Breeding Focus 2021 - Improving Reproduction

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Preface

“Breeding Focus 2021 – Improving reproduction” is the fourth workshop in the series. The Breeding Focus series was developed to provide an opportunity for exchange between industry and research across a number of agricultural industry sectors. With this goal in mind, workshops have included presentations across multiple agriculturally relevant animal species to take participants outside their area of expertise and encourage them to think outside the box. Reproduction is a main driver for profitability and genetic gain. We will discuss existing knowledge, identify gaps and explore genetic and management strategies to improve reproduction further in multiple species.

Successful reproduction is a complex characteristic comprising the formation of reproductive cells, successful mating and fertilisation, embryonic and fetal growth and eventually a successful birthing event. In livestock species, reproduction traits have mostly low heritabilities, which makes it challenging to improve reproduction as part of a multiple trait breeding objective. The complexity arises not just from the cascade of processes required to result in successful reproduction, but the relevant traits are different in males and females and they are influenced through health and fitness, nutrition, climate and other environmental and management factors.

Challenges to the improvement of reproduction can vary widely for different species. For less domesticated species such as abalone, the ability to produce and reproduce the animals in captivity presents a major challenge. In bees, reproduction has not been given great attention and little research has been undertaken to understand the underlying genetics of drone and queen reproduction. However, in all industries reproduction is recognised as the basis for genetic and economic gain. It directly influences the selection intensity that can be applied. It also determines how many animals are not required for replacement and can be sold. In all industries, irrespective of the challenge, cost-effective and easy to measure phenotypes of reasonable heritability are central. New technologies and approaches enable the development of novel phenotypes for genetic improvement which will be combined with a growing amount of genomic data in livestock species and together these developments provide new and exciting opportunities to improve reproduction further.

We would like to thank everyone who has contributed to this event for their time and effort: the authors for their contributions to the book and presentations, the reviewers who all readily agreed to critique the manuscripts. We would like to express a special thanks to Kathy Dobos for her contributions into the organisation of this workshop and the publication. Thank you!

Susanne Hermesch and Sonja Dominik

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Improving reproductive performance in pigs

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Abstract

With the introduction of best linear unbiased prediction (BLUP), pig breeding companies have been able to effectively select for improved reproductive performance in pig production. The improvement in litter size, however, has come at a cost, with an increase in both stillbirths and early neonatal deaths, along with decrease in individual piglet birth weights. Consequently, the potential number of piglets weaned is not reached. To balance these detrimental consequences, breeding companies needed to include alternative traits into breeding objectives. This paper initially explores how traditional litter size traits: total born (TB), number of piglets born alive (NBA), number of piglets alive on day five (LS5) after farrowing have been implemented into breeding programs. Then, we look at how litter size traits have been balanced in breeding programs, by focusing on survival traits, including average piglet birth weight, and pre- and post-weaning survival of progeny. Indirect traits, such as antibody response to vaccination against PRRSV, immune competence and E-coli resistance are also important to maximise sow performance and progeny survival in the presence of disease. Lastly, we briefly discuss the inclusion of sow reproductive traits, such as wean to conception interval and longevity. This paper gives a general overview of how overall reproductive performance has been improved in pig production globally.

Introduction

A key indicator of reproductive performance in pig production is weaned piglets per sow per year, achieved through maximising piglets alive at birth and their ability to survive until weaning, along with the rebreeding performance of sows. Although management and environment largely influence these traits, they are also under the control of genes, and can be improved through selection (van der Lende *et al.* 2002). Over the last three decades, the target number of weaned piglets in commercial herds across the world has increased from 20 to 30 piglets/sow per year and is still increasing (Koketsu *et al.* 2017). This change is largely due to increased litter size following the introduction of best linear unbiased prediction (BLUP) for more accurate selection. Averaged across 28 Australian populations, annual genetic gain was + 0.07 pigs/litter, to +0.18 pigs/litter for the top 25% of herds (Harper *et al.* 2017).

