A genome scan inference to the genetic evaluation of selected and randombred chicken populations

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Essam A. El-Gendy
Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt.

ABSTRACT

The genome scans were obtained for three lines of chickens: genotyping for homozygous naked-necks (line N), homozygous normal feathering (line F) and their randombred population (line C). Lines N and F have undergone massive selection for two generations for increased 6-week body weight. The objective of the study was to evaluate the genetic changes associated with selection or random breeding. Six pooled DNA samples within line and generation were scanned by five decamer RAPD-PCR primers. The averages of allelic bands were 11, 10.6, and 9.6 bands for lines N, F and C, respectively. Bands with polymorphic nature were detected and averaged 71.5, 66.7 and 59.3% of the total allelic bands in the respective lines. The monomorphic alleles averaged 3.3, 8.2 and 8.6%, and line-specific bands were also observed and averaged 9.7, 10.8, and 6.2%. The line-specific bands were mainly attributed to selection and poorly to the random genetic drift. The recognition of monomorphic and line-specific allelic bands revealed the reliable contribution of genome scanning in recognition of line specificity. The change in allele frequency over two selected generations in lines N and F demonstrated allelic bands with downward trend and others with upward trend, concluding that genomic alleles may be employed to monitor the changes in allele frequency over subsequent generations. Allelic coalescence points were estimated and the copies descended from ancestral alleles to the second generation were estimated to be 29.56, 28.20 and 37.56% of the total allelic bands scored in lines N, F and C. Number of gene trees were formed due to the accumulation of transmitted ancestral alleles and totaled 22, 12, and 15 in the respective lines. The estimation of rate of coalescence points and tracing ancestral alleles is of significance for small-sized selected and inbred populations. The results of genomic variability reported in lines N and F indicated that a further selection progress is anticipated in each. The genetic distance between lines N and F after two generations of selection was 1.03, and both were genetically distant from line C by 1.15 and 0.81. The results denote to the significance of genome scanning in the evaluation of breeding programs.

Key words: *Genome scan, genetic evaluation, chicken populations.*

INTRODUCTION

Genomic information provides a unified approach for the variation within and between populations, which is influenced by neither the environmental conditions nor the developmental stages of organisms. Vanhala *et al.* (1998) and Corzo *et al.*, (2004) denoted to the usefulness of molecular information in the evaluation of the genetic variation and divergence. The genomic diversity among different domestic, exotic and commercial breeds and in relation to the environments has been very much explained

by the variation in genomic polymorphism (Plotsky *et al.*, 1995; Vanhala *et al.*, 1998; Sharma *et al.*, 2001; Semyenova *et al.*, 2002; Zhang *et al.*, 2002; Ahlawat *et al.*; 2004; Cuc *et al.*, 2006; and El-Gendy *et al.*, 2006), and conservation plans for domestic populations have been constructed (Romanov and Weigend, 2001). Tremendous genomic researches have targeted the recognition of quantitative trait loci associated with meat production (Dunnington *et al.*, 1992; 1993; Plotsky *et al.*, 1993; Van Kaam *et al.*, 1999; Jennen *et al.*, 2004; Atzmon *et al.*, 2006; Gao *et al.*, 2006; McElroy *et al.*, 2006; and Zhou *et al.*, 2006), and egg production (Schreiweis *et al.*, 2005; and Abasht *et al.*, *2006*). Genomic analyses have been also used to signify population specificity and to detect genetic markers in chicken and turkey lines that have undergone different breeding programs (Dunnington *et al.*, 1991; Zhang *et al.*, 1995; Zhu *et al.*, 1996; El-Gendy *et al.*, 2000; Saleh *et al.*, 2002; Deeb and Lamont, 2003). Such genomic information would be very much helpful to predict the progress in breeding plans. Therefore, the collaboration of genomic and phenotypic information of pedigreed animals is a major breakthrough in poultry breeding to identify the individuals genotyping for maximum productivity (El-Gendy *et al.*, 2000; 2006; Boichard, 2002; Meuwissen and Goddard, 2004; and Zhou *et al.*, 2006).

The objective of this study was to set a genomic inference for the evaluation of the genetic changes in two lines selected for 6-week body weight and a line randomly bred. The selected lines have been formed by an ongoing breeding program aiming to develop an Egyptian native broiler strain.

