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DNA fingerprint variability within and among parental lines and its correlation with performance of F_1 laying hens

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Abstract Genetic diversity within and among nine pure lines of Beijing White Leghorn chickens was determined by DNA fingerprinting using human ministatellite probes 33.6 and α-globin 3'HVR, as well as bacteriophage M13. Within lines similarity coefficients ranged from 0.497 to 0.628, significantly higher than that within a sample of white chicken from a local market. Relationships among lines were established by clustering analysis based on inter-line coefficients of difference calculated from DNA fingerprints of pooled DNA. A complete diallel crossing among the nine pure lines was conducted. By using linear correlation analysis, it was found that the maximum distance between parental lines was positively correlated with egg number, egg production, survival rate and their corresponding heterosis percentages within a pair of reciprocal crosses. Similar relationships were found where only the higher of the reciprocal crosses were used in the analysis. It was also shown that similarity coefficients within a sire line or dam line were positively correlated with 40-week egg number and its heterosis percentage and the heterosis percentage for 40-week egg production, but negatively correlated with the 40-week survival rate of the crossbred populations.

Key words Chicken · DNA fingerprinting · Correlation · Crosses · Production traits

Introduction

Crossbreeding plays an important role in the production of commerical stains of poultry (Qiu and Yang 1985). The advantage of crossbreeding is that the crossbreds can show heterosis for traits of economic importance and trait complementarities between parental lines. To find promising combinations, however, a large number of crosses among parental lines must be tested beacuse of difficulty in predicting the performance of crossbreds. Information on genetic diversity within and among parental lines may help in designing crosses as one could expect more heterosis from more genetically divergent parents (Qiu and Yang 1985).

Traditionally, marker systems based on isozymes and blood proteins have been exploited for the investigation of the genetic structure of populations. However, these markers generally provide limited information beacuse of low degrees of variation. DNA fingerprinting, first described by Jeffreys et al. (1985), can simultaneously detect a large number of hypervariable loci in the genome and make it possible to estimate the genetic diversity representative of the whole genome. It has been proven that DNA fingerprinting is a powerful tool in poultry for investigating genetic diversity within stocks and establishing relationships among stocks (Kuhnlein et al. 1989, 1990; Dunnington et al. 1991, 1994; Haberfeld et al. 1992; Siegel et al. 1992; Grunder et al. 1994). Therefore, DNA fingerprinting analysis may provide useful information for the pre-selection of populations to be used in crossbreeding.

The objectives of the present experiment were to examine genetic diversity within and among nine pure lines of Beijing White Leghorn chickens using DNA fingerprints and to demonstrate relationships between the variability of DNA fingerprints of parental lines and the performance in some production traits of their hybrids.

Materials and methods

Pure lines

Nine pure lines of Beijing Leghorn chickens were established and maintained at Beijing Poultry Breeding Corporation (BPBC), Beij-

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Table 1 Description of pure lines

Line no.	Origin
1, 2, 9	Derived from a commercial strain imported from Romania in 1976. Line 1 was selected according to a complex selection index involving egg number, egg weight, body weight and age at first egg (Zhang 1985). Line 2 was selected for high egg number for 11 successive generations. Line 9 was initially subjected to inbreeding for five generations to reach an inbreeding coefficient of 0.46 and then selected for high egg number for six generations without further inbreeding
3	Derived from a commercial strain, Shaver Starcross 288, and selected for high egg weight since 1973
4, 5, 6, 7	Derived from four Babcook stocks imported from the United States in 1985. Line 4 was selected for high egg number, line 5 selected for high egg production rate, line 6 selected as line 1, and line 7 selected for high egg weight
8	Derived from a commercial strain imported from the United States in 1979 and selected for high egg weight

ing, China. The origin and characteristics of these lines are described in Table 1.

Crossing

The nine parental lines were crossed in all possible combinations, including matings within lines, at the BPBC in 1992. All matings, each involving five males, were made by artificial insemination with 5–10 hens per male. Eggs of a given mating collected over a period of 2 weeks were divided into two equal sets. Offspring hatched from the two sets were separately reared at Zudai Farm and Dongsha Farm (BPBC). All birds were reared under similar conditions. The total number of hens moved to laying cages at 19 weeks of age was 4391 at Zudai Farm and 4312 at Dongsha Farm.

