IMPACT OF GENETIC GROUPS AND HERD-YEAR-SEASON FIXED/RANDOM ON GENETIC PARAMETER ESTIMATES FROM LARGE DATA SETS IN PIGS

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Abstract

Four-trait animal models were used to estimate genetic parameters for lean meat percentage, average daily gain from birth to the end of the test, number of piglets born alive in the first litter and number of piglets born alive in the second and subsequent litters for Czech Large White and Czech Landrace pigs. The models differed by considering herd-year-season as random or fixed and by the presence or absence of genetic group effects. Similar heritabilities and genetic correlations between traits were estimated for all four variants of models giving no reason for preferring one of these variants. However, results from the literature show that treating herd-year-season as fixed effect in the genetic evaluation should be desirable because qualitative genetic material has been more and more concentrated in certain herds. The use of genetic groups in the models seems to be problematic and is probably not really necessary.

Key Words: Pig, genetic parameters, genetic groups, herd-year-season effect

Genetic evaluation of pig dam breeds in the Czech Republic has been based on a four-trait animal model including lean meat content, average daily gain from birth till the end of the test, number of piglets born alive in the first litter and number of piglets born alive in the second and subsequent litters. The herd-year-season effect has been treated as random and genetic groups have been included in the model. Genetic parameters published in WOLF et al. (2005) have been used in the breeding value estimation.

Recently problems have been occurred that the best boars have been concentrated in a low number of herds. This made it necessary to reinvestigate the method of genetic evaluation with special regard to the herd-yearseason effects and genetic groups. The question if herdyear-season effects are to be considered as random or fixed has been intensively discussed in the literature (BABOT et al. 2003, FREY et al., 1997, VISSCHER and GODDARD, 1993). Also the effect of genetic groups on genetic evaluation has been given consideration in the literature (ESTANY and SORENSEN, 1995, KUEHN et al., 2007, PHOCAS and LALOË, 2004).

The objective of the present paper is therefore to investigate the influence of random or fixed herd-yearseason effects and the impact of the presence or absence of genetic groups on the estimates of genetic parameters. Furthermore, the impact of these two factors on the genetic evaluation will be discussed and conclusions will be drawn for the breeding value estimation of Czech pig dam breeds.

Material and Methods

Animals and traits

The analyses were based on performance test data (production and reproduction traits) for the breeds Czech Large White (CLW) and Czech Landrace (CLA)

from 1995 to 2010. The traits considered were lean mean percentage (%) at the end of the performance test estimated from ultrasonic measurements unadjusted for live weight, average daily gain from birth till the end of the field test (in g/d) calculated as weight at end of test divided by age at end of test, number of piglets born alive in a sow's first litter and number of piglets born alive in a sow's second and subsequent litters. These four traits are recently included in the genetic evaluation of pig dam breeds in the Czech Republic.

All data were collected under field conditions. The field test for production traits started at an age of 80 to 88 days and lasted between 56 and 70 days (from 1 January 2003, this interval was changed to 49 to 63 days for gilts; the duration of the test for young boars was not affected). The weight at the beginning of the test was approximately 30 kg. The large data sets used for the routine genetic evaluation as input data were used without further editing. The number of observations and the means and standard deviations for all traits as well as further quantities used as covariates in the calculations are summarized in Table 1. The number of observations was considerably higher in CLW than in CLA (about by a factor of 3).

Statistical methods

For both breeds, four four-trait animal models were calculated to estimate the covariance components. The structure of the models is given in Table 2. The four models differed by considering herd-year-season as fixed or random and by the presence or absence of genetic groups as a factor in the model. The herd-year-season effect was defined in the same way for production and reproduction traits. A flexible allocation of records to herd-year-season classes was applied which was described in detail in WOLF et al. (2005). Genetic groups were formed on the basis of the origin and of the birth year of the animals. The number of genetic groups was 17 in CLW and 10 in CLA.

