UNIVERSIDADE DE LISBOA

FACULDADE DE MEDICINA VETERINÁRIA

THE IMPORTANCE OF DATA ANALYSIS AND THE EFFECT OF SIRE LINE ON THE REPRODUCTIVE AND PRODUCTION PERFORMANCE OF AN IRISH PIG FARM

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Doutora Maria Rodrigues da Costa

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A IMPORTÂNCIA DA ANÁLISE DE DADOS E O EFEITO DA LINHA PATERNA NO DESEMPENHO REPRODUTIVO E PRODUTIVO DE UMA EXPLORAÇÃO DE PORCOS NA IRLANDA

Resumo

Este estudo teve como objetivo analisar o desempenho reprodutivo de uma exploração suína irlandesa e investigar o efeito da mudança da linha paterna no desempenho produtivo dos porcos. Dados relativos ao período de um ano, que contam com 222 porcas gestantes e 375 partos, foram colhidos e parâmetros de ninhada foram analisados por lote, por número de partos e por linha genética.

Os resultados mostraram que o número de partos e o peso médio ao nascimento afetaram significativamente o número de leitões mortos antes do desmame ($P < 0.001$) e o número de porcos desmamados ($P = 0.002$ e $P < 0.001$, respetivamente). A sobrevivência no pré desmame também foi afetada pelo número de partos e pelo peso individual ao nascimento ($P < 0.001$). A mudança de linha genética mostrou diferenças significativas na sobrevivência no pré desmame e no número de leitões mortos antes do desmame ($P < 0.001$), tendo tendência a ser estatisticamente diferente no número de porcos desmamados ($P = 0.064$). As causas de morte no pré desmame, como fome e esmagamento pela porca, também mostraram ser significativamente diferentes entre linhas genéticas ($P < 0.001$ e $P = 0.012$, respetivamente). Baseado nos resultados deste estudo, a mudança na genética da linha paterna não foi uma estratégia de gestão útil para esta exploração, visto ter levado a uma maior taxa de mortalidade pré desmame e um menor número total de porcos desmamados.

Este trabalho realça a importância de ter dados robustos para avaliação corporativa interna, monitorização e tomada de decisões, assim como o efeito da linha paterna no desempenho reprodutivo e produtivo de explorações suínas.

Palavras-chave: análise de dados, efeito parental, suíno, desempenho reprodutivo, produção

A IMPORTÂNCIA DA ANÁLISE DE DADOS E O EFEITO DA LINHA PATERNA NO DESEMPENHO REPRODUTIVO E PRODUTIVO DE UMA EXPLORAÇÃO DE PORCOS NA IRLANDA

Resumo Alargado

Com o aumento do consumo de produtos animais, os produtores pecuários têm sido cada vez mais pressionados a produzirem em maior quantidade e com maior eficiência. Para isso, uma boa análise de dados é fundamental e a seleção genética é uma ferramenta indispensável devido ao seu valor cumulativo e permanente ao longo das gerações, especialmente no sector suinícola.

Este estudo teve como objetivo analisar o desempenho reprodutivo de uma exploração de porcos irlandesa e investigar o efeito da mudança da linha paterna no desempenho produtivo dos leitões. Dados relativos ao período de um ano, que contam com 222 porcas gestantes, 375 partos e 5446 leitões foram colhidos com ajuda de software especializado para recolha e análise de dados em produção suína (PigCHAMP) e parâmetros de ninhada foram analisados por lote, por número de partos da porca e por linha genética paterna.

Em relação ao desempenho reprodutivo, o número médio de leitões nascidos por porca (tamanho da ninhada) por lote (14,5 ± 0,83), por número de partos da porca (14,73 ± 0,750) e por linha genética paterna (14,52 ± 0,198) foi superior à média nacional irlandesa em 2019 e 2020 (14,12 e 14,26, respetivamente). O tamanho da ninhada atingiu o pico nas porcas de 4 e 5 partos, indo de encontro ao reportado pela literatura. O peso médio ao nascimento foi mais baixo nos leitões de porcas com 4 partos, o que reforça a já conhecida relação entre o tamanho da ninhada e o peso medio ao nascimento: quando a capacidade uterina máxima é atingida, um aumento no número total de leitões vai levar a uma diminuição do peso médio da ninhada ao nascimento, e vice-versa. A variação do peso ao nascimento entre leitões de porcas com 4 partos também foi maior do que em leitões de porcas com outro número de partos, o que realça que ninhadas maiores têm uma maior variação no peso ao nascimento entre indivíduos da mesma ninhada. O segundo valor mais baixo do peso médio ao nascimento foi registado em leitões de porcas primíparas enquanto que o maior valor foi registado em porcas de 9 ou mais partos, o que é consistente com achados da literatura que afirmam que o peso ao nascimento é menor em leitões de porcas primíparas e maior em leitões de porcas com elevado número de partos. A mortalidade no período de pré-desmame foi, no geral, superior em relação à média nacional irlandesa (11%), e o menor número de leitões mortos foi registado em porcas com 2 partos, evidenciando a relação entre número de partos e produção de leite: porcas com 2 e 3 partos têm maior produção de leite que outras porcas. A análise estatística mostrou que o número de partos da porca e o peso médio ao nascimento afetaram significativamente o número de leitões mortos antes do desmame (P

<0.001) e o número de porcos desmamados (P = 0.002 e P <0.001, respetivamente). A sobrevivência no pré desmame também foi afetada pelo número de partos da porca e pelo peso individual ao nascimento (P <0.001).

