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Analysis of the Genetic Diversity in the Cairo-Mix Broiler Chicken Using Microsatellite and Start Codon Targeted Markers

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Abstract

Determining the genetic polymorphism is essential for evaluating the outcomes of breeding programs. Thus, the current study aimed at comparing two methods to measure the genetic polymorphism of the cairo-mix broiler hybrid, this was done by using 100 genomic DNA samples. The microsatellite marker method and the start codons targeted (SCoT) marker techniques were used. The results showed that 14 microsatellite loci detected 34 alleles with an average of 2.43 alleles per microsatellite. While ten SCoT loci detected 66 alleles with an average of 6.6 alleles per primer. The effective number of alleles for the microsatellite markers ranged from 1.47 to 2.77 (mcw0217 and adl0266), whereas for SCoT markers, it ranged from 2.38 to 5.55 (SCoT-18 and SCoT-1). Moreover, among the SCoT markers, SCoT-01, SCoT-10, SCoT-40, SCoT-44, and SCoT-50, primers were found to be the most informative and discriminative. The averages of shannon's information index were 0.82 and 1.64 for the microsatellite and SCoT markers, respectively. The mean values of observed heterozygosity were 0.77 and 1.00 for the microsatellite and SCoT markers, respectively. In conclusion, the high genetic diversity of the cairo-mix hybrid indicates that promising results may be expected in future breeding programs. The SCoT markers as a simple and informative technique could be a potent method for studying genetic variation in poultry.

Keywords: *Microsatellite, SCoT, indigenous breeds, broilers, genetic diversity*

Introduction

Selection and breeding programs for chickens using Asian native breeds began in the mid-nineteenth century [1]. Poultry breeding efforts support the commercial breeds to dominate the sector of chicken production leaving the local chicken breeds to be endangered [2]. However, local chicken breeds significantly contribute to the economy of several countries, especially developing countries [3]. In Egypt, the meat production value of indigenous poultry was 1775.8 million dollars, while that of commercial chickens were 2240.3 million dollars (FASTAT 2016). Indigenous chicken strains, in the subtropics, are usually adapted to high environmental temperatures, limited access to water, and require minimal farming input [4-6]. However, these indigenous strains perform poorly due to less genetic improvement, and the selection for production traits would improve herd averages for the traits of interests (FAO 2016). There are four native Egyptian chicken breeds and sixteen synthetic local strains, with very little genetic information known about them [7]. Markers are used to identify intra- and/or inter-population differences. When compared to morphological markers, molecular markers provide possibilities for measuring genetic diversity among populations at the DNA level. The use of genetic markers is significant in many contexts, including gene flow, association mapping, evolutionary history, and genetic diversity [8]. Microsatellites are highly polymorphic co-dominant multi-allelic markers; thus, they are used as excellent markers to determine genetic diversity within and between populations, estimating gene flow, crossover rates, linkage mapping and evolutionary studies [9, 10].

Start Codon Targeted (SCoT) polymorphisms are new repeatable markers based on a short-conserved area in plant genes surrounding the ATG translate start codon [11, 12]. The SCoT polymorphisms [12] are dominant and reproducible markers that use a single 18-mer primer in polymerase chain reaction (PCR) experiments and a high annealing temperature

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(50°C). SCoT markers are beneficial in studying genetic diversity due to their high repeatability and high power for polymorphism detection [13].

SCoT markers have been successfully employed to analyze genetic diversity and structure, identify cultivars, and for quantitative trait loci (QTL) mapping and DNA fingerprinting in wheat, mullet and rice [14-16]. SCoT markers technique is easy and applicable. It has been used extensively in plant genetics studies [12]. In camel breeds, 16 SCoT markers were used to determine the genetic diversity of four Egyptian camel breeds [11]. However, utilizing the SCoT markers in chicken diversity studies is not well established. Therefore, this study may be the first to utilize the SCoT marker technique was used to determine the chicken genetic polymorphism in Egypt. This SCoT marker technique and the microsatellite marker technique were used to compare both efficiencies in identifying the genetic diversity and polymorphism in a novel meat-type chicken, the Cairo-Mix hybrid.

Material and Methods

Ethics statement

The present study has been conducted in accordance with the guidelines of the Ethics Committee of Cairo University Protocol number CU-11-F34-20.

Birds and management

The Cairo-Mix broiler hybrid used in this study was produced through a crossbreeding program that involved the Giza male line with the Cairo female line. The Giza male line was developed by crossing a commercial grandparent male line strain males with females of a synthetic local Bandara strain (developed by crossing the Cornish pure breed males with the synthetic Gemeza local strain). The Gemeza strain was developed by crossing the synthetic Dokki-4 local strain males with the White Plymouth Rook pure breed females. The Dokki-4 local strain was developed by crossing the Fayoumi native Egyptian breed with the Barred Plymouth Rock pure breed females. The Cairo female line was developed by crossing a commercial grandparent's female line strain males with the White Baladi females, a native Egyptian breed. The breeding program, over 15 generations, involved individual selection for attaining a higher 6-week body weight. Also, selection for higher egg production until 42 weeks of age using the independent culling level selection method for the Cairo line.

Since we crossed these 4 chicken breeds (or strains) to get our parental lines, then our final 4-way cross should carry approximately 25% of the genetic makeup of each of the original strains or breeds. Thus, the Cairo – mix hybrid broilers would have the following genetic makeup:
25% Baladi White, native Egyptian breed,
12.5% Cornish, purebreed
6.25% White Plymouth Rock, purebreed
3.25% Barred Rock, purebreed
3.25% Fayoumi, native Egyptian breed
25% Commercial male line strain
25% Commercial female line strain

Individual phenotypic selection for higher 6-week body weight and wider breast width at the same age was practiced over five generations. The Cairo-Mix broilers used in this study were produced by crossing these two parental lines through artificial insemination. Cairo-Mix is a novel Egyptian local broiler hybrid. The average body weight of chicks is 1.34 kg at day 56 of age, with a feed conversion ratio of 2.13. Its dressing percentage is around 65%. White color plumage is dominant (95%) as well as, single comb shape (93%). About 99% of the birds have red earlobes, whereas the rest have white earlobes. Most of the birds (93%) have yellow shanks, while the rest have white shanks. The skin color of the carcass is white (Fig. 1).

Fig.1. Cairo-Mix broiler hybrid

For this study, 300 wing-banded day-old Cairo-Mix chicks were used and reared in a deep litter floor brooder. They were fed on a commercial broiler starter diet (23% protein and 3200 Kcal/Kg ME/ Kg diet) for the first two weeks of age and a commercial broiler finisher diet (21% protein and 3200 Kcal Me/Kg diet) from three to eight weeks of age. The birds had access to ad libitum feed and water.

Blood sample and DNA isolation

One hundred blood samples were collected from chickens in an anti-coagulate buffer [17] from 50 males and 50 females, and stored at 5°C until DNA extraction. Individual genomic DNA were isolated from blood using Genomic DNA Mini kits, microcentrifuge spin-column format (Invitrogen™ K182001, USA) to obtain a pure extracted DNA. A NanoDrop® ND-1000 UV-Vis was used to determine DNA concentration. Spectrophotometer procedure was used to examine the purity of DNA.