For the factor "parity" in the model, 1 to 4 was used for parities 1 to 4, the code 5 summarized parities 5 and 6 and the code 6 summarized parities greater than 6. This was done to keep the number of records for the parity orders reasonably high. Linear regression on live weight was only included for lean meat content, not for daily gain. A quadratic regression on age at farrowing was used for number of piglets born alive in the 1st litter, whereas for the subsequent litters, a quadratic regression on the farrowing interval was included. The model for number of piglets born alive in the 2nd and subsequent litters was a repeatability model and included therefore the effect of parity and the permanent effect of the sow.

All available pedigree information was used. That means, the pedigree was traced back approximately to the year 1980. Restricted maximum likelihood (REML) and optimisation by a quasi Newton algorithm with analytical gradients (NEUMAIER and GROENEVELD, 1998) as implemented in VCE 6 program (GROENEVELD et al., 2008) were used to estimate the variances and covariances. Approximate standard errors of the covariance components were calculated from the Hessian matrix. The number of estimated (co)variances was 19 for herd-year-season fixed and 29 for herd-year-season random. The number of equations to be simultaneously solved was around 1 957 000 for CLW and approximately 670 000 for CLA.

Results

The estimates of residual variances, heritabilities and proportions of variances for further effects in the model are summarized for CLW in Table 3 and for CLA in Table 4. The results were similar for all four models and for both breeds. The lowest residual variances were observed for the model with herd-year-season random and with no genetic groups.

The highest heritability was estimated for lean meat content (LM). The heritability for average daily gain from birth until the end of the field test (ADG) took only values between 0.15 and 0.20 in CLW and between 0.12 and 0.18 in CLA; the lower values were always observed in the models with herd-year-season fixed. The heritabilities for the number of piglets born alive in the first litter (NBA1) and in the second and subsequent litters (NBA2+) were equal or nearly equal (between 0.13 and 0.16) with one exception. The model with genetic groups and herd-year-season fixed yielded a heritability of 0.19 for NBA1 in CLA.

The proportion of variance for the herd-year-season effect was highest for ADG (27 to 28% in CLW and 35 to 37% in CLA) followed by LM (13% in CLW, 12% in CLA) and lowest in NBA1 and NBA2+. In the latter two traits, higher values were estimated for CLA than for CLW. The proportion of variance for the herd-year-season effect was higher in NBA1 than in NBA2+.

The proportion of variance for the common litter effect was highest (22%) and equal for both breeds in ADG for models with herd-year-season fixed. Considering herd-year-season random, this proportion decreased to 16% in CLW and 14% in CLA. The common litter effect caused approximately 10% of the total variance of LM.

The proportion of variance for the permanent environmental effect of the sow was in the range between 3 and 5%. The proportion of the residual variance was higher in the reproduction traits than in the production traits. Whereas in reproduction traits only 13 to 26% of the total variance was explained by known factors, this percentage was 40 to 63% in production traits.

The estimates of the correlations between traits for all random factors in the models are given in for the CLW breed Table 5 and for CLA in Table 6. The highest additive genetic correlations (0.82 to 0.87 in CLW and 0.86 to 0.93 in CLA) were observed between both reproduction traits being in the range. A negative correlation was found between the production traits LM and ADG in all models; this correlation was around $\Box 0.20$ in CLW and between $\Box 0.01$ and $\Box 0.10$ in CLA. The genetic correlations between LM and both reproduction traits were very small (with one exception lower than 0.10) and positive. Small correlations which were mostly negative were observed between ADG and the reproduction traits. Especially in CLW, their absolute value was higher for NBA2+ than for NBA1 ($\Box 0.14$ to \Box 0.18 versus \Box 0.08 to \Box 0.10).

The herd-year-season correlations were also highest between the reproduction traits (0.82 in CLW, 0.92 to 0.93 in CLA). Small positive correlations were estimated between the production traits (0.07 to 0.13 in CLW, 0.10 to 0.17 in CLA). All herd-year-season correlations between production and reproduction traits were positive. The correlations with ADG were higher than the correlations with LM. Whereas the correlations between the reproduction traits and LM were lower in CLA than in CLW (0.07 to 0.16 versus 0.18 to 0.24), the correlations between the reproduction traits and ADG were considerably higher in CLA than in CLW (0.61 to 0.68 versus 0.28 to 0.34).

