# BREEDING AND GENETICS

## Measurement of Genetic Parameters Within and Between Turkey Lines Using DNA Fingerprinting[1]

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**ABSTRACT** An experiment was conducted to estimate genetic parameters in six experimental and five commercial primary breeding turkey lines using DNA fingerprinting. Eighteen individual DNA samples per line were digested with an *Hae*III restriction enzyme and hybridized with Jeffreys' 33.6 probe. The DNA fingerprints were analyzed with computer programs to measure band sharing (BS) and band frequencies. Within lines, BS ranged from 0.39 to 0.62 and reflected the history of the experimental lines. Among lines, BS ranged from 0.21 to 0.33 with an average of 0.26. The BS among the experimental lines reflected known relationships. All lines were subdivided based on indices of population subdivision. About 26 hypervariable loci were estimated from band frequencies. Average heterozygosity and genetic variability estimated from band frequencies were significantly different among lines and displayed a result very similar to the BS among lines. Genetic distance indices among lines were also significantly different and reflected known relationships between the experimental lines. The experimental selected lines displayed lower genetic diversity than did the other lines. The parameters measuring genetic diversity within lines had higher correlation coefficients among them than did the parameters between lines. The computer program used in this study made DNA fingerprinting easier to use in population analysis.

(*Key words*: DNA fingerprinting, computer analysis, genetic diversity, genetic distance, turkey lines)

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## INTRODUCTION

The DNA fingerprinting technique was developed by Jeffreys *et al.* (1985). The technique targets a large number of hypervariable loci that are considered to be distributed over the entire genome. In DNA fingerprinting, simple sequence repeats, such as $(CAC)_5$ (Schafer *et al.*, 1988), and minisatellite sequences, such as Jeffreys' 33.6 and 33.15 (Jeffreys *et al.*, 1985), have been used as probes that hybridize to a large number of restriction fragments of genomic DNA. Because allelic variation in the repeat unit number and mutation in genomic DNA alter the profiles of DNA restriction fragments, the band patterns of DNA fingerprinting display a high degree of polymorphism (Jeffreys, 1987). Different individuals show their unique band patterns in Southern blots. The DNA patterns are highly stable and constant in somatic and germ cells of one individual and inherited in a codominant, Mendelian manner (Cawood, 1989; Bruford *et al.*, 1992).

The DNA fingerprinting technique has been applied in different aspects of animal population genetics (Kuhnlein *et al.*, 1989, 1990, 1991; Hillel *et al.*, 1989, 1991; Dunnington *et al.*, 1990, 1992; Haberfeld *et al.*, 1992; Stephens *et al.*, 1992; Dolf *et al.*, 1993; Plotsky *et al.*, 1993). The technique was demonstrated to be a powerful tool for the study of population genetics. Five potential applications in animal breeding were described by Hillel *et al.* (1993) as follows: identification of genetic distance between related populations; evolution studies in populations selected for quantitative traits; DNA marker-assisted selection; genomic selection; and heterosis. Use of the technique may provide additional methods for improving economic traits in breeding stocks.

The greatest disadvantage of DNA fingerprint analysis is that it is labor intensive and time-consuming, especially when many populations with large sample sizes are analyzed. It is difficult to compare band patterns from different blots or different areas of the same blot distantly apart and almost impossible to compare large number of samples reciprocally by visual inspection without pooling DNA samples (Hillel *et al.*, 1993). Moreover, the use of radioactive materials in the analysis makes the technique more labor intensive and involves health hazards.

Most commercial and some experimental turkey lines have been maintained and selected for decades. Genetic

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diversity is of concern in long-term selected animal lines. It has been estimated that genetic improvement will reach a plateau in about 30 yr with current testing and selection methods (Wheeler and Campion, 1993). Therefore, it is important to measure some important genetic parameters in these lines. This study was designed to estimate genetic parameters within and among experimental and commercial turkey lines based on DNA fingerprints. Computer programs and nonradioactive DNA detection were applied to facilitate the analysis.