Microsatellite markers (MS) statistics

Fourteen, of the original twenty, based on a pilot study, microsatellite DNA markers (Table 1) were used (Thermo Fisher Scientific). PCR reactions were performed in a final volume of 50 µl reaction mixture, composed of 3µl DNA (40 ng/µl), 45µl of

PCR SuperMix 1.1x concentration (Invitrogen, USA), 1.5µl of each primer (10 pmol/µl). The amplification conditions, on a Genemate B960 gradient thermal cycling platform, were as follows: initial denaturation step at 94°C for 3 mins, 30 cycles of amplification (45s of denaturation at 94°C, 60s of annealing at 55°C, 56°C or 60°C based on the optimal annealing temperature for the used primer, 60s of extension at 72°C). This was followed by a final extension at 72°C for 12 min. PCR products were electrophoresed on 1.5% agarose gel containing 0.5 % ethidium bromide then viewed under UV light and documented using the Uvp-BioDoc system the molecular sizes of the PCR-products were determined using a standard ladder DNA marker (100bp).

Start codon targeted (SCoT) analysis.

In the current study, 10 SCoT primers were used. The start codon targeted were brought from Thermo Fisher Scientific [12] (Table 2). Each 20-µl amplification reaction mix included 1 µl (100 ng) of template DNA, 10 µl of Master Mix (Bioline, GmbH, Germany), 1 µl of 25 pmol primers, and distilled sterilized water. Amplification was carried out in a programmed Biometra thermal cycler (version 1.12tp, 2004) using the following protocol: 94°C for 3 min; 35 cycles of 94°C for 1 min, 50°C for 1 min, and 72°C for 1 min; and a final extension at 72°C for 5 min. The resulting amplification products were analyzed by electrophoresis in 1.5% agarose gel in TAE buffer, stained with ethidium bromide, and photographed under UV light. The sequence of the tested primers is provided in Table 2.
The Gel Doc 2000 Bio-Rad system was used for SCoT gel image scanning, and Software v 4.0.1 (BioRad Laboratories, Hercules, Co., USA) was utilized for band scoring and cluster analysis.

Genotyping statistical analysis

The size of the alleles was estimated through comparison with a standard ladder DNA marker. Each allele size was estimated according to its repeated number for each microsatellite marker. The frequencies of different alleles were estimated following the gene-counting method by Nei index genetic diversity. The input files for all genetic software were prepared using Convert version 1.3.1 [18]. POPGENE 3.2 software package [19] was used to calculate heterozygosity (H). The polymorphism information content (PIC) was calculated according to [20] using CERVUS version 3 software [21].

Results

Alleles numbers (Na) and Effective allele number (Ne)

The highest observed number of alleles (Na), presented in Table (3), was 4 alleles at locus ADL0266, followed by 3 alleles at 4 loci: ADL0158, LEI0082, ROS0095, and LEI0112. The mean number of alleles observed over the 14 microsatellite loci for the Cairo-Mix cross is an indication of high allele frequency, which could have been influenced by the genetic improvement of the parents of this cross.

The total effective number of alleles was 28.68 with a mean of 2.05 alleles per loci. Locus ADL0266 showed the highest effective number of alleles 2.77(Table 3). A higher mean effective number of alleles suggests that the original genes were preserved more effectively. The mean effective number of alleles (Ne) in this study confirms the usefulness of locus ADL0266 over other loci used. As expected, the effective number of alleles was lower than the observed number of alleles over all 14 microsatellite markers. comparisons with other studies revealed differences that may plausibly attributable to sample size, markerstaype, and/or populations variation.

The total number of observed alleles (Na) generated by the ten-start codon targeted (SCoT) primers, as presented in Table (4), was 66 with an average of 6.6 amplicons per primer. The lowest number of amplicons (3) was generated by SCoT-18, while the highest number of amplicons (12) was generated by SCoT-10. The highest effective number of alleles was 5.55 alleles at SCoT-1, while the lowest observed number of alleles was 2.38 at SCoT-18. The total number of effective alleles observed by the ten SCoT primers was 41.53 with an average of 4.15 amplicons per primer.

Shannon's Information index (I) and the Polymorphic information content (PIC)

Shannon's Information Index (I) ranged from 0.50 at locus MCW0217, to 1.83 at locus ADL0158 with an average of 0.82. Polymorphic information content (PIC) is one of the most critical indications of genetic marker quality. The PIC for co-dominant markers ranges from 0 (monomorphic) to 1 (polymorphic), as reported by Smith et al. (1997). So, PIC values are divided into three classes: PIC> 0.5 = highly informative, 0.25< PIC< 0.5 = moderate, and PIC < 0.25 = low. The Polymorphic information content (PIC) for this study ranged from 0.38 at loci ADL0188, LEI0094, LEI0120, ADL0292, LEI0079, and MCW0064 to 0.69 at locus MCW0217 with an average 0.49 (Table 3).

The Shannon's information index ranged from 0.94 at SCoT-18 to 2.90 aSCoT-10. The total score was 16.44 with a mean of 1.64. The total number of polymorphic information content was 7.59 with an average of 0.76 per SCoT primer (Table 4). The Polymorphic information content ranged from 0.38 at SCoT-18 to 0.93 at SCoT-10. Allele size ranged from 136 to 1716 (bp). Start codon targeted PIC has traditionally been used to assess the informative capacity of SCoT markers in various germplasm and produced cultivars.

Observed heterozygosity (Ho) and Expected heterozygosity (He)

In Cairo-Mix and with the indicated 14 MS, the observed heterozygosity values were often greater than the expected (anticipated) heterozygosity values. The mean value of observed heterozygosity was 0.77, while, the mean value of the expected heterozygosity was 0.49. The greatest observed heterozygosity value was 1.00 at eight loci, ADL0158, ADL0188, ADL0240, LEI0082, ADL0266, ADL0292, LEI0079, and LEI0112. However, the maximum expected heterozygosity value was 0.64 at three loci, LEI0082, ROS0095, and ADL0266. Out of the 14 microsatellite loci, studied, two loci (LEI0120 and MCW0217) had zero observed heterozygosity, indicating that no individual was heterozygote at these loci.

The observed heterozygosity values were generally higher than the expected heterozygosity values in the Cairo-Mix for all ten SCoT primers. The mean value of observed heterozygosity was 1.00 while the mean value for expected heterozygosity was 0.78. The higher values of observed heterozygosity for all the 10 SCoT primers, are due to the existence of real hybridization in all of these DNA fragments of this local broiler cross, Cairo-Mix.

Average heterozygosity (Ave - Het)

The results presented in Table 3 show that the average heterozygosity ranged from 0.16 at locus MCW0217 to 0.64 at locus ADL0240 and that the mean of the average heterozygosity across markers was 0.48. Our study demonstrated also that five of the fourteen MS markers (ADL0158, LEI0082, ROS0095, ADL0266, and LEI0112) were highly informative and discriminative, and would be appropriate for the analysis of the Cairo-Mix cross.