The estimated correlations caused by the common litter effect between both production traits were near zero in CLW and approximately 0.10 in CLA. The residual correlations between LM and ADG were very low; they took negative values in CLW and positive values in CLA.

Trait	п	Mean	SD
Czech Large	White		•
Lean meat percentage (%)	333357	61.2	2.68
Average daily gain from birth to test end (g/d)	333636	584	76.1
Number of piglets born alive in 1 st litter	39411	10.44	2.497
Number of piglets born alive in 2 nd and subsequent litters	126166	11.28	2.609
End weight in the field test (kg)	333636	88.4	10.95
Age at 1 st farrowing (d)	39411	376	42.3
Farrowing interval (d)	126166	164	24.9
Czech Land	race		
Lean meat percentage (%)	115451	61.3	2.54
Average daily gain from birth to test end (g/d)	115482	618	86.5
Number of piglets born alive in 1 st litter	14120	10.65	2.572
Number of piglets born alive in 2 nd and subsequent litters	39521	11.36	2.733
End weight in the field test (kg)	115482	93.4	12.15
Age at 1 st farrowing (d)	14120	371	40.9
Farrowing interval (d)	39521	166	25.9

Table 1. Number of observations, means and standard deviations for individual traits for the breeds Czech Large White and Czech Landrace

n – number of records, SD – phenotypic standard deviation

Table 2.	Structure	of the	four-trait	animal	models
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Factor	Type of fac- tor	LM	ADG	NBA1	NBA2+
Factors	equal for all mod	lels	•	•	•
Live weight at the end of the test	С	Х	-	-	-
Age at 1 st farrowing linear and squared	С	-	-	Х	-
Farrowing interval linear and squared	С	-	-	-	х
Animal	А	Х	Х	Х	х
Sex	F	Х	Х	-	-
Litter the animal is from	R	Х	Х	-	-
Mating type (AI or natural mating)	F	-	-	Х	х
Breed of the boar	F	-	-	Х	х
Parity	F	-	-	-	х
Permanent effect of the sow	R	-	-	-	х
Factors d	iffering among m	odels			
Herd-year-season:					
Variant 1:	F	Х	Х	Х	Х
Variant 2:	R	Х	Х	Х	х
Genetic group:					
Variant 1:	F	Х	Х	Х	Х
Variant 2:	-	-	-	-	-

Type of factor: C – covariable, A – random with relationship matrix, R – random, F – fixed. Traits: LM – lean meat content, ADG – average daily gain from birth till the end of the field test, NBA1 – number of piglets born alive in a sow's 1^{st} litter, NBA2+ - number of piglets born alive in a sow's 2^{nd} and subsequent litters. 'x' – factor included into the model, '-' factor not included.

Table 3. Estimates of residual variances, heritabilities and proportions of variances of further random effects (with their standard errors) for the four four twit models calculated for the Crock Lana White broad