DNA fingerprinting

Twenty females and ten males were randomly chosen from each parental line for blood samples. Genomic DNA was isolated according to Meng et al. (1993). For investigating genetic diversity within a line, six females and six males per line were individualy fingerprinted. However, pooled DNA of 20 females and 10 males from each line was used for comparisons among lines. For each gel lane, approximately 8 μg of *Hin*fI-digested DNA was loaded. DNA fingerprinting probes used in this experiment were human minisatellites α-globin 3′HVR (Fowler et al. 1988) and 33.6 (Jeffreys et al. 1985) as well as bacteriophage M13 (Vassart et al. 1987). In addition, seven white chickens of unknown origin, purchased at a local market, were similarly analysed by probe 33.6 as a control. Electrophoresis, blotting and hybridization were performed as described previously (Meng et al. 1993).

For all DNA fingerprints, only distiguishable bands larger than 3kb were scored. Pair-wise comparisons of DNA fingerprint lanes were done only within one gel. The similarity coefficient (F) between two DNA fingerprints was calculated as

$$F = 2N_{AB}/(N_A + N_B)$$

where N_{AB} was the number of bands shared by fingerprints A and B, and N_A and N_B were the total numbers of bands present in fingerprints A and B, respectively (Wetton et al. 1987). For the purpose of cluster analysis among parental lines, F was converted to a cofficient of difference (COD)

$$\mathrm{COD} = 1 - \mathrm{F}.$$

Measurements

Daily egg records from the first egg to 40 weeks of age and laying house mortality were recorded. Egg production is defined as egg production per caged hen during the period, which is the average of a cross. The replicate crosses at the two test sites performed quite similarly and so the two sets of data were arithmetically averaged prior to other analyses.
Percentage heterosis (%H) was estimated by

$$\%H = 100(C_{ij} - P_{ij})/P_{ij}$$

where C_{ij} was the performance of the cross between sire line i and dam line j, and P_{ij} was the mid-parent value.

Statistical analysis

The significance of differences among means of similarity coefficients within lines was tested using Duncan's multiple range test at a 0.05 level of significance (Duncan 1955). The cluster analysis, based on coefficients of difference (CODs) between parental lines, was performed using the maximum method described by Johnson (1967).

The reciprocal crosses were classified into several groups according to the inter-line maximum distance with reference to a given probe. We defined the maximum distance between a pair of lines as the COD at which they appeared together in the same cluster of a hierachical clustering. The following trait values for pairs of reciprocal crosses at the age of 40 weeks were averaged within groups: mean egg number: higher egg number, mean egg production (kg), higher egg production (kg), mean survival rate (%), higher survival rate (%) and their corresponding heterosis percentage (Table 2). The mean trait values are the average of a pair of reciprocal crosses, wheares for the higher trait values the better one between a pair of reciprocal crosses is used. The trait values were also averaged within crosses sharing an identical sire line or dam line (Table 3). Simple correlations between the DNA fingerprint data (inter-line maximum distance and F values within sire lines or dam lines) and the trait values were calculated (Montgomery and Peck 1982).

Results and discussion

Genetic diversity within lines

An autoradiogram bearing DNA fingerprints of individual chickens, produced by probe 33.6, is shown in Fig. 1 as an example. The average number of bands greater than 3kb detected by probes 33.6, α-globin 3′HVR and M13, based on fingerprints of 108 individuals, was 28.58 (0.30), 31.81 (0.35), and 36.35 (0.30) (standard errors of mean shown in parentheses), respectively.

The mean similarity coefficient within lines, shown in Table 4, varied with the probe used. This may be because different probes detect different loci with levels of variability. Regardless of the probe used, line 4 had the highest within-line mean similarity coefficient whereas lines 1, 3 amd 8 had the lowest similarity coefficient. With probe 33.6, mean similarity coefficients within lines ranged from 0.483 to 0.589 for the pure lines, significantly higher than that for the market chickens

Table 2 Average trait values within groups classified by inter-line maximum distances[a]

