

## The genetic structure at chromosomes 3, 4 and 5 of the native chicken breeds in Egypt and in relation to the ecology

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### Summary

This study aimed at revealing the genetic structures of native Egyptian chicken breeds, and in relation to the ecology. Five populations with different origins were used. They were Fayoumi (Fay), Sinai Bedouin (SB), White Baladi (WB), Baladi (CE2) and naked-neck Baladi (CE4). PCR was performed on genomic DNA, targeting the microsatellite loci LEI0166 on chromosome 3, LEI0073 and ADL0143 on chromosome 4, and MCW0193 on chromosome 5. WB and Fay had the highest average allele richness ( $A_r$ ) of 7.75 and 6.25 alleles/locus, whereas populations CE2, CE4 and SB had  $A_r$  of 5.5, 5.25 and 4.4 alleles/locus, respectively. The average polymorphic information content was 0.765, 0.592, 0.786, 0.714 and 0.764 in Fay, SB, WB, CE2 and CE4, respectively. The fixation index  $F_{IT}$  averaged 0.567, and indicated that 57% of the variation was accounted for heterozygosity. The  $F_{IS}$  averaged 0.178, and indicated apparent contribution of inbreeding. The value  $F_{ST}$  averaged 0.373, and explained the genetic variations within populations. The results revealed two gene pools for the native Egyptian chickens; the desert gene pool (DGP) from which Sinai Bedouin has been formed, and Nile valley and Delta gene pool (NVDGP) from which Fayoumi, White Baladi, Baladi and naked-neck Baladi have been derived. There were evidences for the gene exchange between the breeds of NVDGP, while no evidences were reported for the gene exchange between DGP and NVDGP.

*Keywords: Ecology, genetic structure, local chickens, microsatellites*

### Introduction

Local chickens although are slowly grown and lowly egg produced (N'dri *et al.*, 2007a, 2007b and Zereu and Lijalem, 2016), they possess major genes that allow for survival under harsh environments (El-Gendy, 2009 and Niknafs *et al.*, 2012). Although local chickens confront the local environmental conditions by their unique genetic background, they have been genetically disused. Mwacharo *et al.* (2013) screened the genomes of 15 chicken populations from Kenya, Uganda, Ethiopia and Sudan. Three distinct autosomal gene pools (I, II and III) were identified. Gene pool (I) was predominantly found in Ethiopia and Sudan, while gene pools (II) and (III) occurred in both Kenya and Uganda. A gradient of admixture for gene pools II and III between the Kenyan coast and Uganda hinterland ( $P = 0.001$ ) was observed, while the gene pool I was clearly separated from the other two gene pools. Also, Abebe *et al.* (2015) studied the genetic diversity, relationship and population structure of 5 local Swedish chicken breeds. There were considerable variations between breeds. Rudresh *et al.* (2015)

studied the variability within and between Indian indigenous chicken ecotypes of six districts. Four ecotypes were genetically identical due to their common ancestral evolution, while two ecotypes formed relatively a different cluster due to a separate common ancestral population.

In Egypt, the winter climate varies from warm to cold, where the diurnal temperature ranges between around 10°C and little above 20°C, with significant reduction to below 10°C during the nighttime. The summer temperature is always at mid-30°C and sometimes exceeds 40°C. The topography in Egypt also contributes to the livestock distribution. The desert atmosphere is dry and the Nile valley and Delta atmosphere is humid. Therefore, it is expected that the native chickens in Egypt are genetically differed to survive these drastic environments.

This study targeted three autosomal regions that have shown to be highly variable in native Egyptian chickens, and aimed at the assessment of the genetic structures of five native chicken breeds in Egypt that have been originally arisen in different ecological zones and the relationship between them.

## **Materials and Methods**

### **Chicken Breeds and Sampling**

Five breeds that have arisen in different ecological zones in Egypt were included in the study. The breeds were Fayoumi, Sinai Bedouin, White Baladi, Baladi and naked-neck Baladi. Fayoumi (Fay) has been developed in Fayoum, a natural oasis lays in the West Desert in the mid-north of Egypt. Sinai Bedouin (SB) is subsisted in the desert of Sinai Peninsula in east of Egypt. White Baladi (WB) has been developed in the faculty of Agriculture, Cairo University during the early 1950s from the village chickens that are commonly found in Nile Delta and valley in north of Egypt. Baladi (CE2) and naked-neck Balasi (CE4) have been developed in the faculty of Agriculture, Cairo University (El-Gendy, 2009) from the village chickens that are commonly spread in Upper Egypt. The populations are retained in about 200-400 females and 40-80 males/population in the respective conservation sites.

### **Microsatellite-PCR analysis and Genome assessment**

The genomic DNA samples were extracted from the blood samples using Promega genomic DNA purification kit (Promega Corporation, Madison, WI, USA), and the extraction procedures were according to the manufacturer's guide. Microsatellite-PCR procedure was performed to screen genomic DNA, using four microsatellite markers (LEI0166 on chromosome 3, LEI0073 and ADL0143 on chromosome 4 and MCW0193 on chromosome 5). The PCR products were separated on 8% polyacrylamide gel electrophoresis (PAGE). Allele richness ( $A_r$ ) and polymorphic information content (PIC) were estimated, and F-statistic and phylogenetic analyses were performed.

