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Internal Traits of Eggs and Their Relationship to Shank Feathering in Chicken Using Principal Component Analysis

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Abstract

Chicken eggs represent an important source of protein to the growing human population and also supply repositories of unique genes that could be used worldwide. The inheritance of shank feathering trait is dominant upon non-feathering shank trait in chicken which is based on two factors: pti-1^{L} and pti-1^{B} that are located on Chromosomes 13, 15, and 24. Using 185 fertile eggs collected from two genetic lines (shank feathering and non-feathering shank) of White Kurdish chicken, we found that egg weight highly ($P < 0.01$) correlated with yolk weight (r^2=0.520, 0.704, respectively), albumen weight (r^2=0.918, 0.835), and shell weight (r^2=0.626, 0.225). The first two principal components explained the greatest variance in both the White with shank feathering (85.6% of total variance) and non-feathering shank (76.5%). Therefore, differences in the component traits of the eggs between the two genetic lines may be influenced by the same gene actions as shank feathering trait. According to these results, the two genetic lines of Kurdish chicken yield significant differences in the internal traits of eggs.

Introduction

Egg quality is an economically important trait for poultry breeding and industry because of its significant influence on the quality and growth of the chicks (McDanniel *et al*., 1978; Altinel *et al*., 1996). Egg quality is also associated with acceptability among the consumers. The egg weight and egg components are affected by genetic and non-genetic factors (Suk & Park, 2001; Tumova *et al*., 2007; Yakubu *et al*., 2008). Local chicken breeds are important sources of protein for growing human populations and also contribute to repositories of unique genes that could be used in other parts of the world. Therefore, it is important to understand differences in egg weight and egg components between local genetic resources. Such comparisons could be used as basis for selection and improvement in programs.

The inheritance of the shank feathering trait has been studied by many poultry researchers including chicken (Danforth, 1919; Lambert & Knox, 1929; Warren, 1949), pidgeon (Wexelsen, 1933), and hawk (Ellis *et al*., 1999). Non-feathering shank is a dominant trait in chicken and it has been proposed that two factors are responsible (pti-1^{L}, pti-1^{B}) (Somes, 1992). Up to date, chromosomes 13, 15, and 24 (Moiseyeva *et al*., 2012) are the candidate chromosomal location for this trait.

Principle Component Analysis (PCA) is a classic technique in data analysis and is the most used multivariate technique available for reducing the dimensionality of a data set. As Rotaru *et al*. (2012) reported, using PCA method in agricultural studies is useful. This method has

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been used by many researchers to study chicken performance (Pinto *et al*., 2006), characterization between breeds (Yakubu *et al*., 2009; Dorji *et al*., 2012), strains (Udeh & Ogbu, 2011), and gene expression (Yeung & Ruzzo., 2001; Ghazalpour *et al*., 2005; Biswas *et al*., 2008). The objective of this study was to estimate the variation in egg weight and egg components using principle component analysis for two genetic lines of the Kurdish local chicken and their relationship with shank feathering.

Materials and Methods

The present study was carried out in the Poultry Production Division of the Agricultural Research Center (Sulaimani, Iraqi Kurdistan) in the Ministry of Agriculture and Water Resources in Kurdistan Government Region-Iraq. Two genetic lines – white with shank feathering (SF) and white with non-feathering shank (NFS) – were used. Chickens were managed under a semi-open system and received 110 g of feed each day. The chicken feed used is described by Abas *et al.* (2014). A total of 185 fertile eggs were collected under a mating ratio of 3 dams: 1 sire (i.e. 12 dams and 4 sires for NFS chicken; 3 dams and 1 sire for SF chicken), comprising 28 eggs collected from SF hens and 157 eggs collected from NFS hens. Eggs were collected when hens were 70-75 weeks of age. Immediately after collection, egg weight and the weights of the yolk, albumen and eggshell were measured for each egg in each genetic line using an electronic balance with 0.01 g sensitivity. After breaking the eggs, yolk was separated from albumen and each of them weighted. Eggshells of broken eggs were washed with water and dried at room temperature for 24 hours. Following this procedure, eggshell weight (with membrane) was measured.

Means, standard errors, and coefficients of variation of egg weight and internal egg measurements were calculated using the descriptive statistic of SPSS /PASW statistics for Windows version 19. One-way analysis of variance was used to test the effect of genetic line on the traits. Pearson's coefficients of correlation (r) among egg weight and the internal egg traits were estimated. From the correlation matrix, data were generated for the principal component factor analysis. Anti-image correlations, Kaiser-Meyer- Olkin measures of sampling adequacy rotation component matrix, and Bartlett's Test of Spherity were computed to test the validity of the factor analysis of the data sets (Jolliffe, 2002). The appropriateness of the factor analysis was further tested using communalities which represent the amount of the variable that is accounted for by the component (Wuensch, 2005).

Results and Discussion

Egg weight and egg components of two genetic lines of white Kurdish local chicken are presented in Table 1. The weights of the egg, yolk, albumen, and eggshell were significantly greater in the NFS eggs compared to the SF eggs. Thus, the two genetic lines differing in shank feather appearance have genetically dimorphic egg sizes.