## MATERIALS AND METHODS

### Turkey Lines

Six closed experimental and five commercial turkey lines were used in the DNA fingerprinting. The RBC1 line was a randombred control population derived from a wide genetic background (McCartney, 1964). The RBC2 line was a randombred control line established from the crossing of two commercial lines of large-bodied turkeys (Nestor *et al.*, 1969). The E line was a subline of the RBC1 line developed by family selection for increased egg production (Nestor, 1980). The F line was a line derived from the RBC2 line by mass selecting for increased 16-wk BW (Nestor, 1977a). The RBC3 line was another randombred control line developed from reciprocal crosses of a commercial sire line and the F line (Noble *et al.*, 1995). The FL line was a line derived from the F line by mass selecting for increased shank width (Nestor *et al.*, 1985).

All randombred control populations were maintained with 36 parental pairs (Nestor, 1977b). Seventy-two parental pairs were used to reproduce the E line. Thirty-six males and 72 females (1 sire mated to 2 dams) were used to reproduce the F line. The 18 best families (four males and four females per family) in the E line were selected to produce offspring for the next generation. The top 36 males and 72 females were chosen in the F line. Thirty-six males and 54 females were selected in the FL line. All parents were mated at random except that full sib matings were avoided to reduce the increase in inbreeding. The E, F, and FL lines had been selected for 36, 25, and 13 generations, respectively.

Five primary breeding turkey lines from a commercial breeder were used. The A and B lines were sire lines selected for growth traits. The C and D lines were large white dam lines selected for a combination of growth and reproduction traits. The G line was a dam line of medium BW and high reproductive performance. Information on line history and selection criteria was not available.

### Probe Preparation

A 1.5-kb inserted fragment of a human genomic clone of Lambda 33.6 (Jeffreys *et al.*, 1985) was purified by gel electrophoresis and elution (Maniatis *et al.*, 1986). The fragment was used as a DNA template for probe production. A Genius 1 DNA labeling and detection kit[3] was used to label the probe by random primed incorporation of digoxigenin-labeled deoxyuridine-triphosphate. The nonradioactive probe can be stored for several months and reused in the hybridization procedures.

### Southern Blot Analysis

Turkey blood samples were randomly collected from 18 males of different families in each line. The DNA isolation method used was reported by Emara *et al.* (1992). Approximately 10 to 15 $\mu$g of DNA from each sample was digested with 15 U of an *Hae*III restriction enzyme[4] for over 3 h in 30 $\mu$L total volume and separated by electrophoresis on 0.8% agarose gels for 36 h at 1.5 V/cm. The DNA in the gels was denatured, neutralized, and blotted to nylon membranes[4] using a Posiblot Pressure Blotter[5] for 2 to 3 h.

Prehybridization and hybridization were conducted according to a method described by Bruford *et al.* (1992) using a 0.25 *M* phosphate buffer containing 1 m*M* EDTA, 7% SDS, and 1% BSA as prehybridization and hybridization solutions. Color development was based on the procedures described in the Genius System User's Guide (Boehringer Mannheim, 1992). The hybridization buffer was reused up to five times. The color development was monitored, and the reactions were stopped when faint bands were visible.

### Computer and Statistical Analysis

Band patterns developed in the membranes were scanned with a computer scanner using a commercially available program, DNA ProScan MW-RFLP.[6] Marking DNA bands was performed on the images amplified 400% to reduce human error. A DNA molecular weight marker ($\lambda$ *Hin*dIII digested) was loaded into lanes in both edges and in the middle of the gel to assist the computer program to correct slight inconsistence of DNA migration among the distantly separated gel lanes and served as a standard for the program to calculate the nucleotide base pair number of each marked band. The DNA fragment sizes from each sample were saved as an individual PRN file using Lotus 123® software[7] with a macro program to speed up the procedure.

