

## DETECTION OF MAJOR GENES AFFECTING GROWTH-RELATED TRAITS IN A BROILER CHICKEN LINE

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### ABSTRACT

In this study the body weight at birthday (BW) and at six weeks of age (BW6) in a commercial broiler chicken line, including 1555 roosters and 12142 hens, were analyzed to detect a single locus affecting growth-related traits by using the Major Gene Index (MGI) method. Based on the selection index method, the commercial broiler line was selected for 19 consecutive years in order to achieve gain in weight in the paternal line and reproductive traits in the maternal line. The goal was to investigate the deviation of offspring-predicted breeding values from parents-predicted breeding values using the MGI method. Trait means were 42.93 and 1861.5 g for BW and BW6, respectively. The MGI values for the entire population of the commercial broiler line at three levels of  $\alpha$  (0.5, 1 and 2) were less than 1 (0.8, 0.72 and 0.77 for BW and 0.91, 0.78 and 0.85 for BW6). The MGI values for candidate individuals were greater than 1, and this index was also increased by the change of  $\alpha$  (0.5-2). The results indicated that 8 of 65 roosters and 115 of 314 hens for BW trait, from 58 roosters and 714 hens as candidates for BW6 trait, 9 roosters and 216 hens were identified as major gene carriers. In conclusion, the MGI approach is suggested to be a useful preliminary step to detect major genes.

**Key words:** body weight; commercial broiler line; major gene index

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### INTRODUCTION

The polygenic model of inheritance is the basis of traditional animal breeding for quantitative traits. This model assumes that a quantitative trait is controlled by many genes with small effects (Falconer and Mackay 1996; Cemal and Karaca, 2005). The great advances are achieved in animal and plant breeding relying on the classical theory. However, in recent decades several genes with major effect on economic traits have been detected in domestic animals. Such loci are called as QTL (Quantitative Trait Loci) or major loci (Cemal and Karaca, 2005). Some of them in poultry are avian dwarf and naked neck genes, which affect body size and heat resistance, respectively (Leroy *et al.*, 1989; Merat, 1990). The maximum likelihood, complex segregation analysis and mixed model methodologies are statistical

methods to detect major genes and to estimate their effects and frequencies using distribution of phenotypes (Ochial *et al.*, 2005). Among these methods segregation analysis is the most powerful method for major gene detection, due to the fact that the whole information about data is considered in the data analysis. This method requires complex calculations for large population. The Major Gene Index (MGI) method is an easier method that has been offered by Karlin *et al.*, (1977) to prevent complex computing. In this method, it is only required to calculate the predicted breeding values of individuals and then to check the deviation between parents and offspring to determine if the candidate individual is a carrier of the major gene (Ochial *et al.*, 2005). In fact, the MGI is a ratio which is a measure of the deviation of the offspring breeding value from the mid-parental breeding value and its deviation from

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Received: February 2, 2015  
Accepted: July 15, 2015

each parental breeding value. This method first was used to analyze human blood pressure data using phenotypic records (Karlin *et al.*, 1979). In later years, the predicted breeding values with Best Linear Unbiased Prediction (BLUP) were used to calculate the index (Famula, 1986). Indeed, the calculated index by BLUP is considered to be more reliable than that by phenotypic data (Ochial *et al.*, 2005). Estimated additive heritability for Body Weights at birthday (BW) and at six weeks of age (BW6) traits of the commercial broiler line were 0.02 and 0.21, respectively (Seraj *et al.*, 2010; Salimi *et al.*, 2011). No any research was conducted for detecting major genes at BW and BW6 traits in the commercial broiler line in spite of the fact, that in the world, investigations were carried out in order to detect major genes for body weight trait at various ages. The aim of this study was to investigate the presence of major genes that affected production traits by the MGI method.

## MATERIAL AND METHODS

### Animals and records

Commercial broiler line was selecting for productive traits over 19 years (1992-2011). The data used in the present study were related to BW and BW6. Records from 14 and 3 generations were applied for the former and the latter case, respectively. Records of three generations were used for BW6, because the number of three generation data at BW6 was approximately the same as the number of 14 generations data at BW. The examined birds included 1555 roosters and 12142 hens. Selection in the paternal line was based on growth-related traits and desired gain selection index scheme. The purpose of selection index in this line was to increase higher growth-related trait.

