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Interval from last insemination to culling: I. The genetic background in crossbred sows

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ABSTRACT

Improving longevity of sows is hampered by the lack of accurate and early recording of factors that contribute to reduced longevity. Besides, phenotypic data of parity number at culling or culling reason are potentially collected in purebred individuals, while these animals are not able to show full potential of their longevity due to EBVs, which makes the culling to take place earlier. In contrast to crossbred animals, of which usually very little information is collected, as phenotypes are expensive and difficult to obtain. Longevity is influenced by several culling reasons of which fertility and leg weakness are known to be the most important, although culling reason is unknown or unreliably recorded in crossbreds. To distinguish different reasons for (in)voluntary culling, interval from last insemination to culling (IL2C) might be able to function as an indicator, which could potentially enable us to breed for sow able to fulfil a complete production cycle. The aim is to quantify and understand the mechanism of parity number at culling by analysing the IL2C, in relation to parity number at culling. The results show that IL2C is a heritable trait that can be used in selection, in addition to parity number at culling. Parity number at culling and IL2C are not significantly correlated, which shows the potential to take both traits into account in breeding. By combining improvement of IL2C with improved longevity, economics and welfare of crossbred sows will even further be increased.

Introduction

Longevity in sows is determined by voluntary and involuntary culling. Improving parity number at culling of sows is hampered by the lack of accurate and early recording of factors causing involuntary culling. While voluntary culling is mainly determined by production ability, involuntary culling has many reasons and usually occurs when this is economically not preferable, e.g. dying during pregnancy or starting-up in early lactation. Preferably sows are culled at the end of the cycle; i.e. after weaning. Culling at any other time point during the cycle incurs costs for the farmer and has welfare implications for the sow.

The heritability of parity number at culling, sometimes defined as stayability (binary), varies from 0.03 to 0.25, and is related with factors such as gilt back fat thickness, size at and age at first farrowing and leg score (Engblom et al., 2009; Serenius et al., 2006b; Serenius and Stalder, 2007). Although it is known that leg weakness and fertility problems affect culling of crossbred sows, leg weakness cannot be related to parity number at culling based on culling reason, as accurate recording of culling reason is often lacking. Data obtained on crossbreds is more informative because culling in purebreds is not only determined by production ability but also based on their genetic ability (their estimated breeding value).

Little is known on the reasons for involuntary culling and the correlation with the time point in a reproductive cycle at which they are culled. Culling around 2–4 weeks after insemination reflect a decision of the farmer not to re-inseminate the sow, i.e. culling for fertility reasons. Culling around 15 or 16 weeks reflects a problem with farrowing, getting lactation started or disability to care for the piglets due to leg weakness or feeding (Dourmad et al., 1994; Lucia et al., 2000).

Interval from last insemination to culling (IL2C) is hypothesised to be a predictor for the culling reason. If being culled at a specific time point in a cycle is heritable and taken into account in breeding, sows can be selected for their ability to fulfil the complete parity until weaning piglets. Therefore, a genetic analysis is performed on IL2C. Little is known about genetic background of IL2C, as to the authors knowledge no literature is available. Therefore, the aim of this study is to quantify and further understand the genetic mechanism of longevity by gaining insight in the interval from last insemination to culling.

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Materials and methods

Population

Data on a total of 111,987 F1 (reciprocal) crossbred sows, 43,973 NNZZ and 68,014 ZZNN (N=Landrace and Z=Yorkshire), were analysed, made available by the pig breeding company TOPIGS BV. The sows were kept on 189 farms in the Netherlands and descended from 24,815 purebred dams and 1372 purebred sires. All sows were born and culled between 2005 and 2012. The time period was chosen to avoid censoring of data from sows born before this period, and culled within the period having incomplete sib information that would not be taken into account e.g. already being culled.

Phenotypes

Longevity is expressed as the parity number of the sow at culling. Longevity varies between 1 and 16 with a mean of 4.3 (SD 2.6). Stayability 2 and 5, often used in the literature and in practice to select in breeding herds at early age, represents the (binary expression of the) ability of a sow to reach a certain parity. Stay2 and Stay5 represent whether the second or fifth parity is reached.

IL2C is expressed as the interval from insemination to culling in number of weeks. IL2C is divided into 5 categories, explaining the two visual peaks of culling in 3 to 6 weeks after last insemination and 19 to 23 weeks after last insemination (Fig. 1), and thereby the period before, in between and after the peaks. For each of these five categories, a binary trait was constructed (culled (1) or not culled (0)).

