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GENETIC AND NON-GENETIC VARIATIONS OF BODY WEIGHT IN IRANIAN NATIVE FOWL AND THEIR CROSSES WITH EXOTIC BREEDS

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ABSTRACT

This study was conducted on a stock of Iranian native fowl and their crosses with improved exotic breeds to evaluate their potential for body weight traits as well as to estimate genetic and phenotypic parameters for those traits, before initiating selection experiments. Four genetic groups were formed consisting of the native fowl and three crosses between native females with two different lines of broiler chickens and one parent stock of layer chickens. Two hatches placed 12 days apart and 4058 chicks were produced. In all genetic groups, body weight (BW) was recorded at 1, 39, 67, 95 and 123 days of age in the first hatch, and at 27, 83 and 111 days of age in the second hatch. Pooled heritability coefficients (sire component) of BW obtained at 1, 39, 67, 95 and 123 days of age in the first hatch and at 27, 83 and 111 days of age in the second hatch were estimated to be 0.48±0.08, 0.23±0.07, 0.24±0.06, 0.18±0.05, 0.14±0.06, 0.37±0.08, 0.20±0.05 and 0.31±0.09, respectively. From the estimates obtained in both hatches, heritability of BW tended to decrease with increasing age. Estimates of pooled genetic and phenotypic correlations of BW among early and late ages were highly significant ($P<0.01$) and positive. The sign of genetic correlations showed that correlations of

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BW taken at ages close together are higher than those separated by greater age. In native fowl and their crosses with meat-type chickens, there were relatively high heritability estimates of body weight at early ages (0.20 to 0.65) as well as their genetic correlations with subsequent ages (0.39 to 1.00). The results of this study indicated that selection on the basis of BW at early ages (27 or 39 days) can be used successfully to improve BW at subsequent ages (111 or 123 days).

تحقیقات کشاورزی ایران

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تنوع ژنتیکی و غیر ژنتیکی وزن بدن در مرغان بومی ایران و آمیخته های آن ها با نژادهای خارجی

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چکیده

این مطالعه برای ارزیابی پتانسیل صفات وابسته به وزن بدن و نیز برآورد پارامتر های ژنتیکی و فنوتیپی صفات مزبوردر یک گله از مرغان بومی ایران و آمیخته های آن ها با نژادهای اصلاح شده خارجی، پیش از اجرای آزمایش های بهنژادی، انجام شد. چهار گروه ژنتیکی متشکل از مرغان بومی و سه گروه آمیخته از مرغان بومی با دولاین متفاوت مرغان گوشتی و یک گروه گله والد مرغان تخمگذار، ایجاد شدند. طی دو مرحله جوجه کشی به فاصله ۱۲ روز، تعداد ۴۰۵۸ قطعه جوجه بدست آمد. وزن بدن در کلیه گروه ها طی سنین ۱، ۳۹، ۶۷، ۹۵ و ۱۲۳ روزگی برای مرحله اول جوجه کشی و طی سنین ۲۷، ۸۳ و ۱۱۱ روزگی برای مرحله دوم جوجه کشی،