A meio do período de tempo a que correspondem os dados utilizados neste estudo, a genética da linha paterna mudou. A linha genética antiga era uma linha selecionada para crescimento rápido e robusto, carne de qualidade e alto valor de carcaça, ao passo que a linha genética nova era uma linha selecionada para robustez, uniformidade, vitalidade, crescimento, resistência ao PRRS, prolificidade e maior peso ao desmame. Com a linha genética nova verificou-se um aumento no número total de leitões nascidos, no tamanho da ninhada, no peso médio ao nascimento e no peso médio ao desmame. No entanto, o número de leitões desmamados diminui e as mortes no período de pré-desmame aumentaram, sendo que a taxa de mortalidade e desmame foram significativamente diferentes entre as duas linhas genéticas (P = 0.009). Além disso, as variações no tamanho da ninhada, no peso médio ao nascimento e no peso médio ao desmame entre indivíduos foram maiores na linha genética nova. Em relação à análise estatística, a mudança da linha paterna mostrou diferenças significativas na sobrevivência no período de pré-desmame e no número de leitões mortos antes do desmame (P <0.001), tendo tendência a ser estatisticamente diferente no número de porcos desmamados (P = 0.064). Estes resultados mostram a existência de um efeito da linha paterna nos parâmetros de ninhada e evidencia que continuar a selecionar geneticamente para maiores tamanhos de ninhada não é uma estratégia útil em termos de produção ou de bem-estar animal. Uma melhor estratégia será manter o tamanho da ninhada em níveis altos e selecionar geneticamente para a sobrevivência dos leitões na linha paterna.

Em relação às causas de morte no período de pré desmame, as únicas causas significativamente diferentes entre genéticas foram fome (P <0.001) e esmagamento pela porca (P = 0.012). O número de mortes por fome foi maior na genética antiga, o que pode estar relacionado com o facto de que, no período de tempo em que esta genética foi utilizada na exploração, ter existido um maior número de porcas com elevado número de partos. Porcas com elevado número de partos têm uma maior redução da função e acessibilidade das tetas, o que pode levar a um consumo de colostro insuficiente. O número de mortes por esmagamento pela porca foi maior na genética nova, o que pode estar relacionado com o aumento do tamanho das ninhadas nesta genética. Ninhadas maiores são um conhecido fator de risco para esta causa de morte. Canibalismo e causas desconhecidas tiveram uma tendência para serem estatisticamente diferentes entre genéticas (P = 0.051 e P = 0.054, respetivamente). Uma explicação possível para estes resultados é a falta de atenção dos trabalhadores da exploração ou registos incorretos, visto que não existiram outros fatores que pudessem ter levado ao aumento destas duas causas de morte.

Apesar da diferença entre genéticas não ter sido significativa, existiu um aumento no número de mortes por síndrome de abdução das patas na linha genética nova. Além do número de mortes por esta causa ter aumentado, os trabalhadores da exploração também reportaram ter existido mais casos desta síndrome no geral. A síndrome de abdução das patas tem uma predisposição genética, o que pode explicar o aumento de casos depois da mudança da linha paterna. O aumento do número de casos desta síndrome também pode ser uma justificação para o aumento do número de mortes por esmagamento pela porca, visto que que esta síndrome é um fator de risco desta causa de morte.

Este estudo realça a importância que o peso ao nascimento, o tamanho da ninhada e o número de partos da porca têm na mortalidade no período de pré-desmame e no número de porcos desmamados, assim como a influência da seleção genética na sobrevivência dos leitões e nos parâmetros de ninhada. Baseado nos resultados deste estudo, a mudança na genética da linha paterna não foi uma estratégia de gestão útil para esta exploração, visto ter levado a uma maior taxa de mortalidade no período de pré-desmame e a um menor número total de porcos desmamados. Este trabalho apoia a teoria de que a linha paterna tem um efeito no tamanho das ninhadas e na sobrevivência dos leitões e reforça a importância de ter um sistema de informação robusto para avaliação corporativa interna, monitorização e tomada de decisões.

Palavras-chave: análise de dados, efeito parental, suíno, desempenho reprodutivo, produção

THE IMPORTANCE OF DATA ANALYSIS AND THE EFFECT OF SIRE LINE ON THE REPRODUCTIVE AND PRODUCTION PERFORMANCE OF AN IRISH PIG FARM

Abstract

This study aimed to analyse the reproductive performance of an Irish farrow-to-finish swine herd and to investigate the effect of a sire line change on the piglets' production performance. Farrowing data over the course of one year, with a total of 222 sows and 375 parturitions, was collected and litter parameters per batch, per parity and per genetic line were analysed.

