



Genetic Diversity and Haplogroup Distribution of Asian Chicken Populations using Mitochondrial DNA sequence

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Abstract

Estimating the genetic diversity and origins is critical for the identification and conservation of valuable animal genetic resources. Mitochondrial DNA (mtDNA) polymorphisms have played a significant role in tracing the origin of specific breeds and the genetic diversity of domestic chicken and other livestock species due to their maternal inheritance, greater rate of substitution relative to nuclear genes, and much lower rate of recombination. In this study, we analyzed the mtDNA D-loop region of 457 genomic DNA samples from 28 Asian chicken populations (Korea: 6, Laos: 4, Bangladesh: 3, Cambodia: 3, Indonesia: 3, Vietnam: 2, Kyrgyzstan: 1, Mongolia: 1, Nepal: 1, Sri Lanka: 1 and White Leghorn, Cornish, Rhode Island Red) from ten Asian countries to clarify their genetic diversity and phylogenetic relationships. In addition, 49 reference data (43 : Oka et al data, 6 : red jungle fowl) were used. We found 82 haplotypes defined by 81 variable sites. Overall haplotype and nucleotide diversity were 0.978 ± 0.01 and 0.0018, respectively. Phylogenetic analyses revealed seven haplogroups (Type A-G). The most of Asian chickens were included in haplogroup A(44.9%), B(22.8%), C(19.3%). Haplogroup F did not belong to any Asian chicken populations (include only 2 reference data). Mongolia chickens were only clustered in haplogroup A and Indonesian chickens did only haplogroup C. About half of Kyrgyzstani chicken populations (43.4%) were clustered in haplogroup E. Vietnamese chicken populations belong to all haplogroup except F. In case of red jungle fowl, *G.g.gallus* and *G.g.bankiva* were clustered in haplogroup C. *G.g.spadiceus* was clustered in haplogroup E or A. As a result, it was possible to identify the mtDNA diversity and origin of Asian chicken populations. In future studies, it is necessary to understand the origin of each haplogroup by adding more reference data and red jungle fowl sequence data. (Keyword : Asian Chicken, Genetic diversity, Genetic Relationship, mtDNA, Haplogroup)

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Introduction

► Since the Convention on Biological Diversity(CBD) in 1992, Importance of animal genetic resources has been increased. So, Many studies on analysis of genetic diversity and relationship among many breeds have been conducted to certify as unique breeds. There are many breeds of chicken in Asia. however, very little information is available concerning the genetic diversity of Asian chicken breeds. Therefore, the present experiment was conducted to characterize genetic diversity and relationship among Asian chicken breeds based on mtDNA D-loop sequences

Material & Methods

► Samples

Nation	Korea	Laos	Bangladesh	Cambodia	Indonesia	Vietnam	Kyrgyzstan	Mongolia	Nepal	Sri Lanka	Transboundary breed
Breeds	6	4	3	3	3	2	1	1	1	1	4

► mtDNA sequences : 1 – 1236bp (D-loop region)

► Data Analysis

- Sequence Alignment : Bioedit Sequence Alignment Editor
- Genetic diversity of populations : DNA Sequence Polymorphism v6.12.03
- Phylogenetic analysis : MEGA 7.0.26
- Haplotype Network : Network 10.0

Results

Table 1. Maternal genetic diversity of Asian chicken populations (D-loop).

Type	POP	N	N. of polymorphic site	N. of haplotype	Haplotype diversity	Nucleotide diversity
Transboundary	RIR	20	8	2	0.100	0.00065
	WLG	19	9	2	0.105	0.00077
	COB	20	11	4	0.668	0.00429
	COR	20	16	4	0.500	0.00299
	AVE	79	11	3	0.343	0.00218
	KNR	20	19	6	0.763	0.00430
	KNY	20	24	7	0.837	0.00658
	KNG	23	23	6	0.794	0.00649
	KNW	16	11	3	0.642	0.00469
	KNB	19	19	4	0.626	0.00640
	KNO	19	21	5	0.789	0.00511
	BGH	8	16	5	0.857	0.00548
	BGD	4	12	3	0.833	0.00542
	BGN	2	9	2	1.000	0.00731
Local	CCH	11	20	7	0.873	0.00647
	CKD	10	0	1	0.000	0.00000
	CKO	9	20	4	0.778	0.00700
	INS	7	3	3	0.524	0.00085
	INK	6	3	4	0.867	0.00119
	ING	6	3	4	0.867	0.00119
	KGG	23	20	5	0.723	0.00642
	LAY	8	17	5	0.857	0.00632
	LAB	10	13	3	0.622	0.00419
	LAC	8	9	3	0.607	0.00206
	LAO	2	2	2	1.000	0.00162
	MGN	62	4	3	0.650	0.00137
	NPS	23	22	11	0.838	0.00472
	SRJ	16	14	6	0.817	0.00308
VNO	24	29	12	0.928	0.00735	
VNH	23	30	14	0.949	0.00070	
Total	AVE	379	14.5	5.12	0.762	0.00425

Table 2. Distribution of mtDNA D-loop haplogroup in 28 Asian chicken populations.