Increased litter size also results in some undesirable consequences for both sows and piglets (Ward *et al.* 2020): both the number of stillborn piglets and pre-weaning mortality increase, leading to ethical concerns (Baxter and Edwards 2018) and economic losses. If the increase in litter size is not accompanied by management alterations, including meeting sow nutritional requirements (Bunter *et al.* 2018), the additional negative effect results in reduced sow longevity, as sows utilise their body reserves to raise piglets during gestation and lactation (Tholen *et al.* 1996). To achieve the full potential of selection for larger litter size, resulting in more piglets weaned, but without the above-mentioned detrimental consequences, additional traits had to be explored. Since the number of weaned piglets is typically not a heritable trait, mostly due to cross-fostering practices, breeding programs had to find alternative approaches to increase this number indirectly. The traits that will be discussed in detail in this paper include average piglet birth weight, piglet survival before and after weaning, E-coli resistance, immune competence and sow traits such as wean to conception interval and longevity.

Strategies to improve litter size

Effective selection for litter size traits was first implemented in the eighties, when BLUP software became available to pig breeders (Bunter 2009). Prior to that, selection for reproductive performance was not very effective, because reproductive traits are lowly heritable, sex-limited traits and do not respond well to simple phenotypic selection. With the use of BLUP, fair comparison of many more individuals was possible: repeated records from both purebred and cross-bred sows and well-structured pedigrees resulted in accurate breeding values for young selection candidates. Large populations and large scale data recording are required to achieve genetic change in litter size traits (Zak *et al.* 2017). To achieve large enough populations, and potentially increase the rate of genetic gain, breeding companies have facilitated an open nucleus breeding program, whereby sows can belong to more than one tier. With this structure, the best individuals from the multiplier (second) tier of the breeding pyramid can also be used in the nucleus (top tier). By having nucleus and multiplication functions within the same breeding facility or farm, sows are able to move between pure (nucleus) and crossbred (multiplier) matings, depending on their genetic merit after reproductive performance has been assessed, without posing a risk to biosecurity. According to James (1977), the rate of genetic gain could increase by 10 to 15%, along with a reduction in inbreeding by 50%, by using this approach. Moreover, data from pedigreed crossbred sows can also contribute to breeding values of nucleus animals. This can be important where the genetic correlation between purebred and crossbred sow performance is <1. Since the majority of commercial sows are crossbred, this is relevant for the pig industry.

Which trait definition?

Selection for increased litter size implies a selection for total number of piglets born (TB), which, by definition included live born and still born piglets. The assumption was that increasing litter size at farrowing would also proportionally increase pigs weaned. Selection for increased TB resulted in an increase of 0.2 piglets per year (Kemp *et al.* 2018) but, at the same time, it was accompanied with an increase in stillbirths, early neonatal deaths and a decrease in individual piglet birth weights. Ultimately, the potential for increasing number of weaned piglets was not fully reached. In order to find a balanced increase in litter size, with a reduction in these detrimental consequences, breeding companies either included additional traits as selection criteria with TB or altered the litter size trait used in breeding programs. Additional or alternative (to TB) traits typically include a combination of: number of piglets born alive (NBA); number of piglets alive on day five (LS5) post-farrowing; number of stillborn piglets (SB); indicator traits such as antibody response to vaccinations; piglet birth weight (APBW); and/or piglet survival traits (the latter two are discussed in the next section of this paper). The decision about which traits to incorporate into breeding programs depends on the ease and accuracy of measurement and cost-benefits. It is relatively accurate to record TB, NBA or SB, as this information is easily obtained from production software, whereas some other traits, such as individual piglet birth weight require additional recording.

In Australia, selection emphasis has been on NBA rather than TB, which resulted in improvements in litter size, with less consequence than TB for stillborn piglets or other birth complications (Bunter 2009). Generally, across studies and populations, heritability for NBA is low, around 0.10 (Bidanel 2011). Several studies have demonstrated that NBA is a genetically different trait for the first vs later parities: the genetic correlation between NBA recorded in first and later parities ranges from 0.50 to 0.65 (Tholen *et al.* 1996; Hermesch *et al.* 2001). In contrast, the genetic correlation between second and third parities was 0.95. The analysis of NBA in the first parity as a separate trait to NBA in later parities is also supported by the basic understanding of how the physiological development of reproductive organs, ovulation rate, fertilisation of oocytes and embryo and foetal survival and development differs with parity (Oh *et al.* 2005).