Two custom computer programs were created using QBASIC® language[8] to compare the restriction band patterns reciprocally. One program was used to measure band sharing (BS) between individuals from the same lines (within lines) and from different lines (between lines) according to the equation:

[3]Boehringer Mannheim, Indianapolis, IN 46250.
[4]Promega Corp., Madison, WI 53711.
[5]Stratagene, La Jolla, CA 92037.
[6]DNA PROSCAN Inc., Nashville, TN 37212.
[7]Lotus Development Corp., Cambridge, MA 02142.
[8]Microsoft Corp., Redmond, WA 98052.

$$BS = \frac{2N_{ab}}{N_a + N_b}$$

(Wetton *et al.*, 1987), where $N_{ab}$ was the number of scored bands shared by samples a and b, $N_a$ and $N_b$ were the total numbers of scored bands in samples a and b, respectively. Another computer program was used to compare six patterns (three from each line in the same blot) from two lines simultaneously. The program counted the total number of different bands and calculated the frequency of each different band in a line.

Bands with differences in size less than or equal to 0.5% were considered the same bands. Because the relationship of DNA fragment size and migration distance in a gel was logarithmic rather than linear, differences of 0.13% × $\log_{10}$ (bp) were also used. The modified differences ranged from about 0.4% for 1.2-kb to 0.5% for 6-kb fragments. Band comparisons using computer analysis and visual inspection did not show a line by method interaction ($P$ = 0.98), although BS levels differed significantly among the methods used. The correlation coefficient between the BS by visual inspection and by computer programs was equal to 0.95. The method using a difference of 0.13% × $\log_{10}$ bp or less of a band was used in the computer analysis because it displayed a higher correlation with the visual inspection than the linear method.

The BS levels were used for relatively unbiased estimates of genetic distance between lines using the equation:

$$D' = -\ln\left(\frac{S_{ij}}{\sqrt{S_i S_j}}\right)$$

adapted by Lynch (1991) from Nei (1972), where $S_{ij}$ is average BS between two populations i and j and $S_i$ and $S_j$ are average BS between individuals within populations i and j, respectively. For testing population subdivision, the equation: $S_{ij}' = 1 + S_{ij} - \frac{S_i + S_j}{2}$ (Lynch, 1991) was used. If two populations are homogeneous, $S_{ij}'$ is equal to 1. In this study, two populations with a $S_{ij}'$ smaller than 0.90 was considered to be subdivided.

Band frequencies (BF) were also used to estimate some genetic parameters. An index of genetic distance between two lines was calculated according to the equation:

$$D = -\ln\left(\frac{1}{N}\sum_{i=1}^{N}\frac{2V_i^{(1)}V_i^{(2)}}{\left[V_i^{(1)}\right]^2 + \left[V_i^{(2)}\right]^2}\right),$$

where N is the number of different bands counted in two lines and $V_i^{(1)}$ and $V_i^{(2)}$ are the frequencies of band i in populations 1 and 2, respectively. The equation was adapted by Kuhnlein *et al.* (1989) from the genetic identity measure of Hedrich (1971). The genetic variability was calculated using the equation:

$$V = 1 - \frac{1}{N}\sum_{i=1}^{N} V_i ,$$

where $V_i$ is the frequency of band i and N is the number of bands counted (Kuhnlein *et al.*, 1989). Heterozygosity ($H_{ub}$ and $H_{bc}$) and the number of loci ($L_{ub}$ and $L_{bc}$) were estimated according to the following equations:

$$L_{ub} = \sum_{k=1}^{A}\left(1 - \sqrt{1 - S_k}\right)$$

(Gilbert *et al.*, 1990),

$$H_{ub} = \frac{2N}{2N - 1}\left(\frac{\sum_{k=1}^{A} S_k}{A - \sum_{k=1}^{A}\sqrt{1 - S_k}} - 1\right)$$

(Stephen *et al.*, 1992),

$$L_{bc} = L_m + \sum_{k=1}^{A}\left(1 - \sqrt{1 - S_k}\right) - \frac{\sum_{k=1}^{A} S_k/\sqrt{1 - S_k}}{8N}$$

(Jin and Chakraborty, 1993),

and

$$H_{bc} = \sum_{k=1}^{A} S_k/L_{bc} - 1$$

(Jin and Chakraborty, 1993),

where $S_k$ is the frequency of the $k^{th}$ band and A, N, and $L_m$ are the total number of different bands, number of individual samples, and unique bands in a line, respectively. Subscripts ub and bc are the abbreviations of unbiased and biased corrected, respectively, indicating two different methods for the same measurement.

