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GENETIC ASSESSMENT OF TWO CHICKEN STRAINS AND TWO JAPANESE QUAIL LINES BY USING CHICKEN AND QUAIL MICROSATELLITE MARKERS RECIPROCALLY

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ABSTRACT: Chromosome homology is highly conserved between chicken (Gallus gallus) and Japanese quail (Coturnix japonica) and a few chromosome rearrangements occurred in the evolution of these two species. Blood samples were collected from chicken strains (21 Silver Montazah and 20 Mandara) and Japanese quail lines (22 Beige and 21 sample Grey). Eight chicken and six quail microsatellite markers were used reciprocally. Highly polymorphic microsatellite markers 12 out of 14 with ratio of 85.7% were successfully worked reciprocally and achieved PCR product in both species. The successful cross-species amplification led to identification of polymorphic markers that will be indispensable for identifying homologous regions on chromosomes. The majority of the loci were highly polymorphic information content (PIC) indicated that the most (12/14) of the selected microsatellite sequences could be serve the genetic diversity on different levels including conservation of such genetic resources, future improvements for these two poultry species and/or understanding different genome arrangement and knowledge interests.

Keywords: genetic evaluation, microsatellite markers, chicken strains, Japanese quail lines.

INTRODUCTION

Birds have a constant number of chromosomes and show relatively low susceptibility to chromosome rearrangements (Kayang et al. 2006). Japanese quail and chicken are closely related. Both species have a karyotype of 2n=78 chromosomes and a similar genome length of 1.2×109 bp (Kayang et al., 2004). Shibusawa et al. (2001) reported that the location and the order of genes in chicken and Japanese quail was similar except for chromosomes 1, 2, 4 and 8. The mapping of microchromosomes by using of STR were problematic because they contained a small number of STR (Kayang et al., 2004). Kayang et al. (2006) showed that the similarity of chicken and Japanese quail genome was 88.4% STR sequences characteristic. The use of the similar microsatellite sequences in closely related species, whose genome is partly mapped, proved to be successful. Such approach offers opportunity for a more rapid sequencing of the Japanese quail genome (Inoue- Murayama et al., 2001; Kayang et al., 2006; Kikuchi et al., 2005).

The chickens used in current study were Silver Montazah and Mandara strains. Mahmoud et. al. (1974) investigated that the cross between RIR males and Dokki 4 females for 3 generations produced Silver Montazah. Mandara strain was initiated from a cross between Alexandria males and selected inbred Dokki-4 females. In first generation females were backcrossed with Dokki-4 males for three subsequent generations (Abd El-Gwad et.al., 1981). Two lines of Japanese quail (Beige and Grey color) were applied in the present work. The present study was designed to assess the genetic diversity between chicken strains and quail lines to find out any potential relationship between them.

MATERIALS AND METHODS

Blood samples and DNA extraction

Blood samples for chicken strains were 21 Silver Montazah and 20 Mandara and for Japanese quail lines were 22 Beige and 21 Grey samples. Whole blood samples were collected separately in tubes containing EDTA as anticoagulant. Blood samples and DNA isolation were carried out as previously described by Roushdy et al., (2009).

Selection of Microsatellite Markers

In the present study, a set of 12 microsatellite markers out of 14 were selected from the researches recommended by Roushdy et al., (2012b and 2016) and from previously reported markers for quails after successful pilot experiment to detect the suitable annealing temperature and other PCR condition in both chicken and quail (Table 1). Some of these markers were already used in different studies to determine the genetic diversity of chicken by Babar et al (2011).

PCR amplification and gel electrophoresis

The amplification conditions with PCR for chicken strains were the cycling conditions included a single initial denaturation at 95°C for 5 min followed by 35 cycles of 95°C for 60 s (denaturation), 47.9-59.5°C for 45 s (annealing), 72°C for 60 s (extension) and a final extension step at 72°C for 15 min. The amplification conditions with PCR for Japanese quail lines were similar conditions except the annealing temperature (51.7-58°C for 45 s) and the number of cycling needed for PCR (30 cycles). PCR products (10 µl) were separated by 10% TBE polyacrylamide gel electrophoresis buffer at 160 V for 6 hours.

