BREEDING FOR REPRODUCTION TRAITS IN CONTEXT OF MULTIPLICATION HERDS EFFICIENCY IN SWINE

Petr Humpolíček, Zdeněk Tvrdoň, Tomáš Urban

Abstract

HUMPOLÍČEK PETR, TVRDOŇ ZDENĚK, URBAN TOMÁŠ: *Breeding for reproduction traits in context of multiplication herds efficiency in swine.* Acta Universitatis Agriculturae et Silviculturae Mendelianae Brunensis, 2013, LXI, No. 3, pp. 647–650

Presented study is a follow-up to the studies focused on effect of different selection pressure applied on two subpopulations of purebred Czech Large White sows on performance in multiplication herds. Higher selection pressure particularly on litter size and number of function nipples, while lower pressure on growth performance was applied in one population. About 1214 farrows of 393 F1 Czech Large White sows were included into statistical evaluation. The mixed linear models using the procedure REML in SAS for Windows 9.1.2. was used. The hypothesis that progeny of sows from hyper-prolific subpopulation breed in multiplier herds have different performance was not confirmed which is in contrast to previous studies. This non-homogeneity can be related to non-additive genetic effects which are caused by crossbreeding while selection methods are based on additive models.

selection, crossbreeding, reproduction

In swine, the selection criteria and breeding methods are mainly focused on the purebred populations in breeding herds but the focus on economic efficiency of multiplier herds are insufficient if we consider profit in swine industry. In spite of this the litter size traits or more generally prolificacy of F1 sows seems to be crucial. Achieving satisfactory reproduction level is complicated by the fact that reproduction traits are influenced by a complex of genetical and internal and external environmental factors. This leads to the problematic advancement even in breeding herds let alone in multiplication herds. During past decades different selection strategies were tested: hyperprolific lines creation (Bidanel and Ducos, 1994), direct selection based on the evaluation of breeding value (Holl and Robinson, 2003), marker assisted selection (Distl, 2007) or introgression (Piyasatian *et al.*, 2008), combination of molecular data into the BLUP-AM procedure (Baruch and Weller, 2009) and genomic selection (Noguera *et al.*, 2009). Mentioned strategies were focused mainly on the progress in purebred populations without regarding the impact on multiplication herds. In previous studies (Tvrdoň and Humpolíček, 2010; Humpolíček and Tvrdoň 2011) it was described that despite maximal selection pressure using hyperprolific line, which can be applied in breeding herds without negative effects, the progress in litter size traits in multiplication herds was insufficient. We noticed that incorporation of some auxiliary selection traits can be very effective. In present study we are concerning that breed specific effect can be crucial if progresses in multiplication herds are taken into account.

MATERIAL AND METHODS

Experimental procedure

In the study the progeny of Czech Large White sows bred at one breeding herd were used. The parental generation breed in breeding herd was divided into either hyperprolific (HP) or normal

(N) subpopulation according to their performance. To be incorporated into the HP subpopulation, the sows had to meet the following criteria: excellent breeding value for litter size (number of piglets born alive in the second and subsequent litters) among the top 15%; have on her first to third litter an average of 12 or more live-born piglets per litter; at least 7 functional nipples on either side, maximal back fat thickness of 12 mm and the sow must be MHS negative (Brenig and Brem, 1992). Sows which failed to meet these criteria belonged to the N subpopulation. Breeding values for individual traits were computed for both populations using the same method. The aggregate breeding values were computed separately for both populations using different weight coefficients. The aggregate breeding value comprises 60% (HP) and 55% (N) of litter size on the second and following litters, 30% (HP) or 40% (N) of average daily gain and 10% (HP) or 5% (N) of lean meat content. In HP subpopulations aggregate breeding values were used for planned mating. The sows of parental generation were mated or inseminated with the purebred boars of Large White breed while the sows of F1 generation were inseminated with purebred Landrase boars. In contrast to the sows from normal population the HP sows were mated or inseminated only with boars with excellent breeding values for reproduction (> 5% of population). These schemes of selection and mating were practised for six years. During this time 393 gilts from F1 generation were moved, at age of six months to the multiplier herd where their performances were recorded and subsequently analysed. All studied sows from F1 generation were bred under the same living conditions.

