DETECTION OF QUANTITATIVE LOCI CORRELATION WITH GROWTH TRAITES IN LOCAL QUAIL USING PCR-RFLP TECHNIQUE

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ABSTRACT

The objective of this study was to investigate the polymorphisms of three loci (SEMA3E, GH and TLX) that related with growth traits in local quail. A total of 720 birds (males and females) from three lines (desert, brown and white) were used. The results revealed that the effects of the line were significant on bird body weight and carcass weight and dressing percentage at 180 days at age. The Best Linear Unbiased Prediction (BLUP) value overall birds for body weight was ranged from -9.2173 to 10.0117, these results showed there were significant differences among high and low BLUP value groups in three quail lines under study. The PCR-RFLP results overall three lines showed that there were three, three and two alleles for SEMA3E, TLX and GH locus, respectively. This alleles gives twelve differences genotypes, the desert male quail with ACABAA genotype and desert female quail with AAABAA genotype (high group) for three loci under study give significantly higher body and carcass weight compared with another groups. In conclusion results showed that there are agreements between BLUP values with PCR-RFLP results to select best birds and the selection process with molecular technique can play a major positive and rapid role to improve and increase growth traits in these lines of local quail in Iraqi Kurdistan region.

Key words: BLUP, growth traits, genes, RFLP, alleles.
INTRODUCTION
Quail is a model animal species due to its small body size, fast growth rate, early sexual maturity, lower cost of care and high reproductive rate (13). Quails have been used to investigate different studies for several purposes since it is closely related to chickens (6). The quail is a sexually dimorphic bird, females have a large body size and require more time to reach sexual maturity than males (25). Producing high-performance poultry lines is the main goal of breeders and farmers, industrially (15). It has been investigated that genetic factors control that both production and reproductive traits (17). Genetic improvement of economic traits of quail procedures for multiple-trait genetic evaluation of livestock requires accurate estimates of genetic and environmental parameters (3). Best Linear Unbiased Prediction (BLUP) is the current method of choice for genetic evaluation of traits. Traditionally, the selection of animals for breeding is based on two types of data, pedigree and phenotypes (2). Therefore, genetic studies of poultry species rely on BLUP in their investigation. The development of molecular biology and particularly DNA base ANDd markers facilitated genetics and animal breeding of livestock studies (11). Molecular genetic markers are important tools to analyze genomes and associate heritable traits with an underlying variation of genomes. In addition, experimental of candidate genes and their effects on the phenotypic traits the basis of marker-associate selection (MAS) (15). The quail has been considered as a model animal in several biological and biomedical studies, the identification of quail genome has been to facilitated various studies and recognize distinct lines of quail (12, 1). The ability of quail to growth and reproductive during certain periods varies greatly due to its diversity among the individuals. It is known that the nature of growth and reproduction are generally influenced by Growth Hormone (GH), steroids and peptides (29). A secreted class 3 semaphorin encoded SEMA3E gene is specific vascular beds to trigger repulsion of endothelial cells, it is also involved to modulate axonal growth and regulate synaptic connectivity for the correct wiring of the central nervous system (CNS) (8). Moreover, Song et al., (31) demonstrated that T-cell leukemia translocation (TLX), also known as Hox11 is considered as an important target in neural development through the progressive regulation of cell cycle in Neural Stem Cells (NSCs). Therefore, the objective of the present study is to identify the genetic polymorphism and best genotypes for quail’s growth using PCR-RFLP for three specific genes (SEMA3E, GH and TLX).

MATERIALS AND METHODS
Measurement of growth and carcass traits
This study was carried out in Grdarasha researches unit, under the supervision and regulations of ethic committee at college of agricultural engineering sciences, Salahaddin University-Erbil. For this purpose 720 newly hatched quail chicks of three local lines, desert (214), brown (250) and white (256) each line were randomly distributed into ten families; the mating system was in a ratio of one male to three females. The estimated BLUP of %10 (top and bottom) form both male and female in local quails according to high and low body weight. The birds were raised under the same living conditions and feeding. A total 144 quail birds were selected for the study (weight and carcass trait), including 72 quails from the high production (H) and low production (L) line for each sex were isolated according to their differences in feather color and body weight. The quails were individually weighed and slaughtered at 6 months by cutting the jugular vein. Blood from each quail were collected for Genomics analysis according to the procedure of Oeywale, (22) as described by (33). The birds were then properly bled (about 4 minutes) and feathers removed manually after dipping in hot water for about two minutes. Dressed percentage were calculated according to procedure and formulae of (6).