Category 1 (week 1–3) explaining involuntary culling before scanning on pregnancy; category 2 (week 4–6) explaining culled sows due to fertility, e.g. scanned empty; category 3 (week 7–18) explaining involuntary culled sows which die or have severe (leg) problems or sows which have problems getting started in early lactation and or leg problems, which enables them not to fulfil parity till weaning; category 4 (week 19–21) explaining sows culled for voluntary reasons (at the end of a cycle); and category 5 (week ≥ 22) explaining sows culled for production reasons and or fertility reasons e.g. not coming into heat for the next cycle (Fig. 1).

Statistical analysis

The logistic regression model to estimate genetic parameters used is:

$$\text{Prob}(Y_{ijkl} = 1) = \exp(\mu + \text{line}_i + \text{farm}_j + \text{YSbirth}_k + \text{sow}_l + e_{ijkl})$$

where Y_{ijkl} represents the IL2C (expressed in culling category 1–5, or as binary trait for each of the culling categories separately (0/1), longevity (expressed as maximum parity) or stayability 2 or 5, binary trait of ability to reach corresponding parity of the lth sow, μ is the intercept of the model. Line$_i$ is the fixed effect of genetic (reciprocal) cross of the lth sow (l= NNZZ, ZZNN), farm$_j$ represents the fixed effect of farm j at which the sow is kept (j=1, 2, …, 189), YSbirth$_k$ accounts for the random year-season effect of birth of the lth sows (k=1, 2, …) and sow$_l$ is the random identification of the lth sow (l=1, 2, …, 111987), and e_{ijkl} represents the random residual. A logistic regression model is also used for the binary traits of culling category 1 till 5. Analyses are performed using SAS (SAS Institute Inc., 2010) and ASReml (Gilmour et al., 2009). Random sows effects are assumed to be distributed as $N(0,A^*\sigma_a{}^2)$. In the logistic regression model the scale of the sow effects is fixed by setting the residual variance to 3.289. As a variation on the above presented model, IL2C is additionally corrected for parity number at culling. Correction for parity number at culling would indicate the IL2C effect without indirect effects due to certain correction between the two traits.

Parity number at culling and culling category 1–5 (cull class) was also analysed using a linear model with the same factors as described in the model above but the residuals were assumed to be distributed as $N(0,I^*\sigma_e{}^2)$.

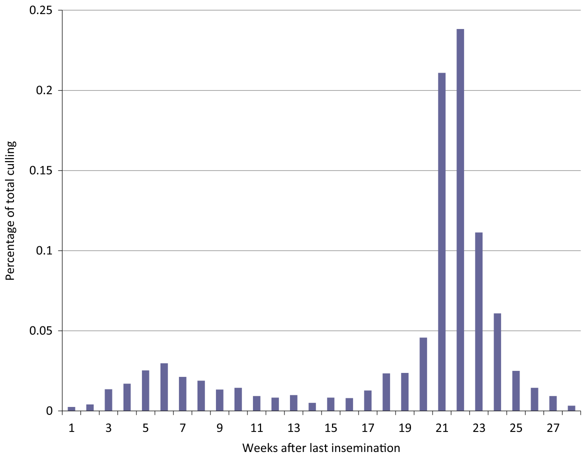

Fig. 1. The interval from last insemination to culling, expressed in weeks. The trait is divided in 5 culling time categories based on two distinct culling peaks in data, in categories 2 and 4.

Results

Production means

The peak production of total piglets born is 14.72 in the 5th parity, while the total number of piglets weaned has a peak production of 11.66 in the 2nd and 3th parity (Fig. 2). The ZZNN crossbred sows show to have to highest average number of piglets born, although the reciprocal NNZZ crossbred sows have a slightly (NS) higher average number of total piglets weaned.

Longevity and stayability

Results show that parity number at culling seems rather normally distributed and has a heritability of 0.16 (Fig. 3). Stayability (stay2 and stay5) both show a heritability of 0.11 (Tables 1 and 2).

IL2C

Analysis revealed (Table 1) that IL2C, expressed as 5 categories, has a heritability of 0.05. Combining parity number at culling and IL2C in bivariate analyses shows the genetic correlation of 0.2 (not significantly different from 0). When IL2C (1–5) is corrected for

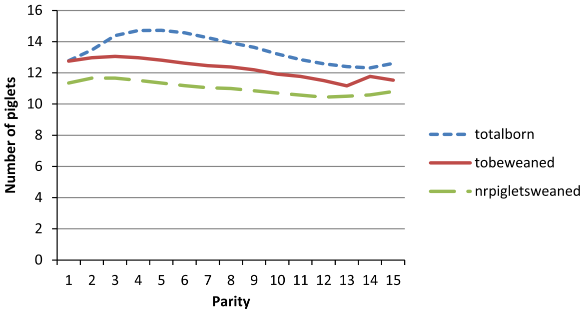

Fig. 2. Number of piglets born, to be weaned and weaned per parity**.** To be weaned contains the number of piglets after crossfostering has occurred.