Genetic improvement for first parity (NBA1) and later parity NBA (NBA2) from a commercial nucleus and multiplier herd in Australia can be seen in Figure 1. A total response of 1.83 piglets in first parity and 2.07 piglets in later parities was achieved between 2006 and 2019 for a Large White herd. In combination with prior response to selection (not shown), observed means for the number of pigs recorded at 21 days have increased from <8 in the 1980's to >10.5 in 2020 (data unpublished from commercial nucleus performance). However, it can be difficult to provide the optimal management and environment for this level of genetic change. For example, Figure 1 (a) shows a negative genetic trend for piglet birth weight (discussed further in this paper). Further, Figure 2 illustrates a detrimental environmental trend for litter size across years in some, but not all, farms which are comparable due to common genetics. Therefore, differences in management practices across farms can result in different changes to phenotypic performance despite common genetic trends. Therefore, it needs to be clearly established what management practices need to be improved to support sows of modern genotypes, and this is beyond the scope of this paper.

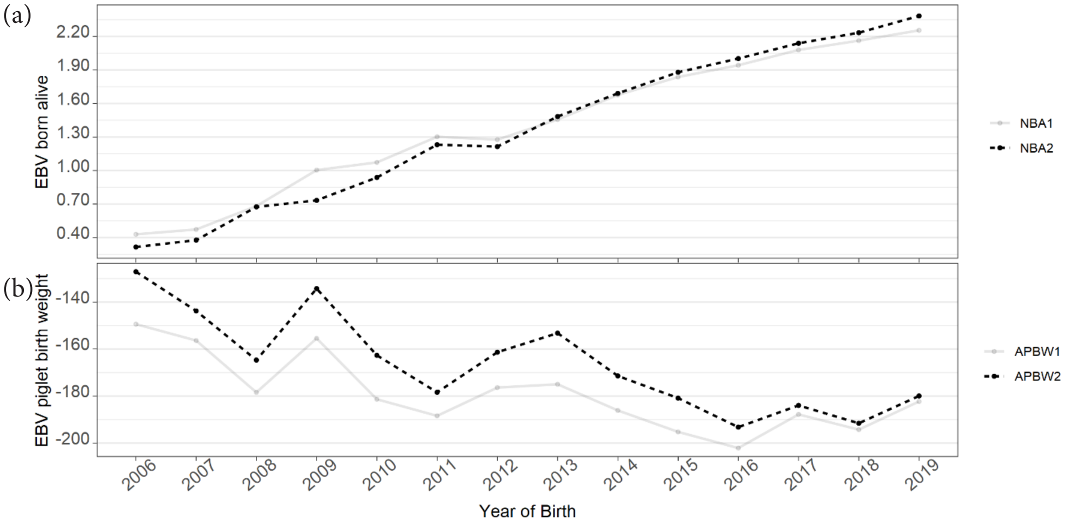

Figure 1. Genetic trend for number of piglets born alive (a) for first parity (NBA1) and later parities (NBA2) and average piglet birth weight (b) for first parity (grams: APBW1) and later parity (grams: APBW2) over time based on year of birth (2006 to 2019)

Figure 2. Approximate environmental trend (phenotypic minus genetic) for number born alive (NBA) for sows across all parities from a single selection line recorded in different production farms (1,2,3,4,5 and 6)

Along with Australian breeders, the primary goal of the much larger Danish pig industry, was also selection for reproductive performance, i.e. litter size. This industry was successful in achieving very large litter sizes through intensive selection across large sow populations, but consequently suffered increased pre-weaning mortality in early lactation. Around 2004, Danish breeding objectives started considering piglet survival and developed a new selection criterion, namely LS5, to ultimately improve the number of piglets weaned. Selecting for LS5 resulted in an overall improvement in total number of piglets born, pre-weaning piglet survival and litter size at weaning (Su *et al.* 2007). However, this strategy has no direct focus on characteristics of the nurse sow to improve piglet survival, as cross–fostered piglets were excluded from the analysis. This could be important in situations where late lactation issues impact piglet mortality (Bunter 2009).

