Genetic Constitutions of Native Ducks in North Vietnam

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Genetic constitutions of the Co and the Bau, which were the Vietnamese native ducks, were investigated on the basis of the blood protein polymorphisms. Blood samples were collected in north Vietnam. Out of 22 loci controlling blood proteins, polymorphisms were observed at nine loci. From a dendrogram and a three-dimension scatter diagram on the first three principal components the Co and the Bau in north Vietnam were genetically similar to each other and the Co in north Vietnam was somewhat different from the Co in south Vietnam. However, these populations of Vietnamese native ducks seemed to be comparatively different from other Asian duck breeds.

Average heterozygosities ($\bar{H}$) of the Co and the Bau in the North Vietnam were 0.105 and 0.113, respectively.

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Key words : Vietnamese native ducks, genetic distance, genetic constitution, the Co, the Bau

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Introduction

A number of ducks are raised in southern area around the Mekong delta and northern area around Hanoi Province of Vietnam. The number is estimated to be about 44millions and ranks as the second after China in the world. The number includes some exotic breeds of ducks such as the Pekin, the Khaki Campbell and the Cherry Valley in addition to native ducks. The exotic breeds including the Pekin grow faster and produce more eggs than the Vietnamese native ducks. The number of the exotic breed ducks is increasing in recent years. However, the Vietnamese native ducks will be sustained in the future because their numbers in Vietnam are great.

There are two breeds in Vietnamese native ducks, namely the Co and the Bau. The former is mainly distributed in the southern area around the Mekong delta and partly in the northern area around Hanoi Province, and the latter is distributed only in the northern area of Vietnam. In 1995, the blood protein polymorphisms of the Co ducks were investigated in the south Vietnam (OKABAYASHI *et al.*, 1998 a, b). It was suggested that the Co was genetically distinct from the North East Asian duck breeds such as the Pekin, the White Tsaiya, the Kairyō Osaka, the Naki Ahiru and the Aokubi

Ahiru, and also from the Indonesian native duck populations and the Khaki Campbell (see also OKABAYASHI *et al.*, 1999). Biochemical genetic studies on the phylogeny of Asian duck breeds and population including Indonesian ducks breeds and populations were reported by TANABE (1994).

This study aims to elucidate the genetic constitutions of the native duck breeds of the Co and the Bau raised in north Vietnam based on the blood protein polymorphisms.

Materials and Methods

Seventy-three blood samples were collected from native ducks in north Vietnam. Of which 45 blood samples were collected from the Co and 28 from the Bau. Ten, ten and 25 of the Co's blood samples were collected at two farms in Hanoi and Bavi, Hanoi Province and a Duck Breeding and Research center in Phu Xuyen, Ha Tay Province, respectively. In the former two farms 50 to 100 of the Co were raised, and 200 of the Co were raised at the Duck Breeding and Research Center. The Bau's blood samples were collected only at the Duck Breeding and Research Center, where more than 500 of the Bau were raised.

The blood was separated into plasma and erythrocyte fractions by centrifugation

Table 1. Gene frequencies of ten loci controlling the

Name of duck No. Population	Number of ducks	<i>Pa-1</i>		<i>Pa-4</i>	
		<i>Pa-1^A</i>	<i>Pa-1^B</i>	<i>Pa-4^A</i>	<i>Pa-4^B</i>
1 Co (NV)	45	0.978	0.022	0.000	1.000
2 Bau (NV)	28	0.929	0.071	0.000	1.000
3 Co (SV)	214	0.523	0.477	0.023	0.886
4 Cirebon (I)	96	0.734	0.266	0.015	0.985
5 Tangerang (I)	101	0.624	0.376	0.038	0.962
6 Tasikmalaya (I)	93	0.672	0.328	0.006	0.994
7 Tagel (I)	91	0.676	0.324	0.000	1.000
8 Magelang (I)	102	0.681	0.319	0.070	0.930
9 Mojokari (I)	95	0.416	0.584	0.016	0.984
10 Mengwi (I)	95	0.553	0.447	0.010	0.990
11 Bogor (I)	33	0.682	0.318	0.000	1.000
12 Lombok	99	0.591	0.409	0.000	1.000
13 Medan (I)	30	0.550	0.450	0.000	1.000
14 Alabio (I)	79	0.817	0.184	0.017	0.983
15 Khaki Campbell (E)	69	0.544	0.457	0.000	1.000
16 Khaki Campbell (J)	158	0.513	0.487	0.000	1.000
17 Pekin (C)	66	0.773	0.227	0.030	0.970
18 White Tsaiya (T)	50	0.610	0.390	0.040	0.960
19 Kairyo Osaka (J)	103	0.718	0.282	0.000	1.000
20 Naki Ahiru (J)	65	0.400	0.600	0.008	0.992
21 Aokubi Ahiru (J)	71	0.563	0.437	0.028	0.972
22 Mallard 1 (J)	51	0.578	0.422	0.000	1.000
23 Mallard 2 (J)	43	0.698	0.302	0.000	1.000

