibit large local migration, and show low fidelity to breeding grounds.

All Siberia populations of species examined also differed considerably in a temporal and spatial context (Table 4). Best it could be revealed for Northern Pintail species: OB84 population was more similar to the Kamchatka population (KAM88) than to populations from the Ob river in 1986 and Kara river in 1985. These results are not very surprising. Four migratory ways cross the Ob and Kara rivers breeding grounds (Scott and Rose, 1996) which can explain the large genetic variability. Regarding the Kamchatka population it appears that the OB84 population was most likely a Middle Asia flyway migrant, rather than European/African, and inhabited Kamchatka in wintering grounds. The genetic data for other Siberian dabbling ducks shows no discrete populations. All three investigated populations of Garganey were genetically different; two Eurasian Wigeon groups from the Ob River formed different populations, but their genetic structure was similar to the Lena river group. Only genetic data of the Northern Shoveler corresponds to ornithological data (Scott and Rose, 1996): Ob River and Kamchatka populations migrate by different flyways; the group from Ob River in 1984 and 1986 had similar genetic structure and formed one population, while the group from Kamchatka differed genetically. Geographic and adaptive variation in different populations of waterbirds is closely associated with the environmental conditions in the different regions of Palaearctic.

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PELDPĪĻU (Anseriformes: *Anas*) PALEARKTIKAS POPULĀCIJU ĢENĒTISKĀ DIFERENCIĀCIJA LAIKĀ UN TELPĀ

Pētīta ģenētiskā diferenciācija 15 asins sēruma proteīnu lokusos starp Palearktikas peldpīļu (*A. acuta, A. clypeata, A. crecca, A. querquedula, A. falcata, A. penelope, A. platyrhynchos*) ģeogrāfiski attālinātām Lietuvas un Sibīrijas populācijām. Noteikti pētīto lokusu alēļu izmaiņu trendi laikā un telpā.