More recently, breeding companies have explored the use of other indicator traits to make advances in litter size, when diseases affecting reproductive performance are endemic. An example of this is the ability of sows to maintain NBA when infected with viral porcine reproductive and respiratory syndrome (PRRSV), which is a heritable trait (Lewis *et al.* 2009). Porcine reproductive and respiratory syndrome (PRRS) induces reproductive failure in sows and results in high mortality rates of piglets in both pre- and post-weaning periods. Porcine reproductive and respiratory syndrome has been reported to be the most economically significant disease in the US (www.thepigsite.co) and globally, but this disease is absent from Australia. A recent study conducted by Sanglard *et al.* (2020) showed that the antibody response to PRRSV vaccination was moderately heritable (0.34) and had favourable genetic correlations with NBA at parity 1 (0.61), pre-weaning mortality at parity 2 (-0.70), number of stillborn at parity 3 (-0.84) and the presence of mummified piglets at parity 3 (-0.83). This study demonstrated that the antibody response to vaccination against PRRSV could be used as an indicator trait to obtain faster genetic progress in litter size and survival at the commercial level, in populations where PRRS is endemic. However, it is unclear if a similar response might be observed in other populations (eg Australia is PRRS free) not affected by PRRS directly.

Strategies to improve piglet survival

As previously mentioned, selection for increased litter size within maternal lines, along with concurrent selection for desirable attributes for growing pigs (e.g. efficient lean growth), has resulted in a number of survival issues for the sow and her progeny. These include a decline in sow longevity, increased still births and pre-weaning piglet mortality (Bunter 2009). This section focuses on how breeding companies have been able to genetically improve survival of progeny.

Selecting for average piglet birth weight (APBW)

In litter bearing species, offspring birth weight is generally a trait of the dam rather than each individual offspring (Alves *et al.* 2018), and is therefore typically evaluated as a sow trait. The antagonistic effect of litter size on birth weight is phenotypically linear, but the magnitude of the negative genetic correlation varies between studies, averaging -0.30 across all parities (Tholen *et al.* 1996). In comparison, the implication of birth weight for piglet survival is non-linear. Individual birth weight is the primary determinant for the pre-weaning survival of individual piglets and is also positively associated with post-weaning growth and survival (Alves *et al.* 2018). Hermesch *et al.* (2001) reported that litter mortality, defined as the number of piglets that died until weaning, also had an unfavourable genetic correlation of -0.46±0.20 with APBW. These results clearly demonstrate, along with moderate heritabilities, ~0.31 (Hermesch *et al.* (2001), that birth weight should be included as a selection criterion in breeding programs to maintain the weight of piglets at birth and improve pre-weaning survival when selecting for increased litter size. However, the relative weighting of both NBA and APBW in the breeding objective needs to ensure the right balance so that heavier pigs are not selected from smaller litters.

The genetic trend in average birth weight using a model that accounted for the effect of litter size on APBW is shown in Figure 1(b). From 2006 to 2016 a reduction of 40 grams per additional piglet born alive was observed for older parity litters (APBW2). Based on estimates of genetic parameters for all traits used as selection criteria, the expected decline in birth weight resulting from increased litter size over the same period was lower at 33.6 grams. This undesirable outcome led to a change in the breeding objective in 2016, to place more emphasis on APBW. Subsequently, there was a 10-gram increase in APBW2 concurrent with a 0.30 increase in NBA2. The change in piglet weight without concurrent selection for NBA and APBW gave a predicted reduction of 47.2 grams per piglet. This outcome demonstrates that with effective data recording it is possible to reduce the magnitude of some detrimental associations between traits, from concurrent selection of traits with antagonistic correlations. However, careful monitoring of results is required as selection progresses.