	Residual variances 1.63 ± 0.010	Fixed No	No
$\begin{array}{c c c c c c c c c c c c c c c c c c c $		1.64 ± 0.010	1.58 ± 0.010
	1798 ± 7	1805 ± 9	1793 ± 7
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	4.54 ± 0.042	4.67 ± 0.047	4.54 ± 0.042
	4.90 ± 0.022	4.92 ± 0.022	4.90 ± 0.020
	Heritabilities		
$\begin{array}{ c c c c c c } DG & 0.20 \pm 0.004 \\ BA1 & 0.13 \pm 0.009 \\ BA2 + & 0.13 \pm 0.005 \\ Proportion \\ M & - \\ DG & - \\ DG & - \\ BA1 & - \\ BA1 & - \\ BA2 + & - \\ Proportio \\ M & 0.09 \pm 0.002 \\ DG & 0.22 \pm 0.002 \\ \end{array}$	0.34 ± 0.004	0.38 ± 0.006	0.36 ± 0.004
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	0.15 ± 0.002	0.20 ± 0.004	0.15 ± 0.002
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	0.16 ± 0.007	0.13 ± 0.008	0.16 ± 0.007
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	0.15 ± 0.003	0.13 ± 0.005	0.16 ± 0.007
$ \begin{array}{c cccc} M & & & & & \\ DG & & & & \\ BA1 & & & & \\ BA2+ & & & & \\ BA2+ & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ DG & & & & & & \\ DG & & & & & & \\ \end{array} $	is of variance for the herd-year-s	ieason effect	
$\begin{array}{c ccccc} DG & - & - & \\ BA1 & - & - & \\ BA2+ & - & - & \\ Proportio \\ M & & 0.09 \pm 0.002 \\ DG & & 0.22 \pm 0.002 \end{array}$	0.13 ± 0.003		0.13 ± 0.003
BA1 - $BA2+$ - $BA2+$ - M 0.09 ± 0.002 DG 0.22 ± 0.002	0.27 ± 0.002		0.28 ± 0.002
BA2+ - $Proportio$ M DG DG 0.22 ± 0.002	0.06 ± 0.002		0.06 ± 0.002
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	0.04 ± 0.001		0.04 ± 0.001
M 0.09 ± 0.002 DG 0.22 ± 0.002	ons of variance for the common l	litter effect	
DG 0.22 ± 0.002	0.08 ± 0.001	0.09 ± 0.002	0.08 ± 0.001
	0.16 ± 0.001	0.22 ± 0.002	016 ± 0.001
Proportion of varian	nce for the permanent environme	ental effect of the sow	
BA2+ 0.05 ± 0.004	0.05 ± 0.002	0.05 ± 0.004	0.04 ± 0.002
Propo	ortion of variance for the residua	ıl effect	
M 0.55 ± 0.006	0.46 ± 0.004	0.53 ± 0.006	0.43 ± 0.004
DG 0.58 ± 0.004	0.42 ± 0.002	0.58 ± 0.004	0.41 ± 0.002
BA1 0.87 ± 0.008	0.78 ± 0.006	0.87 ± 0.008	0.78 ± 0.006
1BA2+ 0.82 ± 0.005	0.77 ± 0.003	0.82 ± 0.005	0.76 ± 0.003

Traits: LM – lean meat content, ADG – average daily gain from birth till the end of the field test, NBA1 – number of piglets born alive in a sow's 1^{st} litter, NBA2+ - number of piglets born alive in a sow's 2^{nd} and subsequent litters

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Factor/Trait		Genetic param	neter estimates	
Herd-year-season	Fixed	Random	Fixed	Random
Genetic groups	Yes	Yes	No	No
		Residual variances		
LM	1.55 ± 0.011	1.46 ± 0.012	1.49 ± 0.012	1.42 ± 0.015
ADG	1846 ± 13	1820 ± 12	1825 ± 14	1808 ± 13
NBA1	4.21 ± 0.071	4.36 ± 0.068	4.43 ± 0.079	4.34 ± 0.069
NBA2+	4.93 ± 0.037	4.90 ± 0.037	4.92 ± 0.037	4.89 ± 0.038
		Heritabilities		
LM	0.32 ± 0.004	0.32 ± 0.005	0.34 ± 0.006	0.34 ± 0.007
ADG	0.17 ± 0.004	0.12 ± 0.003	0.18 ± 0.006	0.12 ± 0.004
NBA1	0.19 ± 0.014	0.14 ± 0.011	0.13 ± 0.014	0.15 ± 0.011
NBA2+	0.15 ± 0.006	0.13 ± 0.007	0.13 ± 0.007	0.15 ± 0.005
	Proportion	ns of variance for the herd-year-sea	son effect	
LM		0.12 ± 0.004		0.12 ± 0.005
ADG		0.35 ± 0.003		0.37 ± 0.005
NBA1		0.10 ± 0.003		0.11 ± 0.006
NBA2+		0.06 ± 0.002		0.08 ± 0.004
	Proporti	ions of variance for the common litt	er effect	
LM	0.10 ± 0.002	0.09 ± 0.002	0.10 ± 0.003	0.09 ± 0.002
ADG	0.22 ± 0.003	0.14 ± 0.002	0.22 ± 0.003	0.14 ± 0.002
	Proportion of varia	ince for the permanent environment	al effect of the sow	
NBA2+	0.03 ± 0.002	0.04 ± 0.002	0.05 ± 0.004	0.04 ± 0.003
	Prop	ortion of variance for the residual e	ffect	
LM	0.58 ± 0.007	0.47 ± 0.006	0.55 ± 0.009	0.45 ± 0.007
ADG	0.60 ± 0.004	0.38 ± 0.003	0.59 ± 0.005	0.37 ± 0.004
NBA1	0.81 ± 0.014	0.76 ± 0.009	0.87 ± 0.014	0.75 ± 0.011
NBA2+	0.82 ± 0.006	0.76 ± 0.005	0.82 ± 0.007	0.74 ± 0.005
Traits: LM – lean meat content, AD0	G – average daily gain from birt	h till the end of the field test. NBA1	l – number of piglets born alive in	a sow's 1 st litter.