Results showed that parity and average birthweight affected significantly the number of preweaning dead piglets (P <0.001) and the number of weaned pigs (P = 0.002 and P <0.001, respectively). Preweaning survival was also affected by parity and individual birthweight (P <0.001). The change in genetic line showed significant differences in preweaning survival and number of preweaning dead piglets (P <0.001) and had a tendency to be statistically different in the number of weaned pigs (P = 0.064). Preweaning death causes such as starvation and crushing by the sow also showed significant difference between genetic lines (P <0.001 and P = 0.012, respectively). Based on the results of this study, changing sire line genetics was not a helpful management strategy for this farm, since it led to higher preweaning mortality and lower total number of weaned pigs.

This work highlights the importance of having robust data for internal benchmarking, monitoring and decision-making and the effect of sire line on the reproductive and productive performances of swine herds.

Keywords: data analysis, paternal effects, swine, reproductive performance, production

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List of Abbreviations

AST - Antimicrobial Sensitivity Testing

BLUP - Best linear unbiased prediction

IgG - Immunoglobulin G

Kg - Kilograms

MFH - Myofibrillar hypoplasia

MMA - Mastitis-metritis-agalactia

No - Number

PCS - Porcine Congenital Splay Leg Syndrome

PDS - Post-partum dysgalactia syndrome

PRRS - Porcine Reproductive and Respiratory Syndrome

SD - Standard deviation

SE - Standard error

1. Internship report

The curricular internship was divided in two different stages: one initial stage in Lisbon, at The Faculty of Veterinary Medicine – University of Lisbon, from September 2019 to January 2020, and a second stage at the Moorepark Animal & Grassland Research Center of Teagasc – Agriculture and Food Development Authority, in Fermoy, Co. Cork, Ireland, from February 14th to May 29th, 2020.

The first stage of the internship was supervised by Professor Telmo Nunes and the intern was able to acquire programming and statistical skills such as learning how to operate data handling programs (like R and Microsoft Office Excel ©) and developing their knowledge in veterinary epidemiology and animal production by solving several exercises proposed by the professor.

The second stage of the internship was supervised by Dr. Maria Costa and the intern was able to experience a different range of activities such as:

- accompanying researchers to pig slaughterhouses and learning how to collect and correctly preserve samples;
- observing and assisting necropsies on pigs;
- revising sanitary inspection issues by going to the slaughterhouse and observing the approved and rejected carcasses;
- visiting farms and discussing pig health and welfare as well as pig farm management;
- performing biosecurity check-ups on pig farms (using the Biocheck.UGhent® scoring system);
- observing and performing artificial insemination in sows;
- attending pig and poultry classes at the University College Dublin as well as attending tutorials about R programming;
- solving and discussing animal production exercises;
- discussing pig related clinical cases;
- participating in weekly discussions of pig related scientific articles in a Journal Club where the intern was able to develop her critical spirit by presenting an analysis of a previously chosen article, pointing out the positive and negative aspects of said article as well as discussing the relevance of the theme the researchers chose to approach;
- laboratorial training in processing samples for microbiological culture and antimicrobial sensitivity testing (AST) analysis.

Due to the COVID-19 pandemic and the international lockdown, practical activities (field visits to farms and slaughterhouses) were interrupted from March 13th 2020 until the end of the internship. All other activities were conducted remotely without any major issues.

2. Introduction

With the global increase in the consumption of animal products, a trend toward large and intensive swine production units has emerged. Herds have been pressured to increase their production efficiency and the number of pigs produced per sow per year. This pressure to maximize production has led to a need for herd managers with high levels of education and specialized swine experience. Consequently, the type of services required by veterinarians has broaden and it is common for veterinary practitioners to perform the role of herd health managers, acting as consultants who can help solve management, environmental and production problems. To help farmers and producers improve production performance, the analysis of herd production records should be performed periodically. This analysis will allow decision makers to understand the reasons behind the results obtained and help them decide which management strategies should be applied to correct possible mistakes (Dewey and Straw 2006).

An important management strategy to improve production and reproduction performance in swine herds is genetic selection. Selection for traits such as survival, vitality, litter size, birth weight and growth has been proved to increase production parameters in the long run. It is known that dams have great potential to improve reproductive traits, therefore, sows have been selected for prolificacy and mothering abilities, while boars have been selected for production performance traits. While the main focus of selection programs in sire lines is growth capacity and carcass traits, there seems to be a paternal effect on litter traits as well. Sire line seems to affect significantly the number of piglets per litter, the number of piglets born alive and the number of weaned pigs per sow (Pedersen et al. 2019; Elbert et al. 2021). Although this effect is known, knowledge about the extension of this effect is limited and little attention has been given to the potential benefits it could bring to reproduction and production performance in swine herds.

2.1. Objectives

This was an observational study that consisted in two main objectives: 1) describing and analysing the reproductive performance of a farrow-to-finish commercial pig farm over the course of one year using farrowing data from multiple batches, and 2) study the effect of a sire line change on the sow and piglets' production performance. The commercial farm used in this study happened to change their terminal sire line genetic in the months preceding the beginning of the traineeship, therefore, the farrowing data of both genetics was used to investigate any relevant differences in parameters that affect reproduction performance and productivity.