MATERIALS AND METHODS

The genetic stocks and experimental design

The genetic stocks used in this study were three chicken lines. Line N which is genotyping for homozygous naked-necks, line F which is genotyping for homozygous normal feathering and line C which represents an Egyptian native randombred population genotyping for naked-necks and normal feathering. Lines N and F have been derived from an entirely heterozygous naked-neck crossbred population and have undergone massive selection for two generations for increased 6-week body weight. Line C has been maintained as a randombred line. Because the objective of the study targeted the line specificity achieved by the ongoing breeding program using genome scanning, the goodness of the results would not as much depend on the number of primers used as it depends on the employment of appropriate primers which evince line specification. However, the overall genetic differences between lines by DNA band patterns may become more explicit by using a plenty of primers, but this was beyond the scope of this study. Also as the genomic differentiation between selected and randombred lines was primarily objected, pooled DNA samples were used. PCR products of all lines, by generation, and recognized by the same primer, along with the DNA marker were separated by electrophoresis on the same agarose gel, to make generation and line comparisons available. The pooled DNA samples have been considered cogent enough to indicate population specificity in chickens (Dunnington *et al.*, 1991; Zhang *et al.*, 1995; 2002; El-Gendy *et al.*, 2000; 2006; and Singh and Sharma, 2002).

Blood collection, DNA extraction and sampling

One-ml blood samples were individually drawn in heparinized 5-ml tubes from the branchial veins of individuals, 10 weeks old, representing both sexes, for each line and generation. The individuals of lines N and F

were those having heaviest 6-week body weights, while individuals of line C were randomly selected. Blood samples were then stored in -20°C until processing of DNA extraction. Upon the collection of all blood samples by line and generation, genomic DNA of each sample has been extracted according to the procedures of Sharma *et al.* (2001). Equal amounts of 10 individual DNA samples, within line and generation, were drawn and put together forming pooled samples, and six samples were made for each.

RAPD-PCR and electrophoresis

DNA samples were subjected to RAPD-PCR analysis using five decamer oligonucleotides arbitrary sequenced primers (Table 1, Operon Technologies, Alameda, CA, USA). The PCR reaction mixture contained 1.30 μl 50 m*M* $MgCl_2$, 5 μl 10X enzymetic reaction buffer (200 m*M* Tris HCl and 500 m*M* KCl, pH = 8.8), 5 μl 10 m*M* dNTPs, 0.23 μl Taq DNA polymerase (5 units/μl), 2 μl primer (15 ng/μl), 2 μl genomic DNA (10 ng/μl). The mixture was increased by sdH_2O to a total volume of 25 μl. Amplification of DNA fragments was carried out using applied biosystem thermocycler-9700 (Applied Biosystem, Foster, CA, USA). PCR protocol included initial denaturation at 95°C for 2 min., followed by denaturation for 40 cycles; each was started at 94°C for 1 min. then the annealing at 35°C for 1 min. and lasted by extension at 72°C for 1 min. The final extension was at 72°C for 5 min. PCR products were loaded along with a standard DNA marker (λ DNA-*Hind III* digested and ΦX174 DNA-*Hae III* digested), on a 1.4% agarose gel (Sigma-Aldrich Co., UK) in 1X TAE running buffer and stained with ethidium bromide. Electrophoresis of the genomic bands was run at 90 volts for 50 min. in a horizontal apparatus (Biometra, Rudolf-Wissell-Stra Be, Goettingen, Germany). The bands were then visualized using an ultraviolet trans-illuminator (Biometra, Rudolf-Wissell-Stra Be, Goettingen, Germany), and exposed to Polaroid films by an ultraviolet illumination camera. The photographs were developed and used to generate the molecular data set.

Parameters under study

The parameters generated from the molecular data set were:

1. ***Allelic band frequency and coalescence points***

   The frequency of allelic bands was estimated, within line and generation. The alleles were traced across generations, for the incidence of coalescence events, and the probability (*P*) of distinct allele coalescences were estimated according to Hedrick (2000), where:

   $$P = [\prod (1-i/2N)]^t [1/2N], \quad i = 1,....n$$

   and *N* denotes to the sample size, and *i* indicates i^{th} allele in *n* sampled alleles, having *n*-1 ancestral alleles in *t*+1 generations.