The BS within lines was used to estimate the genetic diversity of the lines, and the BS between lines were used as indices to compare with the known relationships of the lines. A General Linear Models (GLM) procedure provided in the SAS® software package (SAS Institute, 1988) was used to test the differences in these estimated genetic parameters within lines and between lines. Duncan's multiple range test (Duncan, 1955) was used to separate the means. Unless otherwise stated, significant levels were $P < 0.05$. The SAS® program was also used to test the interactions of line by method and to calculate correlation coefficients among similar measurements, such as BS within lines, genetic variability, and heterozygosity. The BS levels were transformed to other values, namely band differing (BD), using the equation, BD = 1 − BS.

## RESULTS

Colorimetric DNA detection produced clear band patterns in the nylon membranes. Most bands scored

**TABLE 1. Band sharing (BS) between individuals from the same and different lines and indices of population subdivision between the turkey lines[1]**

| Lines[2] | RBC1 | E | RBC2 | F | RBC3 | FL | A | B | C | D | G |
|---|---|---|---|---|---|---|---|---|---|---|---|
| RBC1 | 0.461 | 0.319 | 0.282 | 0.246 | 0.251 | 0.227 | 0.271 | 0.293 | 0.230 | 0.269 | 0.274 |
| E | 0.778 | 0.621 | 0.229 | 0.247 | 0.246 | 0.253 | 0.208 | 0.270 | 0.239 | 0.254 | 0.268 |
| RBC2 | 0.822 | 0.689 | 0.459 | 0.288 | 0.248 | 0.273 | 0.287 | 0.210 | 0.241 | 0.260 | 0.255 |
| F | 0.748 | 0.669 | 0.791 | 0.536 | 0.293 | 0.329 | 0.259 | 0.253 | 0.247 | 0.262 | 0.256 |
| RBC3 | 0.811 | 0.726 | 0.809 | 0.816 | 0.419 | 0.303 | 0.225 | 0.309 | 0.252 | 0.268 | 0.248 |
| FL | 0.738 | 0.684 | 0.785 | 0.803 | 0.835 | 0.517 | 0.243 | 0.239 | 0.269 | 0.260 | 0.271 |
| A | 0.820 | 0.677 | 0.837 | 0.771 | 0.795 | 0.764 | 0.441 | 0.235 | 0.279 | 0.233 | 0.253 |
| B | 0.819 | 0.716 | 0.737 | 0.742 | 0.856 | 0.737 | 0.771 | 0.487 | 0.247 | 0.286 | 0.242 |
| C | 0.803 | 0.732 | 0.815 | 0.783 | 0.846 | 0.814 | 0.862 | 0.807 | 0.393 | 0.261 | 0.271 |
| D | 0.818 | 0.722 | 0.809 | 0.772 | 0.837 | 0.780 | 0.791 | 0.821 | 0.843 | 0.444 | 0.257 |
| G | 0.848 | 0.762 | 0.830 | 0.793 | 0.843 | 0.819 | 0.837 | 0.803 | 0.879 | 0.840 | 0.391 |

[1]BS within (on the diagonal) and between lines (above the diagonal) differed significantly ($P \leq 0.001$). The BS was calculated according to an equation by Wetton *et al.* (1987). The indices of population subdivision (below the diagonal) were calculated using an equation by Lynch (1991).

[2]RBC1, RBC2, and RBC3 = randombred control populations; E = a subline of RBC1 selected for increased egg production; F = a subline of RBC2 selected for increased 16-wk BW; FL = a subline of the F line selected for increased shank width; A and B = commercial sire lines selected for growth traits; C and D = commercial large-white dam lines selected for a combination of growth and reproduction traits; and G = a commercial dam line of medium BW and high reproductive performance.

were between 1.2 and 6 kb in size. The average number of scored bands per sample in a line, ranging from 37 to 40, was not significantly different among lines.

