

Genetic Evaluation of Prolificacy of Two Local Swine Populations Under a Recording and Testing System on Low-Input Smallholder Mixed Farms in Northern Vietnam

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ABSTRACT: Pig keeping forms an integral part of low-input farming by smallholders in the uplands of northern Vietnam. Thus, improving pig genetic resources can have a beneficial impact on their livelihoods. In this study prolificacy of two local pig populations under an on-farm recording and performance testing scheme was genetically evaluated. Heritabilities of 0.17 for number of piglets born alive per litter for the Mong Cai breed and 0.08 for the Ban breed, respectively, suggest that genetic variation is sufficient to improve prolificacy by BLUP based selection. Due to the current market situation a community-based breeding program to enhance litter size appears to be more promising for Ban compared with Mong Cai. It is indicated that improving current pedigree recording is one prerequisite for the implementation of a breeding program for the Ban breed.

Keywords: smallholders; northern Vietnam; pig genetic resources; prolificacy

Introduction

A long-term collaborative research and development project of the National Institute of Animal Science, Vietnam, and the University of Hohenheim, Germany, aims at establishing a community-based pig breeding and marketing program in Son La province, northern Vietnam. The project is targeted at smallholder mixed farmers differing in their distance to urban centres and resource endowment (Lemke et al. (2006)). An on-farm performance and testing scheme (OPTS) has been established and accepted by farmers. It remains to be clarified whether the information generated through OPTS allows for the accurate estimation of breeding values of the target population. No genetic parameters for prolificacy of the indigenous Ban breed, which is widely used by smallholders in the remote uplands of northern Vietnam are available. Thus, this study genetically evaluated prolificacy of two local pig populations under an on-farm recording and testing scheme in northern Vietnam.

Materials and Methods

Study site and animal genetic resources. Data collection was conducted in 11 villages (Ban Bo, Ban Buon, Ban Co, Ban Dau, Ban Duoi, Ban Hiem, Ban Lam, Na Huong, Ot Luong, Pa Dong, Tong Tai) located in Son La province, northern Vietnam, from 2003 to 2012. Not all villages were present in the recording scheme during the complete study period. The villages represent different ethnic groups of northern Vietnam (Thai and H'Mong) and

different production systems (market-oriented vs. resource-driven). Villages differed in their socioeconomic characteristics and the resource endowment resulting in an unequal distribution of pig breeds and their crosses over villages (Lemke et al. (2006)). The study focussed on purebred local Ban and Mong Cai (MC) sows. The Ban breed represents an indigenous genotype which is well adapted to the harsh environment, but limited in its performance potential. The MC breed underwent a governmental breeding program and is considered to be one of the most prolific breeds of Vietnam.

Data. For sows of the Ban and MC breed, respectively, litter traits, i. e. number of piglets born in total per litter, including stillborn piglets and mummies (NBT), number of piglets born alive per litter (NBA), number of dead but fully formed piglets per litter (NSB), and number of piglets weaned per litter (NW) were recorded. Performance data and pedigree recording was conducted by farmers using standardized data sheets, which were collected bi-monthly, cross-checked for plausibility and entered into the PigCHAMP® data base (PigCHAMP, Ames, IA) by project personnel. The data set comprised 975 litters of MC sows and 1 013 litters of Ban sows (table 1).

Table 1. Structure of data for the Ban and Mong Cai (MC) breed.

	Ban	MC
Sows with records	373	239
Sows with pedigree records	73	75
Number of dams	55	49
Number of sires	26	14
Number of litters	975	1 013
Number of piglets born alive	5 968	9 653
Number of piglets weaned	4 531	7 956

Statistical analyses. Analyses were carried out separately for the Ban and MC breed. Fixed effects and two-way interactions were tested by backward selection using the GLMSELECT procedure of SAS 9.3 (SAS Institute Inc., Cary, NC). Fixed effects significant on the 0.05 level were included in the models for genetic evaluation. Parity had 5 levels (parity 1 to ≥5), service boar breed had 4 levels for Ban (unknown, Ban, MC, Large White) and 5 levels for MC (unknown, Ban, MC, Large White, Landrace), and village had 9 levels for Ban and 7 levels for MC. For each trait a repeated records animal model for the estimation of variance components and

breeding values (EBVs) was fitted. The effect of year-season of parity was included as random effect. Seasons were defined as spring (February to April), summer (May to July), fall (August to October) and winter (November to January) as indicated by farmers (Haussner (2013)). The additive-genetic value of animals in the pedigree and the permanent effect of the environment of the sow were also assumed to be randomly distributed. The model can be written in matrix notation as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_{pe} + \mathbf{Z}_3\mathbf{u}_{ys} + \mathbf{e};$$

where \mathbf{y} , $\boldsymbol{\beta}$, \mathbf{u}_a , \mathbf{u}_{pe} , \mathbf{u}_{ys} and \mathbf{e} are vectors of observations, fixed effects, additive-genetic effects, permanent environmental effects, year-season effects and residuals, respectively. \mathbf{X} , \mathbf{Z}_1 , \mathbf{Z}_2 and \mathbf{Z}_3 are the corresponding incidence matrices.