Probes	Groups	Distances	Number of crosses[b]	Egg number (EN)				Egg production (EP)				Survival rate (SR)			
				Mean EN (MEN)	Heterosis for MEN %	Higher EN (HEN)	Heterosis for HEN %	Mean EP (MEP) kg	Heterosis for MEP %	Higher (HEN) kg	Heterosis for HEN %	Mean SR (MSR) %	Heterosis for MSR %	Higher SR (HSR) %	Heterosis for HSR %
33.6	1	0.1624	2	89.74	−6.64	90.23	−3.91	4.95	−5.22	4.95	−1.33	88.10	−0.70	92.23	−0.10
	2	0.1944	4	95.75	2.77	95.83	3.22	5.28	4.66	5.34	5.46	93.64	0.87	94.12	1.40
	3	0.2239	6	91.88	−2.03	93.20	1.86	5.17	−1.45	5.26	2.40	92.94	0.92	93.63	2.27
	4	0.2647	8	90.41	2.31	95.18	4.06	5.13	2.28	5.39	3.53	92.71	1.36	94.23	4.20
	5	0.3335	24	94.78	3.11	96.03	5.42	5.38	3.55	5.46	5.40	95.60	2.50	96.42	3.80
	6	0.3714	28	96.08	5.83	98.49	8.75	5.36	5.65	5.48	8.97	93.63	3.18	94.76	4.31
α-Globin 3′HVR	1	0.1525	2	98.97	5.77	102.03	5.89	5.39	6.14	5.52	7.44	95.16	0.12	96.71	0.64
	2	0.1538	2	93.97	−3.02	96.32	3.52	5.23	−2.9	5.36	4.87	93.83	1.57	94.92	3.19
	3	0.1579	2	95.75	0.91	95.83	1.46	5.28	−0.10	5.34	0.00	93.64	−0.60	94.12	4.44
	4	0.2308	4	90.38	−1.54	96.47	1.04	5.19	−0.73	5.60	1.18	93.43	0.59	94.92	1.81
	5	0.2414	4	89.74	−3.43	90.23	−1.69	4.95	−1.02	4.95	1.07	88.10	0.46	92.23	1.03
	6	0.3061	12	91.16	6.09	93.54	8.35	5.12	5.59	5.22	7.83	92.46	3.25	93.58	4.83
	7	0.3077	6	91.49	2.79	93.15	4.93	5.18	3.07	5.29	4.7	95.13	2.01	95.67	4.12
	8	0.4	40	96.36	4.12	98.75	6.87	5.37	4.41	5.48	7.17	93.39	2.75	94.81	3.85
M13	1	0.1765	2	94.99	0.91	96.95	1.46	5.19	−0.10	5.27	0.00	93.61	−0.60	95.72	4.44
	2	0.2333	2	95.81	5.77	98.35	5.89	5.32	6.14	5.46	7.44	94.45	0.12	95.46	0.64
	3	0.2464	2	89.04	−0.93	91.64	0.50	5.00	0.39	5.20	2.14	95.32	1.89	95.88	2.65
	4	0.3333	4	94.84	−2.58	95.24	2.55	5.32	−2.37	5.36	2.53	94.29	0.43	94.79	2.08
	5	0.3667	6	90.90	−1.14	94.52	0.16	5.14	0.62	5.35	2.12	92.78	1.79	94.03	2.66
	6	0.3871	16	93.67	4.91	95.27	7.27	5.13	4.78	5.19	7.19	92.23	2.95	94.85	4.21
	7	0.4915	12	95.69	7.55	97.84	10.83	5.33	6.88	5.43	9.54	94.83	5.02	96.03	6.75
	8	0.619	28	96.15	2.81	98.96	5.38	5.33	3.39	5.49	6.12	93.67	1.59	94.68	2.73

[a] For the definition of inter-line maximum distance see Materials and methods. A group average is the arithmetic average over all the crosses within a group, whereas that for higher trait values is the arithmetic average of all the crosses with a higher trait value between a pair of reciprocal crosses within a group

[b] The total number of inter-line crosses is 72

Table 3 Mean trait values of crosses sharing an identical sire or dam line[a]

