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The growth pattern of warm-region chickens under prolonged natural severe heating conditions with a reference to association between microsatellite loci on chromosomes 3, 4 and 5 and QTL of growth

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Summary

The objective of this study was to evaluate the growth pattern of native Egyptian chickens under prolonged natural severe heating conditions and to recognize linkage between QTL for growth under heating conditions and microsatellite loci on chromosomes 3, 4 and 5. Two genetic lines were used; line CE1 that has been selected for 6-week body weight for 15 generations and line CE2 as the genetic control. The birds have been exposed to prolonged natural severe heat stress conditions during the growing period from hatch to 20 weeks of age. The diurnal maximum temperature ranged from 28 to 44℃, and the minimum temperature ranged from 16 to 31℃. The diurnal maximum humidity ranged from 24 to100%RH, and the minimum humidity was 4-43%RH. The averages of daily maximum and minimum temperature-humidity index (THI) were 28.8 and 18.6°C. Line CE1 was significantly heavier than line CE2 in all age comparisons. Line differences in growth rates were insignificant and showed retarded growth under the heating conditions in both lines. Four microsatellite loci on chromosomes 3, 4 and 5 showed significant ($P \leq 0.05$) association with many QTL of growth under heating conditions. The allele of 454 bp on locus LEI0166 was associated with QTL that contributed to the phenotypic variance (δ_p^2) of 6-week BW by 26.33%. The alleles of 581, 141 and 171 bp on locus LEI0073 showed linkage to QTL that contributed to growth during the first 4 weeks of age by 19.42-42.02% of δ_p^2. On locus ADL0143, the allele of 423 bp was linked to QTL influencing 8-week BW by 27.07% of δ_p^2. To date, this is the first research that finds association between microsatellite loci and QTLs of growth under natural heat stress conditions.

Keywords: growth performance, heat tolerance, microsatellite alleles, native chickens, QTL

Introduction

In tropical and warm regions, high temperature dominates the climate most of the year, and hence is the foremost cause for retarding growth and reproductive performance in the synthetic broilers and parental stocks. Despite tropical- and warm-region oriented chickens have the genetic compositions that contribute to heat tolerance and have further significance for sustainable development (El-Gendy *et al.*, 2007; van Marle-Koster *et al.*, 2008); they have not been genetically improved in commercial prospect. Purswell *et al.* (2012) studied the growth performance of broilers under temperature-humidity index (THI) of 14.8ºC to 26.9ºC. The results showed that as THI exceeded approximately 21ºC, bird performance significantly declined and body temperature increased up to 1.7°C above the nominal body temperature (41°C).

The whole genome-wide scans with microsatellite markers resulted in the recognition of many QTL that significantly affecting growth, feed efficiency and carcass traits on *Gallus gallus* autosomes GGA1, GGA2, GGA4 and GGA23 (van Kaam *et al.,* 1999a; 1999b). Nassar *et al.* (2015) reported the identification of genomic regions affecting body weight and growth until 20 weeks of age. QTL affecting fatness in chicken were investigated and mapped by Ikeobi *et al.* (2002) and Jennen *et al.* (2004).

Although El-Gendy and Helal (2014) denoted to the existence of linkages between microsatellite loci and QTL for growth in warm-region originated chickens, but to date no research was set to study and detect QTL for growth under natural heat stress conditions. The objective of this study was to evaluate the genetic progress in growth performance of a native Egyptian chicken line selected for high 6-week body weight and its corresponding genetic control line under prolonged natural severe heating conditions and the detection of association between QTL of growth on chromosomes 3, 4 and 5 and microsatellite markers.

Materials and Methods

a. Genetic lines and management

Two native Egyptian genetic lines of chickens were used; line CE1 that has been selected for 6-week body weight for 15 generations, and the genetic control line CE2. A total of 255 chicks of line CE1 and 208 chicks of line CE2 were used. Chicks of both lines were raised together in floor brooding chambers to 6 weeks and in floor rearing pens to 18 weeks of age, in a conventional open house. All chicks received same routine daily managements, including feed, drinking water, light and medications. The indoor circadian natural maximum and minimum environmental temperature and maximum and minimum humidity during the experimental period were monitored, and the temperature-humidity index (THI).

All individuals were weighed at hatch and then biweekly until 18 weeks of age. Biweekly body weight gains (BWG) and growth rates (GR) were calculated. Mortality was also calculated.