2. ***Band sharing (BS),*** which estimates the similarity within lines and generations, according to Wetton *et al.* (1987):

   $$BS = 2(n_{ab}) \div (n_a + n_b)$$

   where, n_{ab} indicates number of bands shared between samples a and b. n_a and n_b indicate the total number of bands in samples a and b, respectively.

3. ***Heterozygosity (H),*** which estimates heterozygosity, by line and generation, for the recognized alleles, according to Ott (1992):

   $$H = 1 - \sum P_i^2, \quad i = 1,....n$$

   where, P_i is the frequency of i^{th} allele in *n* sampled alleles.

4. ***Genomic variability (GV),*** which estimates the genomic variability indices, within lines and generations, using the formula of Kuhnlein *et al.* (1989):

   $$GV = 1 - (1/n \sum v_i), \quad i = 1,....n$$

where, v_i indicates the frequency of band i in the samples under comparison and n indicates the total number of bands scored.

5. ***Genetic distance (GD),*** which estimates the genetic distances between the lines according to Kuhnlein *et al.* (1989):

$$GD = - \ln(I),$$

$$I = 1/n \sum [(2\ v_i^{(a)}.\ v_i^{(b)}) \div ((v_i^{(a)})^2 + (v_i^{(b)})^2)],\quad i = 1,\ldots.n$$

where, I is the genetic identity index for a pair of lines (a) and (b), n is the total number of bands scored in both lines and v_i is the frequency of i^{th} band.

Statistical analysis

Regression of heterozygosity, band sharing and variability on generations was carried out and t-test was used to assess the significance of regression coefficients (SAS, 1999).

RESULTS AND DISCUSSION

Polymorphism and line specificity

A total of 73 allelic bands were amplified by all primers in all lines (Table 1), with averages of 11, 10.6, and 9.6 bands for lines N, F and C, respectively. The band size varied from 118 to 3130 bp. Bands with polymorphic nature were primed in all lines. The percentages of polymorphic bands were high and averaged, overall primers, 71.5, 66.7, and 59.3% in lines N, F and C, respectively. Monomorphic allelic bands were detected and their percentages averaged 3.3, 8.2 and 8.6% in lines N, F and C, respectively. Line-specific bands with different molecular weights were also identified by different primers, and averaged 9.7, 10.8, and 6.2% in lines N, F and C, respectively. The possible causes for specific alleles are mutations, random genetic drift and selection. Because spontaneous mutation rates are typically rather small, 10^{-4} to 10^{-6} per gene per generation (Hartle and Clark, 1989), the tendency of allele frequency to change due to recurrent mutation over a course of two generations would be negligible. According to Jeffreys *et al.* (1988), mutation may result in appearance of new allelic bands at a rate of 1/300 per generation. The mutation rate after two selected generations is 0.007, this means that only 0.7% of the specific bands appeared in this study was due to mutation. The random genetic drift could have been through the errors in sampling process, where the number of sires used to produce the base population was not quite large. The selected lines were also obtained over generations in minimum size, each was formed of 10 sire families having 4-5 dams in each and totaling about 55 parents. The heterozygosity is reduced to $[1-(1/2n)]^t$, in t generations due to random genetic drift (Hartl and Clark, 1989), where n is the effective population size. In this study, the base generation was 100% heterozygous. So, the heterozygosity left in each line after two generations of selection is 0.98. This indicates that only 2% of the line-specific bands may be accounted for random genetic drift. Selection could result in the appearance of line-specific alleles, *via* its role in the changes of allele frequencies. The recognition of monomorphic and line-specific alleles expresses the reliable contribution of genome scanning in revealing line specificity. Polymorphism of 25 to 32% was obtained among Kadaknath and Nicobari Indian breeds (Sharma *et al.,* 2001; and Ahlawat *et al.*; 2004), and averaged 65.2% in Fayoumi, White Baladi and Sinai Bedouin Egyptian breeds (El-Gendy *et al.*, 2006). Polymorphism was 100% of the microsatellite loci found in eight chicken lines greatly differing in the gene pool, three White Leghorn hybrids, three lines native to Finland, a Rhode Island Red line and a broiler hybrid line (Vanhala *et al.*, 1998). In mountain Vietnamese native chickens, Cuc *et al.* (2006) reported a mean number of alleles of 6.41 per locus. The high polymorphism

