

Genetic evaluation of production and reproduction traits in two selected lines of geese under multitrait animal model*

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Heritability of and genetic correlations among production and reproduction traits as well as genetic trends over eight years of selection were estimated in W11 (maternal) and W33 (paternal) lines of geese. Considered was body weight on week 8 (BW8) and week 11 (BW11), number of eggs produced (EP), egg weight (EW), percentage of fertility (PFE), and percentage of hatchability from eggs fertilized (PHC). Multitrait animal model was applied. Moderate to high heritability estimates were obtained for BW8, BW11 and EP in both lines while lower for PFE and PHC. Highest genetic correlations were estimated between PFE and PHC and between the body weight traits. No clear genetic trends for any trait were identified. Generally, unfavourable relationships between productive and reproductive traits have been confirmed.

KEYWORDS: heritability / genetic correlations / genetic trends / geese /
multitrait animal model

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Over last decades the methodology of breeding value prediction has highly been developed. Animal model enables unbiased estimation of variance components in populations undergoing selection provided all relationships and traits included in selection criteria are involved. It makes simultaneous estimation of heritability and genetic correlations possible with implicit correction for fixed effects and genetic trend. Due to increasing consumers' demands also poultry breeders have recognized the need of implementation of more sophisticated statistical methods to breeding value prediction as the more precise evaluation accelerates the genetic gain. Feasibility of accelerating progress through breeding became also considered in waterfowl [Shrestha *et al.* 2004]. To our knowledge the estimates of genetic parameters of reproductive as well as productive traits of geese under multitrait animal model are not, so far, available in literature. Heritability of geese traits estimated *via* single trait animal model was reported by Szwaczkowski *et al.* [2007].

In light of the above the objective of this study was to estimate heritabilities and genetic correlations among production and reproduction traits in two geese lines and evaluate their genetic trends over eight years of selection.

Material and methods

Considered were two lines (W11 and W33) of White Koludzka geese. The breeding programme for both is coordinated by National Research-Breeding Goose Center, Experimental Station Kołuda Wielka of the National Research Institute of Animal Production. Birds were selected based on classical selection index with genetic parameters estimated within generation by Henderson's method III using sire+dam model. The procedure was described by Wężyk [1978].

Both lines originate from White Italian geese. The present W11 is recommended as maternal whereas W33 as paternal line for crossbreeding schemes. The current study was based upon the records of 1707 W11 and 824 W33 birds hatched between 1995 and 2003 year and accounted for the pedigree file. Environmental conditions, mainly feeding and lightening programme did not considerably change over time.

The following production and reproduction traits were considered:

- body weight at week 8 of age (BW8);
- body weight at week 11 of age (BW11);
- number of eggs yielded – egg production until 28th week of egg production (EP);
- egg weight (EW) – mean computed from all eggs laid by the female over week 48, 49 and 50 of age;
- percentage of eggs fertilized (PFE) as evaluated based on seven individual egg incubations (per 3-4 eggs/week);
- percentage of eggs hatched (PHC) from eggs fertilized as evaluated based on seven individual egg incubations (per 3-4 eggs/week).

Table 1. General characteristics of production and reproduction traits in two lines of geese

Line	Trait	Number of observations	Mean	SD
W11	BW8-M (kg) ^a	270	4.29**	0.33
	BW8-F (kg) ^a	2477	3.98**	0.32
	BW11-M (kg) ^b	270	4.90**	0.19
	BW11-F (kg) ^b	2477	4.47**	0.32
	EP (pcs)	2364	46.87**	10.78
	EW (g)	2364	156.83**	13.67
	PFE (%)	1285	75.17 ^{ns}	19.52
	PHC (%)	805	69.23**	19.68
W33	BW8-M (kg) ^a	65	4.58**	0.30
	BW8-F (kg) ^a	1095	4.07**	0.33
	BW11-M (kg) ^b	65	5.29**	0.30
	BW11-F (kg) ^b	1095	4.62**	0.35
	EP (pcs)	994	44.41**	8.27
	EW (g)	335	161.16**	7.57
	PFE (%)	699	75.62 ^{ns}	24.98
	PHC (%)	660	62.40**	22.12

M – males; F – females.

**Significant differences between lines ($P \leq 0.01$); ns – no significant difference between lines.

^{a,b}Significant differences between sexes identified for both body weight traits (joint analysis was performed including fixed effect of sex in the model).

Descriptive statistics of the traits studied are given in Table 1. As expected, the means for productive traits reached significantly higher level in W33 (paternal) line whereas reproduction traits means were higher in W11 (maternal) line. The significance of differences between lines was verified by ANOVA using the GLM procedure of SAS [2002-2003]. Pearson correlation coefficients were calculated with the use of the CORR procedure of SAS [2002-2003].

The following multitrait animal model was employed to estimate variance and covariance components as well as to predict genetic effects:

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

where:

- y – $N \times 1$ vector of observations of t traits;
- b – $pt \times 1$ vector of fixed effects (year of hatching for all traits, sex- for body weight, only);
- a – $qt \times 1$ vector of random additive genetic effects;
- e – $N \times 1$ vector of random errors;
- X – $N \times pt$ known design matrix of fixed effects;
- Z – $N \times qt$ known design matrix of random additive genetic effects;

- I – identity matrix;
 \otimes – Kronecker product;
 N – total number of observations for all traits.

