GENETICAL STUDIES ON NATIVE CHICKENS IN INDONESIA

Y. Yamamoto[1], T. Namikawa,[2] I. Okada, M. Nishibori, S. S. Mansjoer[3] and H. Martojo[3]

Faculty of Applied Biological Science, Hiroshima University, Higashihiroshima-shi 739, Japan

Summary

Phylogenetic analyses were carried out using four Indonesian native chicken breeds; Kampung, Bangkok, Pelung and Kedu. Gene frequencies of four blood group (*A, B, D* and *E*) and eight electrophoretic loci (*akp, Akp-2, Es-1, Amy-1, Alb, Tf, Pas* and *Pa-1*) were examined. Geographical and breed specific trends in the gene frequencies were not found in the local populations of Kampung breed or in four native breeds. The values of average heterozygosity were estimated as 0.35-0.45. Genetic distances among the local populations of Kampung breed and other native breeds were comparatively small. In a cluster analysis, the Bangkok breed and Kampung E population showed distance from another cluster. The coefficient of gene differentiation for local populations of Kampung breed was estimated as 0.099.

(**Key Words**: Blood Group, Protein Polymorphism, Genetic Distance, Coefficient of Gene Differentiation, Indonesian Native Chicken)

Introduction

Four breeds of native chickens, the Kampung, Bangkok, Pelung and Kedu are known in Indonesia. Kampung is the most popular native chicken kept under traditional conditions for egg and meat production. Bangkok is a fighting type chicken, whereas Pelung and Kedu chickens are kept for their fanciness (Mansjoer, 1985). Although a number of improved breeds have been introduced from foreign countries to improve the economic performance of these native chickens, the native breeds still account for 62 percent of population of all chickens reared in Indonesia.

It is an important problem to estimate the genetic constitution of Indonesian native chickens for future practical application. This study was conducted to clarify the genetic constitution at blood group and protein polymorphic loci in the Kampung, Bangkok, Pelung and Kedu breeds of native chickens in Indonesia.

[1] Address reprint requests to Dr. Y. Yamamoto, Faculty of Applied Biological Science, Hiroshima University, Higashihiroshima-shi 739, Japan.

[2] Faculty of Agriculture, Nagoya University, Nagoya 464-01, Japan.

[3] Faculty of Animal Science, Bogor Agricultural University, Bogor, Indonesia.

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Materials and Methods

Chickens and blood collection

Blood samples were collected from Kampung, Bangkok, Pelung and Kedu chickens. The areas surveyed and number of samples collected are shown in table 1. The Kampung is nondescript type of native chickens and can be found all over the country; the Bangkok is a game type chicken which originated in Thailand; the Pelung is bred its song and is kept in east Jeva; and the Kedu is a fancy chicken with black colored plumage and skin and is reared in Kedu village, central Java.

TABLE 1. LIST OF NATIVE BREEDS SURVEYED

Breed	Abbreviation	No. of birds	Sampling area
Kampung	Kamp-A	24	Sumatera
Kampung	Kamp-B	57	Jawa
Kampung	Kamp-C	26	Bali
Kampung	Kamp-D	30	Lombok
Kampung	Kamp-E	20	Sulaweshi
Bangkok	Bang	24	Jawa
Pelung	Pelu	40	Jawa
Kedu	Kedu	38	Jawa

Heparinized blood samples were collected, and separated into plasma and erythrocytes by centrifugation (450 g, for 5 minutes). Erythrocytes were washed with physiological saline by centrifugation three times. Part of the erythrocytes were used for blood typing, while plasma and remaining erythrocytes were stored separately in a freezer (−20℃) for electrophoretic analyses.

Blood typing and electrophoresis

Four blood group systems of *A, B, D* and *E* were tested by hemagglutination. The number of reagents used for blood typing were three for *A*, eleven for *B* and two each for *D* and *E* systems. The nomenclature of blood group alleles used in this study was given by Matsumoto and Okada (1961) and is not necessarily the same as those described by Briles (1964, 1982). Eight loci controlling six kinds of blood proteins were screened for genetic variation by starch or polyacrylamide gel electrophoresis. The list of the genetic loci analyzed in this experiment is given in table 2.