\[
\text{Dressed \% (DP)} = \frac{\text{Carcass yield}}{\text{Live body weight}} \times 100
\]

Sample collection and DNA extraction
Genomic DNA was extracted from the blood of 144 local quails. One mL of blood samples was collected from each bird and then put in a 3mL of anti-coagulant Tris-ethylene di amine tetra acetic acid (EDTA) tube. DNA was then extracted from the blood sample of each bird...
using the DNeasy® blood kit (GeNet Bio, Korea) according to the manufacturer’s instructions. The quantity and quality of DNA was checked by Nanodrop (1000 UK) spectrophotometer and gel electrophoresis.

Selection of the loci and genotyping of the samples

The respective loci were selected according to the chromosome map that was previously constructed by (27). The loci and primers designed for this study were shown in Table 1. The primers were designed based on the sequences submitted to the GenBank by (27), using Primer-Blast of NCBI (http://www.ncbi.nlm.nih.gov). The total reaction volume of PCR was 25 μL consisting 10 μL of Green Master Mix (25 units/mL Taq DNA polymerase 200 μM of each dNTPs and 1.5 mMof MgCl2), 1 μL forward and reverse of primer of each gene, 1 μL of DNA template, and the volume was completed with 12 μL of DNAse free water. The thermocycling conditions for gene 1 (CJA1), and 3 (CJA3) included initial denaturation step at 94 ºC for 5 min, followed by 32 cycles at 94 °C for 1 min, annealing at 60 ºC for 1 min, elongation at 72 ºC for 1 min and a final extension step at 72 ºC for 10 min. For GH gene The thermocycling conditions included an initial denaturation step at 95 ºC for 5 min, followed by 35 cycles of denaturation at 94 ºC for 30 s, primer annealing at 56 ºC for 45 s, elongation at 72 ºC for 1 min, and an extension step at 72 ºC for 5 min. The digestion of 10 μL of PCR product was made using the restriction enzyme (27) with some minor modifications and also based on the instructions of the manufacturer (Thermo Scientific) Table 2. Table 3 shows the restriction enzymes and reaction conditions that were used in the current study. Electrophoresis analysis was made for PCR products using 2.5% agarose gel stained with safe day (Cat. No. B-2010, GeNet Bio, Korea). The agarose gel was run at a constant voltage of 100 V/cm for 45 min. The bands were subsequently visualized by UV transilluminator and the gel photographed (Proxima 2500 Isogene Life science, Netherland). In this study a total of 6 PCR amplicons (2 for each genes) were sent two the commercial company for purificated and sequencing (Macrogen Inc. South Korea). The sequences similarity analysis with previous sequences published in GenBank were performed using the BLAST programme (http://www.ncbi.nlm.nih.gov/BLAST). BLAST analysis approved that all sequences were SEMA3E, TLX and GH gene with 99-100 identities with previous published this genes

| Locus | Chromosomal Location (cM) | Accession Number | Primer Sequence (5’-3’) |
|-------|--------------------------|------------------|------------------------|
| SEMA3E | CJA1 (70.5) | MN542411 | Forward-ATACTCCAGCTGAGTGGGGA  
Reverse-CAGAAGTATGAGGGAGATCAG |
| TLX | CJA3 (165.4) | MN542412 | Forward-ACACTAGGAACATAATGGGCT  
Reverse-TCACCTGTGGCGTTTCAGATT |
| GH | CJA5 (82.3) | MN542413 | Forward-ATCCCCAGGCAAACATCCTCG  
Reverse-CCTGACATCCAGCTCACAT |

Table 2. Name and Reaction conditions of Restriction Enzyme used for each Locus

| Locus | Restriction enzyme | Amount(Unit) | Incubation(°C/h) | Buffer |
|-------|--------------------|--------------|-----------------|--------|
| SEMA3E | Hae III | 5 | 37/3 | R |
| TLX | PstI | 5 | 37/3 | O |
| GH | Msp I | 5 | 37/3 | Tango |