The estimation of variance components was conducted by the restricted Maximum Likelihood (REML) method using VCE version 6.0.2 (Groeneveld et al. (2010)). Estimated breeding values were computed with PEST version 4.2.5 (Groeneveld et al. (1990)). The accuracies of breeding values were derived from the standard errors of EBVs. The genetic trend in NBA was described defining sows born in 2002 as base generation.

Results and Discussion

Estimated genetic parameters and heritabilities for litter traits of the Ban and MC breeds are presented in table 2. Heritabilities were 0.11 and 0.21 for NBT, and 0.08 and 0.17 for NBA for the Ban and MC breed, respectively. The standard errors for the Ban breed were somewhat inflated. The estimate for heritability of NBA of MC sows was considerably higher compared with Duc et al. (1997) and Van and Duc (1999) who reported heritabilities of 0.09 and 0.10 for MC sows raised in larger herds. International purebred breeds showed heritability values of around 0.20 for litter size (Kaufmann et al. (2000); Wolf and Wolfova (2012)) and around 0.10 (e. g. Chen et al. (2003)) to 0.16 (Wolf and Wolfova (2012)) for NBA. Our results indicate that there is sufficient genetic variation for selection on litter size in both local pig breeds, but in case of the Ban breed this outcome is associated with higher uncertainty. On the other hand the estimation of genetic parameters for NSB or NW yielded heritabilities close to zero or high standard errors in the prevailing setting. For NSB the phenotypic variation was relatively low ($\sigma_p^2 = 0.73$ for Ban breed and $\sigma_p^2 = 2.00$ for MC breed, respectively), whereas for NW the residual variation was high for both breeds (table 2). The proportion of variance in NW due to the effect of the permanent environment of the sow was 12% and 6% for the Ban and MC breeds, respectively. High standard errors and low heritabilities could be related to the limited population size under recording and the high environmental variation, especially with regard to the Ban breed. Differences between breeds are further explicable by differences in pedigree information (31% of MC sows with pedigree record vs. 20% of Ban sows with pedigree record) and average number of parities, i. e. repeated measurements per sow (4.2 litters per MC sow vs. 2.6 litters per Ban sow). Cross fostering is only sporadically implemented for MC

piglets, thus the influence on estimates for NW is assumed to be limited.

Table 2. Estimates of variance components[§] and heritabilities (h^2) for number of piglets born in total per litter (NBT), number of piglets born alive per litter (NBA), number of stillborn piglets per litter (NSB), and number of weaned piglets per litter (NW) for the Ban and Mong Cai (MC) breed.

	σ_A^2	σ_{PE}^2	σ_{YS}^2	σ_{RES}^2	h_{SE}^2
NBT					
Ban	0.50	0.30	0.08	3.68	0.11 _{0.08}
MC	2.14	$0.58 \cdot 10^{-9}$	0.48	7.49	0.21 _{0.04}
NBA					
Ban	0.41	0.46	0.01	4.02	0.08 _{0.07}
MC	1.63	$0.60 \cdot 10^{-8}$	0.30	7.70	0.17 _{0.04}
NSB					
Ban	0.02	0.01	0.02	0.68	0.03 _{0.07}
MC	$0.61 \cdot 10^{-11}$	0.03	0.05	1.91	0
NW					
Ban	$0.70 \cdot 10^{-11}$	0.80	0.14	5.75	0
MC	0.25	0.62	0.10	9.66	0.02 _{0.04}