Statistical analysis of the results:

All scored microsatellite data were firstly corrected to estimate each allele size according to its number of repeats for each marker. A Tandem Repeat Analyzer

software package was adopted for this purpose. All possible extracted species figures were carried out employing a Arlequin 3.5 software package after data conversion using CONVERT program. POPGENE software package (Yeh et al., 1999) was used to calculate allele frequencies, observed number of alleles, effective number of alleles.

RESULTS AND DISCUSSION

Microsatellite DNA Polymorphism

Out of 14 microsatellite sequences selected for detecting differentiation and similarity between chicken and Japanese quail only 12 microsatellite markers responded with similarity of 85.7% (12/14) . Three loci out of six for chicken strains were located on chromosome 3 (MCW0126, MCW0127 and LEI0113), two loci located on chromosome 4 (MCW0114 and MCW0167) and one locus located on chromosome 1 (MCW0200). While, one locus was located on each chromosome as follows: GUJ0028, GUJ0029, UBC001, UBC002, UBC004 and UBC005 were located on chromosomes QL08, CJA06, 1, 6, 4 and 3 for quail lines, respectively. Six chicken and six quail highly polymorphic microsatellite markers were successfully worked reciprocally and achieved PCR product in both species. Similar results obtained by Gruszczyńska and Michalska (2013) who investigated that the PCR reaction for 11 chicken microsatellite sequences in Japanese quail yielded a PCR product for 9 STR sequences (9/11) with a percent of 82%.In earlier studies, Pang et al. (1999) used chicken specific primers, amplified only 22.9% of microsatellite sequences in Japanese quail (11 STR sequences out of 48 analyzed), while Innoue-Murayama et al. (2001) only 26.0% (31 out of 120) and Kikuchi et al. (2005) only 8.5% (17 out of 200). Despite this relatively low percentage of successful cross species amplifications, Kikuchi et al. (2005) hold the view that when a cross-species amplification is successful and results in polymorphic markers, these markers can be useful for identifying homologous chromosomal regions.

Microsatellite loci, their chromosome number, primer sequence, Gene Bank accession number and detected annealing temperatures and band size range in bp. are shown in Table (1). Microsatellite loci chosen from MCW (Crooijmans et al., 1996; Groenen et al., 1997) and LEI (Gibbs et al., 1997) were original chicken markers. While, UBC (University of British Columbia) and GUJ were original Japanese quail markers (Kayang et al; 2000 and 2002).

In total, 136 alleles ranged from 7 (MCW0127) to 19 (UCB001) were observed from the 12 loci surveyed in 84 birds. The total number of alleles were 60 and 49 for Silver Montazah and Mandara chicken strains, respectively, and ranged from 2 (GUJ0029) to 8 (UBC005) with a mean of 5 for Silver Montazah and from 2 (MCW0126, MCW0114 and GUJ0029) to 6 (MCW0167 and UCB002) with a mean of 4.10 for Mandara. This average could be informative for such studies according to Barker (1994) who suggested that the average number of alleles per locus in studies of genetic distances must be > 4 to reduce the standard error in the estimation of genetic distances. Similar results were obtained by EL-sayed et al. (2011) who found that total number of alleles per locus over all the populations ranged from 2 (MCW0127) to 10 (MCW0241 and MCW0258) with a mean of 5.5 for Fayoumi and Dandrawi breeds. In Fayoumi native chicken breed (P, G & R), Roushdy et al. (2008) reported that the number of alleles were detected ranged from 3 (ADL171) to 10 (ADL136). While, the total number of alleles for quail lines were 58 and 61 for Beige and Grey lines, respectively and ranged from 2 (MCW0127 and MCW0200) to 10 (UCB001) with a mean of 4.83 for Beige and from 1 (MCW0200) to 8 (MCW0114,