آمار برداری شدند. ضرائب وراثت پذیری ادغام شده (بر اساس پدر) وزن بدن در سنین ۱، ۳۹، ۶۷، ۹۵و ۱۲۳ روزگی برای مرحله اول جوجه کشی و در سنین ۲۷، ۸۳ و ۱۱۱ روزگی برای مرحله دوم جوجه کشی به ترتیب ۰/۴۸ ±۰/۰۸، ۰/۲۳ ± ۰/۰۷، ۰/۲۴ ± ۰/۰۶، ۰/۱۸ ±۰/۰۵، ۰/۱۴± ۰/۰۶، ۰/۳۷±۰/۰۸، ۰/۲۰ ±۰/۰۵ و ۰/۳۱±۰/۰۹ برآورد گردید. این برآورد ها نشان می دهند که در هر مرحله جوجه کشی، اغلب با افزایش سن، ارزش ضریب وراثت پذیری وزن بدن کاهش می یابد. برآوردهای همبستگی های ژنتیکی و فنو تیپی ادغام شده وزن بدن در سنین اولیه و سنین بالاتر همواره مثبت و بسیار معنی دار بود (P<۰/۰۱). علامت همبستگی های ژنتیکی نشان می دهد که این همبستگی ها بین سنین نزدیک به هم بالاتر از مقادیر بدست آمده در فاصله سنی بیشتر است. در مرغان بومی و آمیخته های آن ها با مرغان گوشتی، ضریب وراثت پذیری وزن بدن در سنین اولیه (۰/۲ تا ۰/۶۵) و همچنین همبستگی ژنتیکی آن ها با سنین بالاتر (۰/۳۹ تا ۱/۰۰) به نسبت زیاد بود. نتایج این مطالعه بیانگر این است که انتخاب بر اساس وزن بدن در سنین اولیه (۲۷ یا ۳۹ روزگی) می تواند به طور موثری برای بهبود وزن بدن در سنین بالاتر (۱۱۱ یا ۱۲۳ روزگی) به کار برده شود.

INTRODUCTION

For many years, breeders of broiler chickens have placed their primary selection emphasis on body weight at market age (9). The potential for genetic change in economically important characteristics in chickens depends to a large degree on the magnitude of the genetic variation and heritability of the different characters considered in the selection program. The nature and extent of the relationships among traits also affect the genetic changes resulting from selection (5, 6). An effective breeding plan is based on knowledge of the relative importance of the genetic and environmental variation of economic traits in the population under consideration. Kinney (11) and Chambers (3) reviewed genetic and phenotypic parameters estimates for various performance traits in meat chickens. The heritability of body weight was high and appeared to be similar in magnitude to weight gain heritability (0.35 to 0.53).

Variations in the heritability coefficients for body weight are mostly due to the fact that different methods of estimation give values that contain different proportions of the nonadditive genetics and environmental source of variation and/or because various populations differ in genetic variation for this trait (3, 6, 10). Chambers (3) reported on some broiler type populations and showed that differences between populations have been demonstrated for most traits associated with body weight and meat production such as the Cornish breed and their crosses with other breeds.

The heritability estimates of both body weight and gain based on sire component values were 0.4 to 0.6, whereas estimates based on dam component values were 0.7 (3). The relatively small difference between the paternal variance components and maternal variance components indicates that the heritability of body weight and gain is additive in nature and of moderate to high magnitude (3, 14). Chambers (3) and Marks (14) also pointed out that nonadditive genetics, sex-linked genetics and maternal effects are relatively small for growth traits. Moreover, most researchers have reported that heritability estimates from paternal half sib are expected to be less biased than maternal half sib correlation, because of the confounding of maternal effects or dominance variance with the dam component of variance (1, 2, 10, 11).

The objective of this study was to estimate genetic and phenotypic variation in the native fowl and its crosses with two meat-type and one egg-type chickens. The genetic and phenotypic relationships of body weight in various ages were also examined in order to use body weight at early ages for improving body weight in subsequent ages. The purpose of crossbreeding method, used in this experiment was to insert some of the suitable genes to native fowl population in order to determine the possibility of faster genetic improvement.