Table 3. PCR Product Digestion component for all studied Genes

| Digestion component | Volume |
|---------------------|--------|
| PCR product | 10μl |
| Reaction 10X buffer | 2 μl |
| Nuclease-free water | 17 μl |
| reaction enzyme | 1 μl |
| Final volume | 30μl |

Statistical analysis

Performance (field) data: To analyze the data for quail’s body weight, carcass weight and dressing %, the PROC GLM (General Linear Model) procedure SAS, (28) was utilized. Fixed effects study was using the following model:
\[ Y_{ijkl} = \mu + L_i + S_j + LS_{ij} + \varepsilon_{ijkl} \]

Where: \( Y_{ijkl} \) = body weight, carcass weight and dressing \% for the \( i^{th} \) quail of the \( i^{th} \) line (\( L_i \), \( i=1 \), brown, \( i=2 \), desert and \( i=3 \), white), of the \( j^{th} \) Sex (\( S_j \), \( j=1 \), male and \( j=2 \), female), of the \( k^{th} \) interaction between line and sex (\( K_{ij} \), \( i=1 \), Desert male, \( 2= \) Desert females, \( 3= \) Brown male, \( 4= \) Brown female, \( 5= \) White male and \( 6= \) White female), \( \mu = \) Population mean; \( \varepsilon_{ijkl} \) = random error. It was assumed to be independently and normally distributed with mean zero and variance \( \sigma^2 \varepsilon \). For genetics evaluation of quail (High and low production) for various performance traits, Best Linear Unbiased Prediction (BLUP) procedure described by (28) was applied. The model used for this purpose was the Mixed Model (Fixed + Random effects) of (28) software. The three quail lines were assembled in three groups; high (10%), medium (80%) and low (10%) production, according to the BLUP values

**Molecular analysis**

Genotypes of polymorphic loci were determined by direct counting of the bands. The gene frequencies for each locus in each sample were calculated using the following equations:

\[
p = \frac{2(AB)+AB}{2N} \quad q = \frac{2(BB)+AB}{2N}
\]

where \( p \) = the gene frequency of allele A, \( q \) = the gene frequency of allele B and \( N \) = the total number of birds tested and tested to Hardy-Weinberg ratios using was calculated using GENPOP software version, 3.3 (24). The genotypes effects for body weights, carcass weight and dressing\% were fitted to following equations:

\[
Y_{ijlko} = \mu + A_i + S_j + C_k + P_l + \varepsilon_{ijkl}
\]

Where: \( Y_{ijlko} \) = Body weights, carcass weight and dressing\% of the \( o^{th} \) bird, of the \( i^{th} \) GH (\( A_i \), \( i=1 \), AC, \( i=2 \), AB and \( i=3 \), CC), of the \( j^{th} \) SEMA3E (\( S_j , j=1 \), AB, \( j=2 \), BC and \( j=3 \), CC), of the \( k^{th} \) TLX (\( C_k , k=1 \), AA, \( k=2 \), AB, and \( k=3 \), AC), of the \( l^{th} \) all genes combinations (\( P_l \), \( l=1 \),2,3,4,5,6,7,8,9,10,11,12), \( \mu = \) Population mean; \( \varepsilon_{ijkl} \) = random error. It was assumed to be normally and independently distributed with mean zero and variance \( \sigma^2 \varepsilon \).

**RESULTS AND DISCUSSION**

**Phenotypic evaluation**

**Body weight:** Data presented in Table 4, shows that lines had a significant (\( p<0.01 \)) effects on body weight were (241.30± 9.43), (232.65±7.72) and (225.70± 8.02) for desert, brown and white respectively. On the other hand, the statistical analysis for this trait revealed that the differences between males and females were highly significant (\( p<0.01 \)) on body weight (205.77±5.18) and (260.67±4.12) respectively. While regarding the effect of interaction (sex × line); the findings in Tables 4 showed the significant effects of interaction (sex × line) on body weight and recorded higher interaction between female and lines. Our results were in agreement with a recent study that observed by Al-Kafajy et al., (5) who stated that the desert line had higher significant values of body weight compared with the black and white lines. While sex of the chicks had significant effect on body weight, the higher weights in females could be due to higher weight of reproductive organs such as ovaries and oviducts, could be due to higher weight in females than males (9). Similar findings were also made by (23) who showed the higher significant effect of Sex on body weight (\( P < 0.01 \)) in two strains of Japanese quail.