GUJ0028 and UCB002) with a mean of 5.08 for Grey quail lines. Roushdy et.al. (2016) investigated that total numbers of alleles from two lines of Japanese quail (Beige and Grey color) were 54 based on six microsatellite loci. The mean number of alleles per line varied from 6.00 in Beige to 6.50 in Grey line. Bai et al. (2013) showed that 48 alleles were identified from nine microsatellite markers with an average of 5.3 alleles detected per marker of Chinese yellow quail. Also, Ahmad et al. (2014) studied seven microsatellite markers (ADL0023, ADL0024, ADL0366, UBC0001, UBC0002, UBC0004, and UBC0005) to find out the genetic diversity within two quail breeds (wild quail and Japanese quail). Low estimate was obtained by Sami et al. (2013) who detected 17 alleles for the 3 microsatellite markers examined across chicken and quail populations studied. They found that the mean number of alleles per locus overall 3 studied loci were 2.333 and 4.000 in chickens and quails, respectively, while, number of alleles per locus overall populations ranged between 4 (GUJ0063) and 8 (GUJ0087) with mean of 5.666.

Regarding specific alleles, a total of 68 out of 136 alleles (50 %) were detected overall loci (12 microsatellite loci) versus two species. For Silver Montazah and Mandara chicken strains 18 specific alleles with a mean of 2.25 and 13 with a mean 1.86 were observed, respectively. While For Beige and Grey quail lines 17 specific alleles with a mean 2.43 and 20 with a mean 2.22 were detected, respectively, in Table 2. Consequently, those specific alleles would be utilized as species fingerprint (even one allele for one locus) and could be used to differentiate between the two poultry species (chicken and quail). The present study was higher than that obtained by EL-sayed et al. (2011) who observed that a total of 30 specific alleles out of 83 alleles for Fayoumi (12) and Dandrawi (18) breeds with a ratio of 36.14% were detected overall loci (15 microsatellite loci) versus two breeds. Roushdy et al, (2012a) reported that a total of 32 out of 120 alleles (26.7%) overall loci for the two breeds where, 11 specific alleles were observed for Dandrawi and 2l for Sinai breed. Also, Roushdy et al. (2013b) reported that specific alleles were 7, 5 and 9 alleles with Mamourah, Mandara and Baheij strains, respectively. While, specific alleles were 15 and 18 alleles with Beige and Grey lines, respectively as reported by Roushdy et al, (2016). Fixation index (F_{ST}) overall 12 loci ranged between 0.136 (UBC002) and 0.512 (MCW0200) with mean of 0.252 for chicken and quail species as shown in Table 2. The current results were no much differed from those obtained in British chicken breeds (F_{ST} = 0.25) as previously reported by Wilkinson et al. (2011) and higher than that reported by Roushdy et al. (2016) who observed that a F_{ST} = 0.20. Low value of F_{ST} indicating low level of population differentiation. Higher estimate (F_{ST} =0.50) was observed for Japanese quail as reported by Kim et al. (2007).

Effective number of alleles (ENA) used to corollary the expected heterozygosity. For any given number of alleles the expected heterozygosity (gene diversity) is highest when all the allele frequencies are equal. It means that when the heterozygosity is high we will have the highest effective number of alleles. The lowest mean of ENA was 2.72 and 2.46 for GUJ0029 and MCW0200 when H_E was 0.67 and 0.49 with chicken strains and quail liens, respectively. While, the highest means of ENA were 7.95 and 9.32 for GUJ0028 and UBC001 when H_E were 1.21 and 1.26 with chicken strains and quail liens as shown in (fig.1 and 2). Roushdy et al, (2012a) reported that the lowest effective number of alleles (ENA) was 2.53 for ADL210 when HE was 0.65 while the highest ENA was 6.6 for ADLI76 when H_E was 0.89 for Dandrawi and Sinai breed. Similar results were obtained by Roushdy et al. (2013 a, b

and c) for Dokki-4, Golden Montazah, Silver Montazah, Mamourah, Mandara, Baheij, Matrouh, El-salam and Bandarah strains.