Within lines, BS ranged from 0.39 to 0.62, and the values differed ($P \leq 0.001$) among lines (Table 1). Average BS of the three experimental selected lines (E, F, and FL) was about 0.56, whereas the averages of the randombred control and commercial lines were 0.45 and 0.43, respectively. The BS reflected the history in the three selected experimental and three randombred control lines. Lines E, F, and FL were the only ones significantly different in BS levels. The differences between minimum and maximum BS within these lines were at least 0.28, and the standard deviation of the BS ranged from 0.07 to 0.12.

The BS between lines ranged from 0.21 to 0.33 with a mean of 0.26 (Table 1), which was significantly ($P \leq 0.001$) lower than that within lines. The BS levels among experimental lines were significantly ($P \leq 0.001$) different. They reflected the known relationships between lines (Figure 1). When two randombred control lines were compared to all commercial lines, the RBC1 line had a significantly higher BS (0.29) with the B line than did the RBC2 line (0.21). The RBC1 line had a higher BS with the B line than with the C line. The RBC2 line showed a higher BS with the A line than with the B and C lines. The commercial B line had unexpectedly high BS (0.31) with the RBC3 line, although the B line did not show a high BS with the RBC2 and F lines. Significant differences in BS were also found among the commercial lines. The BS between lines selected for similar traits did not suggest that selection in different lines increased BS between the lines.

Indices of population subdivisions ranged from 0.67 to 0.86 (Table 1). All indices were well below 1, indicating that all lines were subdivided. Indices between experimental lines reflected the history of the lines, such as number of separating generations, selection performed, and genetic bases.

When DNA fingerprints were analyzed based on BF, the percentages of unique bands and total number of different bands scored in a line were significantly different ($P \leq 0.01$) among turkey lines (Table 2). However, the estimated number of the loci was not significantly different among lines or between the two methods of determination. An average of 26 hypervariable loci was estimated. Genetic variability and heterozy-

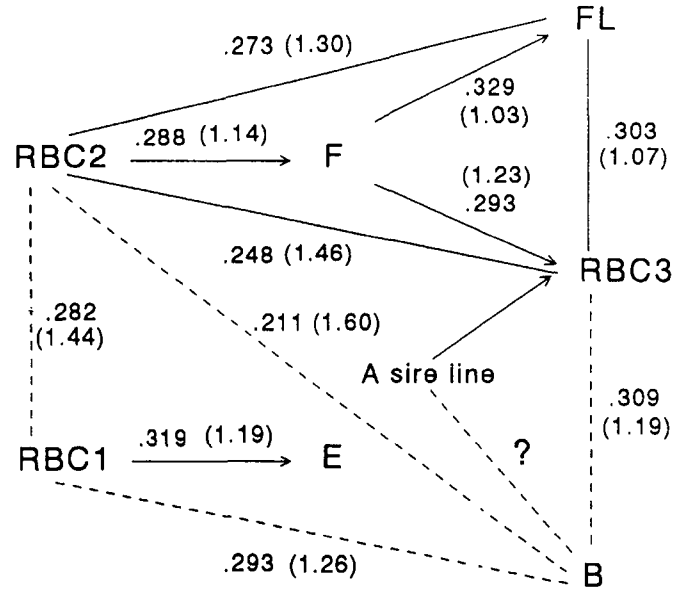


**FIGURE 1.** Relationships of the six experimental turkey lines and band sharing (BS) and genetic distance (in parentheses) between the turkey lines with known and unknown relatedness. Arrows indicate from where lines were derived. Lines show indirect relationships, and dash lines display unknown relationships. RBC1, RBC2, and RBC3 were randombred control populations; E was a subline of RBC1 selected for increased egg production; F was a subline of RBC2 selected for increased 16-wk BW; FL was a subline of the F line selected for increased shank width; B was a commercial sire line selected for growth traits and was included because of the unexpected high BS with the RBC3 line.

