Genetic parameters for piglet survival, litter size and birth weight or its variation within litter in sire and dam lines using Bayesian analysis

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ABSTRACT

Genetic parameters for survival at birth, litter size, birth weight and its variation within litter have been estimated in dam (D1, D2 and D3) and sire lines (S1 and S2) and genetic associations among these traits were examined. Genetic parameters, calculated as posterior means, were estimated at piglet (D1 and D2; 23,565 piglets) and litter level (all lines; 3497 litters) using a Bayesian approach. Posterior means of heritabilities for survival at piglet level (SVBP) were consistently low at 0.01, 0.06 to 0.07 and 0.04 to 0.06 for direct (h^2_d), maternal (h^2_m) and total (h^2_t) genetic effects, respectively, with positive posterior means of correlations between the direct and maternal effect (r_{g-dm}). For survival at litter level (SVBL) heritabilities were between 0.05 and 0.20, with highest estimates in lines with lowest birth weight. For individual piglet birth weight (IBW) heritabilities were substantially higher than for SVBP, ranging from 0.13 to 0.19 (h^2_d), 0.16 to 0.28 (h^2_m) and 0.08 to 0.28 (h^2_t). Heritabilities for average litter birth weight (ALBW) ranged from 0.23 to 0.34, while heritabilities for variation of birth weight within litter (STD) ranged from 0.10 to 0.27. Heritabilities for number born in total (NBT) ranged from 0.11 to 0.16. Genetic associations between SVBL and NBT varied from favourable at 0.39 (D1) to unfavourable at −0.22 (D2). Genetic correlations of SVBL with ALBW and STD were mostly favourable (0.22 to 0.55 and −0.18 to −0.52, respectively) except for SVBL-ALBW in D1 (−0.50) and SVBL–STD in S2 (0.48). In D1 favourable genetic correlations were estimated between direct or maternal effects of SVBP and IBW whereas those for D2 were unfavourable. Consistently negative correlations were estimated between direct effects of SVBP and maternal effects of IBW. Adjustment for NBT resulted in slightly higher h^2_d and h^2_m for SVBP, with unfavourable r_{g-dm}.

Selection for survival is expected to be successful because all lines showed considerable variation for this trait and relatively high heritabilities, in particular in lines with low ALBW. Maternal heritabilities of IBW were mostly at moderate magnitude and thus of interest for selection. For most lines, the correlations between traits indicate that selection on either IBW or ALBW is indirectly increasing survival at birth. The variation in heritabilities among lines indicates that the strategy of selection for an optimal birth weight with lowest variation within litter should be considered per line individually to maximise overall genetic improvement in piglet survival and growth.

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1. Introduction

According to a recent review, piglet mortality from birth to weaning internationally is in the range from 10 to 25% (Alonso-Spilsbury et al., 2007). For the UK, mean stillbirth rate is reported at 6.7%, whereas mean mortality

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of live born pigs before weaning is given at 12.6% (BPEX, 2008). This scale of piglet mortality forms a considerable economic loss for pig producers and raises animal welfare concerns. The recent selection pressure on litter size and lean tissue growth may even increase mortality of piglets if it is not accompanied by selection for survival (e.g. Knap, 2008). In the past, pig producers have tried to increase piglet survival by improving the husbandry conditions for piglets, but a limit in reduction in mortality through these means has apparently been reached (Edwards, 2002). Recently, extensive research has been carried out to examine the potential to increase piglet survival by genetic improvement. Heritabilities of traits related to piglet survival have been estimated, and even though they are generally low, the genetic variation is large enough to provide improvement through breeding (Knol et al., 2002; Su et al., 2008; Roehe et al., 2009). Breeding goal differences, with emphasis on reproduction traits within dam lines and on production traits within sire lines, may result in different genetic parameters between lines (Knol et al., 2002; Kapell et al., 2009).