**Carcass traits**

Carcass traits like any other quantitative traits are largely affected by the interaction between genetic and environmental factors (30). Japanese quail (carcass weight/live body weight) was ranged from 60 to 70 - 75 % depended on slaughter age, line and sex (6). The results of Carcass weight and Dressing percentage of three different line plumage colors are presented in Table 4. In the current study significant differences in Carcass weight among lines were showed. That could be due to genetic variance among studied lines. Nonetheless, no significant differences were observed in dressing percentage. The overall least squares means for Carcass weight and Dressing percentage at 6th month of age were (166.60± 5.26, 161.70± 4.46 and 156.90±
4.09) g and (70.04± 1.34, 70.02± 1.35 and 70.14± 1.34) % respectively in desert, brown and white lines. While the sex effect for this trait was significantly higher (p≤0.01) between male and female. The female (168.63±3.28) was higher than male (154.87±3.90) in Carcass weight but in Dressing percentage trait male (75.55±0.36) was higher than female (64.58±0.37). The effect of interaction (Line×Sex) on Carcass weight and Dressing percentage was significantly (p≤0.01).

Nasr et al. (21) was reported that slaughter and carcass characteristics were signify affected by quail sex. In addition Lotfi et al., (16) was found that Carcass weight was higher in females than males, and also suggested that there are a correlation in between reproductive organs and body weight, therefore the mature female quail weight was higher than in broiler chickens at 42 days of age and consequently, the carcass yield will be lower in Japanese quail. Also, Sabow, (26) indicated significant differences among Japanese quails with different feather colors on slaughter weight and carcass yields at 10 weeks of age.

Table 4. Least Squares Means and Standard Error for different Traits

| Traits         | N. | Body weight(g) | Carcass weight(g) | Dressing percentage (%) |
|----------------|----|----------------|-------------------|-------------------------|
| Overall        | 720| 233.22± 7.72   | 161.75±4.46       | 70.06±1.35              |
| Lines          |    |                |                   |                         |
| Desert         | 214| 241.30± 9.43a  | 166.60± 5.26a      | 70.04± 1.34a            |
| Brown          | 250| 232.65± 7.72ab | 161.70± 4.46ab     | 70.02± 1.35a            |
| White          | 256| 225.70± 8.02b  | 156.90± 4.09b      | 70.14± 1.34a            |
| Sex            |    |                |                   |                         |
| Male           | 356| 205.77±5.18b   | 154.87±3.90b       | 75.55±0.36b             |
| Female         | 363| 260.67±4.12a   | 168.63±3.28a       | 64.58±0.37a             |
| Line×Sex       |    |                |                   |                         |
| Desert Male    | 103| 210.60±10.43b  | 157.10±7.70ab      | 75.43±0.86a             |
| Desert Female  | 111| 272.00±7.59a   | 176.10±6.11a       | 64.65±0.57b             |
| Brown Male     | 127| 208.10±9.15b   | 157.00±7.06ab      | 75.44±0.67a             |
| Brown Female   | 123| 257.20±5.82a   | 166.40±5.43ab      | 64.60±0.84b             |
| White Male     | 131| 198.60±7.61b   | 150.40±5.84b       | 75.79±0.29a             |
| White Female   | 125| 252.80±7.09a   | 163.40±5.22ab      | 64.50±0.55b             |

a,b,c Column means within parameter with common superscripts do not differ (** P<0.01), NS - not significant.

Genetic merit for single trait (BLUP): The estimated Best Linear Unbiased Prediction (BLUP) of local quail for the weight. BLUP values for quail's weight ranged from (0.6527 to 10.0117g, 1.4467 to 8.9887g and 4.2467 to 7.0667g) males and (-8.6613 to -1.6933g, -9.2173 to -2.4293g and -4.3113 to 0.3827) females of desert, brown and white, respectively at six month. These results indicated that there are significant differences of weight trait in between the quails. It means that selection play a crucial role in enhancing weight trait.