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Factor/Pair of traits		Genetic param	ieter estimates	
Herd-year-season	Fixed	Random	Fixed	Random
Genetic groups	Yes	Yes	oN	No
		Additive genetic correlations		
LM – ADG	-0.23 ± 0.014	-0.20 ± 0.008	-0.21 ± 0.014	-0.16 ± 0.005
LM – NBA1	0.03 ± 0.005	0.04 ± 0.008	0.03 ± 0.004	0.05 ± 0.008
LM – NBA2+	0.03 ± 0.010	0.03 ± 0.008	0.02 ± 0.005	0.04 ± 0.009
ADG – NBA1	-0.10 ± 0.027	-0.09 ± 0.013	-0.10 ± 0.011	-0.08 ± 0.012
ADG – NBA2+	-0.17 ± 0.019	-0.18 ± 0.015	-0.17 ± 0.017	-0.14 ± 0.014
NBA1 – NBA2+	0.87 ± 0.023	0.83 ± 0.016	0.87 ± 0.023	0.82 ± 0.015
	Correlati	ions caused by the herd-year-seaso	n effect	
LM – ADG		0.07 ± 0.005	-	0.13 ± 0.006
LM – NBA1	,	0.18 ± 0.010		0.20 ± 0.012
LM – NBA2+		0.22 ±0.011		0.24 ± 0.011
ADG – NBA1		0.33 ± 0.013		0.34 ± 0.015
ADG – NBA2+	,	0.28 ± 0.013		0.34 ± 0.015
NBA1 – NBA2+	,	0.82 ± 0.020		0.82 ± 0.019
	Correlo	ations caused by the common litter	effect	
LM – ADG	-0.01 ± 0.009	-0.01 ± 0.005	-0.01 ± 0.009	-0.01 ± 0.006
	Corr	relations caused by the residual eff	lect	
LM – ADG	-0.02 ± 0.005	-0.03 ± 0.003	-0.03 ± 0.005	-0.03 ± 0.003

Traits: LM – lean meat content, ADG – average daily gain from birth till the end of the field test, NBA1 – number of piglets born alive in a sow's 1^{st} litter, NBA2+ - number of piglets born alive in a sow's 2^{nd} and subsequent litters