reported in chickens in most studies may be correlated with the high percentage of the hyper variable regions found in avian genomes, and may explain the capability of birds to withstand a wide range of environmental conditions. The genetic diversity among Chinese breeds was estimated to be 0.02 to 0.23 (Zhang et al., 2002). Singh and Sharma (2002) reported polymorphism in 21.9% of the bands identified in White Leghorn chickens that have undergone selection. The monomorphic allelic bands were shown in Egg-type and Meat-type, native Indian and Egyptian breeds, revealing breed specificity (Sharma *et al.*, 2001; and El-Gendy *et al.*, 2006). Appearance of new bands upon subsequent generations was reported by Burke and Bruford (1987), when detected novel bands in a house sparrow family and not presented in the parents. The bands were mainly attributed to mutation or incorrect parentage determination. Appearance of bands specific to chicken lines was also reported, when divergent selection was practiced for growth or heat tolerance (Dunnington *et al.*, 1990; and El-Gendy *et al.*, 2000), and their percentages increased as the selection preceded. From the standpoint of breeding, line-specificity assessed by genome banding could be primarily employed as genetic markers in selection. Nakamura *et al.* (2006) reported five microsatellite alleles specific to a dual-purpose native Japanese breed.

Table (1): Summary of polymorphism, monomorphism and line specification in the lines.

Primer	5'–3' Sequence	# Bands				Polymorphism, %			Monomorphism, %			Line-Specification, %		
		MW, bp	N	F	C	N	F	C	N	F	C	N	F	C
A-04	AATCGGGCTG	118-3130	16	12	12	80.0	60.0	60.0	0.0	0.0	5.0	10.0	0.0	10.0
A-014	TCTGTGCTGG	310-2320	9	9	9	58.3	41.7	41.7	16.7	33.3	33.3	25.0	0.0	0.0
B-07	GGTGACGCAG	118-3130	14	14	13	77.8	77.8	61.1	0.0	0.0	11.1	5.6	11.1	5.6
B-019	ACCCCCGAAG	194-2320	8	10	8	80.0	100.0	80.0	0.0	0.0	0.0	0.0	20.0	0.0
G-03	GAGCCCYCCA	234-2320	8	8	6	61.5	53.8	53.8	0.0	7.7	7.7	7.7	23.1	15.4
Mean±SE			11.0	10.6	9.6	71.5	66.7	59.3	3.3	8.2	11.4	9.7	10.8	6.2

N and F, denote to the naked-neck and normally feathered selected lines.
C, denotes to the randombred line.

Table (2): Summary of the incidence of coalescence events and gene trees (GT), and probability of presence of ancestral alleles in the coalescence points (P).

Primer	Line N				Line F				Line C			
	Coalescence events		GT	P	Coalescence events		GT	P	Coalescence events		GT	P
	G_0	G_1			G_0	G_1			G_0	G_1		
A-04	10	16	9	0.0321	1	2	1	0.1593	4	4	3	0.1593
A-014	6	4	4	0.3870	7	6	6	0.3870	4	4	4	0.3870
B-07	3	3	3	0.0760	3	2	2	0.0760	4	5	5	0.1117
B-019	5	2	3	0.4914	1	1	1	0.2963	2	2	2	0.4914
G-03	4	3	3	0.4914	2	2	2	0.4914	1	1	1	0.7286
Total	28	28	22		14	13	12		15	16	15	
Mean	5.6	5.6	4.4	0.2956	2.8	2.6	2.4	0.2820	3.0	3.2	3.0	0.3756

N and F, denote to the naked-neck and normally feathered selected lines.
C, denotes to the randombred line.
G_0, and G_1, denote to the base and first generations.

Table (3): Mean heterozygosity, band sharing, and variability, overall primers, within lines.

Generation	Heterozygosity			Band Sharing			Variability		
	N	F	C	N	F	C	N	F	C
G_0	0.581	0.397	0.321	0.579	0.592	0.638	0.425	0.264	0.214
G_1	0.648	0.305	0.283	0.512	0.702	0.586	0.452	0.203	0.339
G_2	0.678	0.423	0.416	0.469	0.533	0.424	0.505	0.282	0.278
$\alpha + \beta^{'}$	0.54*+0.05	0.35+0.01	0.25+0.05	0.63*-0.06	0.67-0.03	0.76-0.11	0.38*+0.04	0.23+0.01	0.21+0.03

N and F, denote to the naked-neck and normally feathered selected lines.
C, denotes to the randombred line.
$\alpha + \beta$, are the intercept and the slop by which the traits were regressed over generations.
*, indicates significant regression parameter ($P \leq 0.03$).