Lines		Egg number (EN)	Hetrosis for EN(%)	Egg production (EP)(kg)	Hetrosis for EP(%)	Survival rate SR(%)	Hetrosis for SR(%)
Sire	1	93.93(0.93)	3.48(1.52)	5.23(0.05)	4.37(1.35)	94.04(1.03)	2.86(1.26)
	2	93.58(1.40)	1.91(1.84)	5.16(0.09)	1.53(1.92)	94.15(0.34)	0.49(0.28)
	3	94.95(0.60)	−0.08(0.72)	5.34(0.05)	1.34(0.71)	95.19(0.40)	1.70(0.53)
	4	96.06(1.79)	8.28(2.39)	5.33(0.10)	8.12(2.40)	93.59(0.09)	4.42(1.28)
	5	94.86(2.07)	2.49(1.86)	5.24(0.12)	2.06(1.91)	92.47(1.27)	1.14(1.17)
	6	95.59(2.39)	3.98(2.80)	5.27(0.09)	4.51(2.28)	94.58(0.98)	3.01(1.14)
	7	95.15(1.24)	3.03(1.79)	5.37(0.07)	3.01(1.65)	93.00(0.46)	0.56(0.96)
	8	93.57(1.98)	1.03(2.20)	5.27(0.09)	1.46(2.06)	94.48(0.91)	3.52(1.02)
	9	97.44(1.88)	6.15(2.64)	5.33(0.09)	6.25(2.58)	93.63(0.98)	3.23(1.23)
Dam	1	93.98(1.98)	3.54(2.42)	5.22(0.11)	4.11(2.26)	93.34(0.73)	2.10(0.86)
	2	95.27(1.82)	3.78(2.56)	5.33(0.09)	4.91(2.48)	93.71(0.84)	0.19(0.73)
	3	93.31(1.60)	−1.83(1.50)	5.27(0.09)	0.07(1.63)	94.90(0.65)	1.40(0.97)
	4	95.54(1.91)	7.52(2.28)	5.32(0.10)	7.77(2.44)	92.16(1.36)	2.70(1.48)
	5	94.93(1.31)	2.59(1.08)	5.23(0.09)	1.78(1.20)	93.66(0.55)	2.57(0.84)
	6	96.00(1.35)	4.43(1.90)	5.23(0.05)	3.62(1.67)	94.68(0.40)	3.11(0.54)
	7	93.13(1.69)	0.87(2.06)	5.25(0.09)	0.71(1.98)	92.57(0.89)	0.06(0.78)
	8	94.53(1.05)	2.08(1.46)	5.38(0.07)	3.54(1.46)	94.44(0.65)	3.49(0.89)
	9	98.45(1.82)	7.28(2.20)	5.33(0.08)	6.11(1.87)	95.66(0.93)	5.32(1.44)

[a] The number of crosses sharing an identical sire or dam line is eight (exclusive of one within-line cross). Standard errors of means are in parentheses

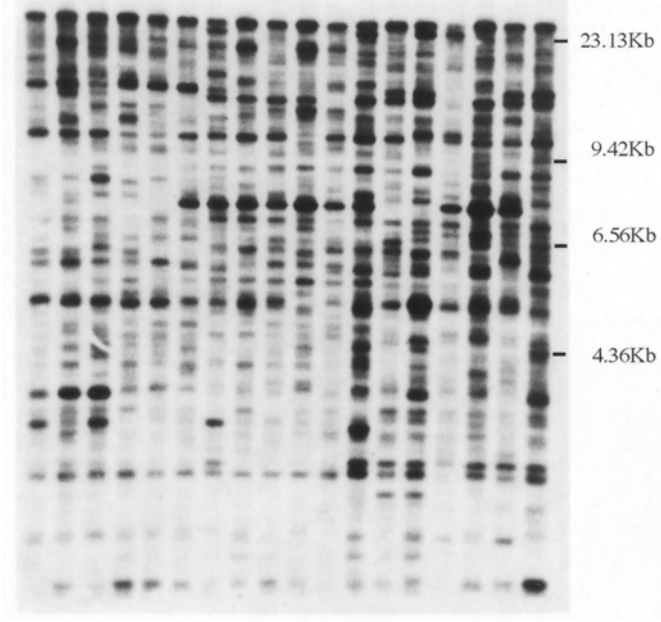

Fig. 1 DNA fingerprints of individual chickens generated with a α-globin 3′HVR probe

(0.253). This result suggested that the genetic background within these lines may be similar. The arithmetic averages of similarity coefficients given by three probes ranged from 0.499 to 0.628.

By DNA fingerprinting Kuhnlein et al. (1990) analysed seven chicken strains with inbreeding coefficients ranging from 0.026 to over 0.98, and obtained within-strain band-sharing probabilities (the same concept as the similarity cofficient used here) ranging from 0.44 to 1.00. Using the calibration curve described by Kuhnlein et al. (1990), it can be deduced that the inbreeding coefficients for the lines we studied here were not high.