Direct selection for pre- and post-weaning survival

In a similar manner, it is also possible to simultaneously improve litter size and enhance the ability of piglets to survive (Mesa *et al.* 2006), despite the unfavourable genetic correlations also between these two traits (Bunter 2009). However, to achieve this, recording information on individual piglets is necessary, using individual identification from birth. Survival of piglets is typically affected by multiple environmental and genetic factors including the piglet's biological dam, the nurse sow, and the genotype of the piglet itself (Knol *et al.* 2002). In order to estimate breeding values for pre-weaning mortality (opposite to piglet survival), Harper *et al.* (2019) tested different strategies and models. They demonstrated that the most suitable model for estimating breeding values for pre-weaning mortality included: 1. direct additive effects of the piglet, 2. common litter effects of both the nurse sow and the biological dam, accommodating the effects of both the lactation and gestation environment experienced by each litter of piglets respectively, and 3. maternal effects, accommodating repeated records and maternal genetic effects of the nurse sow. This study allowed for the accurate separation of direct and maternal effects as >400,000 piglets were recorded for individual cross-fostering and mortality events. Harper *et al.* (2019) also demonstrated that a more parsimonious nurse sow model was appropriate for post-weaning mortality, including the common nurse and biological litter effects, accounting for any carry-over from prior lactation and gestation periods respectively. In contrast Su *et al.* (2007) did not use data for cross-fostered piglets and a biological dam model was used when evaluating litter size at day 5. Analysis of individual survival is enhanced by including systematic effects such as individual birth weight, gestation length, cross-fostering and dam parity details in the model for analysis. Excluding gestation length, birth weight and litter size from models results in an increase in phenotypic variance for pre-weaning mortality and maternally derived variance ratios (Harper *et al.* 2019).

Estimates of variance ratios for direct and maternal pre-wean mortality are 0.02±0.002 and 0.01±0.002 respectively, while the corresponding heritability for post-weaning mortality is 0.02±0.002 (Harper *et al.* 2019). Although these estimates are very low, genetic variation exists and improvements in pre- and post- weaning mortality are possible. The Australian commercial breeding program and sow line showcased in Figure 1 have demonstrated a 3.5%, 1.7% and 1.3% improvement in estimated breeding values for direct and maternal pre-weaning and direct post weaning survival, between 2015 and 2019. For convenience, these differences are expressed as survival, rather than mortality. Correlations between breeding values (not shown) demonstrated that improvements in pre-weaning survival (direct or maternal) were also mirrored by favourable increases in breeding values for litter weight recorded prior to weaning and for post-weaning survival.

Potential of immune competence to improve piglet survival

As noted above, sows that responded well to PRRSV vaccination were genetically more likely to have improved reproductive performance in populations where this disease occurs. Therefore, an alternative to selection based on mortality outcomes is to consider aspects of immune competence generally. Immune competence is the ability of animals to mount an immune response to foreign antigens and render them harmless (Mallard *et al.* 1992). It can be assessed through the combined measures of an animals ability to mount both antibody mediated (Ab-IR) and cell mediated (Cell-IR) immune response (Mallard *et al.* 1992; Wilkie and Mallard 1999). Selection for enhanced overall immune competence has been demonstrated in dairy cattle (Mallard *et al.* 2015) and pigs (Wilkie and Mallard 1999). As a result, overall health and performance improved (Hine *et al.* 2012), by increasing the ability to cope with a variety of disease challenges and through improved responses to commonly used vaccines.

Immune competence generally also has implications for progeny survival (Harper *et al.* 2018). These authors investigated associations between the immune competence phenotype for boars and independent EBVs for their progeny survival. Significant improvement in pre-weaning survival breeding values occurred for progeny of boars with higher Cell-IR and overall immune response (combination of Ab-IR and Cell-IR). However, there was no significant association between progeny survival and boar (sire) Ab-IR only phenotypes. A later study (data not published) evaluated all progeny for mortality and demonstrated an ongoing tendency for increased progeny survival in the post-weaning phase (up to 70 days of age) for sires with high Cell-IR phenotypes.

To explore this further, 87 boars that were evaluated for immune competence phenotypes, as outlined in Harper *et al.* (2018), produced 1571 pure bred daughters that were selected as replacement females in a commercial breeding program. These daughters were assessed for their own reproductive performance in their first litter, along with the number of piglets weaned (NWEAN) being the trait of interest. As sire Cell-IR phenotype increased, NWEAN of daughters in their first litter also improved by 0.37 piglets. The pure- and cross-bred progeny from the daughters first litter (N=11,058) were also evaluated for survival. Logistic regression was performed to analyse individual pre-weaning piglet survival (mortality EBVs expressed as survival for convenience) and the only immune competence phenotype that was found to be significant (p=0.04) was Cell-IR. As sire Cell-IR phenotype increased, a 4% improvement in pre-weaning survival of progeny from their daughters was also observed. These results support that Cell-IR has strong associations with pre-weaning survival, as also outlined in the previously mentioned study (Harper *et al.* 2018). Inherited immune competence attributes positively impact on the reproductive performance of daughters, through improvement in the number of weaned piglets.