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Factor/Pair of traits		Genetic param	leter estimates	
Herd-year-season	Fixed	Random	Fixed	Random
Genetic groups	Yes	Yes	No	No
		Additive genetic correlations		
LM – ADG	-0.10 ± 0.014	-0.06 ± 0.009	-0.03 ± 0.013	-0.01 ± 0.011
LM – NBA1	0.05 ± 0.005	0.09 ± 0.009	0.06 ± 0.007	0.13 ± 0.027
LM – NBA2+	0.01 ± 0.006	0.04 ± 0.007	0.02 ± 0.009	0.08 ± 0.017
ADG – NBA1	-0.03 ± 0.008	-0.02 ± 0.011	-0.08 ± 0.016	0.02 ± 0.015
ADG – NBA2+	-0.08 ± 0.007	-0.06 ± 0.008	-0.03 ± 0.011	0.00 ± 0.017
NBA1 – NBA2+	0.86 ± 0.021	0.88 ± 0.016	0.88 ± 0.020	0.93 ± 0.025
	Correlat	ions caused by the herd-year-seaso	n effect	
LM – ADG	-	0.10 ± 0.005		0.17 ± 0.024
LM – NBA1		0.07 ± 0.008		0.14 ± 0.029
LM – NBA2+		0.10 ± 0.010		0.16 ± 0.024
ADG – NBA1		0.61 ± 0.022		0.64 ± 0.026
ADG – NBA2+		0.65 ± 0.013		0.68 ± 0.018
NBA1 – NBA2+		0.93 ± 0.016		0.92 ± 0.018
	Correl	ations caused by the common litter	effect	
LM – ADG	0.10 ± 0.009	0.10 ± 0.009	0.10 ± 0.012	0.09 ± 0.015
	Cor	relations caused by the residual eff	èct	
LM – ADG	0.08 ± 0.005	0.07 ± 0.005	0.07 ± 0.005	0.06 ± 0.006

Traits: LM – lean meat content, ADG – average daily gain from birth till the end of the field test, NBA1 – number of piglets born alive in a sow's 1^{st} litter, NBA2+ - number of piglets born alive in a sow's 2^{nd} and subsequent litters

Discussion

Contemporary group effects

A question intensively discussed in the literature is if contemporary groups are to be treated as fixed or as random effects. FREY et al. (1997) confirmed the results of ESTANY and SORENSEN (1995) that the model with a random contemporary group effect yields more accurate predictions of breeding values than the model with fixed contemporary group effects. Though a non-random distribution of contemporary groups over families leads to biased genetic evaluations, the authors could show that the prediction of observations was in general more accurate using a model with random herd-year-season effects. Therefore, bias of predicted breeding values with random models was probably small. It is important to emphasise that this result was achieved on the basis of field data, where a significant non-random distribution of contemporary groups over families should be expected.

Our results did not confirm the findings of FREY et al. (1995) that the estimates of additive genetic variance for litter size were considerably higher in the random model. However, similarly as in FREY et al. (1995), low proportions of variance were found for the herd-year-season effect of litter size also in our investigation, especially in CLW.

According to BABOT et al. (2003), the impact of the definition and treatment of contemporary groups in the evaluation model on the genetic response of a pig nucleus is expected to be small. The results of the authors illustrated that treating the herd-year-season effect as random improves the predictive ability of the evaluation model for litter size. However, this does not necessarily lead to significant changes in the selection decisions and in the genetic response achieved. The existence of environmental trends within a population increases the risk of obtaining biased estimators of the genetic means. The bias may be caused by non-random association between the genetic level of the animals and herds. Animals with higher genetic values tend to be located in better herds.

OIKAWA and SATO (1997) compared the robustness of prediction with random and fixed herd models in a simulation study. No difference in empirical accuracy was observed between the prediction models if data included only large herds, whereas for data with small herds, the random herd model had a higher accuracy than the fixed herd model in general. This superiority of the random herd model did not change under selection.

VAN BEBBER et al. (1997) when reviewing the formation of herd-year-season classes in dairy cattle stated that the definition of contemporary group effects is always somewhat arbitrary and has often been a compromise between bias and the effective number of daughters. According to VISSCHER and GODDARD (1993) treating contemporary groups as random recovers some information across contemporary groups, but may cause bias in prediction of breeding values if a non-random association exists between sires and contemporary groups. In that case, the groups should be treated as fixed effects for practical genetic evaluations.