Relationship between parental lines

For ease of inter-line comparisons, a DNA mix approach was adopted as first described by Dunnington et al. (1990). Table 5 shown inter-line CODs obtained with probes 33.6, α-globin 3′HVR and M13, respectively. Beacuse the absolute value of COD for a given comparison was dependent on the probes employed, each set of CODs obtained with a given probe was used to construct a hierachical clustering of nine parental lines (Fig. 2A–C). In Fig 2A, based on data from probe 33.6, the nine lines can be classified into three groups: lines 1, 2, 3 and 9; lines 4 and 5; lines 6,7 and 8. In Fig 2B, based on data from probe α-globin 3′HVR, the nine lines can be classified into four groups: lines 1, 2 and 3; lines 4 and 5; lines 6,7 and 8; and line 9. In Fig. 2C, based on data from probe M13, these lines can be classified into five groups: lines 1 and 2; lines 4 and 5; lines 6,7 and 8; line 3; and line 9. It can be seen that the taxonomic results from different probes are similar, suggesting that any one of probes may be sufficient for establishing reliable phylogenetic relationships among the lines. Although lines 1,2 and 9 have the same origin, line 9 joins the cluster containing lines 1 and 2 quite late in all the hierachial clusterings. Line 9 was once subjected to five generations of inbreeding with mating between sibs or half-sibs, which might have caused it to genetically diverse from lines 1 and 2. Close relationships between lines 4 and 5 or among lines 6,7 and 8 are probably associated either with their common genetic background at an early stage of their formation or with similar selection directions.

Other authors have also demonstrated the power of DNA fingerprinting in estimating phylogenetic relationships of populations in various species (Kuhnlein et al. 1989; Gilbert et al. 1990; Siegel et al. 1992; Castagnone-Sereno et al. 1993). Although different distance indices

Table 4 Similarity coefficients within lines[a]

Lines	No. of pairs	Similarity coefficients			
		33.6	α-globin 3′HVR	M13	Mean
MC	21	0.253[a] (0.017)			
1	30	0.506[bc] (0.015)	0.544[ab] (0.013)	0.446[a] (0.010)	0.499
2	30	0.553[de] (0.012)	0.559[abc] (0.013)	0.568[cd] (0.017)	0.560
3	30	0.484[b] (0.014)	0.530[a] (0.012)	0.476[ab] (0.015)	0.497
4	30	0.589[e] (0.015)	0.653[d] (0.015)	0.642[e] (0.015)	0.628
5	30	0.553[de] (0.013)	0.578[bc] (0.013)	0.601[d] (0.015)	0.577
6	30	0.529[cd] (0.013)	0.563[abc] (0.015)	0.573[cd] (0.012)	0.555
7	30	0.576[e] (0.011)	0.558[abc] (0.015)	0.557[c] (0.015)	0.564
8	30	0.483[b] (0.016)	0.531[a] (0.014)	0.486[b] (0.015)	0.500
9	30	0.533[cd] (0.012)	0.587[c] (0.015)	0.561[cd] (0.016)	0.560

Lines 1–9 are pure lines maintained at the Beijing Breeding Corporation while MC represents a population composed of seven white chickens purchased at a local market. The number of pairs is the number of pair-wise comparisons. Standard errors of the means are in parentheses. With regard to the same probe, similarity coefficients without identical superscripts differ significantly from one another ($P < 0.05$)