Means of allele frequency observed for two chicken strains and two quail lines were shown in Table 3. Mean allele frequencies for Silver Montazah and Mandara chicken strains and Beige and Grey quail lines ranged from 0.13 (UBC005) to 0.50 (GUJ0029) for Silver Montazah and from 0.17 (MCW0167 and UBC002) to 0.50 (MCW0126,MCW0114 and GUJ0029) for Mandara chicken strains, while, ranged from 0.10 (UBC001) to 0.50 (MCW0127 and MCW0200) for Beige and from 0.13(MCW0114 ,GUJ0028 and UBC002) to 1.00 (MCW0200) for Grey quail lines, respectively (Table 3). Similarly, Roushdy et al, (2016) investigated that the highest allele frequency overall loci were 0.68 of allele 060 at locus UBC0005 and 0.33 at locus UBC005 and the lowest ones were 0.02 at locus GUJ0028 (for alleles 099, 108 and 126) and 0.1 at locus UBC001 for Grey and Beige quail lines, respectively. While, low estimate was reported by Bai et al. (2013) who reported that the allele frequencies ranged from 0.014 to 0.289 with alleles 174,160,170 at locus GUJ0028 for Chinese Yellow Quail. According to classification of Botstein et al. (1980), the highly informative markers (PIC) have values >0.50, the reasonably informative markers have PIC value between 0.25-0.50 and the slightly informative markers have PIC value <0.25. The value of PIC for Silver Montazah ranged from 0.44 in locus (GUJ0029) to 0.83 in locus (GUJ0028 and UBC005) and for Mandara ranged from 0.38 in locus (MCW0114) to 0.81 in locus (MCW0167). While, Beige quail line ranged from 0.24 in locus (MCW0127) to 0.85 in locus (UBC001) and for Grey quail line ranged from 0.48 in locus (UBC005) to 0.83 in locus (UBC002) except MCW0200 had no information marker (0.00) for Grey quail line as shown in Table 3. The majority of the loci were highly polymorphic information content except the markers MCW0127 and GUJ0029 for Silver Montazah, MCW0126, MCW0114 and GUJ0029 for Mandara chicken strains, MCW0127 and MCW0200 for Beige and MCW0200 and UBC005 for Grey quail lines had reasonably informative PIC values of 0.46, 0.44, 0.49, 0.38, 0.46, 0.24, 0.49, 0.00 and 0.48, respectively.

These findings were in agreement with Roushdy et al. (2016) who reported that the average of PIC for six markers were 0.66 and 0.71 with Beige and Grey quail line, respectively. Same trend obtained by Roushdy et al. (2013b) who reported that the PIC values were highly informative markers as 0.72, 0.76 and 0.78 for MCW48, ADL176 and MCW51 with Mamourah, Baheij and Mandara strains, respectively. While, Roushdy et al. (2013b) reported that four markers had reasonably informative PIC values 0.44, 0.42, 0.41 and 0.44 for ADL136, ADL171, MCW43 and MCW49, respectively with Mamourah, Mandara and Baheij chicken strains. Also, in Turkish native chicken breeds polymorphism information content was varied from 0.426-0.599 (Kaya and Yildiz. 2008). Roushdy et al. (2013a) reported that the PIC ranged between 0.271 for locus MCW73 and 0.7162 for locus ADL176 with general mean of 0.5545 with Dokki-4, Golden Montazah and Silver Montazah strains. Six markers had highly informative PIC values of 0.55, 0.62, 0.66, 0.53, 0.54 and 0.63 at loci ADL136, ADL172, ADL176, ADL210, MCW49 and MCW51, respectively for Matrouh, El-Salam and Bandarah strains (Roushdy et al. 2013c).

Analysis of Molecular Variance (AMOVA)

The genetic diversity among breeds was assessed by an analysis of molecular variance (F-indices) employing Arlequin

3.51 software package (most widely used for molecular population genetics analysis). The analysis default was treating missing data not exceed 10%, using program standard analysis. Table (4) presents analysis of molecular variance (AMOVA). Variance components proved that the majority of genetic diversity obtained in the current study is represented by within populations (54.03%) rather than others. This result may be due to the variance between two species studied (chicken and quail).