3. Literature review

3.1. Data in swine production and the importance of having robust records for internal benchmarking and monitorization

The use of data in improving decision making and farm productivity is one of the aspects that has generated more interest in swine production in recent years. In the last thirty years, data collection in the swine industry has been poor, making data analysis limited. Previously, most farm activities were basic and mainly focused on the management of tasks, which led to only collecting data about mating, farrowing and weaning in the preweaning period, and body weight, feed intake and mortality per batch in the post weaning period. Integration of data from different sources was also difficult and rare, complicating strategic decision making. To this day, pig data collection still focuses mainly on reproductive key performance indicators, making the progress in data analysis slow. Other reasons for this slow progress include the low added value perceived by farm producers, the good margins that have prevented the need for improvement based on data analysis, the lack of educated professionals in farm data management and the lack of tools adapted to the sector, that facilitate the process of extracting value, benchmarking and monitoring (Piñeiro, Morales, et al. 2019).

However, with the global increase in animal products consumption, farms nowadays are pressured to work more efficiently and that cannot be achieved without adequate data collection, data analysis and good use of the information generated. In the digital era, data collection is easier with new technologies like wireless connection (3G/4G, Wi-Fi, satellite), mobile devices (smartphones and tablets), sensors and cloud computing. With these tools, it is possible to collect more data, and this data is also more reliable and specific. Producers are also becoming more aware that their competitiveness depends on using accurate data appropriately to support decision-making, both for daily decisions and strategic decisions. The importance of good farm management and keeping records in improving pig performance parameters is undeniable. Not only will good farm management improve production, but keeping records will also help farmers detect problems within the farm more easily (Agostini et al. 2015; Benjamin and Yik 2019). Furthermore, without correct records, reducing piglet mortality and improving piglet survival through genetic selection could result in unexpected outcomes (Strange et al. 2013).

According to Piñeiro, Morales, et al. (2019), a swine production company should have a 5-step management program to establish a robust information system (Figure 1). This system will provide the information necessary to support both production efficiency and quality standards, reducing uncertainties in decision-making.

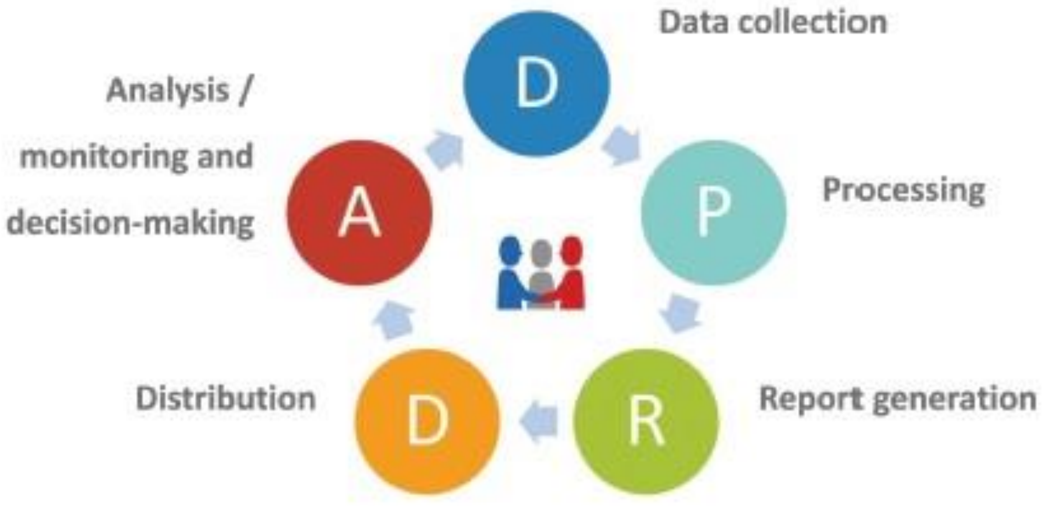


Figure 1 - The five steps of a robust information system (Source: Piñeiro, Morales, et al. 2019).

The first step (data collection) consists in gathering raw information from the farm. This information can be acquired from either human or sensor records. The second step (data processing) consists in creating a corrected database that allows proper information generation. This step includes tasks such as data validation, sorting or aggregation, management of outliers and missing data. The third step (reporting) consists in producing the reports needed for the farm. This step depends on each farm's needs but it can range from creating sow cards and working lists to performing multivariate regression analysis. The fourth step (distribution) consists in getting the right information to the right person at the right time. This is an important step that is not always properly performed, leading to data underuse and poor decision-making. The final step (analytics and decision making), consists in analysing the reports provided to make key decisions in the farm.

Herd data is not only valuable to producers, but it is also of great interest to genetic companies and breeders, since they are able to evaluate performance under commercial conditions and use that information in selection procedures to optimize production related traits (Hollifield et al. 2021).