TABLE 2. LIST OF POLYMORPHIC CHARACTERISTICS ANALYZED

Trait	Locus	Cited from
Blood group	*A*	Matsumoto and Okada (1961)
Blood group	*B*	Matsumoto and Okada (1961)
Blood group	*D*	Matsumoto and Okada (1961)
Blood group	*E*	Matsumoto and Okada (1961)
Alkaline phosphatase	*Akp*	Okada et al. (1980)
Alkaline phosphatase	*Akp-2*	Okada et al. (1980)
Esterase	*Es-1*	Okada et al. (1980)
Amylase	*Amy-1*	Hashiguchi et al. (1970)
Albumin	*Alb*	McIndoe (1962)
Transferrin	*Tf*	Stratil (1968)
Postalbumin	*Pas*	Kuryl and Gasparska (1976)
Prealbumin	*Pa-1*	Tanabe et al. (1981)

Estimation of gene frequency, genetic variability and genetic distance

Gene frequencies were estimated by the direct counting method for the loci known to have only codominant alleles. For the loci including recessive alleles gene frequencies were estimated by the methods presented by Ito and Kanemaki (1987). Genetic variability within population was determined by measuring the average heterozygosity per individual, $\bar{H}$ (Nei, 1978). The average heterozygosity was estimated using the following formula:

$$\bar{H} = \overline{2n\,(1-\Sigma x_i^2)/(2n-1)},$$

where x_i is the frequency of the ith allele at a locus, n is the number of birds of the population concerned, and the bar means the average over all the loci examined. The relative magnitude of genetic differentiation among local populations of the Kampung chickens were estimated using the coefficient of gene differentiation, G_{ST} (Nei, 1973). The coefficient was calculated by the following formula:

$$G_{ST} = (H_T - H_S)/H_T,$$

where H_T and H_S are the average heterozygosity of total population calculated from average gene frequencies of local populations, and the mean of average heterozygosity of local populations, respectively.

The genetic distance was measured by a jackknife method (Mueller and Ayala, 1982) using the following formula:

$$Jr = (1/r)\Sigma\,[rD_r - (r-1)\,D_{r,i}],$$

where D_r is the Nei's genetic distance and $D_{r,i}$ is the same as D_r except that ith locus has been omitted. The Nei's genetic distance was calculated by the method modified for small populations (Nei, 1978).

The dendrogram was constructed from the genetic distance matrix by the unweighted pair-group method of Sneath and Sokal (1973).

Results

The gene frequencies at four blood group loci, *A, B, D* and *E* loci are given in tables 3, 4 and 5. At the *B* locus, many alleles were found at low frequencies. Therefore, some alleles showing similar phenogroups were pooled. The *X* in the notation of phenogroups in table 4 indicates this pooling as described by Okada et al. (1984).

The gene frequencies at the blood group loci showed considerable variations among breeds. For example, at the *A* and *B* loci, the B^{lX} and B^{LX} alleles were detected with low frequencies only in Kampung-B chickens, and the D^{Q} and E^{W} alleles were found with considerable high frequencies at the D and E loci in all the breeds.

The gene frequencies at eight electrophoretic polymorphic loci are shown in table 6. Though the frequencies of *akp*, $Akp\text{-}2^{O}$, Tf^{B} and $Pa\text{-}1^{B}$ alleles were very high in all the breeds, Alb^{A} and Tf^{A} alleles were detected with low frequencies only in Kampung-C and Kedu breeds, respectively. The $Pa\text{-}1^{A}$ allele was detected only in Kampung breeds.

Genetic variability was quantified by measuring the

TABLE 3. GENE FREQUENCIES AT THE BLOOD GROUP *A* LOCUS OF NATVE CHICKENS IN INDONESIA

Breed[1]	No. of birds	Gene frequency						
		A^{FRZ}	A^{FR}	A^{FZ}	A^{F}	A^{R}	A^{Z}	A^{a}
Kamp-A	20	.068	.095	0	.400	.098	.063	.276
Kamp-B	24	.188	.356	.048	0	.408	0	0
Kamp-C	30	.052	.291	0	.290	.111	.054	.202
Kamp-D	26	0	.280	.039	.162	.241	0	.278
Kamp-E	57	.028	.113	.025	.121	.185	.079	.449
Bang	24	0	.229	035	.199	0	.232	.305
Pelu	40	.014	.051	022	.062	.145	.128	.578
Kedu	38	.081	.142	050	.190	.108	.108	.321

[1] See table 1 for the breed abbreviation.