Selecting for E-coli resistance

Enterotoxigenic *Escherichia coli* (*E. coli*) F4 fimbriae adhesions (K88) has long been a major cause of diarrhoea, and ultimately death in sucker and weaned pigs in Australia (van Breda 2017). Typically, *E. coli* is controlled through biosecurity and vaccination of sows to induce maternal antibodies to protect piglets. With larger litter sizes the amount of colostrum consumed and therefore the level of protection of piglets is reduced. However, some pigs are inherently resistant to neonatal *E. coli* diarrhoea, because they lack receptors on their epithelial outer cell wall to which the fimbriae bind (Baker *et al.* 1997). The F4 receptor as reported by Gibbons *et al.* (1977), was inherited as a dominant Mendelian trait, where the dominate allele is susceptible (S), expressed as a receptor for K88 and exhibits clinical infection, while the homozygous recessive (*ss*) pigs lack this receptor. The *ss* genotype does not enable K88 positive coliforms to adhere to the gut of the piglet, resulting in disease resistant animals.

The approach to test and select for *ss* genotype replacement animals was developed after the receptor gene for F4 *E. coli* was located on the pig chromosome 13, as further outlined in the review conducted by Xia *et al.* (2015). Subsequently, this approach was successfully implemented within a large commercial breeding program in Australia. Over an eight-year period (2012 to 2019), replacement gilts and boars with K88 susceptibility were excluded from selection. Actively selecting breeding stock with K88 resistance resulted in a 95% reduction in *E. coli* deaths recorded within the nucleus and multiplication operations. This application required careful consideration of both selection and management activities. For example, *E. coli* resistant (*ss*) sows do not develop and transfer F4-specific antibodies in their colostrum to offspring, and therefore heterozygous (Ss) piglets are un-protected from development of neonatal diarrhea (Fairbrother *et al.* 2005). Therefore, a vaccination program against *E. coli* was implemented during the time period where susceptible litters were possible.

Other sow traits

In production systems, regardless whether in a nucleus or commercial farm, one of the most common reasons for reproductive inefficiency is a prolonged wean to conception interval (WCI). This frequently occurs in sows between their first and second parity, having a detrimental effect on sow longevity, as previously reported in many studies. In order to reduce WCI trait and improve sow productive life, different traits have been investigated. These include: probability of re-mating sows within 7 days after weaning; farrowing interval between the first and second farrowing; and the number of days following the first farrowing to the second mating. Tholen *et al.* (1996) reported heritabilities of 0.10 for both WCI and farrowing interval. The same authors reported small antagonistic genetic correlations between WCI and NBA, APBW or 21-day litter weight in parity 1. These results highlight the necessity of including WCI into breeding programs, to balance litter size, APBW and subsequently a lifetime of reproductive performance. Direct selection for sow longevity or sow productive lifetime is also a possibility (Mote *et al.* 2020), although decisions must be made based on relatives performing in commercial environments, highlighting the need for well-managed data collection and the use of BLUP.

Summary

- Selection criteria representing survival for both sows and piglets in breeding programs is important as increasing reproductive performance can have negative correlated effects.
- Understanding the implications of the different trait definitions for selection criteria (e.g. TB vs NBA) is important for achieving more desirable outcomes.
- Birth weight should be included in breeding programs to maintain the weight of piglets at birth and improve pre-weaning survival while selecting for increased litter size. However, the weighting of both NBA and APBW in breeding objectives should be done with caution to ensure heavier pigs are not selected from smaller litters and requires ongoing monitoring.
- Selecting for pre- and post-weaning survival directly requires extensive data collection to enable accounting for cross-fostering and more accurate separation of direct and maternal effects to calculate estimated breeding values for survival traits. In this scenario, genetic improvement can be achieved directly for piglet survival.
- Immune competence phenotypes of sires have the potential to indirectly improve not only survival of their own progeny but also the maternal performance of their daughters.
- Including litter size, survival and other sow traits, in maternal line breeding objectives allows concurrent selection and simultaneous improvement in all traits even if antagonistic associations exist.

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