3.1.1. Software in swine production

It may be difficult to keep track of the information, especially in smaller farms, where there is a lack of specialized employees. Even when said employees try to have organized hand written records, they can still be easily lost and they are harder to link to historical data. To help farmers with this matter, specialized farm management software has been created and there are now several computerized and mobile applications that allow data acquisition in the field for livestock management. The pros of these software programs are that they are cheap, easy to use by unspecialized employees, can process data at any time, can provide information in real time, are up to date and can be with the farmers at all times, since they can be installed on small devices such as smart phones or tablets (Lantzos et al. 2013). Most software programs are able to run basic farm management tasks, such as sow cards, working lists and a general production summary. However, they have some limitations. They are unable to create new variables, which makes problem solving more difficult; they fail when more complex reports are needed; they were designed for single farm use, not allowing the merging of data from different farms, and farmers and veterinarians are not adequately trained on how to use these programs (Piñeiro, Morales, et al. 2019).

In pig production, some examples of farm management software are Agrisyst PigExpert, PigVision (by AgroVision), D2D PigCom, Quantum and PigCHAMP. These systems are particularly useful and largely used in breeding herds (Taylor 2021).

3.1.2. PigCHAMP

PigCHAMP, which stands for Pig Computerized Health and Management Program, is a software with a reproductive and a grow-finish program that can be used online or on a mobile application. It was created by the University of Minnesota and it was one of the first data collection systems. It provides a powerful analysis due to its multiple useful features, such as: batch data entry for arrivals, pregnancy checks, artificial insemination details, health treatments and weanings; interactive reports that include individual animal performance, death losses and expenses; connectivity to other data sources like genetic programs and feeding systems; easy to export data for further analysis and data sharing with veterinarians and consultants (PigCHAMP 2022). Individual sow records that are manually registered by the farm workers at farrowing can be easily uploaded to the software to create an online database, which makes it easier for breeding herds to compare the reproductive performance between sows and between batches.

3.2. Farrow-to-finish herds

Farrow-to-finish is a type of swine production system that involves breeding and farrowing sows, as well as, feeding the offspring until they reach a designated market weight, which varies from country to country according to industry preferences. In Ireland, the average live weight at slaughter is of, approximately, 115 kilograms. The entire production period takes approximately 11 months, with 5 months for breeding and gestation and up to 6 months to raise the litter to market weight (Linneen et al. 2005; Teagasc 2021).

A farrow-to-finish herd consists, typically, in two subpopulations of animals: breeding sows and growing pigs. Each subpopulation is divided in groups called batches, and the number of individuals per batch is assumed constant. According to their physiological stage, animals evolve through five types of facilities: service rooms, farrowing rooms, nursery rooms and finishing rooms. Farrowing, nursery and finishing facilities are divided into several rooms, ideally managed according to an all-in-all-out strategy, which means all animals in a batch leave the facility at once and enter an empty room simultaneously. Each batch is, therefore, managed independently with limited relationships through environmental components. In service facilities, all the batches are gathered in unique rooms. The two subpopulations (sows and piglets) physically interact exclusively in farrowing rooms (Lurette et al. 2008; Cador et al. 2016). Figure 2 shows an example of the layout of a farrow-to-finish farm and provides an estimate for the time sows and growing pigs spend in each stage.

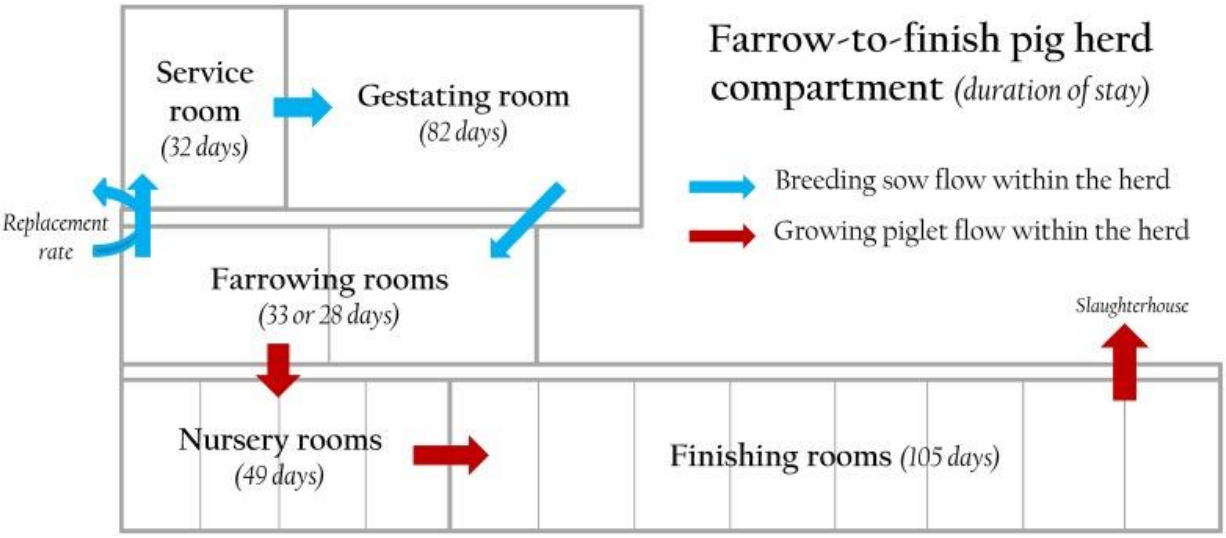


Figure 2 - A farrow-to-finish pig herd facility scheme (Source: Cador et al. 2016).