Several performance traits were recorded in the F1 generation. The prolificacy was specified by the total number of piglets born (TNB; defined as the number of all fully formed fetuses expelled at farrowing, dead or alive), number of piglets born alive (NBA; defined as the number of piglets alive immediately after birth), number of piglets weaned (NW; defined as the number of piglets available on the 28-th day of the piglets' age), age of sows at the first parity (AFP) and number of functional nipples (FN). As the traits describing the growth performance the ultrasonic back fat thickness (BF; Sonomark 100) and lean meat content (LMC; calculated from ultrasonic measurements without any live weight pre-adjustment) and average daily gain from birth to test end (g/day) (ADG) were used.

Statistical Analyses

The mixed linear models using the procedure REML in SAS for Windows 9.1.2. were conducted to estimate the differences between the performance of F1 offspring and the effect of insemination or natural mating on litter size. As very different traits are included in the study, the independent analyses were carried out for each trait. Individual models used to detect the effect of different pedigree are defined in the Tab. I.

RESULTS AND DISCUSSION

Presented study is a follow-up to the studies focused on effect of different selection pressure applied on two subpopulations of purebred Czech Large White sows on performance in multiplication herd (Tvrdoň and Humpolíček, 2010; Humpolíček and Tvrdoň, 2011). In these studies there was described that despite maximal selection pressure, which can be applied in breeding herds using hyperprolific line creation, the progress in litter size traits in multiplication herds was insufficient. In the Tab. II the non-significant differences between the total number of piglets born, number of piglets born alive, number of piglets weaned, age at first farrowing and functional niplets is presented. In previous studies the progress on the growth traits as well as on the number of functional nipples were found. Those results corresponded to the heritability of studied traits when only traits with middle or high heritability coefficient show progress in multiplication herds. Mutually in present study

I: *Specification of models used for detection of differences between sows of HP or N population*

	Litters	Pop	YS	AFF	Dam	Sire	Boar	BF	Mat	PN
TNB	1st	F	F	L	-	-	R	-	F	-
	1st–4h	F	F	L	-	-	R	-	F	F
NBA	1st	F	F	L	-	-	R	-	F	-
	1st–4th	F	F	L	-	-	R	-	F	F
NW	1st	F	F	-	-	-	R	L	F	-
	1st–4th	F	F	-	-	-	R	-	F	F
AFF		F	-	-	R	R	-	-	-	-
FN		F	-	-	R	R	-	-	-	-
BF, LMC &ADG		F	-	-	-	-	-	-	-	-

Note: F – fixed effect; R – random effect; L – linear regression; TNB – total piglets born; NBA – piglets born alive; NW – number of piglets weaned; AFP – age at first farrowing; FN – functional niplets; BF – back-fat thickness; LMC – lean meat content; ADG – average daily gain; Pop – HP or N population; YS – year and season of litter; DAM – dam of sows of F1 generation; SIRE – boar used in parental generation; Boar – boar used in F1 generation; MAT – mating or artificial insemination; PN – Parity number.