Various studies have examined the survivability of piglets at birth and from birth to weaning using linear models based on a restricted maximum likelihood approach (REML) (Knol et al., 2002; Serenius et al., 2004). However, for binomial traits, such as survival (alive or dead), threshold models have been shown to be more appropriate (Sorensen et al., 1995). Software has recently been developed using Bayesian methodology to estimate genetic (co)variances amongst categorical threshold traits, as well as between threshold traits and continuous linear traits. This allows the threshold characteristic of individual piglet survival at birth to be taken into account, and provides an opportunity to examine the precision of estimation of genetic parameters by using Bayesian confidence intervals. Additionally, birth weight and survival at birth have often only been analysed at the litter level, as a trait of the dam, while few studies took the genetic component of the individual piglet into account (Grandinson et al., 2002; Su et al., 2008; Roehe et al., 2009). However, individual piglet birth weight may be closely related to piglet survival and might therefore be used to indirectly improve piglet survival at birth.

The aim of this study was to estimate heritabilities and genetic correlations of survival and weight traits at birth, both at litter level as well as at individual piglet level, for different breeds. These genetic parameters give insight into the efficiency of selection for survival, thus allowing the examination of whether additional selection on piglet birth weight can contribute to improvement of piglet survival at birth over and above direct selection on survival.

2. Materials and methods

2.1. Material

Data on piglet survival, litter size and individual birth weight in several sire and dam lines were provided by the pig breeding company PIC. Data were available for 36,217 purebred piglets born out of 3497 litters between January 2005 and September 2006 on two farms in China and one in Brazil. One farm, in China, was located in a northerly continental, monsoonal climate, the two remaining farms, in China and

Brazil, in a humid subtropical climate. Data included birth weight measured individually on piglets born alive, and for each litter the numbers of piglets born in total, born alive and stillborn was known. Information regarding crossfostering or litters with no piglets born alive was not available. The piglets came from five different purebred lines: dam line D1 (955 litters, average 1.4 litters/dam), dam line D2 (1302 litters, average 1.4 litters/dam), dam line D3 (504 litters, average 1.7 litters/dam), sire line S1 (253 litters, average 1.2 litters/dam) and sire line S2 (483 litters, average 1.3 litters/dam). The three dam lines were bred with the main emphasis on litter size and piglet survival, with additional emphasis on growth rate in D3. Sire line S1 was bred with emphasis on body leanness; sire line S2 with emphasis on growth rate, feed efficiency and growing pig survival.

Four traits were analysed at litter level: percentage survival at birth (SVBL), number born in total (NBT), average birth weight of piglets within litter (ALBW) and standard deviation of birth weight within litter (STD). At individual piglet level, two traits were analysed: individual piglet survival at birth (SVBP) and individual piglet birth weight (IBW). SVBL was calculated as the number of piglets born alive divided by the number of piglets born in total. ALBW was calculated as the sum of all birth weights per litter divided by the number of piglets with known birth weight (stillborn piglets and piglets with missing birth weight were not considered). For STD only litters with a minimum of five piglets with known birth weight were included. Pre-weaning survival after farrowing was not included in this analysis due to very high piglet survival levels (98% on average) on these farms, which led to very low levels of detectable genetic variation in the data.

The quality of pedigree files was checked with Relax2 (Strandén and Vuori, 2006) after which pedigree files were matched per line to the animals in the data set to eliminate redundant animals. No limit was set for the depth of the pedigree and pedigrees consisted of 2929 (D1), 3326 (D2), 1591 (D3), 566 (S1) and 1406 (S2) animals at litter level.

2.2. Statistical analyses

2.2.1. Analysis at litter level

The traits SVBL, NBT, ALBW and STD were analysed for all five lines separately. In addition, to increase the number of observations and decrease the confidence interval of estimates, the two dam lines D1 and D2, with the same breeding goals, were analyzed jointly as D12. In a preliminary analysis, fixed effects were tested per trait and line for significance using the procedures MIXED or GENMOD (SAS, 2002). Based on these analyses parity, gestation length and batch were included in the models. Batches were optimized in preliminary analyses and fitted in the model based on farm, year and quarter of year (starting with January to March). In the dam lines, parities one to five were considered as separate classes, parities six and higher were grouped together. In D12, parities one to seven were considered separate and parities eight and higher were grouped together. In the sire lines, only two parity-classes were significant: either first parity or higher parities. Gestation length was grouped as ≤ 113, 114, …, 117, ≥ 118 for D1 and D2, ≤ 114, 115, …, 117, ≥ 118 for D3, ≤ 112, 113, 117, ≥ 118 for D12, ≤ 113, 114, 115, ≥ 116 for S1 and ≤ 115 or ≥ 116 for S2. All effects were grouped such that sufficiently high numbers of