3.2.1. The sow reproductive cycle

The sow reproductive cycle (147 days in total, with gestation length being 115 days) is made of three different physiological stages to which correspond three different types of facilities. At introduction or after weaning, gilts and sows are moved to service room where they are inseminated 4 days later and remain in this room up to 4 weeks after insemination. Then, batches of sows are moved to the gestating room for 82 days until farrowing entrance. In most commercial indoor farms, a batch of sows farrows every week. Other farms operate in batch systems. In a farm with a 3-week batch system, every 3 weeks a batch of sows joins the farrowing room 5 days before farrowing for acclimatization and gives birth to a batch of piglets. Dams remain with their litter for 4 weeks (lactation period) until weaning. At that time, sows are moved back to the service room to begin a new reproductive cycle starting with sow culling and renewal. Piglets are moved to a vacant nursery room. Finally, each batch of weaned piglets occupies a nursery room until 11 weeks of age before moving to a vacant finishing room until their slaughter age (182 days) (Lurette et al. 2008; Cador et al. 2016).

3.3. Preweaning mortality and herd management

Reducing piglet mortality is not only an important welfare goal in pig production, but it is also a matter of economic improvement for the farm. Litter size continues to increase due to high prolific sows and obtaining litters with 14 to 16 piglets became a common scenario in many countries (Quesnel et al. 2015). In Ireland, the average number of piglets born alive per litter in 2019 was 14.12 and, in 2020, it was 14.26, with the average number of pigs produced per sow per year being 26.8 in 2019 and 27.5 in 2020 (Teagasc 2021). It is, therefore, essential to have good management practices and skilled stockmanship to keep preweaning mortality levels low.

Preweaning mortality can range from 5 to 25% and management practices have been proved to help reduce mortality significantly (Andersen et al. 2007). In commercial swine herds around the world, preweaning mortality usually ranges from 10 to 20%, being around 11% in Ireland, specifically (Koketsu et al. 2006; Teagasc 2021). Most deaths occur around farrowing and during the first few days of life, making the first 72h a critical period (Koketsu et al. 2006). This means that the periparturient period is a particularly important time for management interventions intended to reduce mortality (Pandolfi et al. 2017).

Birthweight, litter size and parity are the most important factors for preweaning mortality. It was shown that piglets with an individual birthweight superior to 1.8 kg had a survival rate of over 90%, while piglets with a birthweight inferior to 700 g had a survival rate of only 33% (Muns et al. 2016). Increased litter sizes have a higher within-litter birth weight variation and higher preweaning mortality rates, although the mean piglet birthweight increases with an increasement in litter size (Milligan et al. 2002). Decreasing birthweight has also been associated with lower survival, as well as, an increase in odds ratios of preweaning mortality (Roehe and Kalm 2000; Fix et al. 2010). Parity and preweaning mortality have been negatively correlated and this might be due to primiparous sows having less colostrum yield than mid parity sows; being more sensitive to environmental factors, and being inexperienced mothers (Marchant et al. 2000; Tummaruk et al. 2010; Ferrari et al. 2014; Quesnel et al. 2015). Moreover, primiparous sows have an immature body size and reproductive cycle, which leads to higher nutrient requirements, fewer piglets born alive and lower colostrum IgG concentrations (Piñeiro, Manso, et al. 2019). Second and third parities tend to have higher colostrum yield than other parities (Devillers et al. 2007) and older sows have a reduced, more variable function and accessibility of teats, with high parity sows having a 41% reduction in the number of functional teats (Vasdal and Andersen 2012).

Furthermore, herd size is also relevant to preweaning mortality. Small-to-mid herds (<570 sows) have more difficulty alleviating the association between increased number of piglets born alive and increased preweaning mortality, since they have less advanced facilities, less human resources and lower level of genetic improvement (Koketsu et al. 2021).

3.3.1. Causes and management solutions to preweaning mortality

The most frequent causes of preweaning mortality are intrapartum stillbirth, low viability, starvation, disease, hypothermia, crushing by the sow and savaging (Spicer et al. 1986; Marchant et al. 2000; Edwards 2002).

Intrapartum stillbirth, low viability and postnatal mortality are all closely linked. Most cases of stillbirth are caused by perinatal asphyxia, which also results in reduced viability and vitality due to metabolic acidosis and hypoxia sequela, increasing the risk of postnatal mortality. Intrapartum stillbirth affects, on average, 0.55 to 0.98 piglets per litter (Dewey and Straw 2006). The incidence of intrapartum stillbirths is also greater in higher parities due to prolonged farrowing caused by excessive fatness and poor uterine muscle tone, which increases the risk of perinatal hypoxia (Zaleski and Hacker 1993; Alonso-Spilsbury et al. 2005). Dystocia, prolonged farrowing and large litter sizes are associated with perinatal asphyxia and are recognized as risk factors for stillbirth and low viability (Rutherford et al. 2013). Management strategies that are effective at reducing stillbirth and improving piglet viability include culling old sows, measures to prevent heat stress, measures to reduce psychological stress around farrowing (for example, provision of nesting materials), intervention to assist dystocic sows and assisting newly born piglets to breathe by clearing the airways or administering oxygen (Kirkden et al. 2013).