Cluster analysis

The phylogenies, by neighbor-joining, procedure categorized various primers into specific clusters and branches based on the proportion of variance explained by microsatellites, and start codon markers (SCoT). Dendrogram cluster analysis (Fig2) indicated that all microsatellites aggregated in one group (except MC0217 and LEI10120 microsatellites), including SCoT-18 and SCoT-55. In these groups, both LEI0094 and MCW0064 markers were identified and separated into further groups far from the others by 0.0325 points. In this cluster, ADL0188, ADL0292, and LEI0079 microsatellite polymorphisms are the same (zero distance). SCoT-18 is the nearest primer to them, while SCoT-55 was the nearest to the ADL0266 marker, (the highest polymorphic microsatellite marker), with a small distance (0.1255) between them. The SCoT-04, SCoT-21, and SCoT-58 primers scored higher polymorphism, aggregated in a separate cluster, and far by 0.0325 points to the microsatellite's groups. In a separate group, SCoT-01, SCoT-40, SCoT-44, SCoT-50, and SCoT-10 primers are the most discriminative and informative of all markers. SCoT-10 primer is the most polymorphic, and informative, and it is separated in a unique cluster. Finally, the least informative markers, LEI0120, and MCW0217 microsatellites aggregated far away from all markers alone in a separate cluster (Fig 2).

Dendrogram using the nearest neighbor hierarchical cluster method, revealed. The genetic relationships and similarities among microsatellites and start codon targeted markers (SCoT) in detecting genetic polymorphism in a novel meat-type hybrid, Cairo-Mix. The number at the node indicates the average distance of a cluster..

Discussion

The highest observed number of alleles (Na) was 4 alleles at locus ADL0266. The mean number of alleles over 14 microsatellite loci indicated high allele frequency, possibly influenced by genetic improvement. Comparison with other studies, variations in allele numbers, likely due to methodological differences, sample size, and genetic background. Ramadan et al. [22] reported that Simple Sequence Repeats (SSR) for loci MCW0064, LEI0120, ADL0240, ADL0273, and ADL0372 had a larger number of alleles in the Cairo line than in the control line. Microsatellites technique play an important role in genetic diversity for being stable, simple, clear, and high specificity [23]. The number of observed alleles was less than what was found (16 - 23) by [24] and differed compared to (4 - 14) as reported by [25] in the Local Turkish Denizli Chicken and (6 – 11) as reported by [26] in Nigerian indigenous chicken. However, the average allele numbers obtained in this study are somewhat lower than these estimates findings (6. 35) of Yacouba et al. [27] using local chicken ecotypes from Burkina Faso. Further, our estimate of the mean number of alleles was higher than those reported in Kenya (1.96) [28].

The total effective number of alleles was 28.68 with a mean of 2.05 alleles per loci. Locus ADL0266 showed the highest effective number of alleles (2.77). A higher mean effective number of alleles suggests better preservation of original genes. Comparisons with other studies revealed differences that may be plausibly attributed to sample size, marker types, and/or population variation. The effective allele numbers are a guide for genetic diversity and mutation flow [23]. When the mean effective number of alleles is higher, it suggests that the population can preserve is original genes and prevent the emergence of new variations, even under the influence of genetic drift and artificial selection. Similar results were previously reported [29, 30]. Furthermore, the mean Ne found in this study (2.05) was much lower than those reported by Olowofeso et al. [26] in Nigerian indigenous chicken (4.45) and Ohwojakpor et al. [31] in chicken populations in

Nigeria's South-South area (6.16). Our estimation was similar to that found in Burkina Faso (2.3) and [27]. The observed differences between the observed allelic number and the effective allelic number could be attributable to sample size, the number or type of markers used, and/or the differences between the examined populations [32]. However, the results were similar to those of many other researchers who documented breed and strain differences in body weight as well as differences in the number of alleles [22].

Ten Start Codon Targeted (SCoT) primers generated a total of 66 observed alleles with an average of 6.6 amplicons per primer. Effective alleles were discussed in relation to inbreeding and genetic diversity. Allele size range and the evolution of genetic diversity were discussed. Based on the data analysis results, the moderate PIC values for marker primers might be attributable to the evolution of genetic diversity [33].

Results showed that Shannon's Information Index ranged from 0.50 to 1.83, with an average of 0.82. The polymorphic Information Content values ranged from 0.38 to 0.69, with an average of 0.49. In Quail, Elkhaiat et al. [34] studied the variation between brown and white quail and their reciprocal cross using microsatellites. Shannon's Information Index ranged from 0.38 to 1.21. These indices provide insights into the informativeness and utility of markers for linkage analysis Comparisons with other poultry breeds' PIC values. It assesses the informativeness and utility of markers for linkage analysis [35, 36]. The PIC for co-dominant markers ranges from 0 (monomorphic) to 1 (polymorphic), as reported by [33]. Thus, PIC values are divided into three classes: PIC> 0.5 = highly informative, 0.25< PIC< 0.5 = moderate, and PIC < 0.25 = low. Several studies have estimated the Polymorphic Information Content (PIC) of different poultry breeds, including an Italian breed (0.54) [37], an Egyptian breed (0.61) [38], a southern Xinjiang chicken breed (0.79) [39], and a Swedish breed (0.56) using 24 MS [40].

In our study, Shannon's Information Index of ten SCoT markers ranged from 0.94 to 2.90, with a mean of 1.64. PIC values ranged from 0.38 to 0.93, indicating a moderate to high informative. Al-Soudy et al., [11] studied the genetic diversity amongst four Egyptian camel breeds using 18 SSRs and 16 SCoT markers. Shannon's Information Index in their study, ranged from 1.78 to 1,88.

Observed heterozygosity values were generally higher than expected, indicating a high level of heterosis. Some loci showed zero observed heterozygosity, possibly due to specific genetic characteristics. Comparisons with other studies and the Hardy-Weinberg equilibrium (HWE) were discussed. The higher mean observed heterozygosity than expected may suggest deviation from HWE. The heterozygosity is a significant display of the chicken population's genetic diversity. The study of Das et al. [41] indicated that out of 24 microsatellite loci, four loci CW0014, MCW0049, MCW0059, MCW0071) across the lines studied and one locus (MCW0041) of the control line demonstrated observed zero heterozygosity (Ho). In the present study, two loci (LEI0120 and MCW0217) demonstrated observed zero Ho, two loci (LEI0094 and MCW0064) demonstrated Ho>0.5. Most of the loci (ADL0273, ADL0240, LEI0082, ADL0158, ADL0188, ROS0095, ADL0266, ADL0292, LEI0079 and LEI0112) demonstrated Ho > 0.75. As most of the loci demonstrated higher Ho probably due to the existence of a large number of heterozygous alleles indicating a high level of heterosis. Sahu et al. [42] demonstrated that ADL0273 have significant effects on some economic traits in chicken.

