Ann. Anim. Sci., Vol. 14, No. 1 (2014) 43–53 *DOI: 10.2478/aoas-2013-0062*

GENETIC PARAMETERS OF CARCASS TRAITS IN DUCKS FROM A CROSSBRED POPULATION*

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Abstract

The aim of this study was to estimate coefficients of heritability as well as genetic and phenotypic correlations among body weight and carcass traits. The dataset contained records of 387 birds from the second crossbred generation. The following traits were recorded: body weight (BW) at 11 weeks, carcass weight (CW), breast muscle weight including superficial and deep muscle (BMW), leg muscle weight including thigh and shank (LMW), wings weight (WW), skin with subcutaneous fat weight (SW), abdominal fat weight (AFW), skeleton with the back muscle and inedible elements (SBM), and liver weight (LW). Estimates of variance components were obtained by the average information – REML algorithm in the ASReml package. Very high slaughter yield (74.90%) was obtained. Generally, the coefficients of heritability were high. The highest one of 0.75 was estimated for body weight at 11 weeks. High coefficients of h^2 were estimated for breast muscle weight (0.69), wings weight (0.70), carcass weight (0.65), skin with subcutaneous fat weight (0.57) and skeleton with the back muscle (0.58), whereas h^2 of liver weight was 0.29. Both phenotypic and genetic relationships between the recorded traits were usually positive. Generally, it seems that the crossbreeding scheme can be perceived as a suitable proposal for the breeding practice.

Key words: body weight, carcass traits, correlations, crossbreeding, heritability

In the European Union countries, ducks play a considerable role in the structure of the waterfowl meat market. In these countries, especially in France and Germany, the intensive duck rearing system is predominant whereas in Poland extensive and

*The research project was supported by Polish Ministry of Science and Higher Education, grant No. N N311 239838.

semi-intensive systems are prevalent. Thus, the system and intensity of fattening together with the genotype of the bird determine the formation of carcass and its meat content and fatness. Over the last decades genetic background of carcass traits has been intensively studied for both livestock and poultry species. It is connected with the major goals of genetic improvement programmes. Long-term selection of meat poultry has resulted in a large increase of carcass yield and reduction in fatness. Commercial hybrids made on the basis of four strains of native Pekin ducks: A-55, P-44, P-55 and F-11 are used for meat production in Poland. In recent years increasing interest in the Pekin type ducks of French origin, hybrids of GL-50 and GL-30 strains, has been observed. Nowadays duck meat production in Poland is based on Pekin ducks (89.50%), Muscovy ducks (5%) and their hybrids, called Mulards. It was estimated that Star 53 H.Y. is the leading stock of Pekin ducks in duck meat production with a share of 60–70%, followed by hybrids originating from native breeding material with 30–40% (Wencek et al., 2012).

Duck meat production aims at reconciling manufacturers' satisfaction (including fast growth rate and good slaughter yield of hybrids) with customer satisfaction (including high meat content in a carcass, particularly in the breast, with low intramuscular and tissue fatness – subcutaneous fat, peri-intestinal fat, abdominal fat). In general, body weight and carcass composition traits can be perceived as highly heritable (Le Bihan-Duval et al., 1999; Rance et al., 2002). Also heritability of some duck carcass traits has been relatively high (Mignon-Grasteau et al., 1998; Xu et al., 2011). It is worth noting that the majority of these studies have been performed on pure lines. Estimates of genetic parameters vary across populations and depend on their structure as well as the statistical approach employed. However, they are sometimes biased, mainly when model assumptions are not valid. One of the main sources of bias of genetic parameter estimates is pedigree incompleteness and when some relationships among individuals are omitted (Roughsedge et al., 2001). In this context, the main advantage of the present study is fully verified pedigree information of a three-generational population. The three-generation crossbred population analysed in the present study is characterized by a complete set of relationships. Moreover, the population structure is relatively balanced. This provides a relatively good basis for the estimation of genetic parameters.

The aim of this study was to estimate coefficients of heritability as well as genetic and phenotypic correlations among body weight and carcass traits.

Material and methods

The experimental procedures were approved by the Local Ethical Commission for Animal Experiments in Poznań (Poland). The research was based on data collected from an F2 cross of lines A-55 and GL-30. The dataset contained records of 387 birds (205 males and 182 females) from the second generation of offspring. The ducks were reared in an enclosed pen. Stocking density was: (i) 6 birds per m^2 of floor space – initially, (ii) 4 birds per m^2 – after 4 weeks of age. Appropriate breeding conditions, considered as standard in duck rearing, were provided by the technological equipment. The ducks were fed *ad libitum* with feed mixtures containing 11.9 MJ metabolizable energy (ME), 19.8% crude protein, 3.6% crude fibre, 1.0% lysine and 0.5% methionine for the first four weeks, and 12.6 MJ ME, 17.6% crude protein, 4.5% crude fibre, 0.9% lysine and 0.4% methionine for the next period of fattening.

