Study on Phylogenetic Relationship Between Wild Japanese Quails in the Weishan Lake Area and Domestic Quails

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ABSTRACT : This paper is based on the 36 wild Japanese quails which migrated to and settled in the Weishan Lake area. The gene frequency of 10 loci encoding the enzymes in viscera and muscle was detected. After collecting the same data about 20 quail colonies in China and other countries, it clusters the 21 quail populations by fuzzy cluster analysis. The study indicates that the wild Japanese quail in the Weishan Lake area is closer to domestic quail for phylogenetic system than wild Japanese quails in Japanese Islands. The paper supports the thesis that the quail domestication area should be further studied. (*Asian-Aust. J. Anim. Sci. 2001. Vol. 14, No. 5 : 603-607*)

Key Words : Wild Japanese Quails In The Weishan Lake Area, Phylogenetic Relationship, Fuzzy Cluster Analysis

INTRODUCTION

Domestic quails, derived from Japanese quails (*Coturnix japonica*), as laying, meat and laboratory animals, have produced a flourishing industry. Now,there are about 1,050 million quails around the world and the development of quail use has a tendency to diversify. Revealing the phylogenetic relationship and hybrid fertility among Japanese quails, common quails (*Coturnix coturnix*)and domestic quails, will lay a foundation for making the quail industry more flourishing, and promote effective protection and exploitation of quail genetic resources. It also can contribute to clarifying quail domestication history and genetic variability (Chang, 1998).

At present, academic circles think that, Japanese quail were domesticated in Japanese Islands about 400 years ago. But recent studies prove that Japanese quail populations cluster alone in the phylogenetic clusters, between wild Japanese quails in Japanese Islands and domestic populations elsewhere in the world (Chang, 1995). That indicates the phylogenetic relationship of domestic quails is distant from that of wild Japanese quails in Japanese Islands (Kimura, 1984). Other studies from Chinese confirmed history showed that, in China, quail domestication history was longer than in Japan. It is at least 1500 years. In the Spring and Autumn Period (770B.C.-476B.C.), The Book of Poetry had many poems which sing the praise of quail, such as "quail's on the jumping". Liji had historical records of "pheasant, hare, quail, common

quail" (Kong, 490B.C.). From the Western Zhou Dynasty to the Warring States (1100B.C.-221B.C.), quail was tribute and often used as a sacrificial offering. In the Sui and Tang Dynasties, quail-fighting came into fashion, and in the Song Dynasty (960A.D.-1279A.D.) the quails were kept in captivity and fed for fight and entertainment. At the capital of the Song Dynasty, KaiFeng, there appeared quail country fair trade, and fried quail. Also in Song Dynasty, a person named Tang Shengwei, quoted the book of YangYi (974A.D.-1020A.D.) which had the records of "In 997A.D., at the time of summer alternated with autumn, one person who lived in the capital loaded a full capacity to the market for sailing". So it can be seen that in the Song Dynasty quail trade was broad in scale. There must have been a domestic quail population near the capital (Xie, 1989). Including these facts, this paper also studies the phylogenetic cluster analysis between wild Japanese quails from the Weishan Lake in China, various kinds of domestic quails, and wild Japanese quails around the Japanese Island. The aim of this paper is to provide new bases for probing the origin of domestic quails and Chinese quails phylogenetic status.

MATERIALS AND METHODS

Materials, sampling methods

Random samples of 36 wild Japanese quails were captured in the Weishan Lake area. Wild Japanese quail in the Weishan Lake area are different in shape but in other traits such as color of feather stripe, beak shape and chirping are the same as domestic quail. This is shown in figure 1.

Sample treatment

Liver, heart and muscle were taken from each quail and homogenized, then spun (15000 rpm) in a

refrigerated centrifuge. Each supernatent in a test tube was kept frozen (Sano et al., 1998) until examined by electrophoresis.