TABLE 4. GENE FREQUENCIES AT THE BLOOD GROUP *B* LOCUS OF NATIVE CHICKENS IN INDONESIA

Breed[1]	No. of birds	Gene frequency												
		B^{AX}	B^{BX}	B^{C}	B^{CX}	B^{DX}	B^{EX}	B^{G}	B^{GX}	B^{IX}	B^{KX}	B^{LX}	B^{M}	B^{MX}	B^{b}
Kamp-A	20	.025	0	0	0	0	.025	.732	.217	0	0	0	0	0	0
Kamp-B	24	.023	.023	0	.023	0	.189	.031	.023	0	0	0	.121	.071	.496
Kamp-C	30	0	0	0	.068	0	.051	.364	.124	0	.132	0	.051	0	.210
Kamp-D	26	.020	.020	0	.020	0	.040	.274	.149	0	.308	0	0	0	.169
Kamp-E	57	.018	.047	.018	.009	0	.093	.217	.077	.012	.085	.044	.241	.029	.110
Bang	24	0	0	0	0	0	.359	.191	.042	0	0	0	.313	0	.095
Pelu	40	0	.013	0	.013	.013	.159	.099	0	0	.026	0	.280	.013	.384
Kedu	38	.135	.014	.030	0	.028	.135	.156	.067	0	.024	0	.204	.015	.192

[1] See table 1 for the breed abbreviation.

TABLE 5. GENE FREQUENCIES AT THE BLOOD GROUP *D* AND *E* LOCI OF NATIVE CHICKENS IN INDONESIA

Breed[1]	No. of birds	Gene frequency							
		D locus				*E* locus			
		D^{QS}	D^{Q}	D^{S}	D^{d}	E^{WY}	E^{W}	E^{Y}	E^{e}
Kamp-A	20	.106	.671	0	.223	.051	.449	0	.500
Kamp-B	24	.173	.418	.120	.289	.043	.669	0	.289
Kamp-C	30	.029	.197	.197	.577	.034	.784	0	.182
Kamp-D	26	0	.484	.169	.347	0	.558	.059	.383
Kamp-E	57	.061	.542	.101	.296	.072	.451	.080	.397
Bang	24	.031	.513	.103	.353	0	.660	.299	.041
Pelu	40	.112	.388	.082	.418	0	.408	.025	.567
Kedu	38	0	.505	.285	.210	.014	.757	0	.229

[1] See table 1 for the breed abbreviation.

average heterozygosity at 12 loci in Kampung, Bangkok, Pelung and Kedu breeds, and they were calculated as 0.448, 0.349, 0.375 and 0.425 respectively. To evaluate genetic differentiation among local populations within Kampung breed, the coefficient of gene differentiation (G_{ST}) was estimated, and the G_{ST} was calculated as 0.099.

Genetic distances between every pair of 7 populations were calculated (table 7). Against an expectation, genetic distances between Kampung local populations were as large as those between breeds. Genetic distance between

TABLE 6. GENE FREQUENCIES AT THE ELECTROPHORETIC POLYMORPHIC LOCI OF THE NATIVE CHICKENS IN INDONESIA

Allele	Breed[1]							
	Kamp-A	Kamp-B	Kamp-C	Kamp-D	Kamp-E	Bang	Pelu	Kedu
Akp	.197	.094	.333	.191	.051	0	.065	.239
akp	.803	.906	.667	.809	.949	1	.935	.761
Akp-2^{a}	.033	.134	.139	.025	.163	.158	0	.027
Akp-2^{O}	.967	.851	.861	.975	.837	.842	1	.973
Es-1^{A}	.387	.377	.519	.621	.450	.250	.337	.342
Es-1^{B}	.597	.550	.463	.276	.375	.604	.575	.500
Es-1^{C}	.016	.132	.018	.103	.175	.146	.088	.158
Amy-1^{A}	.516	.465	.426	.466	.475	.854	.387	.474
Amy-1^{B}	.484	.508	.518	.534	.525	.125	.600	.500
Amy-1^{C}	0	.027	.056	0	0	.021	.013	.026
Alb^{A}	0	0	.037	0	0	0	0	0
Alb^{B}	.677	.789	.630	.756	.825	.896	.600	.632
Alb^{C}	.323	.211	.333	.224	.175	.104	.400	.368
Tf^{A}	0	0	0	0	0	0	0	.026
Tf^{B}	1	.991	.981	.983	.950	.958	1	.947
Tf^{C}	0	.009	.019	.017	.050	.042	0	.027
Pas^{A}	.120	.338	.077	.129	1	.184	.209	.205
Pas^{a}	.880	.662	.923	.871	0	.816	.791	.795
Pa-1^{A}	.129	.061	.130	.069	.100	0	0	0
Pa-1^{B}	.871	.939	.870	.931	.900	1	1	1

[1] See table 1 for the breed abbreviation.