II: *Differences between sows of HP or N population*

N (393)	N	HP
	N	**HP**
	1st litters	
	n = 351	**n = 42**
TNB	9.37 ± 0.24	9.18 ± 0.66
NBA	9.24 ± 0.22	9.24 ± 0.65
NW	8.74 ± 0.20	8.71 ± 0.55
AFF	381.42 ± 3.85	380.39 ± 12.32
FN	14.45 ± 0.05	14.61 ± 0.14
BF	1.04 ± 0.03	1.09 ± 0.05
ADG	587.20 ± 5.03	583.65 ± 10.46
LMC	60.05 ± 0.19	59.58 ± 0.36
	1st–4th litters	
N (1214)	**n = 1 092**	**n = 122**
TNB	9.37 ± 0.24	9.18 ± 0.66
NBA	9.24 ± 0.22	9.24 ± 0.65
NW	9.24 ± 0.09	9.56 ± 0.25

Note: TNB – total number of piglets born; NBA – number of piglets born alive, NW – number of piglets weaned; AFP – age at first farrowing; FN – functional niplets; BF – back-fat thickness; LMC – lean meat content; ADG – average daily gain.

no significant differences were found in any studied traits, the back-fat thickness, lean meat content and average daily (Tab. II), although herd with very similar breed conditions were chosen. Thanks to this choice the effects which play crucial role in breeding and selection as different management, inbreeding level, type of mating (Lewis *et al.*, 2005). Thus, observed non-homogeneity in results must be caused by some other factors.

In swine, purebreds are combined to provide up to five-way crosses. A disadvantage of this structure is that genetic evaluation, by which the selection to hyperprolific line is performed, is predominantly based on an additive genetic model. Unfortunately, production and reproduction traits are influenced not only by additive but by non-aditive effects as well (Ishida *et al.*, 2001). Under these conditions the selection accuracy and consequently progress in production traits are reduced under an additive model. The advantages of dominance effects estimation is valid in population with a large number of dominance relationships that use specialized sire and dam lines (DeStefano and Hoeschele, 1992) as commercial multiplication herds are. The non-homogeneity of presented and previous results can be partially attributed to these non-additive effects which should be incorporated into genetic evaluation. The valuable effect of genetic evaluation with the dominance model was found to be appropriate mainly in case of litter size traits (Angkuraseranee, 2010) and in crossbreed populations (Lutaaya *et al.*, 2001). Other factors can be heterosis effect of sire breeds (Schwab *et al.*, 2010) and maternal effect (Roehe and Kennedy, 1993) which are important parts of total variability so. Genomic selection can solve the problem in the future.

CONCLUSION

Presented study is a follow-up to the studies focused on effect of different selection pressure applied on two subpopulations of purebred Czech Large White sows on performance in multiplication herds. The hypothesis that progeny of sows from hyper-prolific subpopulation breed in multiplier herds have different performance was not confirmed which is in contrast to previous studies. This non-homogeneity can be related to non-additive genetic effects which are caused by crossbreeding while selection methods are based on additive models. Moreover, the results indicate that intensive selection on production and reproduction traits in breeding herds without considering effect in multiplication herds can lead to decreased economic efficiency.

REFERENCES

ANGKURASERANEE, T., 2010: Estimation of additive and dominance variance for reproductive traits from different models in Duroc purebred. *Songklanakarin, J Sci Technol*, 32, 2: 115–117, ISSN 0125-3395.

BARUCH, E., WELLER, J. I., 2009: Incorporation of genotype effects into animal model evaluations when only a small fraction of the population has been genotyped. *Animal*, 3, 1: 16–23, ISSN 1751-7311. DOI 10.1017/S1751731108003339.

BIDANEL, J. P., DUCOS, A., 1994: Genetic evaluation of Large White and French Landrace pigs for prolificacy using an animal model. *J Rech Porcine Franc*, 26, 3: 321–326. ISSN 0021-8812.

BRENIG, B., BREM, G., 1992: Molecular cloning and analysis of the porcine "halothane" gene. *Arch Tierz*, 35, 1–2: 129–135. ISSN 0003-9438.

DeSTEFANO, A. L., HOESCHELE, I., 1992: Utilization of dominance variance through mate allocation strategies. *J Dairy Sci,* 75, 6: 1680–1690. ISSN 1525-3198. http://dx.doi.org/10.3168/jds. S0022-0302(92)77925-9.