Table (4): Genetic distance estimates across generations within the selected lines and between the lines after 2nd selected generation.

Primer	Within Lines, across generations						Between Lines after 2nd selected generation		
	Line N			Line F					
	$G_0 \rightarrow G_1$	$G_1 \rightarrow G_2$	$G_0 \rightarrow G_2$	$G_0 \rightarrow G_1$	$G_1 \rightarrow G_2$	$G_0 \rightarrow G_2$	N → C	F → C	N → F
A-04	0.34	0.57	0.76	2.62	0.74	1.44	1.44	1.79	1.65
A-014	0.33	0.81	1.00	0.00	0.47	0.47	1.81	0.51	1.38
B-07	1.43	1.30	0.73	1.35	1.79	0.87	0.84	0.60	1.20
B-019	0.58	1.24	0.78	1.61	2.17	0.98	0.52	0.33	0.78
G-03	0.78	0.24	0.99	1.49	0.11	1.49	---	---	0.12
Mean±SE	0.69±0.20	0.83±0.20	0.85±0.06	1.41±0.42	1.06±0.39	1.05±0.19	1.15±0.29	0.81±0.33	1.03±0.27

N and F, denote to the naked-neck and normally feathered selected lines.
C, denotes to the randombred line.
G_0, G_1 and G_2, denote to the base, first and second generations.

Estimation of Allelic band frequency and rate of ancestral allele transmission

The change in allelic band frequency over two generations of selection was monitored in lines N (Fig. 1) and F (Fig. 2), revealing allelic bands with downward trend and others with upward trend. The classification of allelic bands according to the change in their frequencies over subsequent generations, can be expressed in the segregation of alleles into selected or unselected allelic bands. So, genomic alleles may be employed to monitor the changes in allele frequency over subsequent generations, and in turn, to evaluate the expected breeding progress. On the other hand, the identified allelic bands were traced from the 2nd generation back to the base generation to examine for coalescence events (Table 2), where genes descended from the same ancestral alleles forming gene trees. Many gene trees appeared in the products of all primers in all lines, and many alleles were vanished. Total number of gene trees, overall primers, was 22, 12, and 15 among lines N, F and C, respectively. Gene trees occur due to the genetic treatment of populations over many generations (Fu and Li, 1999; and Hedrick, 2000), where some alleles are lost while some alleles become more frequent. The smaller the populations, the earlier the appearance of coalescence events and gene trees. Because particular alleles are accumulated over subsequent generations upon selection, the identity of some descended alleles and incidence of coalescence points are probable in lines N and F. Line C has been maintained as a small-sized random-mated population; such mating system indeed permits for inbreeding occurrence, resulting in possible transmission of copies of ancestral alleles across generations forming gene trees. The estimates of probability of incidence of coalescence points were, in general, high and averaged, overall primers, 0.2956, 0.2820 and 0.3756, in lines N, F and C, respectively. This means that

29.56, 28.20 and 37.56% of the allelic bands scored in the second generation of lines N, F and C descended from ancestral alleles forming gene trees. Since the alleles resulted due to mutations was estimated to be 0.7% of the line-specific alleles and the specific alleles correspondents to lines N, F and C averaged 9.7, 11.8 and 6.2% of the total bands scored, the probabilities of incidence of coalescence points due to mutations are 0.0022, 0.0025 and 0.0016, which are extremely low. The high estimates of coalescence points in lines N and F in relation to the short-term selection, although reveal the accumulation of alleles by selection, is expected since the lines are generated in small-sized populations. The conclusion of existence of coalescence events for ancestral alleles might be, however, confounded with being drawn from information generated by pooled DNA samples in the selected lines. In fact, DNA pooled samples were of the individuals showing highest performance in each selected generation which increases the possibility of accumulation of copies of selected ancestral alleles in small-sized selected populations. An experimental plan is already set for the ongoing generations, targeting the coalescence points and gene trees using microsatellites and individual DNA samples. It is concluded that the estimation of allelic coalescence events and tracing ancestral alleles would be very much valuable for small-sized selected and inbred populations as the case of local breeds.