Abbreviations in parentheses mean the countries in which the ducks or mallards were raised
I : Inodonesia, E : England, C : China, T : Taiwan, J : Japan, SV : Vietnam (Southern area), NV

at 3000 rpm for 10min. Both fractions were frozen at -80°C in a laboratory at Faculty of Animal and Veterinary Science of Hanoi Agricultural University. The frozen blood samples were transported to the laboratory at Azabu University School of Veterinary Medicine. Twenty-two kinds of blood proteins were analyzed with horizontal starch gel electrophoresis and horizontal polyacrylamide gel electrophoresis. The detailed description of electrophoresis were given by TANABE (1994). Out of 22 proteins analyzed, nine proteins of plasma prealbumin-1 (*Pa-I*), plasma prealbumin-4 (*Pa-4*), plasma post transferrin-1 (*Ptf-I*), plasma leucine aminopeptidase-2 (*Lap-2*), erythrocyte phospho-hexose isomerase (*PHI*), erythrocyte acid phosphatase-2 (*Acp-2*), erythrocyte esterase-1 (*Es-I*), erythrocyte esterase-3 (*Es-3*), and erythrocyte esterase-4 (*Es-4*) were polymorphic. The other proteins of plasma albumin (*Alb*), plasma prealbumin-2 (*Pa-2*), plasma prealbumin-3 (*Pa-3*), plasma prealbumin-5 (*Pa-5*), plasma transferrin (*Tf*), plasma post transferrin-2 (*Ptf-2*), plasma leucine aminopeptidase-1 (*LAP-I*), erythrocyte acid phosphatase-1 (*Acp-I*), erythrocyte esterase-D₁ (*Es-D₁*), erythrocyte lactate dehydrogenase-A (*LDH-A*), erythrocyte lactate dehydrogenase-B (*LDH-B*) and erythrocyte malate dehydrogenase (*MDH*) were monomorphic. No polymorphisms of erythrocyte esterase-D₂ (*Es-D₂*) were observed in the two duck breeds in north Viet-

blood protein polymorphisms in ducks

<i>Pa-4^C</i>	<i>Prf-I</i>			<i>LAP-2</i>			<i>Es-I^A</i>
	<i>Ptf-I^A</i>	<i>Ptf-I^B</i>	<i>Ptf-I^C</i>	<i>LAP-2^A</i>	<i>LAP-2^B</i>	<i>LAP-2^C</i>	
0.000	0.033	0.967	0.000	0.506	0.000	0.494	0.900
0.000	0.018	0.982	0.000	0.500	0.000	0.500	0.893
0.091	0.101	0.848	0.051	0.785	0.096	0.120	0.639
0.000	0.015	0.980	0.005	0.317	0.017	0.666	0.995
0.000	0.014	0.986	0.000	0.602	0.027	0.371	0.995
0.000	0.000	1.000	0.000	0.328	0.042	0.630	0.984
0.000	0.008	0.992	0.000	0.428	0.021	0.551	1.000
0.000	0.020	0.980	0.000	0.493	0.056	0.451	1.000
0.000	0.015	0.980	0.005	0.305	0.100	0.595	0.988
0.000	0.000	1.000	0.000	0.358	0.041	0.601	0.995
0.000	0.109	0.891	0.000	0.457	0.061	0.483	1.000
0.000	0.050	0.944	0.006	0.347	0.023	0.630	0.988
0.000	0.032	0.952	0.016	0.408	0.067	0.525	0.983
0.000	0.029	0.971	0.000	0.383	0.041	0.577	0.976
0.000	0.035	0.930	0.035	0.455	0.057	0.488	0.977
0.000	0.107	0.844	0.049	0.620	0.054	0.326	0.981
0.000	0.103	0.857	0.040	0.675	0.047	0.277	0.983
0.000	0.100	0.880	0.020	0.781	0.022	0.197	0.919
0.000	0.290	0.710	0.000	0.646	0.071	0.283	0.976
0.000	0.292	0.692	0.015	0.862	0.030	0.108	0.950
0.000	0.120	0.873	0.007	0.803	0.040	0.157	0.986
0.000	0.275	0.716	0.010	0.742	0.039	0.219	1.000
0.000	0.548	0.452	0.000	0.451	0.112	0.437	1.000

as follows.