### Statistical method for detecting major gene

#### Major Gene Index method

Two formulas were used for calculation of the MGI. The MGI was calculated as the below formula for a whole population of the commercial broiler line:

$$\text{MGI}(\alpha) = \frac{\sum_{i=1}^n [ |O_i - 0.5(S_i + D_i)|^\alpha ]}{\sum_{i=1}^n [ |O_i - S_i|^{\frac{\alpha}{2}} |O_i + D_i|^{\frac{\alpha}{2}} ]} \quad (\text{Famula, 1986})$$

where  $O_i$ ,  $S_i$ ,  $D_i$ ,  $n$  and  $k$  – show the offspring breeding value, the rooster breeding value, the hen breeding value, the offspring's number of parents and the known parameter (0.5, 1 or 2), respectively.

The MGI was calculated as the below formula for individual as a candidate of the commercial broiler line:

$$\text{MGI}(P, \alpha) = \frac{\sum_{i=1}^n \frac{1}{k_i} \sum_{j=1}^{k_i} \left[ |a(O_{ij}) - \frac{a(P) + a(M_i)}{2}| \right]^\alpha}{\sum_{i=1}^n \frac{1}{k_i} \sum_{j=1}^{k_i} \left[ |a(O_{ij}) - a(P)|^{\frac{\alpha}{2}} |a(O_{ij}) - a(M_i)|^{\frac{\alpha}{2}} \right]} \quad (\text{Ochial } et al., 2005)$$

where  $P$ ,  $M_i$ ,  $O_{ij}$  indicate individual as a candidate, the  $i$ th mate and the  $j$ th offspring from parents  $P$  and  $M_i$  respectively,  $a$  – is an indicator of a predicted breeding value,  $n$  is the number of mates,  $k_i$  is the number of offspring from parents  $P$  and  $M_i$  and  $\alpha$  is the known parameter (0.5, 1 or 2). Values of  $\alpha$  were recommended as three levels for evaluation of the MGI to emphasize small ( $\alpha = 0.5$ ), moderate ( $\alpha = 1$ ) and large ( $\alpha = 2$ ) deviations by Karlin *et al.* (1979).

In this study, 65 roosters with 30-40 offspring and 394 hens with 6-12 offspring for BW, 58 roosters with 40-60 offspring and 714 hens with 6-16 offspring for BW6 were chosen as a candidate  $P$ . Polygenic model assumes that the deviation of offspring from the mid-parental average is smaller than the deviation from each parent value. The MGI calculation is based on the assumption of polygenic model. Indeed, the MGI is the ratio that its numerator is the deviation of offspring from the mid-parental average and its denominator is the deviation from each parent value. Therefore, if the trait is under polygenic inheritance, the MGI value must be smaller than 1. When the MGI value is greater than 1, it might be expected that major gene is affecting the trait. It should be noted that the MGI value increases by increasing  $\alpha$  (0.5-2).

### Prediction of breeding values

Breeding values for all the birds in the line were predicted using BLUP animal model. Breeding values were calculated by using Bayesian method with Gibbs 3f90 software (Misztal, 1999). The three parameters of Gibbs sampling were: total sampling period of 100000, burn-in period of 5000 and sampling interval of 50. The used animal model was as following:

$$y = Xb + Z_1a + Z_2m + Z_3c + e \quad \sigma_{am} \neq 0$$

where  $y$  – is a vector of observations,  $b$  – is vector of fixed effects (Generation-hatch, Sex, hen age effects for two traits and Age at recording effect for BW6),  $a$  – is an unknown random vector of direct additive genetic effect,  $m$  – is an unknown random vector of maternal genetic effect,  $c$  – is an unknown random vector of maternal permanent environmental effect and

$e$  – is an unknown random vector of residuals. The  $X$ ,  $Z_1$ ,  $Z_2$  and  $Z_3$  are design matrices relating observation to the corresponding effects. More information about Bayesian estimation procedure can be found in Blasco (2001). The software programs SAS/STAT 9.2 (2002-2008), FoxPro (Microsoft Visual FoxPro 9.0) and Excel (Microsoft Excel 2013) were used in this study.