MATERIALS AND METHODS

The present experiment was conducted on chicks produced from Isfahani native fowl population (which is one of several Iranian native fowl populations) as well as the progeny produced from three crosses between native fowl females with exotic breeds of males in the Isfahan Research Center of Native Fowl, Isfahan, Iran. Four genetic groups were formed including: 1) a random sample of a native fowl population (NF), 2) a cross between native fowl females and males of grand paternal parent of broiler lines from Arbor-Acres (B1), 3) a cross between native fowl females and males of grand maternal parent of broiler lines from Arbor-Acres (B2) and 4) a cross between native fowl females and males of parent stock laying chickens from Hy-Line (LL). A system of half sib mating was used to reproduce these genetic groups. The half sib mating system involved mating of one sire to six or seven dams by means of natural matings. Two hatches placed 12 days apart were used and 4058 one-day-old chicks were produced. The number of half sib groups in the B1, B2, LL and NF, used to reproduce those genetic groups were: first hatch 20, 22, 20, 22 and second hatch 21, 22, 21, 22, respectively. The birds were allocated to half sib groups at random. At hatching, all offsprings of both hatches were pedigree wingbanded to sire and then moved to a rearing house. The chicks (both sexes from two hatches), were reared intermingled in an environmentally controlled house until the end of the experiment.

Continuous lighting was provided for the first two days of the experiment, then reduced to 22 h light day^{-1}. After the lst wk, light was decreased at the rate of 2 h wk^{-1} to reach 8 h light day^{-1}. Then, the light was increased 2 h wk^{-1} from 12 wk to the end of the experiment to reach 16 h light day^{-1}. During 0-8 weeks chicks were fed a ration containing 2920 kcal kg^{-1} of ME and 20% CP and from 8 wk to the end of the experiment they were fed on a growing diet containing 2850 kcal kg^{-1} of ME and 17.5% CP. All chicks received water and feed *ad libitum* up to 67 and 55 days of age in the first and second hatches, respectively. In order to control the body weight during laying period, the chickens were fed restricted from 72 and 60 days of age onwards in the first and second hatches, respectively. For the remaining period, they had access to feed for about 4 h day^{-1}. Feeder space was sufficient to allow all chickens to eat simultaneously. The birds were vaccinated against the Newcastle, fowl pox, Gumboro and infectious bronchitis diseases at appropriate ages. Due to insufficient housing space, after 100 days of age, the birds were culled at random about 31% and 48% in the first and second hatches, respectively (approximately equal number per paternal half sib family within all genetic groups).

The body weights (BW) of all offsprings were determined at 1, 39, 67, 95 and 123 days of age in the first hatch and at 27, 83 and 111 days of age in the second hatch. For the purpose of this analysis, only individuals having all records were included.

Heritabilities and genetic correlations were estimated from sire components of variance and covariance calculated from the analyses for each genetic group and also for combination of all data of four genetic groups. In addition, heritabilities were also calculated for each sex with all of the combined data of four genetic groups. Estimates were determined using the least squares and maximum likelihood procedures (7).

The model for the separate analysis of the groups was as follows:

$Y_{ijk}=\mu+sire_i+sex_j+e_{ijk}$

where:

Y_{ijk} is the kth observation of the jth sex and ith sire;

μ is the overall mean;

$sire_i$ is the random effect of the ith sire or sib-group;

sex_j is the fixed effect of the jth sex;

e_{ijk} is the random error associated with the measurement of each individual which is assumed to be randomly and independently distributed, with $\bar{x}=0$ and variance of σ^2.

For the analysis of BW in various ages, the above model was separately submitted for both hatches.

The model for analysis of the combined genetic groups was the following:

$Y_{ijkl}=\mu+group_i+sire_{ij}+sex_k+e_{ijkl}$

where:

Y_{ijkl}, μ, sex_k, and e_{ijkl} are the same as above, and

$group_i$ is the fixed effect of the i^{th} genetic group;

$sire_{ij}$ is the random effect of the j^{th} sire within the i^{th} genetic group.

Amount of the heritabilities and genetic correlations include the following effects (2,, 6): all the additive, one-fourth the additive × additive and sex-linked variance. Standard errors of heritabilities and genetic correlations were estimated by the modified methods of Tallis (21) and Swiger *et al.* (20), as described by Harvey (7). The *t*-test was used for comparisons of least-squares means in all genetic groups and sexes.