In the 11th week of life (before slaughter), body weight was measured (using electronic balance AXIS B15S with 5 gram accuracy) on live birds after 12 hours without access to feed and with permanent access to water. Slaughter and post slaughtering processing were performed under the same standard technological conditions. For good identification, an individual code was installed on each carcass during the whole process. The carcasses were refrigerated for 24 hours at 4°C. Dissection was performed using the method described by Ziołecki and Doruchowski (1989). The carcasses and their components were weighed by electronic balance RADWAG WPT 5C with 0.2 gram accuracy. Except body weight (BW) at the 11th week, the following traits were included: eviscerated carcass (with neck and giblets, without gizzard) weight (CW), breast muscle weight including superficial and deep muscle (BMW), leg muscle weight including thigh and shank (LMW), wings weight (WW), skin with subcutaneous fat weight (SW), abdominal fat weight (AFW), skeleton with the back muscle and inedible elements weight (SBM), liver weight (LW). The pedigree contained 454 individuals, out of which 28 animals were founders (base generation) and 39 animals (generation F1) were selected as parents of the second generation (F2) of offspring. Molecular identification of sex was performed according to the procedure described by Clinton et al. (2001).

Basic statistics describing the data (averages, standard deviations as well as minimum and maximum values for all traits) were estimated with the R package (R Development Core Team 2010). Departures from normal distribution of the analysed traits were verified with the Shapiro-Wilk test statistic. The Wilcoxon rank sum statistic was used to test for differences in the analysed traits between males and females.

Estimates of variance components were obtained by the average information – REML algorithm in the ASReml package (Gilmour et al., 2009). The genetic analysis was done using a two-trait animal model:

$$y = (X \otimes I)\beta + (Z \otimes I)a + e$$

where:

y is the vector of observations,
β is the vector of fixed effect of sex,
a is the vector of random additive genetic effects,
e is the vector of random residual effects,
X and Z are the incidence matrices for fixed and random effects, respectively,
I is the identity matrix,
$\otimes$ denotes the Kronecker product.

Random effects were assumed to be normally distributed with zero means and the following covariance structure:

$$(Co)\,var\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A \otimes G & 0 \\ 0 & \mathrm{I} \otimes R \end{bmatrix}$$

where:

A is the additive relationship matrix with dimensions: 454 × 454,
G is the 2 × 2 matrix of the genetic (co)variances,
R is the 2 × 2 matrix of the residual (co)variances,
a, e and *I* – as above.

Coefficients of heritability of all traits under study were derived from the following formulae:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

where:

σ_a^2 is the additive genetic variance,
σ_e^2 is the residual variance.

Coefficients of genetic correlations between the analysed traits were estimated as:

$$r_g = \frac{g_{12}}{\sqrt{g_{t2} + g_{t2}}}$$

where:

g_{12} is the additive genetic covariance between trait 1 and trait 2,

g_{t1}^2 and g_{t2}^2 are the additive genetic variance of traits 1 and 2.

Coefficients of phenotypic correlations were estimated in an analogous way by taking the phenotypic covariance between the traits and their respective phenotypic variances.

Results

Means, standard deviations, minimum and maximum values for the analysed carcass traits as well as statistical significance of differences in these characters between males and females are presented in Table 1. The experimental duck hybrids after 11 weeks of rearing achieved an average body weight (female and male) of 3111.37 g. The high discrepancy between the minimum (2185 g) and maximum (3995 g) value as well as the relatively high standard deviation (297 g) of this trait may be a result of pronounced sexual dimorphism associated with this species of waterfowl. It was statistically confirmed ($P<0.01$). Very good slaughter yield (74.90%) after slaughter and post-slaughter management was obtained.