## **Results and discussion**

### **Genetic structure of native Egyptian breeds**

**Allele diversity:** The mean allelic richness ( $A_r$ ) was 7.2, 5.0, 6.8 and 4.4 alleles / population at

the microsatellite loci LEI0166, LEI0073, ADL0143 and MCW0193, respectively. White Baladi and Fayoumi had the highest average  $A_r$  of 7.75 and 6.25 alleles/ locus; however Baladi (CE2), naked-neck Baladi (CE4) and Sinai Bedouin had  $A_r$  of 5.5, 5.25 and 4.5 alleles/ locus.

**Polymorphic Information content:** Table (1) presents the polymorphic information content (*PIC*) estimated at different microsatellite loci in different populations. The *PIC* reflects the extent of gene diversity in a population which permits for wide ranges of trait performance. The average *PIC*, overall loci, was 0.765, 0.592, 0.786, 0.714 and 0.764 in Fayoumi, Sinai Bedouin, White Baladi, Baladi and naked-neck Baladi, respectively.

Table 1: Polymorphic information content in the chicken populations

Microsatellite locus	Fay	SB	WB	CE2	CE4	Average
LEI0166	0.75	0.55	0.82	0.969	0.85	0.789
LEI0073	0.71	0.327	0.78	0.83	0.76	0.681
ADL0143	0.84	0.81	0.86	0.65	0.73	0.778
MCW0193	0.75	0.68	0.69	0.41	0.71	0.648
Mean	0.765	0.592	0.786	0.714	0.0764	0.724

Fay, SB, WB, CE2 and CE4 are the abbreviations of Fayoumi, Sinai Bedouin, White Baladi, Baladi and naked-neck Baladi, respectively.

### Relationship between the chicken breeds

**Variation analysis:** The F-statistic analysis was used to recognize the sources of variation between all individuals under study and to assess the extent of the genetic relationships across chicken populations (Table 2). The values of  $F_{IT}$  were in general moderate to high and ranged from 0.297 to 0.860, with an average of 0.567. This indicates that almost 57% of the total genetic variation was accounted for the differences among all individuals of the five populations. It also indicates that heterozygosity is in general high. The  $F_{IS}$  ranged from 0.0 to 0.357 with an average of 0.178, indicating that most of the genetic variation was between populations with apparent contribution of inbreeding.

The  $F_{ST}$  is always given more considerations because it accounts for the level of genetic differentiation between populations. In this study,  $F_{ST}$  values ranged from 0.297 to 0.454, and the average was 0.373. This explains approximately 63% of the genetic variations to be between chicken populations. The results of F-statistic analysis reveal that many of the ecotype breeds are genetically differentiated from each other and show less genetic relationships.

Table 2: The F-statistic analysis

Microsatellite Locus	$F_{IT}$	$F_{ST}$	$F_{IS}$
LEI0166	0.649	0.454	0.357
LEI0073	0.860	0.420	0.143

ADL0143	0.464	0.320	0.212
MCW0193	0.297	0.297	0.000
Mean ± SE	0.567±0.121	0.373±0.038	0.178±0.063

**Phylogenetic analysis:** The phylogenetic dendrogram for the chicken populations was constructed (Figure 1), and reflected the geographical origin of the breeds. The breeds were clustered into two groups. Sinai Bedouin formed a group and the other breeds formed another group. Fayoumi was in a separate branch, while White Baladi, Baladi and naked-neck Baladi had arisen from the same genetic node in two branches. One branch was mutated to form White Baladi. The other branch formed a base population that has been split to form Baladi and naked-neck Baladi. The phylogenetic analysis reveals that the native Egyptian chicken breeds form two separate gene pools according to their ecological origin; the desert gene pool (DGP) from which Sinai Bedouin has been formed, and Nile valley and Delta gene pool (NVDGP) from which Fayoumi, White Baladi, Baladi and naked-neck Baladi have been derived. There were evidences for the gene exchange between the breeds of NVDGP, while no evidences were reported for the gene exchange between DGP and NVDGP.

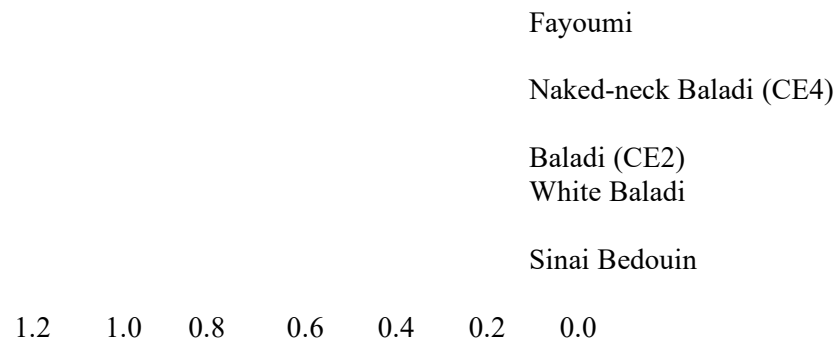


Figure 1: The phylogenetic dendrogram of the native Egyptian chicken breeds

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