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Our knowledge of hens' reproductive breeding value is limited upon selecting birds for flock reproduction*

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Influence of two sources of information on the accuracy of fertility and hatchability proofs in laying hens was studied on a Rhode Island White-based maternal strain record. Five- or three-generation pedigree and including or not including the laying performance as correlated traits were varied to create four variants of analysis tested against the reference – five-generation, multiple-trait, and *post factum* reproduction record of the selected generation. The upper limit of the rank correlation between the reference ranking and the best possible ranking reached 0.9. A significant increase in the accordance of the BLUP proof rankings with the reference one was attributed to the multiple-trait approach while the pedigree depth exerted a lesser impact on the reproduction proof accuracy. It is concluded that, with low heritable reproduction traits, five-generation pedigree should be recommended to the three-generation pedigree and the laying performance, possibly enriched with other early recorded traits, should accompany the breeding value prediction of the reproduction complex.

KEY WORDS: fertility / hatchability / laying performance / multiple-trait / proof accuracy

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Selection criteria in many farm species evolve rapidly from just production, related to output and income, to production plus adaptation complex to account also for inputs and costs inevitable in a breeding enterprise [e.g. Sewalem *et al*. 1998, Hartmann *et al*. 2002]. Reproduction is a vital component of that complex. The problem of reproduction is particularly important in maternal strains of laying hens designated to produce crossbred terminal progeny, in the possibly most efficient way. With the usual, yearly cycle of production in laying hens we have, however, to rely on the birds' breeding value for reproduction only predicted from the performance of the previous generations. A possibility of improving the reliability of the proofs lays in the multiple-trait approach, when analysing data with missing observations [Kovac and Groeneveld 1990, Hoeschele *et al*. 1995]. Indeed, at the moment of selecting hens for reproduction of the flock or for production of terminal progeny, we have the initial production of the candidate birds already measured. Yet, the quality of this source of information depends greatly on the power of genetic correlations between traits of production and those of reproduction. Age at first egg and egg weight are the routinely recorded traits which correlate moderately with fertility and hatchability [Rozempolska-Rucińska *et al*. 2007] and can be considered upon breeding value estimation for reproduction.

The purpose of this study was to test the influence of the pedigree depth and single- or multiple-trait analysis approach on ranking of hens by their breeding value for reproduction, to formulate recommendations for the breeders.

Material and methods

The data of body weight at 18 weeks age (BW18), age at first egg (AFE), 15 weeks egg laying rate (LR15) and mean egg weight from the 34th week of collection (EW34) were individually recorded for nearly 4800 hens in each generation of a Rhode Island White-based maternal strain, at a commercial farm producing crossbred birds for egg production. The birds were maintained in individual cages in a three level battery.

Some 500 hens were selected for reproduction of the flock in each generation and for them numbers of eggs set, eggs fertilized (FE), chicks hatched from set eggs (CSE) and chicks hatched from fertilized eggs (CFE) were recorded. Four hatches were run annually.

Prior to REML runs for estimation of the (co)variance components and BLUP [Madsen, Jensen 2000] runs for the breeding value prediction the significance of factors in the models had been verified with the least-squares analysis of variance. The final set of effects accounted for in the statistical classification is presented in Table 1.

Table 1. Factors fitted in the statistical models for particular traits

Effect	Type[a]	Trait		
		BW18[b], AFE[b], LR15[b], EW34[b]	FE, CSE	CFE
year * hatch of origin	F	x		
year of reproduction	F		x	x
no. of eggs set	C		x	
no. of eggs fertilized	C			x
individual additive genetic	A	x	x	x

[a]Type of effect: A – random additive genetic associated with the relationship matrix, F – fixed, C – fixed covariate.
[b]Analysed in multiple-trait variants I, II and IV – Table 2.

The following terminology was accepted to describe the further used notions:

– "selected generation" – generation from which hens of known initial laying performance are selected for reproduction;
– "reference breeding value" – breeding value predicted with the broadest information *i.e.* 5 generations, accomplished reproduction, multiple-trait approach;
– "approximated breeding value" – breeding value predicted on the reproductive performance of relatives from previous generations.

Altogether five variants of analysis with varying information were tested, as shown in Table 2. Variants II and IV allow obtaining the most reliable proofs in the practice reality when results on, respectively, five or three generations are included in the analysis.

Table 2. Characteristic of variants employed for (co)variance components/breeding value prediction

Varied feature	Variant				
	I	II	III	IV	V
No. of generations	5	5	5	3	3
No. of generations of recorded reproduction	5	4	4	2	2
Reproduction records of selected generation	yes	no	no	no	no
Multiple-trait (laying performance)	yes	yes	no	yes	no
No. of hens of known laying performance record	24246	24246	24246	14326	14326
No. of hens of known reproduction record	2584	2052	2052	1037	1037
No. of birds in pedigree	24800	24800	24800	14837	14837

The quality of ranking of birds according to their breeding value for reproduction, as obtained with different approaches, was assessed with the Spearman rank correlations, taking results of variant I as the reference.