RESULTS AND DISCUSSION

Results of analyses of variance of body weights in the native fowl, their crosses and the combined data are presented in Table 1. The random effect of the sire in each genetic group and in combined data was responsible for a large proportion of variance in most ages. Highly significant sex differences ($P<0.001$) were also observed at one-day-old BW of native fowl but was not significant for their crosses with exotic breeds ($P<0.05$). Effect of sex on BW at one-day-old was highly significant ($P<0.001$) in the combined data which may be due to variations between the four genetic groups. Effect of sex in the higher ages of all groups was also very significant ($P<0.001$). This effect was an important source of variation in all genetic groups. In combined data, BW at 39 days of age was significant at $P<0.05$ between males and females. Least-squares means of BW showed that in all ages, males were heavier than females (Table 2). It is well known that a sex difference in body weight occurs soon after hatching and becomes greater as the age increases (3, 5). From an endocrinological point of view, it is evident that body weight is positively correlated with the pitutary size (4). Therefore, the effect of sex on BW appears to be responsible for at least part of the difference in body weight.

Table 1. Analysis of variance for body weights of the native fowls (NF) and their crosses (B1 and B2 with meat-type and, LL with egg-type chickens).

Source	Mean squares[†]						Mean squares[†]			
	df	1d	39d	67d	95d	123d	*df*	27d	83d	111d
Group B1										
Sire	19(18)[§]	63.5***	10005***	66743**	83510^{ns}	109325*	20(20)[§]	14033***	114844***	119307***
Sex	1	0.008^{ns}	144201***	9469834***	31371042***	44537004***	1	33445***	9804505***	7699639***
Residual	521(383)	9.39	4177	30833	53230	65022	423(222)	2772	37939	43625
Group B2										
Sire	21	37.2***	12082***	97358***	114487**	122110*	21	8468***	58802*	82715**
Sex	1	11.5^{ns}	361686***	10861528***	31644557***	4516322***	1	77942***	14923683***	10958919***
Residual	512(375)	12.6	3387	29201	50797	71879	530(258)	2887	34720	42161
Group LL										
Sire	19	36.5***	2734*	27705***	46338***	56858***	20(19)	2958*	36762**	41102**
Sex	1	0.05^{ns}	109941***	3139862***	7305932***	10441673***	1	71472***	3205018***	3273523***
Residual	427(261)	9.70	1605	10845	15881	16879	362(159)	1812	16020	18062
Group NF										
Sire	21	46.1***	9847***	37897**	72031***	74987**	21	5011***	39130*	38448^{ns}
Sex	1	118.6***	238407***	3448440***	10319156***	13091791***	1	81814***	4171177***	3113457***
Residual	553(351)	7.70	1799	18627	25690	36620	552(292)	1804	22529	27090
Combined data										
Group	3	161.8*	6061435***	52223140***	93452245***	75063670***	3	4069225***	61592811***	40989423***
Sire:group	80(79)	43.3***	9058***	60355***	87081	90873***	82 (81)	7628***	63767***	69963***
Sex	1	52.0***	817612*	25191576***	74286518***	106139804***	1	258745***	29822559***	23532030***
Residual	2016(1373)	9.84	2791	23648	40220	55473	1870(934)	2329	29394	35180

*, **, ***, Significant at P<0.05, 0.01 and 0.001, respectively.

ns Nonsignificant (P>0.05).

† In the first and second hatch, respectively.

§ *df* in parentheses shows *df* for 123 and 111 days of age in the first and second hatch, respectively.