Multiloci electrophoresis

Starch gel electrophoresis was used to determine the variations from 10 loci encoding the enzymes in viscera and muscle viz alcohol dehydrogenase (Adh), esterase (Es), esterase-D (Es-D), α-glycerol dehydrogenase (α-Gpd), phospho-glucose isomerase (Pgi), 6-phosphogluconate dehydrogenase (6-Pgd), malate dehydrogenase (Mdh-I ,Mdh-II)and mannose phosphate isomerase (Mpi-I, Mpi-II). The types of the variations were determined according to the standards universally accepted in the countries neighboring China (Suzuki, 1991).

Statistical analysis

The frequency and variance of genes were estimated according to sample structure and sample size of the populations. The following two formulae were used to calculate the reliability that ensures the estimate not to deviate from the true value more than 0.5 times (β) and the relative deviation when the reliability reaches 0.9545 (η).

$$\beta = \int_0^\lambda \frac{2e^{-\frac{\lambda^2}{2}}}{\sqrt{2\pi}} d\lambda; \qquad \eta = 2\left[V\left(P^{\frac{1}{2}}\right)\right] \cdot P^{-1}$$

In the above formula, P and V (p) stand for gene frequency and gene variance, respectively; λ is the standardized deviation of the estimate and is suitable for the first formula when its standardized deviation is

$$\lambda = 0.5P \div [V_{(P)}]^{\frac{1}{2}}$$

Phylogenetic relationship cluster: According to the frequency of the genetic loci 7 in each population, the following formula was used to describe the fuzzy consistency relationship matrix of the similarity between populations and to compose the fuzzy similarity relation. Thus population cluster is achieved

Figure 1. Domestic quails (LEFT) and wild Japanese quails in the Weishan Lake area (RIGHT)

(Chang et al., 2000).

$$\mu_R(x,y) = \frac{1}{2}\ln\left(J_{x,y} / \sqrt{J_x \cdot J_y}\right) + 1$$

In the above formula, Jx, Jy and Jx,y stand respectively for population X, population Y and the probability average among loci of the same alleles acquired at random from the first two populations;

$\mu_R(x,y)$ stands for the membership function under the fuzzy consistency relation R between X and Y populations.

Quotation of source materials

In the above phylogenetic relationship clusters, the data information and the frequency distribution of 7 loci in 20 colonies are shown in tables 1 and 2. Data of this type are reported by other researchers with the same techniques.

RESULTS

Accuracy and reliability of the estimate of gene frequencies of wild Japanese quail in the Weishan Lake area are shown in table 3.

Of the 10 loci tested, 7 have polymorphism. It is seen from table 3 that the reliability of estimate of 12 alleles reached 0.95 apart from Pgi^A, Adh^C, α-Gpd^B, Es^C and 6-Pgd^A, and their reliability is 0.5704, 0.6922, 0.6156, 0.7776 and 0.8444, respectively. So these data may serve as statistical analysis of phylogenetic relationship.

Phylogenetic clusters

The internal and external data are quoted, phylogenetic clusters are performed as standard genetic distance based on gene frequency of 7 allozyme polymorphic loci in 21 quail populations.

Figure 2 shows the phylogenetic relationship among 21 quail populations in China and other countries, the base of which is the fuzzy similarity matrix.

From figure 2 we can see that on the value level of 0.970, the 21 populations are classified into two groups, one is wild Japanese quails, the other is all kinds of domestic populations and wild Japanese quails in the Weishan Lake area.This is consistent with the results of Zheng Huiling (1997). Wild Japanese quails do not cluster with domestic quails until the value level comes to 0.967. For this reason wild Japanese quails in Weishan Lake area and domestic quails share the same origin in fairly recent times, compared with wild Japanese quails and domestic quails.