## RESULTS AND DISCUSSION

Descriptive statistics of the studied traits was included into the Table 1. The MGI for a whole population at three levels of  $\alpha$  (0.5, 1 or 2) is shown in the table 2. The MGI values in Table 2 were less than 1; the whole population was under polygenic inheritance. However, the calculation of the MGI for individuals, as candidate for presence of a major gene, confirmed some of them as a carrier of a major gene. Descriptive details of predicted breeding values and the MGI for candidate roosters carrying major gene are shown in Table 3, and for candidate hens carrying major gene are shown in Table 4. Only hens as carriers of major gene with more than 10 offspring for BW and hens as carriers of a major gene with more than 14 offspring for BW6 are shown in Table 4 due to the high number of hens' carrying major gene. As mentioned before, when the MGI value is greater than 1, regardless of value of  $\alpha$ , and when the index increases by increasing of  $\alpha$  (0.5-2), the candidate individual can be considered as a carrier of the major gene. Accordingly, among 65 roosters for BW and 58 roosters for BW6, the individuals shown

in Table 3 were considered to be carriers of a major gene. Also, of the hens tested in this investigation, 115 of 314 hens were identified to be carriers of major genes for BW, and 216 out of 714 hens were identified to be carriers of major genes for BW6 (all of them are not shown in Table 4). The rooster number 73904 and his offspring have desirable predicted breeding values for BW. Additionally, the rooster number 115386, 117544, 119758 and 121040 and their offspring have desirable predicted breeding values for BW6. The hen number 75910, 65823, 65372 and 91263 and their offspring have desirable predicted breeding values for BW and the hen number 116441, 115385, 120313 and 119763 and their offspring have the same feature for BW6 (not shown in Table 4). According to these results, these roosters and hens could have segregation of a major gene with favorable effects on each trait.

There is number of researchers, who have reported about major genes in poultry. Navarro *et al.* (2006) found segregation of a major gene in the genetic control blood oxygen saturation in a commercial broiler line using segregation analysis. Ochial *et al.* (2005) showed impact of a major gene on age at sexual maturity and egg production traits in a selected laying line by using the MGI method. Alijani *et al.* (2010) investigated major gene affecting the age at first laying, body weights at the end of eight weeks and 12 weeks, average egg weight during 84 days of laying and number of eggs laid during egg production period traits in Mazandaran and Azerbaijan rural poultry. They found segregation of a major gene for all traits in Mazandaran population and for average egg weight trait

**Table 1: Descriptive statistics of studied traits in the commercial broiler line**

Trait	Number of records	Trait means (g)	Standard deviation (g)	Maximum value (g)	Minimum value (g)	Coefficient of variation (%)
BW	7441	42.93	4.14	58	28	9.63
BW6	8478	1861.56	355.81	2861	542	19.11

**Table 2: MGI values for the entire population of the commercial broiler line**

Trait	MGI (0.5)	MGI (1)	MGI (2)
BW	0.883	0.728	0.774
BW6	0.913	0.789	0.856

**Table 3: Descriptive details of Predicted Breeding Values (PBV) and Major Gene Index (MGI) for roosters carrying major gene**

P Rooster	N. Offspring	BW6					P Rooster	N. Offspring	BW				
		PBV	PBV of offspring	MGI (0.5)	MGI (1)	MGI (2)			PBV	PBV of offspring	MGI (0.5)	MGI (1)	MGI (2)
115140	44	-181.69	-108.50	1.01	1.02	1.07	54211	30	-0.62	0.23	1.07	1.14	1.20
115386	55	68.85	47.19	1.01	1.04	1.14	65231	35	-0.67	-0.50	1.03	1.08	1.17
117544	59	49.48	33.05	1.00	1.02	1.06	73125	30	-0.26	-0.14	1.05	1.11	1.25
118236	42	-79.37	-11.51	1.03	1.19	1.37	73904	35	0.53	0.23	1.10	1.12	1.14
119758	48	131.05	71.41	1.01	1.04	1.20	78199	32	-0.22	-0.32	1.00	1.06	1.29
120263	54	-52.75	36.31	1.03	1.08	1.17	87732	32	-0.14	-0.14	1.03	1.06	1.31
121040	49	137.47	124.19	1.06	1.12	1.19	108670	31	0.03	-0.19	1.07	1.16	1.33
122519	59	-78.36	-53.57	1.02	1.05	1.06	-	-	-	-	-	-	-