As shown in Table 1, when combined data were used, a significant group difference (P<0.01) in BW was occurred in all ages except for BW at one-day of age (P<0.05). There was significantly higher BW in crosses of B1 and B2 than NF and lower BW in cross LL compared with NF (Table 2). On the other hand, BW traits in crosses between NF with broiler lines were about 50-60% higher than NF, while crosses with layer chicks were about 10% lower. Overall, the BW of native fowl in this study was heavier than that reported for the native fowl by some investigators (8, 18), while it was lower than that reported by others (8, 17). Effects of crossbreeding between indigenous domestic fowl with exotic breeds were in agreement with those of Horst (8), Makarechian and Nik-Khah (13), and Omeje and Nwosu (18), but it should be noted that those results varied depending on the genetic distance between exotic and native populations. In an investigation on crossbreeding of Nigerian fowl and exotic breeds, Omeje and Nwosu (18) showed that heterosis was a significant factor for body weights.

Studies on the crossbreeding of native fowl with improved exotic breeds have been made by many commercial and governmental breeding farms with the objective of developing a new breed adapted to the tropical areas (16), but reports of these studies are not available, perhaps due to commercial secrecy.

Heritability estimates of BW at various ages are given in Table 3. Estimates of pooled heritabilities from combined data agreed closely with the average estimates obtained from the literature (4, 11), especially for weights before 12 weeks of age. The heritabilities of BW for crosses of B1 and B2 generally decreased with increasing age, while the heritability of crosses with layer-type chickens increased. In addition, the heritabilities for BW of native fowl varied from age to age, but generally decreased with increasing age as did for the crosses B1 and B2. The pooled heritability estimates of overall groups by sex at various ages showed a consistent difference, where in all ages but one age (83 d), the heritability for BW of females was higher than for males. The heritabilities obtained showed that there are more additive genetic variance on BW for females than males (2, 6). Siegel (19) reported that the differences between the heritabilities of BW for males and

Table 2. Least- squares means (± SE) of body weights in the native fowls and their crosses†.

		First hatch						Second hatch		
Groups	Obser.§	1d	39d	67d	95d	123d	Obser.§	27d	83d	111d
Overall means	2101(1457)	36.9±0.2	329±2.2	976± 5.7	1332± 6.8	1659± 8.4	1957(1020)	295±2.0	1160± 6.1	1525±11.0
Genetic group										
B1	542(403)	37.1^{b}±0.3	433^{a}±4.5	1291^{a}±11.6	1753^{a}±13.8	2108^{a}±16.3	445(244)	378^{a}±4.4	1510^{a}±12.5	1928^{a}±18.8
B2	535(398)	37.5^{a}±0.3	411^{b}±4.4	1206^{b}±11.4	1640^{b}±13.6	1999^{b}±15.9	553(281)	373^{a}±4.0	1435^{b}±11.4	1830^{b}±17.8
LL	448(282)	36.1^{c}±0.3	223^{d}±4.5	655^{d}±11.7	913^{d}±14.0	1220^{d}±17.9	384(180)	200^{c}±4.5	799^{d}±12.8	1104^{d}±20.6
NF	576(374)	37.0^{b}±0.3	249^{c}±4.2	753^{c}±10.7	1021^{c}±12.8	1308^{c}±15.8	575(315)	230^{b}±3.9	898^{c}±11.3	1240^{c}±17.5
Sex group										
Male	1129(647)	37.1^{a}±0.2	349^{a}±2.5	1089^{a}± 6.5	1525^{a}± 7.9	1940^{a}±10.1	841(206)	307^{a}±2.5	1288^{a}± 7.6	1220^{a}±15.6
Female	976(810)	36.8^{b}±0.2	309^{b}±2.6	864^{b}± 6.7	1139^{b}± 8.3	1377^{b}±11.0	1116(814)	283^{b}±2.3	1033^{b}± 6.9	1330^{b}±10.7

† Means followed by the same letter in each column are not significantly different at P<0.05 (*t*-test).

§ No. of observation in parentheses shows numbers of observations for 123 and 111 days of age in the first and second hatch, respectively.

Table 3. Heritability estimates (±SE) of body weights in the native fowls, their crosses and combined data.