TABLE 7. MATRIX OF GENETIC DISTANCE BETWEEN EVERY PAIR OF BREEDS[1] CALCULATED BY NEI'S EQUATION

	Kedu	Pelu	Bang	Kamp -E	Kamp -D	Kamp -C	Kamp -B
Kamp-A	.030	.049	.079	.214	.046	.032	.050
Kamp-B	.022	.019	.046	.092	.051	.032	
Kamp-C	.024	.048	.089	.173	.021		
Kamp-D	.031	.066	.077	.166			
Kamp-E	.153	.165	.180				
Bang	.052	.085					
Pelu	.033						

[1] See table 1 for the breed abbreviation.

Kampung E and other populations were estimated as 0.163, and this value was especially larger than those between every pair of other populations.

The dendrogram drawn from the genetic distances among the 7 populations is given in figure 1. Though the populations of Kampung A, B, C and D formed same cluster, Kampung E population formed another cluster. Except for Kampung populations, Bangkok breed was also comparatively separated from other populations.

Discussion

Though genetic differentiation between local populations or strains within breeds was found in farm animals and chickens (Sandberg, 1967; Nozawa, 1970; Okada et al., 1989), few studies of genetic differentiation

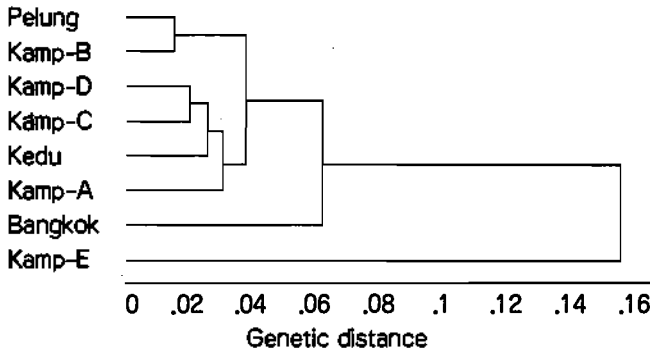

Figure 1. Dendrogram drawn from matrix of Nei's genetic distance.

in native chickens, especially the chickens indigenous to developing countries, have been reported (Maeda et al., 1992, Yamamoto et al., 1991). Maeda et al. (1992) analysed blood proteins collected from five local populations in Nepal, described that the five chicken populations formed a different cluster from Sri Lanka and Bangladesh chicken populations. Yamamoto et al. (1991) also analysed blood groups for the same Nepalese chicken populations, and found the coefficient of gene differentiation was comparable to those of other native chickens.

In the present study, local populations within the Kampung breed did not constitute a group in the same cluster (figure 1). The Kampung E population sampled from Sulaweshi island belonged to a different cluster from other Kampung populations. Genetic distances between Kampung E and other Kampung populations were larger than those of several Japanese indigenous breeds reported by Okada et al. (1989). As shown in figure 1, close relationships among Kampung, Pelung and Kedu were observed. Pelung and Kedu breeds are raised in the limited areas of Java island and their population sizes were generally small. They may have some genetic influences from Kampung breed when their original breeds were developed.

The coefficients of gene differentiation, G_{ST}, were estimated for six Japanese and one Bangladesh indigenous breeds and for two improved breeds of chickens, they were calculated as 0.016-0.14, 0.004 and 0.21-0.24, respectively (Okada et al., 1989). The G_{ST} value of Nepalese indigenous breed was also calculated as 0.128 (Yamamoto et al., 1991). Although the G_{ST} value of Kampung breed was approximately the same as those of Japanese and Nepalese indigenous breeds, it was generally less than half the value of improved breeds such as White Leghorn and Rhode Island Red.

The $\bar{H}$ values of Indonesian native breeds were estimated as 0.35-0.45 (table 6). These estimates were also the same as those of Japanese indigenous breeds and Bangladesh native fowls (Okada et al., 1989).

The present results suggest that it is difficult to declare the Kampung chicken is a finished breed.

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