**Table 4: Descriptive details of Predicted Breeding Values (PBV) and Major Gene Index (MGI) for hens carrying major gene** (Only hens as carriers of major gene with more than 10 offspring for BW and hens as carriers of major gene with more than 14 offspring for BW6)

P Hen	N. Offspring	BW6					P Hen	N. Offspring	BW				
		PBV	PBV of offspring	MGI (0.5)	MGI (1)	MGI (2)			PBV	PBV of offspring	MGI (0.5)	MGI (1)	MGI (2)
122776	14	34.48	112.65	1.13	1.17	1.71	60123	11	0.13	-0.17	1.04	1.10	1.22
116451	15	22.56	57.32	1.02	1.07	1.20	60723	10	-0.21	-0.30	1.02	1.06	1.12
116547	15	105.51	-5.56	1.08	1.20	1.57	65006	10	-0.12	-0.62	1.06	1.15	1.31
116913	14	-205.49	-126.10	1.04	1.12	1.32	65052	10	-1.27	-0.55	1.05	1.07	1.11
117038	14	1.08	53.05	1.07	1.09	1.10	73846	12	0.65	0.59	1.02	1.08	1.21
117466	14	59.04	127.36	1.02	1.04	1.05	77475	12	0.13	0.02	1.07	1.14	1.29
117781	14	16.96	49.08	1.00	1.01	1.02	93324	10	-0.43	-0.64	1.09	1.13	1.14
118444	16	72.50	111.69	1.00	1.03	1.09	-	-	-	-	-	-	-
118731	15	55.04	7.72	1.00	1.01	1.02	-	-	-	-	-	-	-
120456	14	-23.37	-25.05	1.02	1.05	1.08	-	-	-	-	-	-	-
120848	16	-47.23	-50.10	1.02	1.03	1.04	-	-	-	-	-	-	-
121974	14	-139.77	-36.87	1.02	1.07	1.27	-	-	-	-	-	-	-

in the Azerbaijan population using segregation analysis. The results of present study are consistent with the data of Alijani *et al.* (2010) for body weight trait. Szawczkowski *et al.* (2001) suggested that existence of a major gene in egg weight and body weight traits, age at the first egg and egg production were caused by polygenic inheritance model in the Polish Rode-

Island Red layer line. In this study, BW and BW6 traits were found to be influenced by a major gene, which was consistent with the results of Szawczkowski *et al.* (2001). The MGI method could be used for detecting major genes that contributed more than 20 % of phenotypic variation of a particular trait, but it cannot estimate the gene and genotypic frequency. However,

its simplicity, low cost and less time-consuming make the MGI method to be suitable as a preliminary step for major gene detecting before applying advanced Bayesian methods or molecular techniques. Detection of a major gene has several useful applications like its great impact on improvement of the efficiency of animal breeding programs by their positive effects on economical traits (Argente *et al.*, 2003), especially on low heritability traits or the traits that can only be measured in one sex (Falconer and Mackay, 1996) and their effect in our understanding of the biology of economical traits (Jennen *et al.*, 2004). Therefore, as the segregation of major gene using the MGI method for two traits was verified, the segregation of major gene in the line, investigated by the Bayesian marker-free segregation analysis methods, might be considered as the most powerful statistical method. This method is also able to estimate the effect of a major gene on interested traits as well as allelic frequency.

## CONCLUSION

The purpose of this study was to investigate the presence of major genes affecting BW and BW6 traits related to a commercial broiler line in Iran by the MGI method as a simple, low cost and less time-consuming one. Analysis of the phenotypes of BW and BW6 for a commercial broiler chicken line using the MGI method suggested that the major gene can significantly affect BW and BW6 traits. The MGI values at three levels of  $\alpha$  (0.5, 1 or 2) for some of candidate roosters and hens were greater than 1 (shown in Tables 3 and 4) and the index was increased by increasing  $\alpha$  (0.5-2) in the individuals that were carriers of a major gene. Nowadays, despite an increase of genomic selection application in genetic improvement of economically important animal, identification of major genes is also important issue because of their great impact on improvement of animal breeding programs, on our understanding of the biology of traits and functional genomics step. Results of this paper provide a basis to support further molecular genetic studies about the genetic effects on BW and BW6 traits.

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