The present estimates were similar to the estimates reported for MCW0005, MCW0014, and MCW0016 in Rhode Island Red (RIR) chickens [43]. Findings of Das et al. [41] that ranged from 0.5053 (MCW0059) to 0.8421 (MCW0004) in the selected RIR line. Also, the estimated means of the (Ho) and (He) in the Cairo-Mix are similar to those reported by [44, 45]. The differences, observed in different studies, might be due to their different genetic base, loci studied and chicken breeds /lines /strains. Also, most of the Swedish chicken breeds, with relatively lower effective population sizes, had lower observed homozygosity than expected [46].

In contrast with the finding of Das et al. [41] the Ho mean observed was more than the He means indicating that this population is not within the Hardy-Weinberg equilibrium (HWE). Lower observed heterozygosity, than expected, indicates a higher rate of inbreeding [40]. The absence of homozygosity may be caused by the presence of heterozygous alleles at the same locus [47]. Keeping breeds in tiny groups and small isolated flocks causes heterozygosity loss over several generations [48].

Observed heterozygosity values were generally higher than expected, indicating real hybridization in the Cairo-Mix.Comparisons with heterozygosity values in other breeds were provided. In the Kinda and Hedem breeds, the average observed heterozygosity ranged from 0.39 to 0.73. A lack of heterozygosity within a breed is caused by the existence of homozygous alleles at the same locus [47]. Keeping breeds in small populations will cause more observed homozygosity than expected. This is a sign of genetically related individuals mating, genetic drift, and non-random mating [46]. Al-Soudy et al [11] using the SCOT marker in the Egyptian Camel breed, A data binary matrix was created using the banding profiles that the SCoT markers had produced, taking into account whether the bands were present (1) or absent (0). Al-Soudy et al. [11] showed that the bulked genomic DNA for the four

breeds of camels as well as the banding profile produced by 12 of the 16 SCoT primers. As can be seen, 153 amplicons in all, with an average of 9.56 bands per primer, were produced. Seventy-five of the 153 bands were polymorphism, resulting in a polymorphism rate of 49%. Across the four Egyptian camel breeds, the number of polymorphic amplicons ranged from zero (SCoT-08) to twelve (SCoT-15), with an average of 4.6 bands per primer. The polymorphism percentage with the highest value was found in the SCoT-15 marker (92.3%). The SCoT-08 marker, on the other hand, showed (0%) polymorphic amplicons.

Average heterozygosity ranged from 0.16 to 0.64.Five markers were highlighted as highly informative and discriminative for the Cairo-Mix cross. Comparisons with other studies on genetic diversity in chicken populations were provided. Heterozygosity levels represent genetic variation within races [49]. When the breed is under the Hardy-Weinberg equilibrium, the genetic diversity is comparable to the estimated homozygosity. Zanetti et al. [37] used 20 microsatellite markers on Italian native chickens and found that the mean observed and anticipated heterozygosity were 0.35 and 0.33, respectively. In addition, Cendron et al. [50] discovered that Italian native chickens exhibit limited genetic diversity in comparison to commercial stocks.

Cluster analysis is an example approach that is designed to assign random data into groups (clusters) to identify common patterns and improve understanding [51]. A cluster can be defined as a group of markers closely together, which is expressing similar results. Clustering the polymorphic genetic results revealed that variation and diversity resulted from primers: SCoT-01, SCoT-40, SCoT-44, SCoT-50, and SCoT-10 primers are highly indicated to study polymorphisms in the future breeding improvement plans.

Conclusion

The high genetic diversity of the Cairo-Mix hybrid indicates that promising results should be expected in future breeding programs. The selection for production traits would improve herd averages for the traits of interest. The SCoT markers as a simple and informative technique could be a potent method for studying genetic variation in poultry.

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Conflict of interest statement

There is no potential conflict of interest to declare.

Authors’ contributions

F.K. R. Stino: designed the experiment and critically revised the article; E. M. El-Komy; M.I. El Sabry: growing the flock and drafting and revising the article; O. S. Rashed: establishing the flock and growing the chicks; Mona M. A. Ghaly: maintaining and selecting the breeding flocks, growing the flock, and drafted the article. G. S. Ramadan: Lab. Work, data analysis, and drafted the article.

Data availability statement

Available upon reasonable request.

TABLE 1. Microsatellite markers (ID), their distribution on chicken chromosomes, sequences, annealing temperature and traits associated with the indicated genetic loci.

Marker	Ch	Forward (5` − 3`) Reverse (3` -- 5)	AT °C	Traits associated with the genetic loci	References
MCW0064	8	CTTCAAGAGCCATAGGTGGT TCTCAGCACTACAAAATACACAG	**55**	Body weight 28, 42, 56-day, Abdominal fat weight, Drumstick weight, Breast and leg meat weight, spleen %.	[52]
ROS0095	28	CCCTCCCTCTGTGCTCTG AGCTGCTTTGAAGGAGAAACC	**55**	Body weight (day of first egg), Skin fat weight, Abdominal fat weight, carcass weight, and Tibia width.	[53, 54]
ADL0240	12	ACC TGG GAG ATT GGA TTC CGT CCC GTC CTG ANT GTT TG	**56**	Drumstick %, Breast muscle %, and Leg bowing.	[55]
LEI0120	15	CGTAACACATGCAACTCAAT TTAGAATGAAAAGGCTGTTCC	**55**	Growth (8-46) days, Body Weight 35. 42, 46 days, Abdominal fat %, Drumstick and thigh %, Tibia bone mineral density, carcass weight, spleen weight & spleen %.	[54, 55]
ADL0292	5	TTAGAATGAAAAGGCTGTTCC AAA TGG CCT AAG GAT GAG GA	**55**	Body weight (40 days), Conformation score, Body depth, Chest width, Breast muscle weight, Feed conversion ratio, Weight of the front half of the carcass, Abdominal fat percentage, Shank growth, Gizzard weight, Marek's disease-related traits.	[54, 56,57]
LEI0079	1	AGGCTCCTGAATGAATGCAT TCATTATCCTTGTGTGAAACTG	**60**	Body Weight, 21,35, 42, 56, 63, 77, and 84 days. Carcass weight, Breast muscle, wing weight, heart, spleen, and gizzard weight.	[53, 58]
LEI0082	5	TATCCATACAGTACCCTCCT CCTTAGCTGGCTCAGTGGATG	**55**	Body Weight 42, 112, and 200-days, carcass weight, Conformation score, Breast percentage, Dressing percentage, breast muscle, the weight of the front half of the carcass, Drumstick weight,	[59, 60]
ADL0273	Z	GCC ATA CAT GAC AAT AGA TGG TAG ATG CTG AGA GGT GT	**55**	Body Weight, Number of eggs, Femur bone mineral density, Marek's disease-related traits.	[61,62]
ADL0158	10	TGG CAT GGT TGA GGA ATA TAG GTG CTG CAC TGG AAA TC	**56**	Body Weight (ascites conditions), Body Weight 14, 28-day, spleen, liver, Abdominal fat %, Heart %.	[6,41]
MCW0217	18	GATCTTTCTGGAACAGATTT CTGCACTTGGTTCAGGTTCTG	**60**	Body weight (1, 35, and 56-day), Abdominal fat weight & %, breast, and spleen %, weight.	[54,56]
ADL0188	1	CAC TTC CAG TAT TAA CGT GTG GAC ACA ATG AGT TCC TC	**55**	Body weight, 21, 42, 63-day, Breast and leg meat weight, Abdominal fat weight, shank length Breast color, Tibia marrow diameter, and Shank length.	[54,62]
ADL0266	4	GTG GCA TTC AGG CAG AGC AAT GCA TTG CAG GAT GTA TG	**56**	Body weight 42, 63, and 112-days. Growth (21-42), (42-63), and (46-112) days. Spleen, liver, and egg weights, conformation score, tibia-marrow diameter, thigh meat to bone marrow, and creatine kinase level.	[63]
LEI0094	4	GATCTCACCAGTATGAGCTG TCTCACACTGTAACACAGTGC	**55**	Body weight 21.42.and 112 days, Growth (46-112) days, breast muscle, thigh muscle, abdominal fat, and egg weight, and Marek's disease-related trait.	[64,65]
LEI0112	15	GGGAACATACAGGGTGCTG TATCATACCAGCGCAGCTCTG	**56**	Body weight 14, 21, 28, 42-days, and carcass weight,	[55]