Starvation occurs when the piglet’s colostrum intake capacity is affected. Factors that influence colostrum intake by the piglet include litter size, piglet vitality, low birth weight, birth order, sow nutrition, splay leg and the ability of the piglets to reach the udder, stimulate a teat and suckle (Devillers et al. 2007). Insufficient milk production or lactation failure in sows is also an important cause for death by starvation, accounting 6 to 17% of preweaning mortality. Furthermore, post-partum dysgalactia syndrome (PDS), also known as mastitis-metritis-agalactia (MMA), is a condition with considerable prevalence among herds and causes lactation failure usually during the first three days after farrowing (Muns et al. 2016). Management strategies to reduce the risk of death by starvation include cross-fostering (preferably in the first 12-24 hours after birth to allow piglets sufficient colostrum intake from their birth sow while also preventing the disruption of teat hierarchy establishment and preventing the piglets from missing nursing episodes), split suckling, assistance to suckle and milk supplementation (Wensley et al. 2021).

Disease in piglet mortality includes infectious and non-infectious diseases. Important infectious diseases in piglet mortality include enteritis, pneumonia and systemic infections, such as sepsis and polyarthritis. Non-infectious diseases include congenital diseases (with splay leg being particularly relevant), anaemia and leg and foot injuries, which can cause lameness when infected. Management strategies that help prevent infectious diseases include applying biosecurity measures, good hygiene of the farrowing house (all-in all-out management, removal of faeces and dirty bedding, cleaning and disinfecting), vaccination of the sow, assistance of weaker piglets with feeding and a warm, draft-free environment. Specific management strategies to prevent systemic infections include ensuring that procedures such as teeth resection and tail docking are hygienic, prophylactic use of antibiotics and the use of nonabrasive floors, which helps reduce leg and foot injuries. Anaemia can be reduced by ligating the umbilical cord after birth and splay leg can be treated by taping the legs (Kirkden et al. 2013).

Although hypothermia is rarely recorded as a primary cause of death in commercial pig herds, it might lead to death by other causes such as starvation, crushing and disease (Edwards 2002). The ambient temperature of the farrowing house is normally below the lower critical temperature of the newly born piglets. The new born pig is poorly insulated and maintenance of its homeothermic balance depends essentially on its capacity to produce heat. Piglets do not possess brown adipose tissue and rely almost exclusively on shivering thermogenesis for thermoregulatory purposes. For this reason, they initially use their energy reserves to maintain body temperature, so it is essential that they consume colostrum promptly. Piglets with low birth weight have a higher risk of suffering from hypothermia due to low energy reserves and a poor ability to compete at the udder (Herpin et al. 2002). Management strategies to prevent hypothermia include a heated creep area, floor heating, floor mats or bedding and radiant heat lamps (Baxter et al. 2011; Andersen and Pedersen 2016).

Crushing is mainly due to the sow’s behaviour and the farrowing house system and design, with large litter sizes also playing an important role, since they create an increase in the number of fights at suckling and, therefore, an increase in the risk of death by crushing and starvation. Conventional farrowing crates were designed to prevent crushing however sows kept in these crates show signs of an impaired welfare state (increased heart rate, stress-hormone responses, negative or abnormal behaviour) and crushing continues to happen since the piglets can still be trapped underneath the sow. Loose farrowing systems may prevent crushing but it has no real effect on piglet mortality since piglets still die due to other causes. Recommended management strategies to reduce death by crushing of the sow include modifications to the pen or crate design with a safe zone for piglets to retreat, the use of neoprene mats, which helps reduce the temperature gradient between the piglet and the floor surface, and provision of nest material to encourage maternal behaviour. There is, however, no evidence that these measures have a real effect on piglet mortality (Muns et al. 2016).

Savaging is an aggressive behaviour directed at piglets by the sow, which results in injury or death. Savaging is most common in gilts and is thought to be associated with new and stressful events such as the change of environment, fear of contact with humans or fear of the new born piglets. Savaging occurs predominantly around the time of farrowing. Management strategies that are effective to control this problem are supervision of a trained stockperson after farrowing, separating the sow from the piglets if necessary and culling savaging sows, since this behaviour tends to persist across parities (Harris et al. 2003; Harris and Gonyou 2003). Some other measures that can help are sedation of the sow and inspection for signs of mastitis, since this causes pain and, therefore, aggressive behaviour (Fangman and Amass 2007).

3.3.1.1. The importance of stockmanship

In order to minimize the factors influencing preweaning mortality, good stockmanship is essential. This refers not only to the technical competence of the stockperson but also to the nature of their relationship with the animals in their care. When the sow fear levels are high, aggression levels and nervousness increase and so does the risk of being savaged or crushed. Farrowing day and the first two days after farrowing are usually the focus of stockhandlers because good farrowing supervision with immediate assistance to the sow and piglets helps reduce preweaning mortality, especially the number of stillbirths. However, there is evidence that consistent positive handling can decrease the fear of humans and, consequentially, the factors leading to other causes of preweaning mortality, such as savaging and crushing. A suitable training program is highly beneficial in helping improve a stockperson’s attitudes and behaviour towards the animals, which will also result in decreased sow fearfulness and stress. Skilled labour is more important than extra labour in a farm. Furthermore, when compared with farms with unspecialized workers, farms with trained stockhandlers have showed a 5% increase in weaned pigs per year (Baxter et al. 2013; Jääskeläinen et al. 2014).