[§] σ_A^2 : additive-genetic variance

σ_{PE}^2 : variance of permanent environmental effects

σ_{YS}^2 : variance of year-season effects

σ_{RES}^2 : residual variance

Before the practical implementation of a breeding program further genetic, organizational and economic considerations are necessary. Firstly, correlated responses of productive, reproductive and fitness traits when selecting on NBT or NBA are unknown for the Ban and MC breeds. To date most of these traits cannot be accurately measured and recorded on-farm. Secondly, the importance of litter size for the economic profit of smallholders is not known, although they consider this trait as relevant for breed choice and in need to be improved (Roessler et al. (2009); Herold et al. (2010); Roessler et al. (forthcoming)). Thirdly, the profitability of a selection program on litter traits has to be evaluated under the given limitations in (financial) resources. Previous model simulations for selection on four traits in both breeds and considering different crossbreeding schemes question the financial sustainability of such a breeding program (Roessler et al. (2009); Herold et al. (2010)). Yet, it was noted that costs for the science-driven OPTS may be considerably higher than for a commercial breeding program (Herold et al. (2010)). During the monitoring and research period the genetic trends for NBT and NBA were around zero for both breeds (figure 1), suggesting that traditional breeding and culling practices hardly contribute to genetic improvement of prolificacy in both breeds. It is interesting to note that EBVs of MC sows were more volatile than those of Ban sows. This could be explained by the higher influx of external breeding material for MC compared with the Ban breed.

The accuracy of EBVs was higher for the MC breed compared with the Ban breed and higher for sows compared with boars (table 3). It can be concluded that EBVs for Ban have to be considered as preliminary, but for MC sows accuracies of about 71% and 65% for NBT and

NBA, respectively, indicate that sows can be adequately discriminated according to their genetic merit.

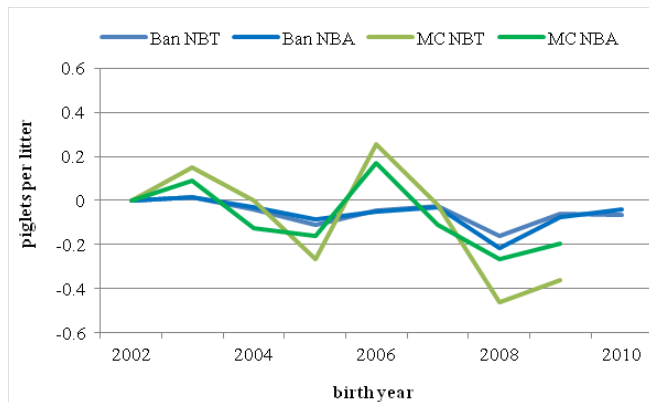


Figure 1: Genetic trends number of piglets born in total per litter (NBT) and number of piglets born alive per litter (NBA) for the Ban breed (birth year cohorts 2002-2010) and the Mong Cai (MC) breed (birth year cohorts 2002-2009).

Table 3. Accuracies (r_{IT}) of estimated breeding values for number of piglets born in total per litter (NBT) and number of piglets born alive per litter (NBA) for males and females of the Ban and Mong Cai (MC) breed.

		Accuracy in %		
		N	NBT	NBA
Ban	male	26	30	27
	female	376	44	39
MC	male	14	56	53
	female	243	71	66

Genetic improvement is a long-term investment whereas smallholders keeping only 1-2 sows are dependent on immediate returns. Thus, generating profit from marketing is essential and determines farmers' willingness to adopt new technologies (Winter and Doyle (2008)) and to participate in the breeding program. The pork markets in the region are highly dynamic and increasingly demand lean meat. Consequently farmers shifted to the use of "super lean" Piétrain x Duroc crosses as sire breeds. The demand situation for MC purebreds and crossbreds decreased recently due to their high fat percentage, but meat from pure Ban and Ban crosses fetches high prices in niche markets. Thus, at present a breeding program focussing on the improvement of prolificacy of the Ban breed appears to be more promising and acceptable for farmers as compared with the MC breed. Genetic gain in litter traits of the Ban breed would be limited due to low heritabilities and limited selection intensity. Elevating pedigree recording at least to the current level of MC might improve the situation. For this purpose boar keepers and breeders have to be trained in pedigree recording and husbandry-related aspects. Institutional support in data recording, planning of mating and genetic evaluation has to be ensured for a long-term

period, whereas cost-benefits have to be critically monitored. In designing the breeding program it should be considered to link several villages to allow for higher selection intensity and to avoid inbreeding (Gizaw et al. (2009)). Then a breeding program to enhance prolificacy of the local Ban breed can contribute to improve the meat production potential of Ban and ultimately improve livelihoods of remote mixed smallholder farmers.

Conclusion

In conclusion genetic variation in litter traits of local Vietnamese Ban and MC populations allow for BLUP based selection on prolificacy in the frame of a smallholder community-based breeding program. Due to the current marketing situation setting up a breeding program for the Ban breed only is more promising, but pedigree recording remains to be improved to achieve an adequate accuracy of EBVs. For this, especially village boar keepers and breeders have to receive institutional and technical support.

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