Table 1. Means, standard deviations (SD), minimum, and maximum values for body weight and carcass traits of F2 duck cross after 11 weeks of rearing, along with significance testing between males and females for each trait

Trait	Mean±SD	Min	Max	Sex
Body weight (g)	3111.37± 296.67	2185.0	3995.0	**
Weight of eviscerated carcass (with neck and giblets – without gizzard) (g)	2330.36±231.45	1566.6	2948.6	**
Breast muscle weight (g)	331.47±44.96	210.8	487.6	**
Leg muscle weight (g)	238.56±28.88	162.6	335.0	**
Weight of wings (with skin) (g)	251.82±24.27	189.4	328.8	**
Weight of skin with subcutaneous fat (g)	676.32±108.45	247.0	967.0	**
Abdominal fat weight (g)	45.96±13.77	2.8	100.6	NS
Weight of skeleton with the back muscles (g)	550.48±70.17	262.2	830.6	**
Liver weight (g)	69.82±12.59	34.4	115.4	**

**$P<0.01$, NS – non significant difference.

When analysing the weight of tissue components and their percentage in the carcass of hybrids, good carcass conformation should be noted. It is expressed in the high content of the most desirable element of carcass – breast muscle (331.47 g) and slightly lower content of leg muscle (238.56 g). In all, muscles made up 24.46% of eviscerated carcass with neck and giblets – without gizzard. The average values of other examined dissection traits of experimental duck hybrids were within the range of values obtained for this poultry species. Males and females differed significantly ($P<0.01$) with respect to all of the analysed traits, except abdominal fat weight. Statistical significance of sexual dimorphism influenced the relatively large standard deviation of these traits. Furthermore, trait variability obviously resulted from crossbreeding effects as well. It should be recalled that all birds recorded were kept under the same environmental conditions and fed on feed mixtures with the same nutritional value. Thus it can be hypothesized that a large proportion of the observed variability was determined by genetic effects.

Estimated coefficients of heritability as well as genetic and phenotypic correlation along with their approximated standard errors are listed in Table 2. The highest heritability coefficient of 0.75 was estimated for body weight at 11 weeks. This trait is complex as it partly consists of other traits included in the analysis. This may explain its large genetic variability. However, heritability estimates for other traits varied. High coefficients of h^2 were estimated for breast muscle weight (0.69), wings weight (0.70), carcass weight (0.65), skin weight (0.57) and skeleton with the back muscle (0.58). Some coefficients of heritability were relatively low. For instance, h^2 of liver weight was 0.29. Moreover, standard deviations of these estimates were relatively large. They were mainly influenced by population size.

Table 2. Estimated coefficients of heritability (diagonal), genetic (lower diagonal) and phenotypic (upper diagonal) correlations between carcass traits in an F2 duck cross

	BW	CW	BMW	LMW	WW	SW	AFW	SBM	LW
BW	0.75±0.18	0.92±0.01	0.65±0.06	0.68±0.04	0.75±0.04	0.67±0.05	0.37±0.08	0.70±0.04	0.53±0.06
CW	0.99±0.01	0.65±0.17	0.69±0.05	0.70±0.04	0.73±0.04	0.71±0.05	0.43±0.07	0.74±0.04	0.50±0.06
BMW	0.69±0.14	0.65±0.15	0.69±0.17	0.65±0.05	0.60±0.04	0.22±0.09	0.07±0.09	0.54±0.06	0.37±0.06
LMW	1.00±0.02	1.00±0.03	0.88±0.09	0.51±0.16	0.68±0.04	0.29±0.08	0.14±0.08	0.56±0.05	0.46±0.06
WW	0.90±0.06	0.90±0.07	0.98±0.06	0.91±0.07	0.70±0.17	0.29±0.09	0.08±0.09	0.67±0.04	0.48±0.05
SW	0.60±0.17	0.65±0.16	–0.13±0.27	0.28±0.27	0.22±0.26	0.57±0.17	0.65±0.05	0.30±0.08	0.18±0.08
AFW	0.33±0.25	0.35±0.26	–0.29±0.27	0.06±0.31	0.13±0.29	0.72±0.14	0.47±0.16	0.07±0.08	0.11±0.08
SBM	0.88±0.08	0.89±0.07	0.79±0.13	0.94±0.06	0.97±0.04	0.22±0.27	0.09±0.30	0.58±0.17	0.49±0.05
LW	0.64±0.21	0.47±0.26	0.66±0.23	0.80±0.17	0.94±0.10	–0.18±0.33	–0.39±0.32	0.91±0.11	0.29±0.14

BW – body weight, CW – carcass weight, BMW – breast muscle weight including superficial and deep muscles, LMW – leg muscle weight including thigh and shank, WW – wings weight, SW – skin with subcutaneous fat weight, AFW – abdominal fat weight, SBM – skeleton with the back muscles and inedible elements weight, LW – liver weight.