Haplo group	Korea	Laos	Bangladesh	Cambodia	Indonesia	Vietnam	Kyrgyzstan	Mongolia	Nepal	Sri Lanka	Leghron	Cornish	Rhode	Total
A	42 (36.2)	6 (21.4)	8 (57.1)			9 (19.2)	12 (52.2)	62 (100)	22 (95.6)	14 (87.5)	1 (5.3)	29 (72.5)		205
B	35 (30.2)	10 (35.7)		2 (6.7)		7 (14.9)			1 (4.4)	2 (12.5)	18 (94.7)	10 (25)	19 (95)	104
C	24 (20.7)	8 (28.6)	6 (42.9)	18 (60)	19 (100)	13 (27.7)								88
D	13 (11.2)					6 (12.8)	1 (4.4)							20
E	2 (1.7)	4 (14.3)		4 (13.3)		9 (19.2)	10 (43.5)					1 (2.5)	1 (5)	31
F														
G				6 (20)		3 (6.4)								9
Total	116	28	14	30	19	47	23	62	23	16	19	40	20	457

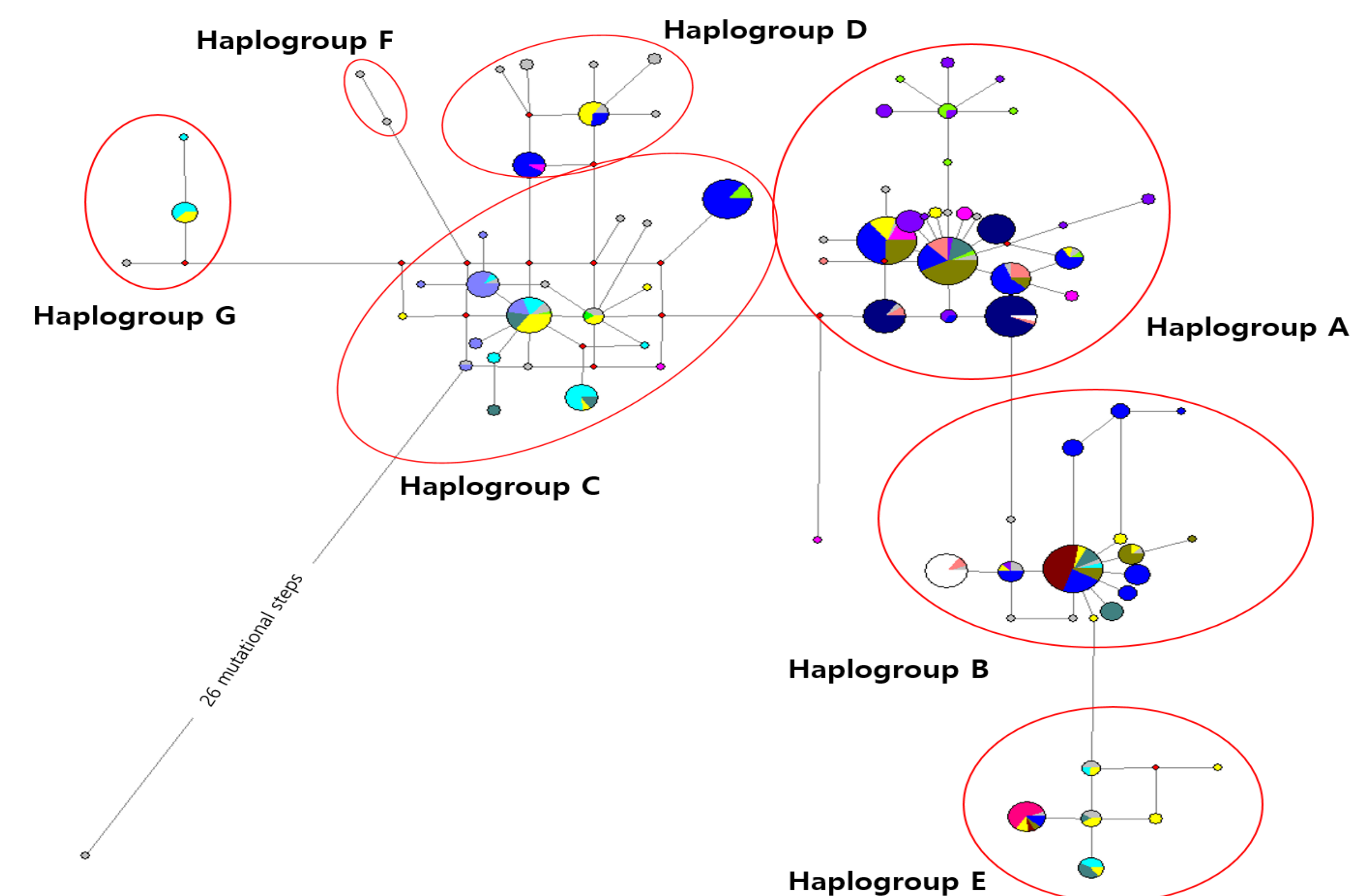


Figure 1. Median-joining network of 28 Asian chicken populations

Conclusion

► The knowledge obtained regarding Asian chicken breeds in 10 country as estimated by mtDNA D-loop sequences may also be useful as an initial guide in defining objectives for designing future investigations of genetic variation and developing conservation strategies.

Reference

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