Sewall Wright invented a set of measures called F statistics for departures from HWE for subdivided populations (Weir and Cockerham, 1984). F stands for fixation index, where fixation being increased homozygosity. A pair wise difference among chicken strain and quail lines was 0.719 based on among species F index (F_{IS}), when F_{IS} value increased genetic diversity decreased. While, among individual within populations differences versus total variance was the lowest fixation indices (F_{ST}= 0.249) indicating low level of subpopulation differentiation. F_{ST} is a measure of population substructure and is most useful for examining the overall genetic divergence among subpopulations (Subpopulation within the total population).

Population structure Wright's F Statistics F_{IT} is not often used. It is the overall inbreeding coefficient of an individual relative to the total population (Individual within the total population). Population fixation index was 0.789 of variation referring to low differences within individuals versus total variance (F_{IT}). This result agreed well with Roushdy et al. (2016) who detected that variance components proved that the majority of the genetic diversity obtained among individuals within populations was 64.67% with Fixation indices (F_{IS}= 0.80), (F_{ST}= 0.201) and (F_{IT}=0.848) for Beige and Grey quail lines. Similarly, Roushdy et al. (2013c) reported that the majority of genetic diversity within individuals was 55.46% for Matrouh, El-Salam and Bandarah strains. Also, Roushdy et al. (2012a) reported that the majority of genetic diversity obtained by within individuals 55.35% and Fixation indices were FIS=0.345, FST= 0.155 and FIT=0.446 for Dandrawi and Sinai breeds. While, EL-Sayed et al. (2011) observed that the majority of genetic diversity obtained within individuals was 86.44%, while Fixation indices were F_{IS}=0.098, F_{ST}= 0.041 and F_{IT}=0.135 for Fayoumi and Dandrawi breeds.Cluster analysis based on Nei's genetic distance indicated that the studied populations formed two main groups (Fig. 3). The 1st group included Silver Montazah and Mandara chicken strains and the 2nd group harbored Beige and Grey quail lines. Although genetic analyses can reveal the extent of biodiversity in chicken breeds (Nassiri et al., 2007; Semik and Krawczyk, 2011) additional information on specific adaptations, distinct phenotypes, performance level, demography (including effective population size, and geographical distribution) and descriptive databases are required for adequate assessment of each breed when deciding on conservation and breeding programs (Groeneveld et al. 2010). The combining of generated molecular genotypic data (such as microsatellites) and appropriate statistical analysis program must be concerned to identify and interpret the relationships of genetic and phenotypic variations of the resource breeds. Ultimately, this approach can lead to the detection of DNA markers that can be applied for genetic improvement of populations in marker-assisted selection schemes of poultry breeding (Lamont; 2003). When a cross-species amplification is successful and results in polymorphic markers, these markers can be useful for identifying homologous chromosomal regions.

CONCLUSION

It could be concluded that , the 12 microsatellite markers were recommended to assess molecular genetic structure and similarity of two poultry species (chicken and quail). The results could be serve the genetic diversity on different levels including conservation of such genetic resources, future improvements for these two poultry species and/or understanding different genome arrangement and knowledge interests.

Table (1): Microsatellite loci used, their chromosome number, primer sequence, gene bank accession no. annealing temperatures detected and size range estimated in bp.