*The traits in Table 1, refer to those traits associated with the genetic loci responsible for meat production in chickens from previous studies, Ch: chromosome number, AT: Annealing Temperature.

TABLE 2. Names, sequences, GC % and Annealing Temperature, of SCoT primers.

Primer	Sequence 5'-3'	GC%	AT °C
SCOT-01	CAACAATGGCTACCACCA	50	50
SCOT-04	CAACAATGGCTACCACCT	50	50
SCOT-10	CAACAATGGCTACCAGCC	56	50
SCOT-18	ACCATGGCTACCACCGCC	67	50
SCOT-21	ACGACATGGCGACCCACA	61	50
SCOT-40	CAATGGCTACCACTACAG	50	50
SCOT-44	CAATGGCTACCATTAGCC	50	50
SCOT-50	ACAATGGCTACCACTGGG	56	50
SCOT-55	ACAATGGCTACCACTACC	50	50
SCOT-58	ACAATGGCTACCACTAGG	50	50

TABLE 3 Genetic parameters measured in the Cairo-Mix hybrid using 14 259 microsatellite markers

Markers	Na	Ne	I	PIC	Ho	He	Ave Het
ADL0158	3.00	2.63	1.83	0.49	1.00	0.56	0.56
ADL0188	2.00	2.00	0.69	0.38	1.00	0.56	0.50
ADL0240	2.00	1.72	0.61	0.53	1.00	0.56	0.64
ADL0266	4.00	2.77	1.16	0.49	1.00	0.64	0.61
ADL0273	2.00	1.72	0.61	0.68	0.80	0.53	0.45
ADL0292	2.00	2.00	0.69	0.38	1.00	0.56	0.50
LEI0079	2.00	2.00	0.69	0.38	1.00	0.56	0.50
LEI0082	3.00	2.38	0.94	0.60	1.00	0.64	0.58
LEI0094	2.00	1.72	0.61	0.38	0.60	0.47	0.42
LEI0112	3.00	2.38	0.94	0.50	1.00	0.64	0.58
LEI0120	2.00	2.00	0.69	0.38	0.00	0.00	0.25
MCW0064	2.00	1.72	0.61	0.38	0.60	0.47	0.42
MCW0217	2.00	1.47	0.50	0.69	0.00	0.00	0.16
ROS0095	3.00	2.17	0.88	0.60	0.80	0.64	0.51
Total	34.00	28.68	11.45	6.86	10.80	6.83	6.68
Mean	2.43	2.05	0.82	0.49	0.77	0.49	0.48
SD	0.65	0.37	0.20	0.13	0.35	0.21	0.13

Na=Observed number of alleles; Ne=Effective number of alleles; I=Shannon's Information index; PIC=Polymorphic information content; Ho=Observed heterozygosity; He=Expected heterozygosity; Ave Het=Average heterozygosity.

TABLE 4. Genetic parameters measured on the Cairo-Mix hybrid using 10 SCOT markers

Primer	Na	Ne	I	PIC	Ho	He	Ave-He	Allele size range (bp)
SCOT-01	9	5.55	1.96	0.89	1	0.86	0.82	440-765
SCOT-04	4	3.38	1.28	0.79	1	0.74	0.71	175-1334
SCOT-10	12	5.12	2.90	0.93	1	0.85	0.81	216-761
SCOT-18	3	2.38	0.94	0.38	1	0.61	0.58	200-1716
SCOT-21	4	3.38	1.28	0.74	1	0.74	0.71	224-647
SCOT-40	9	5.44	1.91	0.89	1	0.86	0.82	252-791
SCOT-44	8	4.87	1.80	0.85	1	0.84	0.80	136-1362
SCOT-50	8	4.54	1.74	0.85	1	0.82	0.78	139-971
SCOT-55	4	2.98	1.19	0.50	1	0.70	0.67	380-1114
SCOT-58	5	3.89	1.44	0.77	1	0.78	0.74	218-939
Total	66	41.53	16.44	7.59	10	7.8	7.44	---
Means	6.6	4.15	1.6	0.76	1	0.78	0.74	---
S.D.	2.83	2.98	1.10	0.38	0.17	0	0.08	---

Na = the Observed number of alleles; Ne = Effective number of alleles I = Shannon's Information index; PIC= Polymorphic information content; Ho = Observed heterozygosity; He = Expected heterozygosity; Ave-Het= Average heterozygosity.