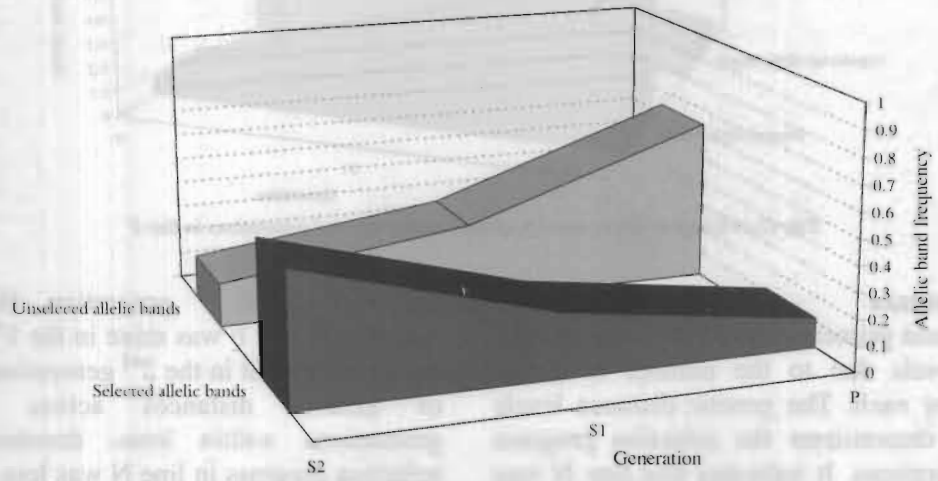

Fig. (1): Change in allelic band Frequency over selected generations in line N

Heterozygosity, variability and similarity

The heterozygosity within line N steadily increased over subsequent generations and reached to 0.678, in the 2nd selected generation (Table 3), whereas it tended to fluctuate, with less magnitude, within lines F and C and reached to 0.423 and 0.416. The coefficients of regression of heterozygosity on generations in all lines was not however significant. In line N, the intercept was positive and significant ($P<0.027$), revealing high heterozygosity in the base generation. Vanhala *et al.* (1998) reported a mean heterozygosity of 0.67, in a broiler line *versus* 0.29, in a White Leghorn line. Also, heterozygosity varied from 0.627 to 0.668 in three mountain native Vietnamese

chickens (Cuc *et al.*, 2006). Also, increasing trends were observed for the genomic variability within lines N and F over subsequent generations and averaged, overall primers, 0.505 and 0.282 after two generations of selection *versus* a fluctuating trend in line C. The fluctuation trend in line C is anticipated for such a random-mated line. Similar trend of molecular variation was also observed by Vanhala *et al.* (1998), attributing it to the small sizes of populations under study. Although the similarities within lines, estimated by band sharing indices, seemed in declining trends over subsequent generations in all lines, the corresponding regression coefficients were not significant. The insignificance pattern of the regression coefficients of heterozygosity, genomic variability and similarity is possible over a course of only two generations. The results of genomic variability reported in lines N and F denote that a further selection progress is anticipated in each line.