**TABLE 2. Frequencies of unique bands, number of different bands and hypervariable loci, genetic variability (V), and heterozygosity in the turkey lines**

| Turkey lines[1] | Unique bands | Different bands | V[2] | Locus number | | Heterozygosity | |
|---|---|---|---|---|---|---|---|
| | | | | $L_{ub}$[3] | $L_{bc}$[3] | $H_{ub}$[4] | $H_{bc}$[4] |
| | (%) | (n) | | | | | |
| RBC1 | 36.1[a] | 72[a] | 0.507[a] | 25 | 23 | 0.528[abc] | 0.630[a] |
| E | 16.3[c] | 56[b] | 0.375[c] | 28 | 26 | 0.334[d] | 0.386[d] |
| RBC2 | 29.3[ab] | 76[a] | 0.474[ab] | 28 | 26 | 0.512[abc] | 0.572[ab] |
| F | 24.3[b] | 68[a] | 0.420[bc] | 29 | 27 | 0.420[cd] | 0.439[cd] |
| RBC3 | 33.3[ab] | 73[a] | 0.489[a] | 25 | 24 | 0.565[a] | 0.594[ab] |
| FL | 25.1[b] | 66[a] | 0.442[ab] | 27 | 25 | 0.445[bcd] | 0.480[bcd] |
| A | 33.2[ab] | 77[a] | 0.477[ab] | 28 | 26 | 0.530[abc] | 0.532[abc] |
| B | 29.0[ab] | 70[a] | 0.459[ab] | 27 | 25 | 0.481[bc] | 0.502[bcd] |
| C | 33.1[ab] | 76[a] | 0.488[a] | 25 | 24 | 0.622[a] | 0.633[a] |
| D | 30.7[ab] | 72[a] | 0.495[a] | 26 | 24 | 0.514[abc] | 0.609[a] |
| G | 36.1[a] | 76[a] | 0.498[a] | 25 | 23 | 0.631[a] | 0.626[a] |

[a–d]Means within a column with no common superscript differ significantly ($P \leq 0.05$).

[1]RBC1, RBC2, and RBC3 = randombred control populations; E = a subline of RBC1 selected for increased egg production; F = a subline of RBC2 selected for increased 16-wk BW; FL = a subline of the F line selected for increased shank width; A and B = commercial sire lines selected for growth traits; C and D = commercial large-white dam lines selected for a combination of growth and reproduction traits; and G = commercial dam line of medium BW and high reproductive performance.

[2]The genetic variability was calculated from an equation by Kuhnlein *et al.* (1989).

[3]There were no differences among the lines ($P > 0.05$). Locus number, $L_{ub}$ and $L_{bc}$, were calculated based on equations by Gilbert *et al.* (1990) and Jin and Chakraborty (1993), respectively.

[4]Heterozygosity, $H_{ub}$ and $H_{bc}$, were calculated based on equations by Stephens *et al.* (1992) and Jin and Chakraborty (1993), respectively.

gosity estimated from BF were also different ($P \leq 0.01$). The two methods used to estimate heterozygosity gave significantly different values, but there was no line by method interaction. Indices of genetic variability and heterozygosity displayed a result very similar to that of BD within lines. Correlation coefficients among calculated BD levels within lines, genetic variability, and heterozygosity were highly significant ($P \leq 0.0002$). The correlation coefficients ranged from 0.89 to 0.98 (Table 3). Using the GLM procedure, no significant interaction of line by method was detected among these parameters.

**TABLE 3. Correlation coefficients among parameters estimated from DNA fingerprints of individuals in the same or different turkey lines[1]**

| | Between lines[2] | | | | Within lines[3] | | |
|---|---|---|---|---|---|---|---|
| | $S_{ij}'$ | D′ | D | | V | $H_{ub}$ | $H_{bc}$ |
| BD | –0.61 | 0.81 | 0.84 | BD | 0.92 | 0.98 | 0.92 |
| $S_{ij}'$ | | –0.96 | –0.64 | V | | 0.89 | 0.96 |
| D′ | | | 0.76 | $H_{ub}$ | | | 0.91 |

[1]The correlation coefficients among estimated parameters were significant (all $P \leq 0.001$ except for $S_{ij}'$ vs BD and $S_{ij}'$ vs D, which were $P \leq 0.015$).

[2]BD = band differing calculated by 1 – band sharing (BS) between lines, where BS was calculated using an equation by Wetton *et al.* (1987); $S_{ij}'$ = population subdivision index calculated with an equation by Lynch (1991); D′ = genetic distance index estimated from BS according to Lynch (1991); and D = genetic distance index estimated from band frequencies based on an equation by Kuhnlein *et al.* (1989).