: Vietnam (Northern area).

nam. Polymorphisms of the enzyme were observed only in mallard 1 (migrating mallard, see TANABE, 1994). The symbols of the loci controlling the proteins were shown in the parentheses.

Genetic distances between the duck populations were calculated according to the method shown by NEI (1972). To elucidate the genetic relationship of the duck population, a dendrogram was drawn by UPG method of SNEATH and SOKAL (1973) and a three-dimension scatter diagram was drawn on the first three principal components calculated by variance-covariance matrix of allele frequencies. The heterogeneity of duck populations was estimated from the average heterozygosity ($\bar{H}$) calculated from the average over 22 loci of heterozygosity per locus ($1-q_i^2$).

Results

Out of 22 protein loci analyzed, only nine were polymorphic. The frequencies of the alleles at the ten loci including *Es-D₂* locus in the Co and the Bau ducks in the north Vietnam are given in Table 1. For comparison, the allele frequencies in the other duck breeds and mallard populations cited from OKABAYASHI *et al.* (1998a) are also listed in Table 1. In the comparison between the Bau and the Co in the north Vietnam, the Bau

Table 1. (continued)

Name of duck No. Population	Number of ducks	<i>Es-1</i>	<i>Es-3</i>		<i>Acp-2^A</i>
		<i>Es-1^B</i>	<i>Es-3^A</i>	<i>Es-3^B</i>	
1 Co (NV)	45	0.100	0.444	0.556	0.067
2 Bau (NV)	28	0.107	0.500	0.500	0.161
3 Co (SV)	214	0.362	0.388	0.612	0.051
4 Cirebon (I)	96	0.005	0.684	0.316	0.088
5 Tangerang (I)	101	0.006	0.614	0.386	0.124
6 Tasikmalaya (I)	93	0.017	0.629	0.371	0.346
7 Tagel (I)	91	0.000	0.571	0.429	0.189
8 Magelang (I)	102	0.000	0.665	0.335	0.017
9 Mojokari (I)	95	0.013	0.505	0.495	0.051
10 Mengwi (I)	95	0.005	0.380	0.620	0.301
11 Bogor (I)	33	0.000	0.333	0.667	0.313
12 Lombok	99	0.012	0.436	0.564	0.153
13 Medan (I)	30	0.017	0.862	0.138	0.128
14 Alabio (I)	79	0.024	0.428	0.572	0.075
15 Khaki Campbell (E)	69	0.023	0.546	0.454	0.244
16 Khaki Campbell (J)	158	0.019	0.613	0.387	0.181
17 Pekin (C)	66	0.017	0.605	0.395	0.354
18 White Tsaiya (T)	50	0.081	0.380	0.620	0.224
19 Kairyo Osaka (J)	103	0.025	0.418	0.583	0.264
20 Naki Ahiru (J)	65	0.050	0.385	0.615	0.163
21 Aokubi Ahiru (J)	71	0.015	0.319	0.681	0.194
22 Mallard 1 (J)	51	0.000	0.628	0.373	0.059
23 Mallard 2 (J)	43	0.000	0.390	0.611	0.138

showed higher frequencies of $Pa-I^B$ and $Acp-2^A$ than the Co, but other allele frequencies in the Bau were similar to those in the Co.

Significant differences of allele frequencies between the south Vietnam and the north Vietnam in the Co were found at $Pa-I$, $Lap-2$, $Es-I$, and $Es-4$ loci. Higher frequencies of $Pa-I^B$ and $Es-I^B$ than the Co in the north Vietnam were found in the Co in south Vietnam. $Pa-4^C$, $Ptf-I^C$, $LAP-2^B$ and $Acp-2^o$ were observed at lower frequencies in the Co in south Vietnam, while the alleles were not observed in the same breed in north Vietnam.

A dendrogram showing the genetic distance between duck populations is given in Figure 1, and a three dimension scatter diagram drawn from principal component scores of the population is given in Figure 2. The Co and the Bau in north Vietnam were located at near position to each other. Both populations also showed near relationship to the Co in south Vietnam, but remote relationship to the other Asian duck breeds.