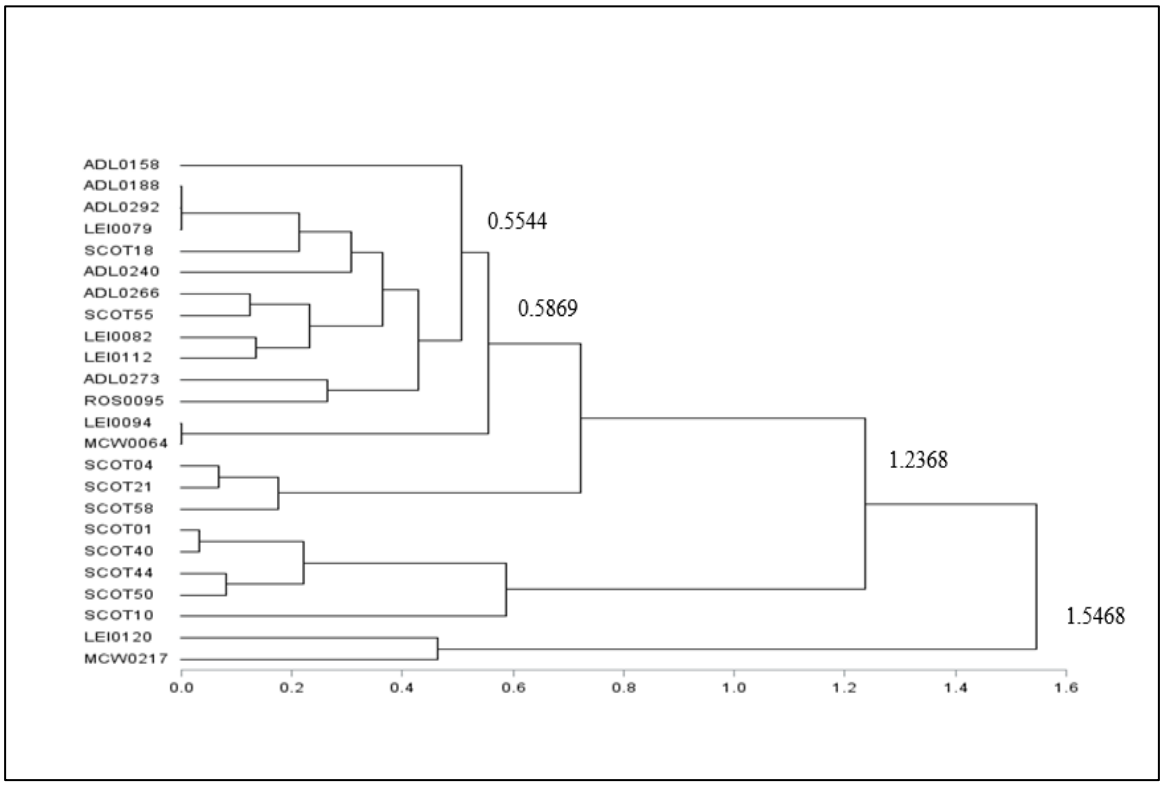

Fig. 2. The genetic relationships and similarities among microsatellites and start codon targeted markers (SCoT) in detecting genetic polymorphism in a novel meat-type hybrid, Cairo-Mix. The number at the node indicates the average distance of a cluster.

References

1. Boelling, D., Groen, A.F., Sørensen, P., Madsen, P. and Jensen, J. Genetic improvement of livestock for organic farming systems. *Livestock Production Science*, **80**(1-2)79-88(2003).
2. Granevitze, Z., Hillel, J., Chen, G.H., Cuc, N.T.K., Feldman, M., Eding, H. and Weigend, S. Genetic diversity within chicken populations from different continents and management histories. *Animal genetics*, **38**(6),576-583. (2007).
3. Yoshimura, Y. and Barua, A. Female reproductive system and immunology. *Avian Reproduction: From Behavior to Molecules*, pp.33-57(2017).
4. El Sabry, M.I., Romeih, Z.U., Stino, F.K., Khosht, A.R. and Aggrey, S.E. Water scarcity can be a critical limitation for the poultry industry. *Tropical Animal Health and Production*, **55** (3), 215(2023).
5. El-Sabry, M.I.M., Atta, A.M.M., Tzschentke, B., Gharib, H.B.A. and Stino, F.K.R. Potential use of Interleukin-2-rich supernatant adjuvant in Fayoumi hens. *European Poultry Science,* **76** (3) 162-167(2012).
6. Kaya M. and Yıldız M. A. Genetic diversity among Turkish native chickens, Denizli and Gerze, estimated by microsatellite markers. *Biochemical Genetics*, **46**, 480-491(2008).
7. Hassanane, M.S., Hassan, A.A., Ahmed, F.M., El-Komy, E.M., Roushdy, K.M. and Hassan, N.A. Identification of Mx gene nucleotide dimorphism (G/A) as genetic marker for antiviral activity in Egyptian chickens. *Journal of Genetic Engineering and Biotechnology*, **16**(1), 83-88(2018).
8. Bamshad, M.J., Wooding, S., Watkins, W.S., Ostler, C.T., Batzer, M.A. and Jorde, L.B. Human population genetic structure and inference of group membership. The American *Journal of Human Genetics*, **72**(3), 578-589(2003).
9. Abdul-Muneer, P.M. Application of microsatellite markers in conservation genetics and fisheries management: recent advances in population structure analysis and conservation strategies. *Genetics Research International*, **1**, 691759(2014).
10. Vieira, M.L.C., Santini, L., Diniz, A.L. and Munhoz, C.D.F. Microsatellite markers: what they mean and why they are so useful. *Genetics and Molecular Biology*, **39**, 312-328. (2016).
11. Al-Soudy, A., El-Sayed, A., El-Itriby, H. and Hussein, E. Assessment of the genetic diversity, breeds structure and genetic relationships in four Egyptian camel breeds using microsatellite and start codon targeted (SCoT) markers. *Journal of Biodiversity & Endangered Species*, **6**(001) 1-8 (2018).
12. Collard, B.C. and Mackill, D.J. Start codon targeted (SCoT) polymorphism: a simple, novel DNA marker technique for generating gene-targeted markers in plants. *Plant Molecular Biology Reporter*, **27**,86-93(2009).
13. Amirmoradi, B., Talebi, R. and Karami, E. Comparison of genetic variation and differentiation among annual Cicer species using start codon targeted (SCoT) polymorphism, DAMD-PCR, and ISSR markers. *Plant Systematics and Evolution*, **298**, 1679-1688 (2012).
14. Cabo, S., Ferreira, L., Carvalho, A., Martins-Lopes, P., Martín, A. and Lima-Brito, J.E. Potential of Start Codon Targeted (SCoT) markers for DNA fingerprinting of newly synthesized tritordeums and their respective parents. *Journal of Applied Genetics*, **55**, 307-312(2014).
15. MAM Elian, S., A Hussein, B., F Abdelghany, M. and Soliman, H. M. Molecular characterization of four Mullet species based on SCoT and ISSR markers. *Egyptian Journal of Aquatic Biology and Fisheries*, **25**(1),1-23 (2021).
16. Mulpuri, S., Muddanuru, T. and Francis, G. Start codon targeted (SCoT) polymorphism in toxic and non-toxic accessions of Jatropha curcas L. and development of a codominant SCAR marker. *Plant Science*, **207**, 117-127 (2013).
17. Ramadan, G.S. Molecular markers as a tool for selection in local Egyptian chickens (Doctoral dissertation, Ph. D. THESIS, Fac. Agric., Cairo Univ., Egypt).(2019).
18. Glaubitz, J.C. Convert: a user- friendly program to reformat diploid genotypic data for commonly used population genetic software packages. *Molecular Ecology Notes*, **4**(2), 309-310(2004).
19. Yeh, F.C., 1999. POPGENE (version 1.3. 1). Microsoft window-bases freeware for population genetic analysis. http://www. ualberta. ca/~ fyeh/.(1999).
20. Botstein, D., White, R.L., Skolnick, M. and Davis, R.W. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics*, **32**(3),314(1980).
21. Kalinowski, S.T., Taper, M.L. and Marshall, T.C. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology*, **16**(5), 1099-1106 (2007).
22. Ramadan, G.S., Moghaieb, R.E., El-Ghamry, A.A., El-Komy, E.M. and Stino, F.K.R. Microsatellite marker associated with body weight in local Egyptian broiler line Cairo B-2. *Bioscience Research*, **15**(4), 3188-3201(2018).
23. Zhang, X., He, Y., Zhang, W., Wang, Y., Liu, X., Cui, A., Gong, Y., Lu, J., Liu, X., Huo, X. and Lv, J., Development of microsatellite marker system to determine the genetic diversity of experimental chicken, duck, goose, and pigeon populations. *BioMed Research International*, **1**, 8851888(2021).
24. Hillel, J., Groenen, M.A., Tixier-Boichard, M., Korol, A.B., David, L., Kirzhner, V.M., Burke, T., Barre-Dirie, A., Crooijmans, R.P., Elo, K. and Feldman, M.W. Biodiversity of 52 chicken populations assessed by microsatellite typing of DNA pools. *Genetics Selection Evolution*, **35**, 1-25(2003).
25. Özdemir, D. and Cassandro, M. Assessment of the population structure and genetic diversity of Denizli chicken subpopulations using SSR markers. *Italian Journal of Animal Science*, **17**(2), 312-320(2018).