Locus	**Chr.**	**AT.**	**Primers Sequence**	**Gene Bank Accession no.**	**Band Size** (bp)
MCW0126	3	57.9	5'-TGGTGTACAGCACAGGCAACA-3' 3'-ACAGAGGAAGCCTGAATGAGT-5'	G31961	100-422
MCW0127	3	59.5	5'-TGCAATAAGAGAAGGTAAGGTC-3' 3'-GAGTTCAGCAGGAATGGGATG-5'	L43646	100-267
LEI0113	3	51.7	5'-ATGGGATGCTGGAAAGGGGT-3' 3'-TTCTGCAAACCCTATGTTGGGC-5'	X82853	375-663
MCW0114	4	59.5	5'-AGCAAACTGCTCAGTGCTGTG-3' 3'-GCGTTGAAAGTAGTGCTTCCG-5'	L43641	206-521
MCW0167	4	47.9	5'-GATCCCAAAACAAATGCACAC-3' 3'-CTTACATGAGTGCTATCTGCT-5'	L43665	90-140
MCW0200	1	54.8	5'-GAGACATTGCAAATACTCAGC-3' 3'-TAGTCAGGGAGTTCAGGAAGG-5'	G31982	55-280
GUJ0028	QL08	57.2	5'-TGAACAAAGCAGAAAGGAGC-3' 3'-CCTTACCTACATGAAACGTC-5'	AB035838	70-196
GUJ0029	CJA06	51.7	5'-GAGCATTTCTAGTCTGTCTC-3' 3'-ATACACAGGTAAGGAAACC-5'	AB035839	50-149
UBC001	1	48	5'-TCTCTAAAATCCAGCCCTAA-3' 3'-AGCTCCTTGTACCCTATTGC-5'	AF121113	110-470
UBC002	6	58	5'-CAGCCAATAGGGATAAAAGC-3' 3'-CTGTAGATGCCAAGGAGTGC-5'	AF121114	120-274
UBC004	4	51.7	5'-TCCTTGGGCAGTAGTTTCAA-3' 3'-CTCCCATGTTGCTTCTTTAG-5'	AF121115	220-290
UBC005	3	51.7	5'-GGAACATGTAGACAAAAGC-3' 3'-AGTAGTCCATTTCCACAGCCA-5'	AF121117	60-177

Table (2): Number of alleles observed for each locus within each species, total no. of alleles, specific alleles and pairwise proportion of different alleles between populations (F_{ST}).

Locus	No. of alleles per species				No.of specific alles				Total no. of alleles per locus	FST
	Silver Montazah	Mandara	Beige	Grey	Silver Montazah	Mandara	Beige	Grey		
MCW0126	4	2	4	3	2	0	2	1	9	0.270
MCW0127	3	4	2	3	0	0	2	1	7	0.392
LEI0113	5	4	6	4	4	3	2	0	14	0.219
MCW0114	5	2	4	8	4	1	1	5	15	0.299
MCW0167	7	6	5	5	1	0	0	1	10	0.137
MCW0200	4	4	2	1	1	1	2	1	8	0.512
GUJ0028	7	5	9	8	1	2	0	0	14	0.197
GUJ0029	2	2	4	5	0	0	1	2	8	0.295
UBC001	4	5	10	7	0	1	7	4	19	0.149
UBC002	6	6	5	8	0	3	0	3	13	0.136
UBC004	5	4	4	5	1	2	0	0	8	0.154
UBC005	8	5	3	4	4	0	0	2	11	0.276
Mean	5	4.10	4.83	5.08	2.25	1.86	2.43	2.22	11.33	0.252
Total	60	49	58	61	18	13	17	20	136	

Table (3): Allele frequency mean and PIC observed for two chicken strains and two quail lines.