DISCUSSION AND CONCLUSIONS

Phylogenetic clusters are one of the bases of

Table 1. Abbreviation, sampling source and data source of 21 quail populations in China and other countries

Population abbreviation	Sampling source	Data source
Wo85	Wild Japanese quail, captured in Kochi,Japan in 1985	Kimura and Fujii, 1989
WSHI	Wild Japanese quail, captured in Shizioka,Japan	Kimura et al., 1984
NS-I	Laboratory quail, bought from Aishi,Japan	Sano, 1995
WK83	Wild Japanese quail, captured in Kagoshima,Japan in 1983	Kimura et al., 1984
WK84	Wild Japanese quail, captured in Kagoshima,Japan in 1984	Kimura and Fujii, 1989
WK85	Wild Japanese quail, captured in Kagoshima,Japan in 1985	Kimura and Fujii, 1989
WK86	Wild Japanese quail, captured in Kagoshima,Japan in 1986	Kimura and Fujii, 1989
SZOR	Laying quail, bought from S farmer in Aishi,Japan	Sano, 1995
BNN	Laying quail, bought from B farmer in Aishi,Japan	Sano, 1995
NKG	Laying quail, bought from N farmer in Aishi,Japan	Sano, 1995
SZK	Laying quail, bought from Japan	Sano, 1995
FRA2	French quail,bought from Tokyo	Sano, 1995
GIANT	Meat quail from Canada	Cheng et al., 1992
K-FR	Laboratory quail with heavy weight from France	Sano, 1995
KES	Laboratory quail with heavy weight from Esthonia, bred by Environmental Research Institute of Japan	Sano, 1995
SC-T2	Laboratory quail with heavy weight from Shizioka, Japan	Sano, 1995
UBC-T	Laboratory quail with heavy weight from Canada	Cheng et al., 1992
WH89	Re-uncultivated quail of Hawaii, bought from UBC University of Canada	Sano et al., 1995
CH-K	Laying quail of Korea, bought from XianYang, China	Zheng, 1997
CH-G	Laying quail of Germany, bought from XianYang, China	Zheng, 1997
WSH	Wild Japanese quail, captured in the Weishan Lake area	This study, 2000

Table 2. The gene frequencies of allozyme polymorphism loci in viscera and muscle of 21 quail populations in China and other countries