26. Olowofeso, O., Wheto, M., Durosaro, S.O., Bankole, K.O., Adepoju, D.A. and Folarin, O.V. Combined exclusion probabilities of ten microsatellite markers used with Nigerian chicken populations. European International *Journal of Science and Technology*, **5**(4), 21-32(2016).

27. Yacouba, Z., Isidore, H., Michel, K., Isidore, G.B., Boureima, T., Vinsoun, M., Maurice, K., Ousseni, B., Moussa, Z., Valerie, B.Y.M. and Romdhane, R. Genetic diversity and population structure of local chicken ecotypes in Burkina Faso using microsatellite markers. *Genes*, **13**(9), 1523(2022).

28. Okumu, O.N., Ngeranwa, J.J.N., Binepal, Y.S., Kahi, A.K., Bramwel, W.W., Ateya, L.O. and Wekesa, F.C. Genetic diversity of indigenous chickens from selected areas in Kenya using microsatellite markers. *Journal of Genetic Engineering and Biotechnology*, **15(**2), 489-495 (2017).

29. Bakare, I.O., Ilori, B.M., Wheto, M., Egbeyale, L.T., Sanda, A.J. and Olowofeso, O., Genetic diversity and gene flow among three chicken populations in Nigeria using microsatellite markers. *Agriculturae Conspectus Scientificus,* **86(**2), 173-181(2021).

30. Liu, G.Q., Jiang, X.P., Wang, J.Y., Wang, Z.Y., Liu, G.Y. and Mao, Y.J. Analysis of genetic diversity of Yangzhou chicken by microsatellite markers. *Int. J. Poult. Sci.*, **7**, 1237-1241(2008).

31. Ohwojakpor, O., Olowofeso, O., Adebambo, O.A. and Onagbesan, O.M. Genetic diversity of chicken populations in South-South region of Nigeria using microsatellite markers. *Egyptian Poultry Science*, **32**, 263-271(2012).

32. Ajayi, F.O. Nigerian indigenous chicken: A valuable genetic resource for meat and egg production. *Asian Journal of Poultry Science,* **4**(4), 164-172(2010).

33. Smith, J.S.C., Chin, E.C.L., Shu, H., Smith, O.S., Wall, S.J., Senior, M.L., Mitchell, S.E., Kresovich, S. and Ziegle, J. An evaluation of the utility of SSR loci as molecular markers in maize (Zea mays L.): comparisons with data from RFLPs and pedigree. *Theoretical and Applied Genetics*, **95**, 163-173(1997).

34. Elkhaiat, I., El-Kassas, S., Eid, Y., Ghobish, M., El-Komy, E., Alagawany, M. and Ragab, M. Assessment of variations in productive performance of two different plumage color varieties of Japanese quail and their reciprocal crosses. *Tropical Animal Health and Production*, **55**(3), 195(2023).

35. Guo, X. and Elston, R. Linkage information content of polymorphic genetic markers. *Human Heredity*, **49**(2), 112-118(1999).

36. Osman, S.A.M., Sekino, M., Nishibori, M., Kawamoto, Y., Kinoshita, K., Yamamoto, Y. and Tsudzuki, M. Genetic variability and relationships of Japanese native chickens assessed by means of microsatellite profiling approach-Focusing on the Oh-Shamo (Japanese Large Game) and its related breeds. *The Journal of Poultry Science*, **41**(2), 94-109(2004).

37. Zanetti, E., De Marchi, M., Dalvit, C. and Cassandro, M. Genetic characterization of local Italian breeds of chickens undergoing in situ conservation. *Poultry Science*, **89(**3), 420-427(2010).

38. Eltanany, M., Philipp, U., Weigend, S. and Distl, O. Genetic diversity of ten Egyptian chicken strains using 29 microsatellite markers. *Animal Genetics*, **42**(6), 666-669 (2011).

39. Azimu, W., Manatbay, B., Li, Y., Kaimaerdan, D., Wang, H.E., Reheman, A. and Muhatai, G. Genetic diversity and population structure analysis of eight local chicken breeds of Southern Xinjiang. *British Poultry Science*, **59**(6), 629-635(2018).

40. Abebe, A.S., Mikko, S. and Johansson, A.M. Genetic diversity of five local Swedish chicken breeds detected by microsatellite markers. *PLoS One*, **10**(4), e0120580 (2015).

41. Das, A.K., Kumar, S., Rahim, A., Debnath, J. and Kokate, L.S. Investigating genetic heterogeneity using microsatellite markers after long term selection for egg production in Rhode Island Red chicken. *Indian Journal of Animal Sciences*, **90**(10), 1387-1391(2020).

42. SAHU, A.R., Kumar, S. and Jain, S.K., Association of diversity in microsatellite genotypes with layer traits in Rhode Island Red chicken. *Research Square,* **1**(2) 1-20 (2022).

43. Vanhala, T., Tuiskula-Haavisto, M., Elo, K., Vilkki, J. and Maki-Tanila, A. Evaluation of genetic variability and genetic distances between eight chicken lines using microsatellite markers. *Poultry Science*, **77**(6), 783-790 (1998).

44. Chatterjee, R.N., Niranjan, M., Sharma, R.P., Dange, M. and Bhattacharya, T.K. Estimation of genetic heterogeneity of chicken germplasm being used for development of rural varieties utilizing DNA markers. *Journal of Genetics*, **89**(2), e33-e37(2010).

45. Rajkumar, U., Gupta, B.R. and Reddy, A.R. Genomic heterogeneity of chicken populations in India. Asian-*Australasian Journal of Animal Sciences*, **21**(12), 1710-1720 (2008).

46. Gebeyehu, S.T. Genetic mapping on local Swedish chicken breeds. PhD thesis. *European Master in Animal Breeding and Genetics*, pp56. (2021).