Table 5 Inter-line coefficients of difference obtained with different probes

Lines/probes		2	3	4	5	6	7	8	9
1	33.6	0.1733	0.1944	0.3043	0.3690	0.3239	0.2603	0.3429	0.2676
	3′HVR[a]	0.1525	0.2203	0.3725	0.3103	0.3333	0.2069	0.3462	0.2453
	M13	0.2333	0.5410	0.6190	0.5385	0.5938	0.4754	0.5362	0.4237
2	33.6		0.1642	0.3143	0.3714	0.3429	0.2857	0.3433	0.2121
	3′HVR[a]		0.2414	0.3200	0.2982	0.2830	0.2632	0.3333	0.2692
	M13		0.4915	0.5410	0.5238	0.5806	0.4237	0.4627	0.4915
3	33.6			0.3231	0.3333	0.2239	0.2174	0.2121	0.1940
	3′HVR[a]			0.4000	0.3333	0.2453	0.1579	0.2549	0.3077
	M13			0.3871	0.2813	0.3333	0.3667	0.3536	0.4333
4	33.6				0.2647	0.2286	0.3429	0.3134	0.2941
	3′HVR[a]				0.1579	0.3061	0.3061	0.2340	0.3478
	M13				0.1765	0.3538	0.3871	0.2857	0.5161
5	33.6					0.2285	0.2867	0.2836	0.2941
	3′HVR[a]					0.2857	0.2857	0.2800	0.3962
	M13					0.2239	0.2500	0.2500	0.4063
6	33.6						0.2286	0.2239	0.2647
	3′HVR[a]						0.2308	0.1600	0.3617
	M13						0.3333	0.2464	0.4098
7	33.6							0.2239	0.2353
	3′HVR[a]							0.1538	0.2516
	M13							0.2941	0.3667
8	33.6								0.2308
	3′HVR[a]								0.2444
	M13								0.3824

[a] 3′HVR, α-globin 3′HVR

are used for constructing phylogenetic trees, most, if not all, of them are based on band frequencies in populations by evaluating the DNA fingerprinting patterns of individuals. We show here that the coefficient of differences among populations, obtained by evaluating DNA mixes of populations, can be directly used for constructing phylogenetic trees. This approach is both simple and fast.

Correlation between inter-line variability and the performance of F_1 hens

The correlation coefficients between inter-line maximum distance and some 40 week production traits of F_1 hens are listed in Table 6. With probe 33.6, the maximum distance was positively and significantly correlated with higher egg number and the heterosis for mean survival rate ($P < 0.01$) as well as the heterosis percentages for higher egg number, higher egg production and higher survival rate ($P < 0.05$); the correlations between the maximum distance and mean egg number and its heterosis percentage, mean egg production and its heterosis percentage and higher egg production are also positive and the correlation coefficients are high but not statistically significant at the 0.05 level of probability. With the α-globin 3′HVR or M13 probes, there was a trend for the maximum distance to be positively correlated with all the traits, although most of their coefficients were not statistically significant. Thus we con-

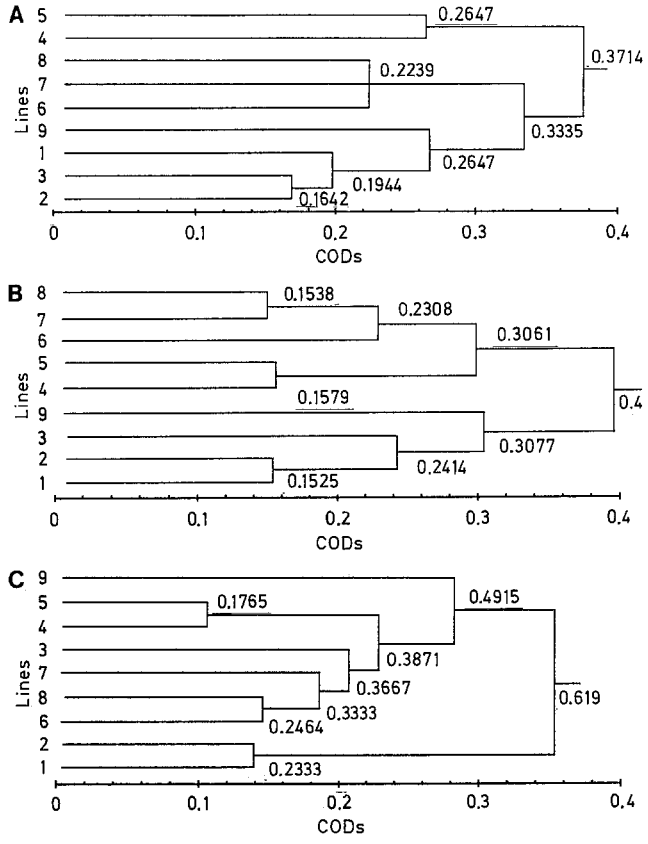

Fig. 2A–C Hierarchical clustering of nine pure lines of Beijing White Leghorn chickens. The cluster analyses, based on coefficients of difference (CODs) between parental lines (Tables 5), were performed using the maximum method described by Johnson (1967). The COD at which two lines or clusters first join together is written on the figure, which is also defined as the maximum distance between a pair of lines. **A** probe 33.6; **B** probe α-globin 3′HVR; **C** probe M13