Populat-	Adh^A	Adh^B	Adh^C	EsD^A	EsD^B	Es^A	Es^B	Es^C	Pgi^A	Pgi^B	$6\text{-}Pgd^A$	$6\text{-}Pgd^B$	$6\text{-}Pgd^C$	$6\text{-}Pgd^D$	$\alpha\text{-}Gpd^A$	$\alpha\text{-}Gpd^B$	$Mpi\text{-}I^A$	$Mpi\text{-}I^B$	$Mpi\text{-}I^C$	$Mpi\text{-}I^D$
Wo85	0.029	0.942	0.029	0.000	1.000	0.088	0.912	0.000	0.059	0.941	0.029	0.647	0.324	0.000	1.000	0.000	0.059	0.912	0.029	0.000
WSHI	0.019	0.081	0.000	0.024	0.976	0.024	0.928	0.048	0.000	1.000	0.024	0.571	0.405	0.000	1.000	0.000	0.000	0.905	0.095	0.000
	0.067	0.333	0.000	0.433	0.567	0.150	0.833	0.017	0.333	0.667	0.133	0.600	0.050	0.217	1.000	0.000	0.000	1.000	0.000	0.000
NS-I	0.067	0.933	0.000	0.000	1.000	0.150	0.850	0.000	0.033	0.967	0.050	0.683	0.250	0.017	1.000	0.000	0.033	0.917	0.050	0.000
WK84	0.026	0.974	0.000	0.079	0.921	0.105	0.895	0.000	0.105	0.895	0.026	0.737	0.237	0.000	0.974	0.026	0.026	0.974	0.000	0.000
WK83	0.050	0.950	0.000	0.050	0.950	0.200	0.775	0.025	0.000	1.000	0.075	0.700	0.225	0.000	0.950	0.050	0.025	0.950	0.025	0.000
WK85	0.056	0.944	0.000	0.074	0.926	0.111	0.889	0.000	0.111	0.889	0.093	0.648	0.259	0.000	0.958	0.042	0.019	0.907	0.074	0.000
WK86	0.700	0.000	0.300	0.383	0.617	0.167	0.817	0.017	0.350	0.650	0.167	0.567	0.067	0.199	1.000	0.000	0.050	0.950	0.000	0.000
SZOR	0.682	0.318	0.000	0.288	0.712	0.151	0.834	0.015	0.288	0.712	0.091	0.409	0.212	0.288	1.000	0.000	0.061	0.939	0.000	0.000
BNN	0.717	0.283	0.000	0.350	0.650	0.183	0.784	0.033	0.183	0.817	0.116	0.467	0.150	0.267	1.000	0.000	0.048	0.952	0.000	0.000
NKG	0.694	0.306	0.000	0.306	0.694	0.145	0.839	0.016	0.274	0.726	0.097	0.468	0.113	0.322	1.000	0.000	0.083	0.917	0.000	0.000
	0.571	0.381	0.048	0.090	0.910	0.227	0.705	0.068	0.137	0.863	0.064	0.205	0.423	0.308	1.000	0.000	0.237	0.763	0.000	0.000
SZK	0.375	0.625	0.000	0.150	0.850	0.500	0.393	0.157	0.050	0.950	0.050	0.275	0.375	0.300	1.000	0.000	0.250	0.750	0.000	0.000
FRA2	0.200	0.800	0.000	0.450	0.550	0.100	0.900	0.000	0.250	0.750	0.050	0.050	0.500	0.400	1.000	0.000	0.250	0.750	0.000	0.000
GIANT	0.575	0.425	0.000	0.425	0.575	0.350	0.650	0.000	0.175	0.825	0.400	0.200	0.125	0.275	1.000	0.000	0.150	0.850	0.000	0.000
K-FR	0.545	0.455	0.000	0.159	0.841	0.341	0.659	0.000	0.273	0.727	0.045	0.341	0.364	0.250	1.000	0.000	0.023	0.977	0.000	0.000
K-ES	0.900	0.100	0.000	0.225	0.775	0.425	0.350	0.225	0.075	0.925	0.000	0.050	0.700	0.250	1.000	0.000	0.100	0.900	0.000	0.000
SC-J2	0.000	1.000	0.000	0.000	1.000	0.026	0.974	0.000	0.125	0.875	0.025	0.425	0.000	0.550	1.000	0.000	0.275	0.725	0.000	0.000
UBC-J	0.457	0.543	0.000	0.314	0.686	0.071	0.929	0.000	0.200	0.800	0.297	0.216	0.351	0.135	1.000	0.000	0.162	0.838	0.000	0.000
	0.538	0.463	0.000	0.300	0.700	0.087	0.800	0.112	0.587	0.412	0.188	0.262	0.287	0.250	1.000	0.000	0.287	0.712	0.000	0.000
WH89	0.274	0.661	0.065	0.343	0.657	0.286	0.671	0.043	0.041	0.959	0.115	0.590	0.295	0.000	0.950	0.050	0.466	0.534	0.000	0.000

determining the scope of breed, judging the possibility of identical genes controlling similar body shapes in different populations, analysing the population characteristic of genetic coadaptation, and devising breeding strategy.

It can calculate genetic distance from gene frequency. The accuracy depends on the scale of sample and the loci tested. When the scale is definite, the more loci tested, the higher the reliability the results would have. From 18 allele frequencies of 7 loci we calculated the genetic distance among 21 populations. Although this is relative genetic distance,