47. Dakin E., Avise J. Microsatellite null alleles in parentage analysis. *Heredity*, **93**(5), 504-509(2004).

48. Young, A.G. and Clarke, G.M. Genetics, demography and viability of fragmented populations. *The Canadian Field-Naturalist.,* **118** (3),478-480 (2004).

49. Melo, R.C.D., Trevisani, N., Pereira, T.C.V., Guidolin, A.F. and Coimbra, J.L.M. Heterozygosity level and its relationship with genetic variability mechanisms in beans1. *Revista Ciência Agronômica*, **48**, 480-486(2017).

50. Cendron, F., Perini, F., Mastrangelo, S., Tolone, M., Criscione, A., Bordonaro, S., Iaffaldano, N., Castellini, C., Marzoni, M., Buccioni, A. and Soglia, D. Genome-wide SNP analysis reveals the population structure and the conservation status of 23 Italian chicken breeds. *Animals*, **10**(8), 1441(2020).

51. Han, J., Pei, J. and Tong, H. Data mining: concepts and techniques: Morgan kaufmann, 2022.

52. Zhou, H., Deeb, N., Evock-Clover, C.M., Ashwell, C.M. and Lamont, S.J. Genome-wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. II. Body composition. *Poultry Science*, **85**(10), 1712-1721(2006).

53. Podisi, B.K., Knott, S.A., Burt, D.W. and Hocking, P.M. Comparative analysis of quantitative trait loci for body weight, growth rate and growth curve parameters from 3 to 72 weeks of age in female chickens of a broiler–layer cross. *BMC Genetics*, **14**, 1-11(2013).

54. Abdalla, B.A., Chen, J., Nie, Q. and Zhang, X. Genomic insights into the multiple factors controlling abdominal fat deposition in a chicken model. *Frontiers in Genetics*, **9**, 262 (2018).

55. Griffin, D.K., Robertson, L.B., Tempest, H.G., Vignal, A., Fillon, V., Crooijmans, R.P., Groenen, M.A., Deryusheva, S., Gaginskaya, E., Carré, W. and Waddington, D. Whole genome comparative studies between chicken and turkey and their implications for avian genome evolution. *BMC Genomics*, **9**, 1-16(2008).

56. Zhou, Z., Yao, D., Qiu, Y. and Yang, D. Microsatellite instability in Marek's Disease Virus infected primary chicken embryo fibroblasts. *Virology Journal*, **9**, 1-5 (2012).

57. Choi, N.R., Seo, D.W., Jemaa, S.B., Sultana, H., Heo, K.N., Jo, C. and Lee, J.H. Discrimination of the commercial Korean native chicken population using microsatellite markers. *Journal of Animal Science and Technology*, **57**, 1-8(2015).

58. Xu, Z., Nie, Q. and Zhang, X. Overview of genomic insights into chicken growth traits based on genome-wide association study and microRNA regulation. *Current Genomics*, **14**(2), 137-146(2013).

59. Heifetz, E.M., Fulton, J.E., O'Sullivan, N.P., Arthur, J.A., Wang, J., Dekkers, J.C.M. and Soller, M. Mapping quantitative trait loci affecting susceptibility to Marek's disease virus in a backcross population of layer chickens. *Genetics*, **177**(4), 2417-2431(2007).

60. Severing, E.I., van Dijk, A.D., Stiekema, W.J. and van Ham, R.C. Comparative analysis indicates that alternative splicing in plants has a limited role in functional expansion of the proteome. *BMC Genomics*, **10**, 1-13 (2009).

61. Heifetz, E.M., Fulton, J.E., O'Sullivan, N.P., Arthur, J.A., Cheng, H., Wang, J., Soller, M. and Dekkers, J.C. Mapping QTL affecting resistance to Marek's disease in an F6 advanced intercross population of commercial layer chickens. *BMC Genomics*, **10**, 1-17(2009).

62. Goto, T. and Tsudzuki, M. Genetic mapping of quantitative trait loci for egg production and egg quality traits in chickens: A review. *The Journal of Poultry Science*, **54**(1), 1-12(2017).

63. Rowe, S.J., Pong-Wong, R., Haley, C.S., Knott, S.A. and De Koning, D.J. Detecting parent of origin and dominant QTL in a two-generation commercial poultry pedigree using variance component methodology. *Genetics Selection Evolution,* **41**, 1-11(2009).

64. Cho, S.H., Lee, S.S., Manjula, P., Kim, M., Lee, S.H., Lee, J.H. and Seo, D. Population structure analysis of Yeonsan Ogye using microsatellite markers. *Journal of Animal Science and Technology*, **62**(6), 790(2020).

65. Cui, W., Jin, X., Guo, Y., Chen, C., Zhang, W., Wang, Y., Lan, J. and Zhu, B. Development and validation of a novel five-dye short tandem repeat panel for forensic identification of 11 species. *Frontiers in Genetics*, **11**, 1005(2020).

تحليل التنوع الوراثي في دجاج اللحم الهجين (كايرو ميكس) باستخدام علامات الميكروساتلايت وعلامات استهداف كودون البدء

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الملخص

يُعتبر تحديد التعدد الجيني أمرًا أساسيًا لتقييم نتائج برامج التربية. ولذلك، هدفت الدراسة الحالية إلى مقارنة طريقتين لقياس التعدد الجيني في هجين دجاج اللحم كايروميكس، وذلك باستخدام 100 عينة من الحمض النووي الجينيDNA تم استخدام طريقة علامات الميكروساتلايت وتقنيات علامات استهداف كودون البدء .(SCoT) أظهرت نتائج 14 موقعًا للميكروساتلايت اكتشاف 34 أليلًا بمتوسط 2.43 أليلًا لكل ميكروساتلايت، بينما اوضحت نتائج عشرة مواقع اكتشاف 66 SCoTأليلًا بمتوسط 6.6 أليلًا لكل بادئ. تراوح العدد الفعال للأليلات لعلامات الميكروساتلايت بين 1.47 و2.77 للمواقع (mcw0217) و(adl0266) بينما تراوح لعلامات SCoT بين 2.38 و5.55 للمواقع (SCoT-18) و-SCoT (1). علاوة على ذلك، كانت المواقعSCoT-01 ، SCoT-10، SCoT-40، SCoT-44، و SCoT-50 هي الأكثر إفادة وتمييزًا بين علامات SCoT .كانت متوسطات مؤشر المعلومات لشانون 0.82 و1.64 لعلامات الميكروساتلايت و SCoTعلى التوالي. كما كانت القيم المتوسطة للتنوع الوراثي الملحوظ 0.77 و1.00 لعلامات الميكروساتلايت و SCoTعلى التوالي. في الختام، يشير التنوع الوراثي العالي في هجين كايروميكس إلى أنه يمكن توقع نتائج واعدة في برامج التربية المستقبلية. وتعد علامات SCoT كطريقة بسيطة وغنية بالمعلومات أداة قوية لدراسة التباين الوراثي في الدواجن.

الكلمات الدالة: الميكروساتلايت، SCoT، السلالات المحلية، دجاج اللحم و التنوع الوراثي.