Average heterozygosities ($\bar{H}$) of the Vietnamese native and other Asian duck breeds including mallard populations are given in Table 2. The estimates of average heterozygosity were ranged from 0.098 to 0.154. The estimate (0.105) of the Co in north

<i>Acp-2</i>		<i>PHI</i>		<i>Es-4</i>		<i>Es-D₂</i>	
<i>Acp-2^B</i>	<i>Acp-2^o</i>	<i>PHI^A</i>	<i>PHI^B</i>	<i>Es-4^A</i>	<i>Es-4^B</i>	<i>ES-D₂^A</i>	<i>ES-D₂^B</i>
0.933	0.000	0.711	0.289	0.444	0.556	0.000	1.000
0.839	0.000	0.714	0.286	0.446	0.554	0.000	1.000
0.926	0.023	0.670	0.330	0.560	0.441	0.000	1.000
0.734	0.179	0.783	0.217	0.843	0.157	0.000	1.000
0.637	0.239	0.750	0.250	0.843	0.157	0.000	1.000
0.521	0.133	0.740	0.260	0.837	0.163	0.000	1.000
0.612	0.199	0.853	0.147	0.791	0.209	0.000	1.000
0.824	0.159	0.811	0.189	0.817	0.183	0.000	1.000
0.588	0.361	0.515	0.485	0.796	0.204	0.000	1.000
0.538	0.160	0.455	0.545	0.643	0.357	0.000	1.000
0.473	0.214	0.618	0.382	0.462	0.539	0.000	1.000
0.602	0.245	0.625	0.375	0.753	0.247	0.000	1.000
0.540	0.333	0.650	0.350	0.450	0.550	0.000	1.000
0.676	0.250	0.962	0.038	0.597	0.403	0.000	1.000
0.498	0.258	0.900	0.100	0.464	0.536	0.000	1.000
0.448	0.371	0.607	0.393	0.504	0.496	0.000	1.000
0.314	0.333	0.443	0.557	0.474	0.526	0.000	1.000
0.588	0.192	0.082	0.918	0.417	0.583	0.000	1.000
0.378	0.358	0.208	0.793	0.568	0.432	0.000	1.000
0.552	0.286	0.482	0.518	0.361	0.640	0.000	1.000
0.534	0.272	0.223	0.777	0.381	0.619	0.000	1.000
0.734	0.268	0.069	0.931	0.469	0.531	0.020	0.980
0.415	0.447	0.456	0.544	0.379	0.621	0.000	1.000

Fig. 1. A dendrogram drawn by UPG method based on Nei's genetic distance between duck populations.

Vietnam was lower than that (0.152) of the Co in south Vietnam, which was at the least level among the populations investigated until now. The value (0.113) of the Bau was also low.

Fig. 2. A three dimension scatter diagram drawn based on the first three principal components.

Discussion

According to DANG (1998)'s review, the Co and the Bau may differ somewhat each other in mature body weight and adult plumage color. In recent years, exotic duck breeds such as the Pekin, the Cherry Valley and the Khaki Campbell have been introduced into Vietnam.

Scientific reports on the Co could not been available until the genetic investigation on the Co in south Vietnam was started in 1995. Genetic constitutions of the Co in south Vietnam and its phylogenetic relationships with other Asian ducks were reported by OKABAYASHI *et al.*, (1998ab). Recently, genetic constitutions of Japanese native ducks were also investigated by OKABAYASHI *et al.*, (1999). They suggested that genetic constitutions of the Co differed from those of the North-east Asian duck populations consisting of the Pekin, the Naki Ahiru, the Aokubi Ahiru, the Kairyō Osaka and the White Tsaiya, and is distinct from those of the Indonesian native ducks and the Khaki Campbell. The present study with our previous study (OKABAYASHI *et al.*, 1998a) show that the genetic positions of the three populations in north and south Vietnam locate between the duck breeds in northeast Asia and those in Southeast Asia including of Indonesian ducks and the Khaki Campbell.

However, in the present study genetic constitutions of the Co in north Vietnam were somewhat different from the Co in south Vietnam. Vietnam is narrow from east to west and very long beyond 1100 km from north to south. Central area of Vietnam

Table 2. Average heterozygosities of the duck populations

No. populations	Name of duck	Number of ducks	Average heterozygosity
1	Co (NV)	45	0.105
2	Bau (NV)	28	0.113
3	Co (SV)	214	0.152
4	Cirebon (I)	96	0.125
5	Tangerang (I)	101	0.123
6	Tasikmalaya (I)	93	0.127
7	Tagel (I)	91	0.118
8	Magelang (I)	102	0.136
9	Mojosari (I)	95	0.135
10	Mengwi (I)	95	0.139
11	Bogor (I)	33	0.147
12	Lombok	99	0.114
13	Medan (I)	30	0.151
14	Alabio (I)	79	0.098
15	Khaki Campbell (E)	69	0.137
16	Khaki Campbell (J)	158	0.154
17	Pekin (C)	66	0.149
18	White Tsaiya (T)	50	0.144
19	Kairyo Osaka (J)	103	0.151
20	Naki Ahiru (J)	65	0.150
21	Aokubi Ahiru (J)	71	0.136
22	Mallard 1 (J)	51	0.128
23	Mallard 2 (J)	43	0.179