Results and discussion

Rozempolska-Rucińska *et al*. [2007] estimated the heritability coefficients for FE, CSE and CFE at 0.33, 0.26 and 0.15, respectively (Tab. 3). The heritabilities can be considered as moderate and thus call for the use of additional information sources to increase the accuracy of the reproduction proofs.

Table 3. Heritability coefficients (h^2) for the examined traits and *genetic correlations* between the complexes of traits [Rozempolska-Rucińska 2007]

Production		Reproduction		
		fertilized eggs	chicks hatched from eggs	
			set	fertilized
	h^2	**0.33**	**0.26**	**0.15**
Body weight	**0.55**	*-0.11*	*-0.08*	*-0.04*
Age at first egg	**0.48**	*0.01*	*0.19*	*0.33*
Initial laying rate	**0.10**	*-0.14*	*-0.07*	*0.01*
Egg weight	**0.53**	*-0.24*	*-0.25*	*-0.20*

Bennewitz *et al*. [2007], when applying a Bayesian threshold model approach, arrived at heritability coefficients of 0.067, 0.126, and 0.136 for FE, CSE, and CFE, respectively. Since the fertility and hatchability traits follow, in fact, the binomial distribution, approximation of that distribution with the normal distribution, as in the study of Rozempolska-Rucińska *et al*. [2007], could have resulted in higher estimates. Additionally, the data on hatchability were pooled within a hen and thus, the permanent environment component could also contribute to the overestimation of heritability.

Rankings of the BLUP proofs for number of fertilized eggs, number of chicks hatched from set eggs and number of chicks hatched from fertilized eggs, obtained with different variants of the analysis, are compared in Table 4. The accordance of the ranking of the reference breeding values with the ranking produced by the best of the realistic approaches (5 generations, multiple-trait) reached only 0.89 and was equal for all the traits. Such a split of rankings is, however, inevitable and the breeders should realize that the decision taken at selecting birds for reproduction may be very much imperfect. This split is further deepened when giving up accounting for correlated traits (variant III) – the accordance of fit with the reference ranking drops for the hatchability rates below acceptable levels (to 0.74 and 0.63). The beneficial effect of the multiple-trait approach was achieved despite generally low genetic correlations between reproduction and production traits. The highest absolute value of a correlation (0.33) was that between age at first egg and hatching rate from fertilized eggs (Tab 3).

Zięba *et al.* [1998] concluded that the three-generation pedigree was sufficient for the purpose of breeding value estimation of laying performance. That, however, regarded traits of higher heritability and additional information contributed to the reliability of the proofs in a much lower extent. In the present study the more

Table 4. Rank correlations between the reference BLUP solutions and alternative solutions for studied reproduction traits

Variant	Trait		
	FE	CSE	CFE
II	0.89	0.89	0.88
III	0.85	0.74	0.63
IV	0.82	0.79	0.74
V	0.80	0.68	0.56

extensive model of the two three-generation models applied (IV and V) produced rank correlations of only 0.74 to 0.82, with the reference proofs. When the information from correlated traits was neglected the correlation coefficients dropped to as low as 0.68 and 0.56 for the hatching rates (Tab. 4). The fertilization rate – trait of the highest heritability coefficient of the studied traits – was, naturally, the least susceptible to the changes of the information sources.

Unless more generations are included and/or other marker traits of higher correlations with the examined reproduction traits are considered, 0.9 seems to be the upper limit of the accordance between the reference ranking and the approximated breeding value ranking, in the five-generation analysis. It is unlikely, although not impossible, that the breeders seek improvement of the accuracy reaching deeper into the pedigrees. Alternatively, research aiming at scanning early recorded traits, in search of those of high genetic correlations with the reproduction complex, could be recommended, as the correlated traits contribute more to the accuracy of the proofs than the pedigree depth.

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S t r e s z c z e n i e

Wpływ jakości dwóch źródeł informacji na dokładność oceny wartości hodowlanej pod względem stopy zapłodnienia i wylęgu analizowany był na danych z użytkowości matecznej linii niosek wywodzącej się z rasy *Rhode Island White*. Pięcio- lub trzypokoleniowy rodowód oraz wykorzystanie lub nie informacji o skorelowanej użytkowości nieśnej utworzyły cztery warianty analizy, których wyniki porównywane były z wynikami oceny odnośnej, uzyskanymi w najbardziej rozbudowanej analizie, uwzględniającej *post factum* wyniki reprodukcji pokolenia selekcjonowanego. Górna granica korelacji rangowej między wynikami oceny referencyjnej a wynikami testowanych wariantów analizy wyniosła 0,9. Istotny przyrost zgodności uszeregowania wartości hodowlanych BLUP, odnośnych z testowanymi, powodowany był głównie wykorzystaniem informacji o cechach skorelowanych. Głębokość rodowodu miała mniejsze znaczenie. Wnioskuje się, że w ocenie niskoodziedziczalnych cech reprodukcji powinny być wykorzystywane rodowody głębsze niż w przypadku cech produkcyjnych, a zwłaszcza uwzględniana powinna być skorelowana użytkowość nieśna, wzbogacona możliwie o inne cechy, mierzone wcześnie w życiu.