cluded that the greater the distance between two parental lines, as estimated by DNA fingerprinting, the better the performance of their F_1 cross with respect to egg number, egg production and survival rates. In other words, the greater the variability of DNA fingerprints between two parental lines, the better the performance of their hybrids. For example, lines 2, 4, 6 and 9 are classified into different clusters (see Fig. 2), and crosses 4 × 2, 9 × 4 and 6 × 9 gave the best performance among the 72 inter-line crosses with respect to 40-week egg number and egg production as well as for heterosis for these two traits.

It is noted that the correlation between maximum distance and a given trait was dependent on the probe used. An extensive pedigree analyses in humans revealed that only 1.2% of DNA fingerprint bands were co-detected by two probes (Jeffreys et al. 1991). Bruford and Burke (1994) also demonstrated in chickens that probes 33.6, 33.15, α-globin 3′HVR and M13 HVR detected almost independent sets of loci. So, it seems that the probe-dependence of the correlations is essentially locus-dependent.

Correlation between intra-line variability and the performance of F_1 hens

The correlation coefficients between the similarity coefficients within sire line or dam line and some 40-week production traits of F_1 hens are listed in Table 7. Regardless of the probe used, similarity coefficients within a sire line or dam line are positively correlated with egg number, heterosis for egg number and for egg production in the F_1 generation. Crosses involving a line with a higher similarity coefficient produced more eggs and showed stronger heterosis for both egg number and egg production. For instance, for the best three

Table 6 Correlation coefficients between inter-line maximum distance and performance of crosses[a]

40 week traits	Correlation coefficient (Regression equation[b])		
	Probe 33.6	Probe α-globin3′HVR	Probe M13
Mean egg number	0.779	0.615	0.504
Heterosis for mean egg number (%)	0.791	0.373	0.315
Higher egg number	0.940** (= 87.84 + 29.93COD$_m$)	0.607	0.667
Heterosis for higher egg number (%)	0.893* (= − 8.74 + 46.35COD$_m$)	0.436	0.522
Mean egg production (kg)	0.674	0.556	0.519
Heterosis for mean egg production(%)	0.697	0.445	0.367
Higher egg production(kg)	0.714	0.278	0.618
Heterosis for higher egg production(%)	0.810* (= − 4.85 + 34.54COD$_m$)	0.390	0.559
Mean surival rate(%)	− 0.184	0.458	0.588
Heterosis for mean survival rate(%)	0.968** (= − 2.85 + 16.26COD$_m$)	0.771* (= − 1.55 + 11.55COD$_m$)	0.596
Higher survival rate(%)	0.012	0.592	0.670
Heterosis for higher survival rate(%)	0.890* (= − 2.38 + 19.45COD$_m$)	0.407	0.299

[a] The linear correlations are based on data listed in Table 2. For the definition of the mean trait values and the higher trait values see Materials and methods. *, $P < 0.05$; **, $P < 0.01$

[b] A regression equation is developed only when the correlation is statistically significant. The COD$_m$ in the equations symbolizes the maximum distance between a pair of lines

Table 7 Correlation coefficients between the similarity coefficients within parental lines and the performance of crosses[a]

Parental lines	40-week traits	Correlation coefficients (regression equations[b])		
		Probe 33.6	Probe α-globin 3′HVR	Probe M13
Sire	Egg number	0.356	0.594	0.491
	Heterosis for egg number(%)	0.638	0.896** ($=-31.34+61.2F_s$)	0.626
	Egg production(kg)	0.132	0.237	0.105
	Heterosis for egg production(%)	0.483	0.818** ($=-25.86+52.01F_s$)	0.471
	Survival rate(%)	−706* ($=102.2-15.54F_s$)	−0.463	−0.559
	Heterosis for survival rate(%)	−0.154	0.431	0.038
Dam	Egg number	0.171	0.470	0.439
	Heterosis for egg number(%)	0.480	0.764* ($=-30.64+59.97F_d$)	0.566
	Egg production (kg)	−0.125	0.098	0.051
	Heterosis for egg production(%)	0.346	0.701* ($=-22.78+46.57F_d$)	0.421
	Survival rate(%)	−0.665* ($=104.5-19.85F_d$)	−0.442	−0.343
	Heterosis for survival rate(%)	−0.249	0.257	0.074