Average heterozygosity was estimated from average of heterozygosity in each locus over twenty two loci.

is especially narrow from east to west, and mostly dry and arid mountainous land, where is not suitable to keep ducks, because ducks can live only in wet waterful areas. Most of ducks in Vietnam are raised in northern plain area around Hanoi Province and southern plain area around the Mekong delta. As the distance between the northern and the southern areas is too long for the migration of the population, genetic exchange of the Co ducks between northern and southern area seems to be little. Further, it was possible that the Co had crossed with the Bau in north Vietnam. In this study, the Co and the Bau in north Vietnam were found to be rather similar genetic constitutions. The Bau originates in Cho Ben, Hoa Binh Province, Vietnam, and might be genetically differ from the Co due to DANG (1998). The Co has a smaller body size and produces less eggs than the Bau. It was possible to cross the Bau to the Co to improve growth rate and egg production. However, the body sizes of both the duck breeds apparently so differed to each other that the crossbreeding might not be possible in the populations of the Co and the Bau ducks in north Vietnam at least in recent years. The present study suggests the presence of considerably high genetic random drifts among the duck populations in north and south Vietnam, because a

close genetic relation was observed between the Co and the Bau in north Vietnam than between the Co in north Vietnam and that in south Vietnam. It should be note worthy that the duck breeds of Vietnam had not been pedigree-bred, and they can be called populations instead of breed although their external features are similar.

The average heterozygosities of ducks and mallards were ranged from 0.098 to 0.179, and the values were at same levels compared with those in Asian native horse and dog populations but at higher level than those of water buffalo and Asian native goat populations (NOZAWA, 1994). In poultry similar estimates of 0.078 to 0.162 in Indonesian, Lanka, Fijian and Bangladesh native chickens (MAEDA *et al.*, 1987) were reported. A range from 0.098 to 0.179 of the average heterozygosities of ducks and mallards estimated in the study is considered to be at a medium level of the estimate. Lower estimates of $\bar{H}$ in the Co in north Vietnam might be caused by small size breeding systems. However, the same reason might not be true in the Bau, since the local population size of the Bau from which blood samples were collected was exceptionally large as more than 500 in north Vietnam. The other reasons for the low estimate in the Bau may be considered as a bottle-neck effect or sampling error. Comparatively large estimate of the Co in south Vietnam might be caused by larger population size breeding system. Average heterozygosity varies due to population size and reproduction systems of the population. More informations on actual numbers of male and female in mating and breeding history of the populations will be necessary in the field studies.

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ベトナム北部における在来アヒルの遺伝子構成

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ベトナムのハノイ市を中心とした北部地域において飼養されている在来アヒル Co と Bau について 22 種類の血液タンパク質の遺伝的変異を調べた。また、ベトナム在来アヒルをはじめ他のアジア産アヒルにおいても平均ヘテロ接合体率を推定した。ベトナム北部の在来アヒルにおいて多型を示したのは 22 タンパク質のうち 9 種類(座位)であった。マガモのみに多型の見出されている *Es-D₂* を含めた 10 座位における遺伝子の頻度を基に調査した集団の間で Nei の遺伝的距離を求め、それに基づいて枝分かれ図を描いた。また、遺伝子頻度の分散共分散行列に基づく行列から主成分分析を行い、その第一～三成分を基にして三次元の散布図を描いた。ベトナム北

部における Co と Bau の遺伝子構成は全体的によく似通っていた。また、北部の Co と南部の Co とはその遺伝子構成がやや異なっていた。枝分かれ図ならびに散布図から、北部の Co と Bau とは互いに比較的近い位置にあり、またベトナム南部の Co とはすこし離れていたが、これらの 3 集団はともに東北アジア産アヒルともインドネシア産アヒルとも少し離れたところに位置することが分かった。ベトナム北部の Co と Bau の $\overline{H}$ はそれぞれ 0.105 および 0.113 であった。

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キーワード: ベトナム在来アヒル, 血液タンパク質多型, 遺伝的距離, 遺伝子構成