Table 3. The estimates of gene frequencies and their reliability and precision

Loci	Alleles	n	P	V (Ps)	η	λ	β
Adh	Adh^A	31	0.274	3.32×10^{-3}	0.4206	2.38	0.9827
	Adh^B	31	0.661	3.73×10^{-3}	0.1848	5.41	1
	Adh^C	31	0.065	1.01×10^{-3}	0.9779	1.02	0.6922
Es	Es^A	31	0.286	3.40×10^{-3}	0.4708	0.45	0.9857
	Es^B	31	0.671	3.68×10^{-3}	0.1808	5.53	1
	Es^C	31	0.043	6.86×10^{-4}	0.8209	1.22	0.7776
α-Gpd	α-Gpd^A	30	0.95	8.19×10^{-4}	0.0602	16.60	1
	α-Gpd^B	30	0.05	8.19×10^{-4}	1.145	0.874	0.6156
6-Pgd	6-Pgd^A	32	0.115	1.64×10^{-4}	0.7043	1.42	0.8444
	6-Pgd^B	32	0.590	3.90×10^{-3}	0.2112	4.72	1
	6-Pgd^C	32	0.295	3.35×10^{-3}	0.3924	2.55	0.9892
Mpi-I	Mpi-I^A	32	0.466	4.01×10^{-3}	0.2718	3.68	1
	Mpi-I^B	32	0.534	4.01×10^{-3}	0.2372	4.21	1
Es-D	Es-D^A	30	0.343	3.88×10^{-3}	0.3632	2.75	1
	Es-D^B	30	0.657	3.88×10^{-3}	0.1899	5.27	1
Pgi	Pgi^A	30	0.041	6.78×10^{-4}	1.2701	0.79	0.5704
	Pgi^B	30	0.959	6.78×10^{-4}	0.0543	18.42	1

it can serve as phylogenetic classification.

Wild Japanese quails and wild common quails are distributed widespread in the east of China, Central Plains and northwest China. At the east of the Central Plains, two species are distributed dominantly. Shandong, Anhui and the north of Jiangsu, which circled the Weishan Lake are good places to stay on for wild quails. Every year after White Dews

Figure 2. Phylogenetic structure of 21 quail populations in China and other countries

(October), wild quails migrate from northeast, and before Rain Water (April) Wild quails migrate from South China. The local peasants own the custom of catching the quail, the super skill of distinguishing the breed and training the quail.

China and Japan are separated only by a strip of water. Cultural exchange has a distant source and a long stream. In the Sui and Tang Dynasties, with the return of students studying abroad, envoys to Sui and Tang Dynasties and learned monks, the custom of quail-fighting spread from China to Japan. Chinese quail culture had some effect on that of Japan. Based on this historical background, this paper can serve as one of the bases for research on quail origin.

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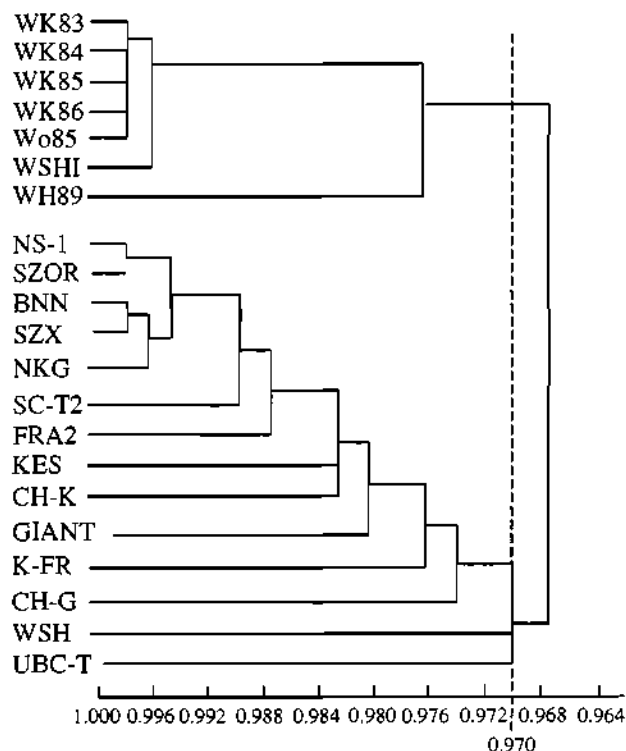Kimura, M. and S. Fujii. 1989. Genetic variability within and between wild and domestic quail populations. Jpn.

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