Molecular characterization of local quail: Allele and genotype frequency in local quail populations: The respective loci were successfully amplified using stated primer pairs. PCR product sizes were differed from 412 to 776 bps. After cutting with the appropriate enzymes, one to four different fragments for each locus were observed Table 5. Figure 1A, B and C shows restriction products of particular samples for each locus. Polymorphism was observed for each primer (SEMA3E, GH and TLX) loci. One sequences for each genes obtained were deposited in the GenBank under accession numbers (MN542411, MN542412 and MN542413) for SEMA3E, TLX and GH respectively.

Table 5. Fragment and Restriction products size for all Genes

| Locus  | Size of PCR Product (bp) | Enzyme | Cut | Lengths of Restriction Fragments (bp) |
|--------|-------------------------|--------|-----|--------------------------|
| SEMA3E | 412                     | Hae III| +   | 412/ 362/50/ 335/77      |
| TLX    | 546                     | PstI   | +   | 546/ 404/142             |
| GH     | 776                     | Msp 1  | +   | 776/ 529/241             |
Genotype and number of bands for each loci was shown in Table 6. For the SEMA3E locus three different alleles (A, B and C), three genotypes (AB, BC and CC) with an approximate size of 412 bps as dominant PCR product were observed in Figure 2A, while three different alleles such as A, B and C and also three genotypes namely AA, AB and AC were found for the TLX locus, a single amplification product of approximately 546 bp was obtained. Figure 2B. Results obtained from the digestion showed the presence of polymorphism in GH gene fragment at 776 bp-sized quail research was to produce two types of alleles (A and C) with three genotypes (AA, AC and CC) Figure 2C. The allele frequencies of SEMA3E, GH and TLX loci for males and females in three local lines ranged from A: 0.083-0.750, B: 0.000-0.333 and C: 0.208-0.583 respectively. The allele frequency for A; males and females in TLX loci had the highest frequencies (0.667 and 0.750) and the least was of SEMA3E loci (0.000 and 0.083). For allele B; males and females (0.333) had the highest in SEMA3E loci and the least frequencies in TLX was (0.000-0.167). Frequency of C; 0.583 and 0.500 of males and females was recorded in SEMA3E and GH loci respectively and the least was 0.167-0.250 in TLX Loci. The genotypic frequencies of males and females were higher for AA in TLX (0.562 and 0.445), AC (0.50 and 0.486) GH and BC (0.523) SEMA3E genes compared to the (AB and CC) genotypes. While, genotypic frequency in TLX was higher AA (0.562 and 0.445) in males and females compared to AB and AC genotypes as given in Table 7. These results agree with Bozkaya et al. (7) that detected the possibility of using each SEMA3E and TLX loci to study recombination frequencies in the Japanese quails populations out of the eight loci studied (SEMA3E, IFR1, HAL, LOC396025, UGP2, LOC396192, TLX and BMP5), polymorphism was detected in the SEMA3E and TLX loci; five of their loci were regarded as monomorphic and one locus (HAL) wasn’t amplifiable by PCR. Deef et al. (10) indicated that the PCR-RFLP was performed in terms of revealing the genetic characterization and also genetic relationship of the five species of quails. The Common quails are found to be Coturnix coturnix, bobwhite quail Colinus virginianus, and three quails belong to Coturnix japonica including panda quail, Japanese quail, dotted white quail. Highly polymorphic restriction profiles were recorded from the analysis of fragments that were generated by digestion of PCR products with the restriction enzyme NlaIII. A wide variability in intra specific SEMA3E and TLX genes was obtained among the respective quails. Previous studies on allele frequencies have been used the same method as in the current study, their results have varied among populations from 0.000 to 1.000 (19). Allele and genotype frequencies were observed in the analyzed samples are shown in Table 5. To our knowledge, there is no previous study examining the polymorphism of the respective loci in other populations of Japanese quails. Despite Sasazaki et al., (27) mapped out the loci on the CJA1 and CJA3, no data on allele frequencies or heterozygosity were reported by those researchers. Therefore, results from the current study were extensively compared with those that have been reported on other loci or species and GH.
Figure 1. Polymerase chain reaction based restriction fragment length polymorphism profiles of A) SEMA3E; B) TLX and C) GH of pulled samples in three local lines. L: DNA marker, DMH: desert male high production, DML: desert male low production, BMH: brown male high production, BML: brown male low production, WMH: white male high production, WML: white male low production, DFH: desert female high production, DFL: desert female low production, BFH: brown female high production, BFL: brown female low production, WFH: white female high production and WFL: white female low production