[a] The linear correlations are based on data listed in Tables 3 and 4. *, $P<0.05$; **, $P<0.01$

[b] A regression equation is developed only when the correlation is statistically significant. The F_s or F_d in the equations symbolize the similarity coefficient within the sire line or within the dam line, respectively

inter-line crosses (i.e., crosses 4 (♂) × 2(♀), 9 × 4 and 6 × 9, with respect to 40-week egg number and egg production as well as heterosis for these two traits) both sire lines and dam lines had a high similarity coefficient. However, the intra-line similarity coefficient was negatively correlated with 40-week survival rate in the F_1 generation. At present we have no explanation for this. Since egg-production traits are of the greatest importance in laying hens, lines with a high similarity coefficient should be selected as parent lines in making commercial crossbreds.

As mentioned above, the performance of the F_1 generation was affected by the genetic distance between parental lines, and so crosses between two lines with a high similarity coefficient did not always result in a good performance. For example, crosses between lines 4 and 5, both of which had a high similarity coefficient, showed poor performance beacuse the two lines were closely related as revealed by DNA fingerprinting.

With regard to reciprocal effects, some authors reported that a cross between two lines had strong heterosis only when the line of higher genetic homogeneity was used as the sire line (Kovalenko and Bondarenko 1979; Chen 1986). We found that correlation coefficients between the similarity coefficients of sire lines and the production traits of crosses were not significantly different from those between the similarity coefficients of dam lines and the production traits of crosses ($P>0.05$). It seems that no general rule exists for the choice of sire line based merely on intra-line genetic similarity, although a pair of reciprocal crosses may differ greatly in performance. For example, the hetrosis percentages for 40-week egg number and for egg production of cross 9 × 4 were 20.61% and 21.37%, respectively, whereas those of cross 4 × 9 were 11.73% and 11.20%, respectively. Therefore, the choice of sire line between two lines should rely on the result of a reciprocal crossing test.

Conclusions

Most lines or stocks of chickens available today are formed by successive artificial selection for specific traits of economic importance. Accurate estimates of genetic diversity within lines or stocks and of relatedness between lines or stocks are important both for the maintenance of lines and stocks and the development of superior commerical cross strains. Such estimates can be obtained by exploiting the power of DNA fingerprinting, as demonstrated by other authors (Kuhnlein et al. 1989, 1990; Dunnington et al. 1991, 1994; Haberfeld et al. 1992; Siegel et al. 1992). In the present experiment, we have examined genetic diversity within and among nine pure lines of Beijing White Leghorn chickens by DNA fingerprinting and our results were consistent with the known history of the lines.

Modern poultry production has paid much attention to strain or line crosses mainly in order to take advantage of heterosis. It has been shown that both dominance and epistasis are important in hetrosis for egg-production traits in Leghorn strain crosses (Fairfull et al. 1987). Compared to related strains, genetically distant strain are more likely to have different fixed alleles at the same loci and hence their crosses should give a higher degree of heterosis. Furthermore, heterosis should be greater if both parental strains have a higher degree of homozygosity. Genetic diversity estimated by DNA fingerprinting is to a large extent representative of the whole genome and may be associated with heterosis for some traits. Our study has demonstrated that the variability of DNA fingerprints within and among parental lines is correlated with some production traits of laying hens from line crosses. Other authors have previously found some DNA fingerprint bands that were associated with specific traits in farm animals (Georges

et al. 1990; Dunnington et al. 1993; Plotsky et al. 1993). Therefore, it is likely that some minisatellites have co-evolved with genes controlling quantitative traits.

Correlation coefficients between the variability of DNA fingerprints in parents and the performance of F_1 laying hens obtained in our experiment might be biased because crosses between lines formed under identical selection criteria were included in the analysis. Nevertheless, in cases where the correlation coefficients are statistically significant ($P < 0.05$) (Tables 6 and 7) the performance of crosses in some traits could be predicted based simply on DNA fingerprint variability within or among parental lines by developing a linear regression equation. For example, we obtained a regression equation relating mean heterosis for 40-week egg production of F_1 hens (H_p) to the similarity cofficient of a sire line (F_s) with the α-globin 3'HVR probe as $H_p = -25.864 + 52.01F_s (P < 0.01)$.

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