Genetic groups

ESTANY and SORENSEN (1995) found no evidence that genetic groups improved the predictive ability for litter size. However, group effects were shown to affect inferences about genetic trend, particularly in Landrace, where genetic group composition changed consistently over the years.

KUEHN et al. (2007) showed that breeding units must be sufficiently connected for comparing predicted breeding values among animals in different management units. The introduction of genetic groups in the model reduces the bias of predicted breeding value only if a high degree of connectedness between herds is ensured. If, for example, imported animals from a certain breeding organisation are located only in one herd or in a very limited number of herds, estimated breeding values will be biased.

PHOCAS and LALOË (2004) found when investigating models for the evaluation of AI beef sires in France that including fixed genetic group effects led to an overestimation of selection response under BLUP selection across groups despite the unbiasedness of the estimation, i.e. despite the correct estimation of differences between genetic groups. Also SCHAEFFER (2006) detected problems when using genetic groups and concluded that phantom parent groups are not really necessary.

Conclusions

No clear decision for one of the four models presented in this study is possible. There are arguments both for and against fixed and random contemporary group effects. Originally random herd-year-season effects were justified in the Czech herd book breeding programme as it could be assumed that there were no significant differences in the distribution of genetic material over herd. However, it seems that genetic differences between herds have been considerably increased more recently so that a fixed contemporary group effect is probably more justified. Concerning genetic groups, we agree with SCHAEFFER (2006) that they are not really necessary, at least not in herd book breeding programmes where it is difficult to ensure a high degree of connectedness between herds.

References

- BABOT D., NOGUERA J.L., ALFONSO L., ESTANY J.: Fixed or random contemporary groups in genetic evaluation for litter size in pigs using a single trait repeatability animal model. J. Anim. Breed. Genet., 120 (2003), 12-22.
- ESTANY J., SORENSEN D.: Estimation of genetic parameters for litter size in Danish Landrace and Yorkshire pigs. Anim. Sci., 60 (1995), 315-324.
- FREY M., HOFER A., KÜNZI N.: Comparison of models with a fixed or a random contemporary group effect for the genetic evaluation for litter size in pigs. Livest. Prod. Sci., 48 (1997), 135-141.
- GROENEVELD E., KOVAČ M., MIELENZ N.: VCE User's Guide and Reference Manual, Version 6.0 (2008). Available from ftp://ftp.tzv.fal.de/pub/ latest_vce/doc/ (accessed Aug 1, 2011).

- KUEHN L.A., LEWIS R.M., NOTTER D.R.: Managing the risk of comparing estimated breeding values across flocks or herds through connectedness: a review and application. Genet. Sel. Evol., 39 (2007), 225-247.
- NEUMAIER A., GROENEVELD E.: Restricted maximum likelihood estimation of covariances in sparse linear models. Genet. Sel. Evol., 30 (1998), 3-26.
- OIKAWA T., SATO K.: Treating small herds as fixed or random in an animal model. J. Anim. Breed. Genet., 114 (1997), 177-183.
- PHOCAS F., LALOË D.: Should genetic groups be fitted in BLUP evaluation? Practical answer for the French AI beef sire evaluation. Genet. Sel. Evol., 36 (2004), 325-345.
- SCHAEFFER, L.R.: Phantom genetic groups and genetic trend (2006). Available from http://cgil.uoguelph.ca/ dcbgc/Agenda0609/phantom.pdf (accessed Sep 7, 2011).
- VAN BEBBER J., REINSCH N., JUNGE W., KALM E.: Accounting for herd, year and season effects in genetic evaluations of dairy cattle: a review. Livest. Prod. Sci., 51 (1997), 191-203.
- VISSCHER P.M., GODDARD M.E.: Fixed and random contemporary groups. J. Dairy Sci., 76 (1993), 1444-1454.
- WOLF J., ŽÁKOVÁ E., GROENEVELD E.: Genetic parameters for a joint genetic evaluation of production and reproduction traits in pigs. Czech J. Anim. Sci., 50 (2005), 96-103.

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