***b. Genome analysis**:*

DNA was extracted from blood samples and microsatellite-PCR procedure was performed to scan individual genomic DNA samples, using 4 microsatellite primers targeting 3 autosomal chromosomes. The genomic bands were separated on polyacrylamide gel electrophoresis.

***c. Genome and Statistical analysis**:*

PCR products were visualized and photographed using Gel Documenter and the DNA images were analyzed to derive the genome data. The growth performance data set was statistically analyzed using the GLM procedure of SAS. The genome data were combined with the growth data, and the association analysis was applied to the combined molecular and phenotypic data sets.

Results and Discussion

a. Growth Performance

Body weights of the genetic lines under prolonged natural severe heating conditions are shown in figure (1). The selected line CE1 was significantly ($P \leq 0.05$) heavier than its corresponding genetic control line CE2 at hatch and during the whole growing period under study. Figure (2) presents the results of biweekly growth rates. During the 0-2 week period, line CE1 grew in a rate significantly ($P \leq 0.05$) faster than the corresponding control line CE2, thereafter the significance of line differences along the growing period were inconsistent. Figure

(3) shows that the mortality rates in both lines were very close, without distinctive difference during the growing period. Until 12 weeks of age, the mortality rates in both lines were minimal and less than the normal range known for broiler chicks and reached to 0.67% in either line during the 10-12 week period. The mortality has increased during the 12-14 week period to reach 5.40 and 5.15% in lines CE1 and CE2 respectively, and then gradually declined to 3.8 and 3.2% in both lines respectively. The results of growth performance explain the growth patterns of different genetic lines under prolonged natural severe heating conditions. Although line CE1 had significant and greater growth performance than line CE2 due to selection pressure, birds of both lines showed retarded growth.

Figure 1: Biweekly body weights (BW) of the selected line (CE1) and control line (CE2) under prolonged natural severe heating conditions

Figure 2: Biweekly growth rates (GR) of the selected line (CE1) and the control line (CE2) under prolonged natural severe heating conditions

Figure 3: Biweekly mortality of the selected line (CE1) and control line (CE2) under prolonged natural severe heating conditions

b. Genome Banding and Association Analysis

Four microsatellite loci were recognized in both lines CE1 and CE2. The results indicated the presence of several microsatellite alleles that were significantly associated with many QTL of growth under heating conditions (Table 1). On chromosome 3, locus LEI0166 significantly ($P \leq 0.05$) contributed to 30.70% of δ_p^2 in 4-wk BW, 26.33% of δ_p^2 in 6-wk BW and 16.74% of δ_p^2 in 8-wk BW. The alleles of 581, 141 and 171 bp on locus LEI0073 on chromosome 4 showed significant to highly significant contribution to the growth during the first 4 weeks of age, however the allele with 534 bp was associated with QTL significantly contributed to the growth

during 6 and 8 weeks of age. ADL0143 locus on chromosome 4 was associated to QTL with significant ($P \leq 0.05$) contribution by 14.17% of δ_p^2 in 6-wk BW, by 27.07% of δ_p^2 in 8-wk BW. The association of the MCW0193 locus with QTL influencing growth measurements was obvious, and there was a significant contribution to δ_p^2 in 4-wk BW by 20.36% in δ_p^2 and in 6-wk BW by 11.83% of δ_p^2.

Table 1: The association between microsatellite alleles and QTLs of growth, referred by percentage contribution in the phenotypic variance

Microsatellite locus	Band size (bp)	QTL	Contribution to δ_p^2, %
LEI0166	287	4-wk BW	30.70 *
	454	6-wk BW	26.33 *
	454	8-wk BW	16.74 *
LEI0073	581	4-wk BW	31.55 **
	581	2-4 wk BWG	42.02 *
	141	4-wk BW	28.75 **
	141	0-2 wk GR	19.42 *
	171	4-wk BW	28.84 **
	171	2-4 wk BWG	34.96 *
	171	2-4 wk GR	27.87 *
	534	6-8 wk BWG	22.87 *
	534	6-8 wk GR	24.53 *
ADL0143	349	6-wk BW	14.17 *
	349	8-wk BW	20.48 **
	423	8-wk BW	27.07 **
	423	6-8 wk BWG	31.83 *
MCW0193	325	4-wk BW	20.36 *
	461	6-wk BW	11.83 *

*, significant (P ≤ 0.05), **, significant (P ≤ 0.01)

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