As expected, both phenotypic and genetic relationships between the recorded traits were usually positive. In general, the genetic and phenotypic correlations showed a similar magnitude for respective pairs of traits. However, in the case of leg muscle weight the genetic dependencies of some traits (body weight, carcass weight), seemed to be overestimated. The carcass weight tends to have high positive phenotypic correlations (at least 0.34) with others traits. Standard errors of these phenotypic correlation coefficients were relatively small. In the case of other traits, phenotypic correlations were more variable. It can be assumed that body weight is also strongly correlated with particular body components. It was confirmed for a majority of traits.

Although the majority of phenotypic and genetic correlations for respective pairs of traits were similar, estimates for some of them were quite different (Table 2). For instance, skin with subcutaneous fat weight and abdominal fat weight were negatively genetically correlated with breast muscle weight and liver weight. Moreover, abdominal fat weight had a negligible positive genetic correlation with leg muscle weight (0.06) and wings weight (0.13). It should be stressed that for the above mentioned estimates of genetic correlations, their standard errors were relatively large. On the other hand, another group of trait pairs showed strong positive genetic correlations. Estimates of rG were close to 1 (i.e. body weight with leg muscle weight). It seems that these parameters might have been overestimated.

Discussion

The body weight of experimental duck hybrids after 11 weeks of rearing achieved similar values to the parameters obtained in the studies on meat traits of Pekin type ducks (Kokoszyński, 2011). Other authors found a lower level of this trait, but for a shorter (7- or 8-week) period of rearing. Biesiada-Drzazga et al. (2012) found that Star ducks 53 H.Y. (♂GL-50 × ♀GL-30) had the following body weights: (i) 2751.1 g after 7 weeks of rearing, (ii) 3075.1 g after 8 weeks of rearing. Furthermore, Kokoszyński and Korytkowska (2003) revealed differences in duck body weight indicative of the sexual dimorphism manifesting itself from 3 to 4 weeks of age. This corresponds with the findings of Bochno et al. (2005) and Witkiewicz et al. (2006). In the current research the ratio of weight of eviscerated carcass with neck and giblets (without stomach) to preslaughter body weight, or slaughter yield of experimental population, was very high and reached nearly 75%. In most studies regarding the evaluation of slaughter value of Pekin ducks after 8 weeks of rearing, this parameter did not exceed 70% (see e.g. Łukaszewicz et al., 2011). On the other hand, Kokoszyński (2011) reported that the dressing percentage of Star 53 H.Y. slaughtered at 7 and 8 weeks of age was 71.25% and 72.98%, respectively. In the light of the cited papers and our own investigation, it may be postulated that together with a prolongation of ducks rearing period, a decrease of the rate of body weight gain and a change in the tissue composition of carcass is observed, which has a positive effect on slaughter yield (Bochno et al., 2005).

The most valuable tissue of the poultry carcass is the muscle tissue. Many studies have proven (e.g. Mazanowski et al., 2003) that muscle weight is mainly affected by the weight of breast and leg muscle. The total share of these muscles, expressed as a percentage of eviscerated carcass shows the meat content (the possibility of good use for meat of assessed individuals). In the cited studies, breast muscle ranged from 13.7 to 18.5%, whereas leg muscle ranged from 10.5 to 14.4% of the eviscerated carcass with neck. In the current research the content of the discussed muscle types was at the lower range of values obtained by other authors. It was 14.22% for breast muscle and 10.24% of carcass for leg muscle. Undoubtedly, this was associated with a longer rearing period of ducks (11 weeks) in the present work. In accordance with the physiology of ducks and their tendency to subcutaneous fat deposition in order to prevent overcooling while living in natural water conditions, during this period the proportion of muscle content in the carcass decreased in favour of skin with subcutaneous fat. The present study reported that the content of skin with subcutaneous fat reached 29.02%, whereas in a shorter rearing period of broiler ducks it ranged from 24.1% to 25.8% or 26.9% combined with abdominal fat (Bochno et al., 2005; Łukaszewicz et al., 2011). However, according to Mazanowski and Książkiewicz (2004) the content of skin with subcutaneous fat of 7-week-old A-55 sire strain was 28.8%.

Wawro et al. (2004) comparing the slaughter value of Pekin ducks and Muscovy ducks found that the abdominal fat content was 1.15% in male Pekin ducks at 7 weeks of age and 1.90% in Muscovy ducks at 12 weeks of age. Moreover, a similar proportion of abdominal fat content (1.97%) was characteristic of hybrid carcass of Pekin ducks after 11 weeks of rearing, as demonstrated in the current study.

The weight of liver, among giblets, is significantly important in duck rearing because of the tradition of fattening this poultry species for fatty livers (foie gras). Force-feeding is currently not practiced in Poland, but it is still used in many countries, including the European Union. The experimental hybrids of ducks were characterized by high liver weight (69.82 g on average), which accounted for 3% of the carcass. All of the analysed meat performance traits except the abdominal fat content, were dependent on the ducks' sex.