Table 1. Egg weight and egg components of the genetic lines

Weights (g)	Shank feathering N = (28)			Non-feathering shank N = (157)			*P*-value
	Mean	S.E.	C.V.	Mean	S.E.	C.V.	
Egg	57.77	0.82	18.94	62.15	0.33	17.58	<0.0001
Yolk	19.02	0.31	2.62	20.18	0.17	4.70	0.007
Albumen	33.69	0.67	12.64	36.22	0.25	9.64	<0.0001
Shell	5.07	0.14	0.53	5.76	0.07	0.68	<0.0001

Egg weight was positively correlated with the egg components in both genetic lines ($P < 0.01$). An increase of weight in any of the internal components will invariably lead to a corresponding increase in the total egg weight. According to Harms & Hussein (1993), albumen weight is more closely associated with egg weight than yolk weight because the yolk weight is affected more heavily by the environment rather than by genetics (Oluyemi & Roberts, 2000). Kaiser–Meyer–Olkin (KMO) measure of sampling adequacy was mediocre for both SF and NFS lines (0.558 and 0.535, respectively). While the overall significance of the correlation matrices tested by Bartlett test sphericity for egg internal traits of SF (chi-square

= 10.746, $P < 0.05$) and NFS (chi-square = 13.824, $P < 0.01$) were significant, this implied that PCA was applicable to the data sets.

Table 2 presents the Eigen values, percentage of the total variance, and communalities of the egg component of the two genetic lines of Kurdish local chicken. The communalities represent estimates of variance in each variable accounted range (0.752-0.977, 0.598-0.946 in FS and NFS, respectively). The Eigen values showed the amount of variance out of the total variance explained by each factor. Two principal components were extracted from SF with Eigen values of 1.701 for the first principal component (PC1), and 0.845 for the second principal component (PC2), and together accounted for 84.86% of the total variance. In NFS, the two principal components were extracted with Eigen values of 1.33 for PC1 and 0.934 for PC2 and together accounted for 75.46% of the total variance.

The first two principal components explain a high percentage of the total variance (Table 2). Moreover, differences in egg components between the two genetic lines may be due to the genetic makeup. The first principal component (PC1) had the highest correlation with shell weight in SF eggs and albumen weight in NSF eggs (Table 2).

Table 2. Eigen values and percentage of total variance along with the rotated component matrix and communalities of the egg components of the genetic lines

Traits	Shank feathering			Non-feathering shank		
	PC1	PC2	Communality	PC1	PC2	Communality
Yolk weight (g)	0.589	0.793	0.977	0.688	-0.497	0.721
Albumen weight (g)	0.788	-0.443	0.817	0.765		0.598
Shell weight (g)	0.856		0.752	0.521	0.821	0.946
Eigen value	1.701	0.845		1.33	0.934	
% of total variance	56.70	28.161		44.34	31.125	

Pearson's coefficients of correlation between egg weight and egg internal traits for the two genetic lines are given in Table 3. The correlation coefficients ranged from 0.178 to 0.918 in FS genetic line and from 0.074 to 0.835 in NFS genetic line. The correlation between egg weight and all egg internal measurements were positive in both genetic lines. The highest correlation ($P < 0.001$) was observed between egg weight and albumen weight in both genetic lines, while correlation between albumen weight and yolk weight in both lines were low (0.178 in SF and 0.247 in NFS). Correlation coefficients of eggshell weight with albumen weight were higher than yolk weight in both genetic lines.

Table 3. Correlation coefficients between egg components

Traits	Shank feathering				Non-feathering shank			
	EW	YW	AW	SW	EW	YW	AW	SW
Egg weight	1				1			
Yolk weight	0.520**	1			0.704***	1		
Albumen weight	0.918***	0.178 ns	1		0.835***	0.247**	1	
Shell weight	0.626***	0.319 ns	.523**	1	0.225**	0.074 ns	0.158*	1

*** Correlation is significant at the 0.001 level; ** Correlation is significant at the 0.01 level; * Correlation is significant at the 0.05 level; ns Correlation is not significant.
EW= Egg weight; YW= Yolk weight; AW= Albumen weight; SW= Shell weight

Conclusion

We conclude that yolk, albumen, and shell weights are significantly different between the genetic lines of Kurdish local chicken. This finding can help us characterize these genetic lines and find the genes responsible for shank feather appearance.

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بررسی صفات داخلی تخم مرغ و ارتباط آن‌ها با پردرآوری ساق پا در مرغ با استفاده از روش تجزیه به مولفه‌های اصلی

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چکیده

تخم مرغ منبع پروتئینی مهمی در جوامع بشری و همچنین منبع ذخیره ژنی است که می‌تواند در سرتاسر دنیا استفاده شود. توارث‌پذیری صفت پردرآوری ساق پا در مرغ غالب است که بستگی به دو عامل pti-1^L و pti-1^B دارد که روی کروموزوم‌های ۱۳، ۱۵ و ۲۴ قرار دارند. با استفاده از ۱۸۵ تخم مرغ بارور از دو لاین ژنتیکی مرغ کردی سفید (ساق پای پردار و ساق پای لخت)، ما دریافتیم که همبستگی وزن تخم مرغ با وزن زرده (به ترتیب با r^2 برابر با ۰/۵۲ و ۰/۷۰۴)، با وزن سفیده (به ترتیب با r^2 برابر با ۰/۹۱۸ و ۰/۸۳۵)، و با وزن پوسته (به ترتیب با r^2 برابر با ۰/۶۲۶ و ۰/۲۲۵) بالا است ($P < ۰/۰۱$). دو مولفه اصلی اولیه نشان داد که بیشترین واریانس در مرغ-های کردی سفید با ساق پای پر درآور و لخت به ترتیب ۸۵/۶ و ۷۶/۵ درصد بود. بنابراین ، اختلافات در ترکیبات تخم مرغ در بین دو لاین ژنتیکی ممکن تحت تاثیر عمل ژن‌های مشابه با صفت پردرآوری ساق پا باشد. برطبق نتایج این آزمایش، صفات داخلی تخم مرغ در دو لاین ژنتیکی مرغ کردی اختلاف معنی‌داری با همدیگر دارند.

کلمات کلیدی
مرغ
پردرآوری ساق پا
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