[3]BD = 1 – BS within lines; V = genetic variability calculated according to Kuhnlein *et al.* (1989); $H_{ub}$ = unbiased estimate of heterozygosity calculated using an equation by Stephens *et al.* (1992); and $H_{bc}$ = bias corrected estimate of heterozygosity based on an equation by Jin and Chakraborty (1993).

Estimated genetic distance ranging from 0.38 to 0.92 and from 1.03 to 1.79 based on BS and BF, respectively (Table 4). Indices between the experimental lines reflected their relationships and history (Figure 1). Indices estimated from BS within and between lines appeared to be better indicators of genetic differences between lines than those from BF. On the other hand, indices from BF seemed to show relatedness between lines better than those from BS according to the base population, selection method, and separating generations.

Correlations among indices of genetic distance, BD between lines, and indices of population subdivision were also significant (Table 3). The correlation coefficient between subdivision indices and indices of genetic distance estimated from BS levels was –0.96. The indices of population subdivision had similar correlation coefficients with the BD levels and the indices of genetic distance estimated from the BF (–0.61 and –0.64), as did the BD with the indices of genetic distance estimated from BS and BF (0.81 and 0.84). The correlation coefficient between the two indices of genetic distance was 0.76.

## DISCUSSION

The experimental lines used in the present study were maintained for genetic research. All were closed populations. The history of the lines has been well documented including population sizes, generations, selection criteria, genetic bases, and mating systems. Randombred

**TABLE 4. Indices of genetic distance estimated from band sharing and band frequencies of DNA fingerprints between individuals from different turkey lines[1]**

| Lines[2] | RBC1 | E | RBC2 | F | RBC3 | FL | A | B | C | D | G |
|---|---|---|---|---|---|---|---|---|---|---|---|
| RBC1 | | 0.518 | 0.489 | 0.703 | 0.560 | 0.766 | 0.509 | 0.481 | 0.616 | 0.516 | 0.438 |
| E | 1.19 | | 0.846 | 0.848 | 0.729 | 0.806 | 0.923 | 0.711 | 0.726 | 0.726 | 0.609 |
| RBC2 | 1.44 | 1.77 | | 0.544 | 0.570 | 0.579 | 0.450 | 0.812 | 0.567 | 0.552 | 0.508 |
| F | 1.46 | 1.41 | 1.14 | | 0.481 | 0.470 | 0.630 | 0.703 | 0.620 | 0.622 | 0.581 |
| RBC3 | 1.46 | 1.79 | 1.46 | 1.23 | | 0.429 | 0.647 | 0.380 | 0.476 | 0.476 | 0.490 |
| FL | 1.47 | 1.59 | 1.30 | 1.03 | 1.07 | | 0.677 | 0.744 | 0.518 | 0.613 | 0.506 |
| A | 1.34 | 1.85 | 1.30 | 1.32 | 1.50 | 1.42 | | 0.679 | 0.400 | 0.641 | 0.495 |
| B | 1.26 | 1.50 | 1.60 | 1.42 | 1.19 | 1.31 | 1.65 | | 0.572 | 0.486 | 0.590 |
| C | 1.24 | 1.82 | 1.34 | 1.25 | 1.23 | 1.18 | 1.03 | 1.29 | | 0.470 | 0.369 |
| D | 1.44 | 1.55 | 1.44 | 1.40 | 1.30 | 1.28 | 1.56 | 1.25 | 1.42 | | 0.483 |
| G | 1.28 | 1.73 | 1.36 | 1.20 | 1.33 | 1.21 | 1.21 | 1.35 | 1.17 | 1.37 | |

[1]The indices of genetic distance between the lines were calculated using an equation by Lynch (1991) based on band sharing and an equation by Kuhnlein *et al.* (1989) based on band frequencies. The numbers above and below the diagonal space were estimated from band sharing and band frequencies, respectively.