Locus		Chicken strains		Quail lines	
		Silver Montazah	**Mandara**	**Beige**	**Grey**
MCW0126	Frequency mean	0.25	0.50	0.25	0.33
	PIC	0.68	0.49	0.64	0.65
MCW0127	Frequency mean	0.33	0.25	0.50	0.33
	PIC	0.46	0.72	0.24	0.58
LEI0113	Frequency mean	0.20	0.25	0.17	0.25
	PIC	0.75	0.69	0.70	0.67
MCW0114	Frequency mean	0.20	0.50	0.25	0.13
	PIC	0.73	0.38	0.59	0.78
MCW0167	Frequency mean	0.14	0.17	0.20	0.20
	PIC	0.79	0.81	0.61	0.68
MCW0200	Frequency mean	0.25	0.25	0.50	1.00
	PIC	0.54	0.63	0.49	0.00
GUJ0028	Frequency mean	0.14	0.20	0.11	0.13
	PIC	0.83	0.77	0.73	0.58
GUJ0029	Frequency mean	0.50	0.50	0.25	0.20
	PIC	0.44	0.46	0.60	0.77
UBC001	Frequency mean	0.25	0.20	0.10	0.14
	PIC	0.68	0.75	0.85	0.82
UBC002	Frequency mean	0.17	0.17	0.20	0.13
	PIC	0.81	0.80	0.65	0.83
UBC004	Frequency mean	0.20	0.25	0.25	0.20
	PIC	0.63	0.56	0.61	0.67
UBC005	Frequency mean	0.13	0.20	0.33	0.25
	PIC	0.83	0.70	0.50	0.48
	PIC means overall loci	**0.67**		**0.62**	

Table (4): AMOVA analysis of chicken and quails strains based on microsatellite DNA variation.

Source of variation	d.f.	S .S.	Percentage variation	Fixation indices
Among populations	3	132.217	24.88	FIS= 0.71932
Among individuals within populations	80	387.950	54.03	FST= 0.24881
Within individuals	84	66.500	21.08	FIT= 0.78916
Total	167	586.667		

F_{IS} Fixation indices (Among populations)
F_{IT} Fixation indices (Within individuals)
F_{ST} Fixation indices (Among individuals within populations)

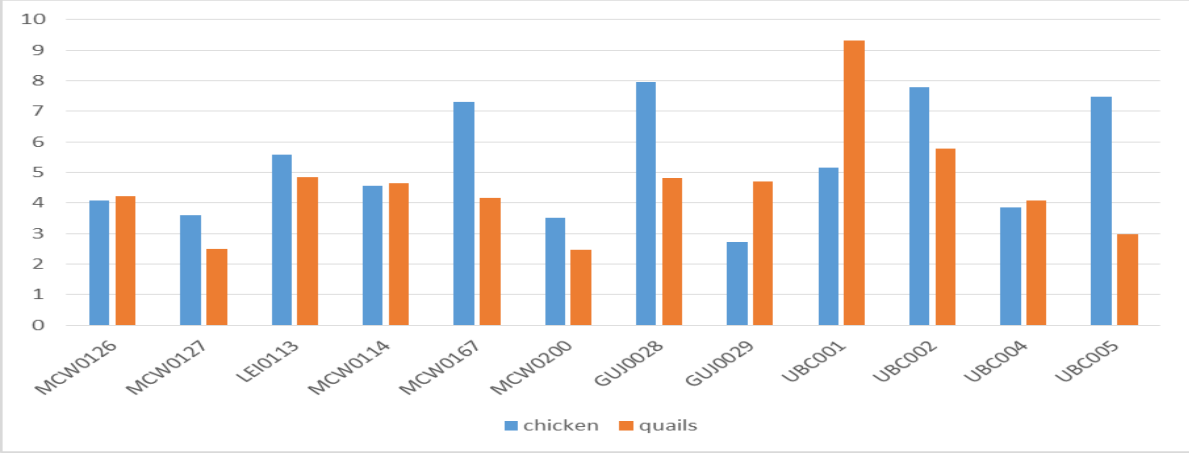

Figure (1): Mean effective no. of alleles (ENA) for chicken strains and quail lines.