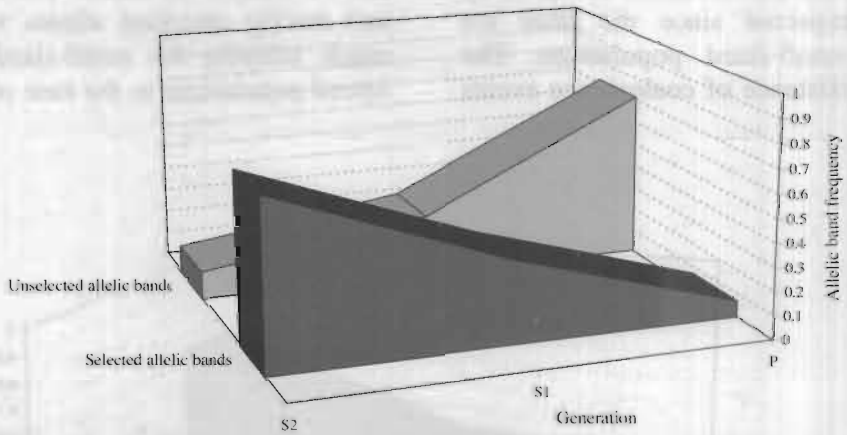

Fig. (2): Change in allelic band frequency across selected generations in line F

Genetic distance

Different primers showed different genetic distance levels due to the number of bands amplified by each. The genetic distance levels (Table 4), demonstrate the selection progress across generations. It indicates that line N was 0.69 genetically distant from the base population after one generation, and has achieved a genetic distance of 0.83 by the second generation. The results also reveal that line F has responded to selection, achieving genetic distances of 1.41 and 1.06 after one and two generations of selection, respectively. This reflects that line N showed more response to selection in the 2nd generation compared to that achieved in the 1st generation. However the progress in line F was more in the 1st generation compared to that in the 2nd generation. The trend of genetic distances across subsequent generations within lines, denotes that the selection progress in line N was less than in line F. The genetic distance between lines N and F after two generations of selection was 1.03, and both were genetically distant from the line C by 1.15 and 0.81, respectively. Thus, selection has segregated the populations into truly two different lines. The genetic distances estimated by Vanhala *et al.* (1998) among eight different Finnish native chicken lines confirmed the specific genetic features of them. Also Sharma

et al. (2001) and Ahlawat *et al.* (2004) reported least genetic distances between Indian native breeds and farthest distances between the natives and the exotics or commercial strains. The estimated genetic distances thus reliably expressed the response of the populations to selection and random breeding.

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الملخص العربي

إستخدام المسح الجينومى فى التقييم الوراثى لعشائر دجاج تحت ظروف الإنتخاب أو التزاوج العشوائى

عصام عباس الجندى

قسم الإنتاج الحيوانى – كلية الزراعة – جامعة القاهرة – الجيزة – جمهورية مصر العربية

تم إجراء تقييم للخصائص الوراثية المصاحبة للإنتخاب أو التزاوج العشوائى عن طريق المسح الجينومى بإستخدام RAPD-PCR لثلاث عشائر (خطوط) دجاج: الخط (N) وهو لدجاج أصيل عارى الرقبة، الخط (F) وهو لدجاج أصيل للتربيش الطبيعى، العشيرة (C) وهى تمثل القطيع المحلى المصرى ويحمل التراكيب الوراثية المختلفة لنمو ريش الرقبة. خضع الخطان N وF للإنتخاب الفردى لوزن الجسم عند عمر 6 أسابيع لجيلين وخضعت العشيرة C للتزاوج العشوائى كنموزج للقطعان المحلية. كانت متوسطات عدد المقاطع الأليلية 11، 10.6، 9.6 فى العشائر N، F، C، وكانت نسب المقاطع لمواقع متعددة المظاهر (polymorphism) تمثل 71.5، 66.7، 59.3% بينما كانت المقاطع لمواقع وحيدة المظهر (monomorphism) تمثل 3.3، 8.2، 8.6%، وكانت نسب المقاطع المحددة للعشيرة تمثل 9.5، 10.8، 6.2%. وجد أن المقاطع المحددة للعشيرة ترجع أساسا إلى الإنتخاب وبدرجة قليلة إلى الإنجراف الوراثى العشوائى. كما أن التعرف على مقاطع لمواقع وحيدة المظهر أو محددة للعشيرة يدل على إمكان إستخدام المسح الجينومى لدراسة خصائص العشائر. وجد أن تكرار المقاطع الوراثية خلال جيلين من الإنتخاب فى الخطين N، F قد إتخذ إتجاه تكرارى هابط لبعضها وإتجاه تكرارى صاعد للبعض الأخر مما يدعم إمكان إستخدام المسح الجينومى فى قياس التغير فى تكرار الأليلات عبر الأجيال. كانت نقاط الإلتحام الأليلي تمثل 29.56، 28.20، 37.56% من كل المقاطع الأليلية للعشائر N، F، C، وكان عدد الأشجار الجينية المتكونة نتيجة إنتقال الأليلات الجدود عبر الأجيال هو 22، 12، 15، ويعتبر تقدير معدل الإلتحام الأليلى وتتبع إنتقال الأليلات الجدود ذات أهمية كبيرة فى العشائر الصغيرة تحت ظروف الإنتخاب أو التزاوج العشوائى حيث تتزايد إحتملات حدوث التربية الداخلية. أشارت النتائج إلى إمكان تحقيق نتائج إيجابية عند إستمرار الإنتخاب فى الخطين N، F، وكانت المسافة الوراثية المقدرة بينهما 1.03 وكانت بين كلا منهما وبين العشيرة C على التوالى 1.15، 0.81.