[2]RBC1, RBC2, and RBC3 = randombred control populations; E = a subline of RBC1 selected for increased egg production; F = a subline of RBC2 selected for increased 16-wk BW; FL = a subline of the F line selected for increased shank width; A and B = commercial sire lines selected for growth traits; C and D = commercial large-white dam lines selected for a combination of growth and reproduction traits; and G = a commercial dam line of medium BW and high reproductive performance.

control lines were also maintained along with the selected lines. These lines were excellent models for evaluating the applications of DNA fingerprinting in studies of animal populations.

The parameters estimated from DNA fingerprints of individuals from the same lines, such as BD, genetic variability, and heterozygosity, were highly correlated with correlation coefficients close to 1. The high correlation coefficients among them suggested that these parameters were virtually the same measurement. Genetic variability and heterozygosity are measurements of genetic diversity in a population. Therefore, BS between individuals from the same population can also serve as an index to evaluate the genetic diversity in a population.

Unlike the parameters within lines, most parameters estimated from individuals of two lines did not have high correlation coefficients among the parameters. All correlation coefficients were smaller than 0.85 except the one between indices of population subdivision and genetic distance based on BS (0.96). Based on the correlation coefficients, indices of population subdivision and genetic distance probably were the same measurement. According to the results and the information provided on the experimental lines, it appeared that these two indices measured the overall difference of two populations, which may be used for evaluating population subdivision. The BS between individuals from different lines and indices of genetic distance from BF may measure different parameters. The BS seemed to be the superior indicator of relatedness between populations than other parameters, and indices of genetic distance based on BF better reflected genetic distance.

The selected experimental lines, especially E, exhibited a reduction in genetic diversity relative to the commercial lines and experimental control lines. Inbreeding differences may have been involved in line differences in genetic diversity. The BS of DNA fingerprints in chicken strains was associated with the known inbreeding of the strains, though they were not related in a linear manner (Kuhnlein *et al.*, 1990). A similar result was found in sheep populations (Hermans *et al.*, 1993). In future selection experiments, mating individuals with low BS between them instead of random mating may reduce the rate of decrease in genetic diversity of populations.

Pairwise comparisons of DNA fingerprints among several chicken lines derived from the same or different base populations have been performed by Dunnington *et al.* (1991). Closed lines divergently selected from the same base populations had higher BS levels than those of unrelated lines. A similar result was found in the present experiment where the BS reflected the known degrees of relationships very well. Therefore, high BS levels between some of these lines (e.g., RBC1 and B, RBC3 and B, A and C, and B and D) with unknown relationships suggested that the lines have genetic material in common.

Based on a limited sample of available turkey lines, the average BS among the lines was 0.26. Dunnington *et al.* (1994), in an extensive survey of broiler chicken sire and dam lines and parental stocks of white egg layers, measured an average BS of 0.26. Thus, it appears that turkey lines may not be more closely related than chicken lines.

All lines were subdivided according to indices of population subdivision. The result was reasonable based on history of the experimental lines. The experimental lines had been closed and maintained for more than ten generations. Although some lines were derived from the same genetic base, the lines had undergone different selection pressure on a long-term basis.

Although the total number of different bands significantly varied among lines, the numbers of hypervariable loci estimated by two methods did not differ. This result seems to be theoretically reasonable, because the hypervariable loci should be consistent within a species.

The computer programs significantly reduced the time needed and provided higher stringency for analyz-

ing DNA fingerprints than visual inspection. Using the computer programs, the band comparisons were completed in a few hours, whereas it probably would take a person several months to finish using visual inspection. Images of band patterns can be amplified to reduce subjective error in marking bands. One disadvantage of the computer program is that bands with different color intensity cannot be treated differently. However, this appeared not to be a major problem because the BS from visual inspection and from computer analysis were highly correlated and no line by method interaction was detected. Future improvement to include the information of color intensity is possible for the computer program. Therefore, the computer analysis is an excellent substitute for tedious visual inspection.

In summary, the results obtained from the analysis of DNA fingerprints reflected the known information of experimental turkey lines. The DNA fingerprinting is an excellent technique for measuring genetic parameters within and between animal lines. The computer programs greatly facilitated the DNA fingerprinting analysis.

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