Figure 2. Digestion of PCR products of A) SEMA3E; B) TLX and C) GH of pulled samples in three local lines. L: DNA marker, DMH: desert male high production, DML: desert male low production, BMH: brown male high production, BML: brown male low production, WMH: white male high production, WML: white male low production, DFH: desert female high production, DFL: desert female low production, BFH: brown female high production, BFL: brown female low production, WFH: white female high production and WFL: white female low production
Table 6. Band number and Fragments size (Bp) for GH, SEMA3E and TLX Genes in Local Quails

| Population/group | Genotype and No. of band | GH band Size bp | SEMA3E band Size bp | TLX band Size bp |
|------------------|--------------------------|-----------------|---------------------|-----------------|
| DMH              | AC                       | 3               | 776+539+237         | AB              | 2               | 336+412         | AA              | 1               | 546             |
| DML              | AC                       | 3               | 776+539+237         | CC              | 2               | 335+77          | AB              | 2               | 546+404         |
| BMH              | CC                       | 2               | 539+237             | BC              | 2               | 362+50          | AC              | 3               | 546+404+142     |
| BML              | AA                       | 1               | 776                 | BC              | 2               | 362+50          | AC              | 1               | 546             |
| WMH              | AB                       | 3               | 776+539+237         | BC              | 2               | 335+77          | AA              | 3               | 546+404+142     |
| WML              | AC                       | 3               | 776+539+237         | BC              | 2               | 335+77          | AB              | 2               | 546+404         |
| DFH              | AA                       | 1               | 776                 | AB              | 2               | 336+412         | AA              | 1               | 546             |
| DFL              | CC                       | 2               | 539+237             | CC              | 2               | 335+77          | AA              | 1               | 546             |
| BFH              | AC                       | 3               | 776+539+237         | BC              | 2               | 362+50          | AC              | 3               | 546+404+142     |
| BFL              | CC                       | 2               | 539+237             | BC              | 2               | 362+50          | AC              | 3               | 546+404+142     |
| WFH              | AC                       | 3               | 776+539+237         | CC              | 2               | 335+77          | AA              | 1               | 546+404+142     |
| WFL              | AC                       | 3               | 776+539+237         | CC              | 2               | 335+77          | AC              | 3               | 546+404+142     |

Table 7. Allele and Genotype Frequency of SEMA3E, GH and TLX Genes in male and female of Local Quail

| Locus | Sex | Allelic frequency | Genotype frequency | Overall |
|-------|-----|-------------------|--------------------|---------|
| SEMA3E| Male| 0.083 0.333 0.583 | 0.113 0.523 0.364 |
|       | female| 0.083 0.333 0.583 | 0.113 0.523 0.364 |
|       | Overall| 0.083 0.333 0.583 | 0.113 0.523 0.364 |
| TLX   | Male| 0.666 0.167 0.167 | 0.444 0.278 0.278 |
|       | female| 0.750 0.000 0.25  | 0.562 0.000 0.438 |
|       | Overall| 0.708 0.083 0.208 | 0.501 0.143 0.356 |
| GH    | Male| 0.500 0.500 0.25  | 0.500 0.25 0.25  |
|       | female| 0.417 0.583 0.174 | 0.486 0.340 0.294 |
|       | Overall| 0.458 0.542 0.210 | 0.496 0.294 0.294 |

Table 8. The mean of high and low level on Body weight, Carcass weight, and Dressing percentage traits in Local Quails as influenced by the different Genotypes