The following parameters describing genetic and phenotypic structure of the population were estimated:

- heritability coefficients;
- genetic correlation coefficients;
- phenotypic correlation coefficients;
- genetic trends.

In order to achieve convergence of iteration process SIMPLEX and AIREML were combined. The DXMUX programme [Meyer 2001] was used. Genetic trends were derived as changes in mean predicted breeding values over time. Standard deviations of heritability estimates were approximated according to the formula described by Smith and Graser [1986].

Results and discussion

The estimates of genetic parameters for the populations studied are listed in Tables 2 and 3. Except for PFE and PHC, moderate to high heritability coefficients (h^2) were estimated in both lines.

There are very few papers referring to genetic parameters of breeding geese. Larzul *et al.* [2000] reported the h^2 of body weight at the age of 8 and 11 weeks to reach 0.64 and 0.68, respectively, with genetic correlations of 0.92, being similar to those estimated for geese bred in Canada where h^2 of body weight at different ages ranged from 0.41 to 0.77 [Shrestha and Grunder 2006], and in Poland, where the respective h^2 was found to vary from 0.35 to 0.51 [Rosiński 2000]. Lower heritability of body weight (0.18) was reported by Yeh *et al.* [1999] for White Roman geese in Taiwan. Szwaczkowski *et al.* [2007] applying a single trait animal model, estimated

Table 2. Heritability estimates (bolded and underlined) with standard errors and genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients among production and reproduction traits in W11 geese

Trait	BW8	BW11	EP	EW	PFE	PHC
BW8	<u>0.64</u> (± 0.05)	0.67	-0.10	0.24	-0.01	-0.03
BW11	0.45**	<u>0.50</u> (± 0.05)	-0.05	-0.02	-0.20	-0.15
EP	0.20**	0.29**	<u>0.47</u> (± 0.06)	-0.63	0.37	0.20
EW	0.12**	0.12**	-0.29**	<u>0.49</u> (± 0.06)	-0.22	-0.25
PFE	0.04	0.04	0.19**	-0.07*	<u>0.08</u> (± 0.05)	0.96
PHC	0.03	-0.05	0.03	-0.05	0.91**	<u>0.09</u> (± 0.06)

Table 3. Heritability estimates (bolded and underlined) with standard errors and genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients among production and reproduction traits in W33 geese

Trait	BW8	BW11	EP	EW	PFE	PHC
BW8	<u>0.76</u> (±0.09)	0.67	0.30	0.61	-0.31	-0.49
BW11	0.72**	<u>0.46</u> (±0.08)	0.02	0.44	-0.02	-0.29
EP	-0.01	0.32**	<u>0.30</u> (±0.09)	0.84	-0.51	-0.25
EW	0.35**	0.39**	0.32**	<u>0.23</u> (±0.14)	-0.48	-0.48
PFE	0.00	-0.05	0.01	0.08	<u>0.02</u> (±0.08)	0.85
PHC	-0.02	-0.08*	0.02	0.05	0.90**	<u>0.05</u> (±0.08)

**P≤0.01.

the direct heritability of body weight in geese to range between 0.0001 and 0.55 depending on the model used.

Different body weight h^2 estimates given by different authors result from population structure (selected vs unselected), environmental conditions (domesticated vs wild birds), algorithm employed and statistical vs genetic model used [Larsson 1993, Rosiński *et al.* 2000, Szwaczkowski 2007].

Heritabilities of egg production traits estimated in the current report (Tab. 2 and 3) are higher than those (0.21-0.40) shown by Rosiński [2000] and Shrestha and Grunder [2006]. Lowest heritability estimates were obtained for reproductive traits (PFE and PHC). It corresponds with the report by Shrestha and Grunder [2006]. Low h^2 values determine a limited possibility of genetic gain in these traits. Lower estimates could also result from deviations from normality observed for these traits which may cause overestimation of residual variance. From theoretical perspective threshold animal model would be more appropriate for studies on fertility-related traits. However, linear-threshold analysis still creates many methodological and computational problems. Moreover, some authors [Jamrozik *et al.* 1991, Varona *et al.* 1999] did not confirm advantage of threshold model over linear one to analyse a discrete reproduction characters. Another approach proposed [e.g. Szwaczkowski *et al.* 2000] is data transformation with the use of the Bliss degree that can be directly applied for single trait analysis. In case, however, of multitrait analysis, a multidimensional normal distribution should be assumed. Thus, simultaneous transformation of all traits studied should be done.

In this study genetic correlations were mostly in accordance with phenotypic ones. As expected, the highest genetic and phenotypic correlations were found between two reproduction traits – fertility (PFE) and hatchability (PHC). Relatively high positive correlations have been observed for BW8 and BW11. Positive relationships were estimated between body weight and egg weight as well.