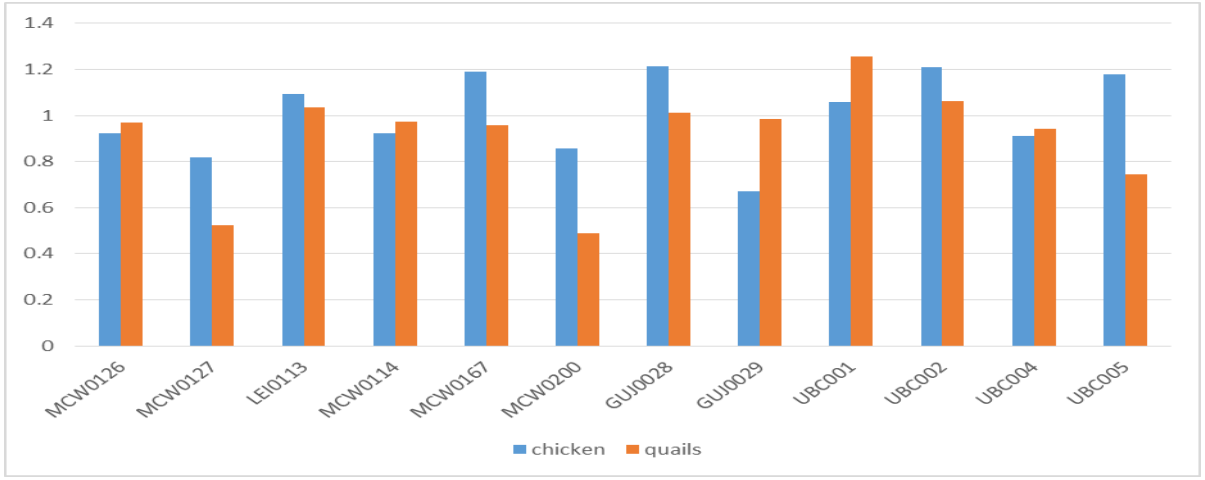

Figure (2): Expected heterozygosity for chicken strains and quail lines.

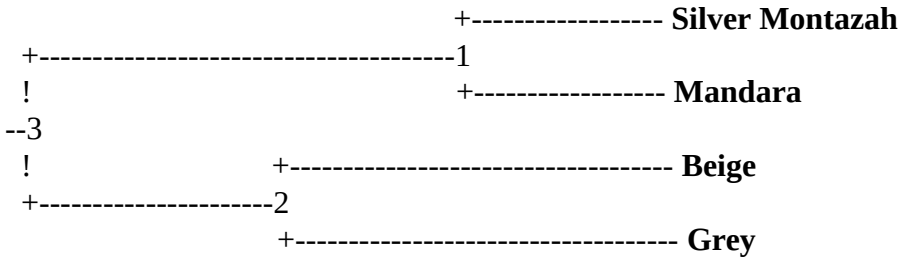

Figure (3): Dendrogram Based Nei's (1978) Genetic distance of two chicken strain and two quail lines produced by UPGMA clustering based on Nei's genetic distance using 12 microsatellite loci.

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الملخص العربى

التقييم الوراثى لسلالتين من الدجاج وخطين من السمان الياباني بالاستخدام المتبادل للواسمات الجزيئية الخاصة بالدجاج والسمان

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إن الكرموسومات الموجودة في كلا من الدجاج ونظيرتها الموجودة بالسمان الياباني متشابهة الي حد كبير مع وجود اختلافات بسيطة في الترتيب الكروموسومي لهذين النوعين . تم اخذ عدد 21 عينة دم من دجاج المنتزة الفضي و20 عينة من دجاج المندرة و22 عينة من خط السمان البيج و21 عينة من خط السمان الرمادي. إستخدم عدد ثمانية واسمات وراثية خاصة بالدجاج وستة من الواسمات الوراثية خاصة بالسمان الياباني بشكل متبادل. أظهرت النتائج نجاح تطبيق 12 واسم جزيئي من اجمالي 14 واسم جزيئي بنسبة 85.7% بشكل متبادل في النوعين. أعطت الواسمات الجزيئية نتائج ناجحة في تحيد المناطق المتماثلة علي الكروموسومات بشكل متبادل علي النوعين.ولقد اشارت نتائج ال (PIC) الي إمكانية إستخدام 12 من 14 واسم جزيئي يمكن استخدامهم لاعطاء اشكال عديدة من التنوع البيولوجى علي مختلف المستويات بما في ذلك الحفاظ علي الموارد الوراثية وإدخال تحسينات مستقبليا لهذة الانواع ومعرفة الاختلاف في الترتيب الجيني لتلك السلالات.