| Population/group | Genotype for all genes | Body weight (g) | Carcass weight(g) | Dressing percentage (%) |
|------------------|------------------------|-----------------|-------------------|-------------------------|
| DMH              | ACABAA                 | 251.00± 2.65c   | 184.33± 8.99ab    | 75.84± 1.79a            |
| DML              | ACCCAC                 | 173.00± 3.61d   | 129.67± 2.03d     | 76.26± 0.44a            |
| BMH              | CCBCAC                 | 243.33± 2.73c   | 182.33± 3.97a     | 74.97± 0.62a            |
| BML              | AABCAC                 | 176.67± 10.48d  | 131.67± 7.33d     | 75.90± 0.13b            |
| WMH              | AABBAC                 | 230.33± 1.45c   | 174.33± 2.03b     | 65.96± 1.08bc           |
| WML              | ACBCAC                 | 173.67± 4.09d   | 130.33± 2.69d     | 63.49± 0.29cd           |
| DFH              | AABAAA                 | 299.33± 10.41a  | 197.67± 10.14a    | 61.74± 0.82d            |
| DFL              | CCACCA                 | 244.67± 1.20c   | 155.33± 1.45c     | 60.94± 0.29cd           |
| BFH              | ACBAC                  | 281.00± 6.56ab  | 192.33± 6.74ab    | 68.41± 0.91b            |
| BFL              | CCABAC                 | 240.00± 3.51c   | 150.00± 1.00c     | 62.53± 1.17d            |
| WFH              | ACBACA                 | 277.67± 6.17b   | 184.00± 4.51ab    | 66.26± 0.15bc           |
| WFL              | ACCACAC                | 235.33± 2.52c   | 151.33± 1.86c     | 61.74± 0.82d            |

a,b,c Column means within parameter with common superscripts do not differ (** P < 0.01). DMH: desert male high production, DML: desert male low production, BMH: brown male high production, BML: brown male low production, WMH: white male high production, WML: white male low production, DFH: desert female high production, DFL: desert female low production, BFH: brown female high production, BFL: brown female low production, WFH: white female high production and WFL: white female low production.
Genotypes associations with body weight traits in local quails

The effects of genetic (RFLP) markers on studied economic traits in local quail are illustrated in Table 8. There was a significant association between RFLP patterns and live weight at 6th month of age, carcass weight, and dressing percentage. The best genotype for local quail at three loci in the present study was AAABAA in body weight (299.333 g), carcass weight (197.667 g) in the DFH population. While, higher the dressing percentage was (76.264%) was recorded in CCBCAC genotype in the BMH population. This result showed that the selection play a major role to increase body weight, carcass weight and dressing percentage of local quail. Also, the desert quail had the highest in body weight and carcass weight when it compared to brown and white lines and females are highest than males, while in carcass weight the males was higher than females. Furthermore, The ACCCAB genotype had the lowest body weight (173 g) and Carcass weight (129.667 g) of and DML population and ACCCAC genotypes had the lowest dressing percentage (61.749%) of the WFL population. The effect of selection for quail of high and low body weight, Carcass weight and dressing percentage revealed the variance in between males and females within and between three lines of local quails. The variation in quantitative trait is controlled by several genetic loci called quantitative trait loci (QTL). While to select animals for selective breeding programmers, genetic markers for QTL that are linked to the trait gene (34). Data collected from PCR-RFLP and the use of MspI enzyme observes the effect of GH gene polymorphic of quail on weight. Polymorphism of this gene showed different effects on the patterns of body weight in which the average weight of male quail is relatively lower than the female quail (29). the results by Nasirifar et al. (20) detected four distinctive alleles (A, B, C, and D) and four different genotypes (AA, AB, AC, and AD) in population of Japanese quails in GH marker site, which could be detected by MspI restriction enzyme showed a significant (P<0.05) association between RFLP patterns with live weight and carcass weight. Carcass weight of the AB birds was lower than that of other genotypes. Through employing PCR-RFLP technique researchers have been able to notice a difference in poultry species as chickens, ducks, quail, rabbits, and turkeys (4). while Zhu et al., (37) detected a significant correlation between GH gene and quality of meat in Anka and Rugao hens Furthermore, Zhang et al. (36) observed a positive link between intron 1 of GH gene, and composition of body and fatness in duck. In contrast, polymorphism of GH and productive traits in Mazandaranian native poultry were found to be not correlated (14). Results from the current study indicated that there was a significant association between three genes and the composition of carcasses in local quail. These results can also be a valuable index to properly select and to genetically improve local quail. Finally, further researches and experiments are recommended in order to clarify direct interaction of polymorphism of three genes with growth and carcasses composition traits in local quail.

CONCLUSION

It is concluded that a great genetic variation exist among the three lines studied. Candidate genes SEMA3E, TLX and GH genes were successfully amplified in local quail, indicating that these regions are conserved and some genotypic profiles of the above candidate genes were found to be associated with growth trait in local quail and could be used as a potential marker for selection for body weight in the production of local quail lines.

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