Significant phenotypic correlations were also found between both body weights and EW, whereas the sign of relationship between EP and EW and egg production

was inverse between the lines. Correlations between EP and FER or PHC were inconsistent which confirms results of Shrestha and Grunder [2006] concerning fertility (0 to -0.40) and hatchability (0.38 to -0.12). Generally, the antagonistic correlations between productive and reproductive traits were found in the other species of poultry [Szwaczkowski 2003] and livestock [Roxström *et al.* 2001, Jagusiak 2005]. More negative associations between productive and reproductive traits were found in paternal W33 compared with maternal W11 line. It seems that goose breeding programmes need to consider both production and reproduction traits if fertility is to be maintained and further increased production achieved.

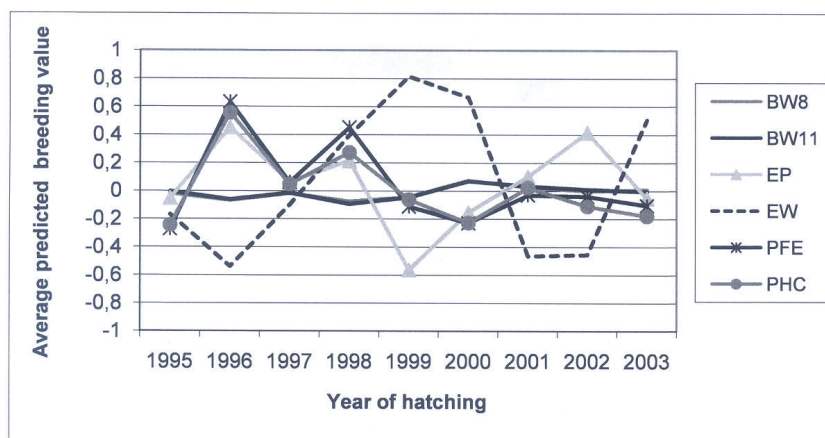


Fig. 1. Genetic trends in W11 geese.

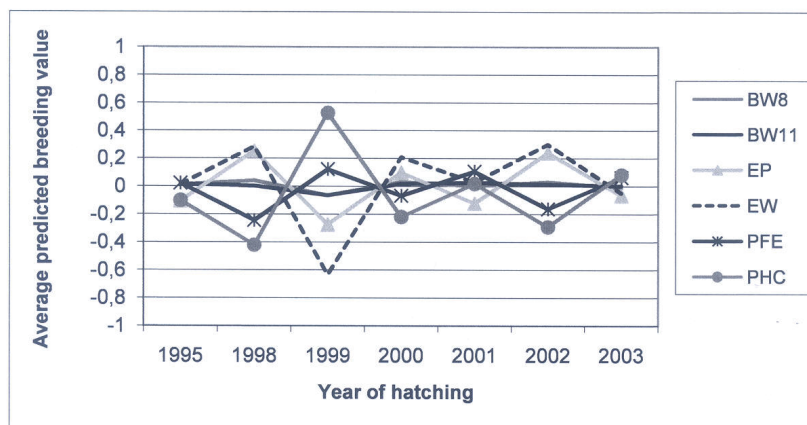


Fig. 2. Genetic trends in W33 geese.

In neither line regularities of changes in mean breeding values were recorded (Fig. 1 and 2). Genetic trend randomly fluctuated around zero.

Currently, genetic parameters in the analysed populations are estimated within generation based on sire+dam model. Such approach ignores information from previous generations and relationships between birds other than full and half-sib families. Genetic relationship between traits is taken into account in the selection index. However, it is not properly accounted for in predicting of breeding value. Suboptimal methods of prediction the breeding value may contribute to low selection accuracy and reduced genetic gain expressed as lack of clear genetic trend for the studied traits. Therefore, as suggested by many authors for other species, the multitrait animal model methodology (including both productive and reproductive characters) should be implemented for breeding value prediction in geese. To enable across-generation evaluation the unique and consistent numbering of birds would be necessary.

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Wielocechowa ocena wartości genetycznej gęsi pod względem cech produkcyjnych i reprodukcyjnych

Streszczenie

Oszacowano odziedziczalność i korelacje genetyczne między cechami produkcyjnymi w dwóch rodach gęsi (BW8 i BW11). Ponadto wyznaczono trendy genetyczne i fenotypowe dla badanych cech, które obejmowały: masę ciała w 8 i 11 tygodniu życia (BW8 i BW11), nieśności (EP), masę jaja (EW), procent zapłodnienia (PFE) i procent wylęgu z jaj zapłodnionych (PHC). Analizę przeprowadzono za pomocą wielocechowego modelu zwierzęcia. Współczynniki odziedziczalności dla masy ciała i nieśności przyjęły średnie wartości w obu rodach. Najniższe wartości h^2 uzyskano dla cech reprodukcyjnych. Najwyższe dodatnie korelacje wykazano wśród cech reprodukcyjnych (PFE i PHC) oraz dwóch pomiarów masy ciała (BW8 i BW11). Trendy genetyczne we wszystkich badanych cechach były niewielkie i nieukierunkowane. Generalnie, przeprowadzone badania potwierdziły istnienie niekorzystnych zależności między cechami produkcyjnymi a reprodukcyjnymi.