Sex differences for body weight as well as carcass weight and its components in some species of poultry have been reported by many authors (Mignon-Grasteau et al., 1998; Le Bihan-Duval et al., 1998; Zerehdaran et al., 2007). These traits are determined by a combination of genetic and physiological factors. Mignon-Grasteau et al. (1998) estimated different direct and maternal genetic variances for male and female body weight in Muscovy ducks. Greater competition between males, different nutritional needs and different hormonal effects can affect some carcass components (e.g. Le Bihan-Duval et al., 1998). As has already been mentioned, birds analysed in the present study were kept in one group. Therefore competition effects can be considered in the interpretation of the results obtained. Generally, averages of the studied traits correspond with the ones for ducks in the 11th week of life, reported among others by Larzul et al. (2006). They showed that differences in body weight depended on the population. Similar remarks appeared also in other studies (Kisiel and Książkiewicz, 2004). However, as reported by Kokoszynski and Bernacki (2010) a long-term selection aimed at improvement of the same traits in different populations contributed to their very similar levels, especially live weight at slaughter and some carcass components.

It should be recalled that the investigated population was crossbred. By definition, performance traits in such a population are expected to be higher compared to purebred ones. Thus, estimated coefficients of heritability could also be expected to be higher. This was confirmed in a number of studies (e.g. Brun and Larzul, 2003).

As noted before, heritabilities of the majority of traits (except liver weight) exceeded 0.5. For purebred populations of Muscovy ducks, a considerable share of genetic variance in the total variance has been demonstrated (Hu et al., 1998). Xu et al. (2011) found heritabilities equal to 0.53 and 0.50 for body weight (at 7 weeks) and breast muscle weight, respectively. Whereas Etancelin et al. (2010) estimated lower heritability for mule duck traits measured at 10 weeks of age. Relatively high estimates of h^2 were reported for other poultry species (Rance et al., 2002).

On the other hand, it is well known that body weight, and in consequence, carcass composition, is also determined by genetic and permanent environmental maternal effects. Furthermore, the crossbreeding variances (dominance, epistatic) could also have biased the estimated coefficients of heritability. Thus, heterosis effects are expected (Larzul et. al., 2006). Unfortunately, from a methodological perspective, estimation of nonadditive and maternal genetic variances seems unrealistic in the context of a relatively small size of the studied population. Some authors (e.g. Clement et al., 2001) showed that ignoring maternal genetic effects (if they are considerable) leads to an overestimation of direct heritability. However, other studies suggest negligible maternal heritabilities for carcass traits. For instance, Grosso et al. (2010) reported that for some carcass traits maternal heritabilities did not exceed 10% of direct heritability. It should be stressed that the above mentioned studies were performed on large populations, including thousands of recorded individuals. Le Bihan-Duval et al. (2001) excluded maternal effects from the model for some carcass traits when the number of recorded individuals was smaller.

However, moderate coefficient of heritability was obtained for liver weight. One might have expected that they are affected by empirical distribution of these characters. Small sample size and departure from normality led to overestimation of residual variance. Thus, heritability estimates for these traits could be underestimated.

Estimated phenotypic correlations were in agreement with the biological background of particular recorded traits. As noted before, they were usually positive and high. Similar results for duck populations were generally reported by Xu et al. (2011) and Etancelin et al. (2010). However, by contrast to the results of the present study, Xu et al. (2011) usually obtained higher genetic than phenotypic correlations for the respective pairs of traits.

Two genetic correlation estimates (BW – LMW, WW – BMW) achieved maximum values. This indicates overestimation of the parameters. Analogous problems were reported by Le Bihan-Duval et al. (1998). It seems that two probable reasons can be considered. Estimation of correlation assumes two-dimensional normal distribution of the traits studied. As previously mentioned, the assumption does not hold for some traits. It is worth mentioning that a two-dimensional normal distribution is not directly determined by a uni-dimensional normal distribution for the two traits. In fact, from a practical point of view, the joint assumption often requires verification. However, it can be perceived as a serious source of bias of correlation estimates, especially when genetic relationships are evaluated. The second reason is likely to be connected with the number of recorded individuals.

In general, the F2 experimental duck hybrids were characterized by a high level of meat performance traits, namely slaughter yield (74.89%), meat content (24.44%) – including breast muscle (14.22%), and a relatively large liver (69.82 g). It seems that the crossbreeding scheme can be perceived as a suitable proposal for breeding practice.

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Accepted for printing 7 X 2013