DISTL, O., 2007: Mechanisms of regulation of litter size in pigs on the genome level. *Reprod Domest Anim,* 42, 2: 10–16. ISSN 1439-0531. DOI 10.1111/j.1439-0531.2007.00887.x.

HOLL, J. W., ROBINSON, O. W., 2003: Results from nine generations of selection for increased litter size in swine. *J Anim Sci,* 81, 3: 624–629. ISSN 1525-3163

HUMPOLÍČEK, P., TVRDOŇ, Z., 2011: Realized effect of different selection criteria applied in breeding herds on performance in multiplier herds. *Livestock Sci,* 137, 1: 264–267. ISSN 1871-1413. DOI 10.1016/j.livsci.2010.10.008.

ISHIDA, T., KUROKI, T., HARADA, H., FUKUHARA, R., 2001: Estimation of additive and dominance genetic variances in line breeding swine. *Asian Austral J Anim,* 14, 1: 1–6. ISSN 1976-5517.

LEWIS, T. W., WISEMANi, J., WOOLLIAMS, J. A., 2005: Genotype by mating type interaction for litter size in Landrace and Large White sows. *Anim Sci,* 81, 3: 331–335. ISSN 1740-0929. DOI http://dx.doi.org/10.1079/ASC50290331.

LUTAAYA, E., MISZTAL, I., MABRY, J. W., SHORT, T., TIMM, H. H., HOLZBAUER, R., 2001: Genetic parameter estimates from joint evaluation of purebreds and crossbreds in swine using the crossbred model. *J Anim Sci,* 79, 12: 3002–3007. ISSN 1525-3163.

NOGUERA, J. L., RODRIGUEZ, C., VARONA, L., TOMAS, A., MUNOZ, G., RAMIREZ, O., BARRAGAN, C., ARQUEL, M., BIDANEL, J. P., AMILLS, M., OVILO, C., SANCHEZ, A., 2009: A bi-dimensional genome scan for prolificacy traits in pigs shows the existence of multiple epistatic QTL. *BMC Genomics,* 10, 636: 1–12. ISSN 1471-2164. DOI 10.1186/1471-2164-10-636.

PIYASATIAN, N., FERNANDO, R. L., DEKKERS, I. C. M., 2008: Introgressing multiple QTL in breeding programmes of limited size. *J Anim Breed Genet,* 125, 1: 50–56. ISSN 1439-0388. DOI 10.1111/j.1439-0388.2007.00677.x.

ROEHE, R., KENNEDY, B. W., 1993: Effect of selection for maternal and direct genetic-effects on genetic improvement of litter size in swine. *J Anim Sci,* 71, 11: 2891–2904. ISSN 1525-3163.

SCHWAB, C. R., BAAS, T.J., STALDER, K. J., 2010: Results from six generations of selection for intramuscular fat in Duroc swine using real-time ultrasound. II. Genetic parameters and trends. *J Anim Sci,* 88, 1: 69–70. ISSN 1525-3163. DOI:10.2527/jas.2008-1336.

TVRDOŇ, Z., HUMPOLÍČEK, P., 2010: Impact of hyper-prolific population generation on the reproduction of sows in multiplication herds. *Arch Tierz,* 53, 2: 176–183. ISSN 0003-9438.

Address

Ing. Petr Humpolíček, Ph.D., Polymer Centre, Faculty of Technology, Tomas Bata University at Zlin, nám. T. G. Masaryka 5555, 762 72 Zlín, Czech Republic; Centre of Polymer Systems, Tomas Bata University in Zlín, nám. T. G. Masaryka 5555, 762 72 Zlín, Czech Republic, Ing. Zdeněk Tvrdoň, Ph.D., NAVOS, Co. Czech Republic, doc. Ing. Tomáš Urban, Ph.D., Department of Animal Morphology, Physiology and Genetics, Mendel University in Brno, Zemědělská 1, 613 00 Brno, Czech Republic, e-mail: humpolicek@ft.utb.cz