	First hatch					Second hatch		
Groups	1d	39d	67d	95d	123d	27d	83d	111d
Combined data	0.48±0.08	0.23±0.07	0.24±0.06	0.18±0.05	0.14±0.06	0.37±0.08	0.20±0.05	0.31±0.09
Genetic group								
B1	0.71±0.22	0.20±0.11	0.17±0.10	0.08±0.07	0.13±0.10	0.65±0.22	0.35±0.16	0.53±0.24
B2	0.30±0.13	0.39±0.15	0.36±0.15	0.20±0.11	0.15±0.11	0.29±0.13	0.11±0.08	0.28±0.17
LL	0.29±0.14	0.12±0.10	0.26±0.13	0.32±0.15	0.58±0.24	0.14±0.11	0.27±0.14	0.51±0.27
NF	0.64±0.20	0.59±0.19	0.15±0.09	0.26±0.19	0.23±0.14	0.26±0.19	0.11±0.08	0.12±0.12
Sex group								
Male		0.23±0.08	0.20±0.07	0.11±0.06	0.18±0.11	0.32±0.10	0.27±0.10	0.26±0.31
Female	0.63±0.13	0.59±0.12	0.40±0.10	0.40±0.10	0.40±0.11	0.44±0.10	0.18±0.07	0.37±0.11

females could be caused by a major gene located on the sex chromosome. However, Merritt and Gowe (15) and Leenstra (12) found higher heritability estimates for BW weight of males than females.

All estimates of the genetic correlation between BW at different ages were large, significant ($P<0.01$) and positive (Table 4). The largest correlation was found between BW at 95 and 123 days of age. As shown by Chambers (3), lower correlation values result when the weights are separated by greater differences in age. Chambers (3) also reported that there is a high genetic correlation among juvenile body weights. Phenotypic correlations were also significant ($P<0.01$) and positive between BW at ages of recording (Table 4), but were consistently lower in magnitude than the corresponding estimates of genetic correlations. The results of the present experiment show a large association between body weights obtained at various ages prior to sexual maturity at both the phenotypic and genotypic levels. Similar results were reported by Siegel (19). Apparently some of the genes which influence juvenile weight at one age may also have a large effect on juvenile weight at other ages. This effect can be considered as pleiotropism (6).

Table 4. Genetic (r_G) and phenotypic (r_P) correlations for body weights in the native fowls, their crosses and combined data†.

		Genetic groups			
Ages	Combined data	B1	B2	LL	NF
39 and 67 *d*					
r_G(±SE)	0.87±0.07	0.87±0.17	0.84±0.12	0.96±0.22	>1.0
r_P	0.54	0.52	0.59	0.44	0.58
39 and 123 *d*					
r_G(±SE)	0.65±0.16	0.80±0.28	0.39±0.46	0.87±0.21	0.50±0.26
r_P	0.43	0.40	0.46	0.42	0.49
67 and 123 *d*					
r_G(±SE)	0.73±0.14	>1.0	0.21±0.44	1.0±0.09	1.0±0.18
r_P	0.64	0.58	0.64	0.63	0.66
95 and 123 *d*					
r_G(±SE)	0.94±0.07	0.99±0.15	--------	0.91±0.10	0.99±0.06
r_P	0.79	0.71	0.81	0.72	0.82
27 and 111 *d*					
r_G(±SE)	0.93±0.11	0.94±0.11	0.90±0.28	------	1.0±0.30
r_P	0.44	0.50	0.32	0.53	0.51
83 and 111 *d*					
r_G(±SE)	0.94±0.09	1.0±0.11	0.91±0.21	0.85±0.17	0.86±0.33
r_P	0.64	0.59	0.58	0.72	0.76

† All correlation coefficients were significant at $P<0.01$ (H_0: $r = 0$).

Results of this study indicate that selection to improve BW at a particular age should be based on selection of that age or on the age where body weights are genetically highly correlated. In addition, better performance in crosses of B1 and B2 suggests that to improve the BW of native fowl, they could be crossed with high growth rate broiler strains and then selected *inter se*.

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