3.4. Genetic selection in pig production

In pig production, strategies to mitigate health and welfare issues, such as genetic predisposition of undesirable traits, are essential to economic success. Research suggests that selection of traits like piglet survival and litter size increasement can be achieved through genetic selection and, around two decades ago, the introduction of the best linear unbiased prediction (BLUP) facilitated selection for traits of lower heritability, making substantial improvements in several animal production traits (Rutherford et al. 2013). Even though the heritability of these traits is generally low, making genetic improvement occur at low rates, the genetic variations are large enough to provide improvements through breeding (Roehe et al. 2009).

3.4.1. Effects on piglet survival and preweaning mortality

In the past, pig producers have tried to increase piglet survival by improving the husbandry conditions, reaching only a limited reduction in mortality (Edwards 2002). Since environmental factors can be inconsistent, genetic selection for piglet survival has gained attention due to its cumulative and permanent value across generations.

Preweaning mortality has low heritability and has only been slightly correlated genetically with post-weaning mortality, suggesting that mortality before and after weaning are controlled by different genes. Heritability of mortality traits increases with age, therefore, selection for survival after weaning could be more effective than selection only for survival before weaning (Dufrasne et al. 2014). Moreover, stillborn mortality doesn’t seem to be genetically correlated with mortality after birth until weaning, which means that perinatal and postnatal preweaning mortality are also under different genetic control and should be treated as different traits in a selection program (Strange et al. 2013).

Perinatal mortality increases with total number of born piglets and is reduced by maternal heterosis (crossbred sows) (Varona et al. 2020). It also seems to be highly related to the piglet shape and size (Baxter et al. 2009). Moreover, selection against perinatal mortality (up to day 5) yields slightly higher heritabilities than later preweaning mortality and has a high, positive genetic correlation with the number of weaned pigs as well as moderate, positive genetic correlations with survival rate at birth (Su et al. 2007; Su et al. 2008).

3.4.1.1. Correlations with litter size, birth weight and parity

Selection for survival has not been genetically correlated to litter size increasement or growth performance. Nonetheless, it has been proven that it is possible for breeding companies to select for both survival and litter size increasement (Merks et al. 2012) as well as there is a possibility of selection for both survival and growth (Dufrasne et al. 2014). It is possible to increase litter size in about 0.4 piglets per generation through genetic selection (Sørensen et al. 2000), but increased litter sizes have been associated with higher piglet mortality (Varona et al. 2020).

The chance of survival increases with the increasement of birth weight, however, researchers have concluded that breeding for increased birth weight will not necessarily result in higher overall survival rate (Grandinson et al. 2002; Su et al. 2008). High birth weight variation within-litter has been associated with lower survival chances and more variable weaning weights. Moreover, larger litters increase within-litter birth weight variation and decrease survival chances (Milligan et al. 2002). Improvement of litter size and birth weight seems to be possible, however, there is a limit in how far both litter size and birth weight can be increased simultaneously due to their negative correlation. When the maximum uterine capacity is reached, an increase in either total number of piglets born or average litter birth weight will lead to a decrease in the respective other trait. Furthermore, selection on individual birth weight instead of average litter birth weight seems to be a more successful strategy for piglet survival improvement (Kapell et al. 2011).

Different parities have different genetic correlations with litter parameters and should, therefore, be considered as different traits. The first parity seems to be genetically different from later parities, having lower genetic correlations for traits such as number of born alive piglets and total number born (Lopez and Seo 2019). The number of born alive piglets peaks at middle-aged sows and number of born dead piglets increases significantly in older parities. Birth weight seems to be lower in gilts and higher in older sows, while litter size seems to peak in middle-aged sows. Piglets with low birth weight and from sows of sixth parity or older have significantly lower chances of survival (Milligan et al. 2002).

3.4.1.2. Direct effects, maternal effects and sire line effects

Piglet survival is controlled both by the genes of the piglet (direct genetic effects) that are involved in vitality, health and growth, and by the genes of the dam (maternal genetic effects) that affect milk yield and other mothering abilities. These genetic effects are especially important in postnatal mortality. A recent study showed that the maternal genetic effects are the main limiting factor for improving piglet survival, with direct genetic effects having more a secondary role. This implies that breeding programs should emphasize selection pressure on the maternal genetic effects for a higher chance in piglets’ survival (Nguyen et al. 2021).

Breed also seems to be genetically relevant, with studies showing clear differences among breeds in several litter parameters and in the expression of direct and maternal genetic effects (Su et al. 2007; Su et al. 2008; Ibáñez-Escriche et al. 2009). Moreover, using Duroc boars as terminal sire lines seems to reduce piglet mortality (Pedersen et al. 2019).

In breeding programs, reproduction traits are usually the focus of dam lines while production traits are usually the focus of sire lines. That is also why most research on sire lines is linked to growth and carcass traits. However, there seems to be a sire line effect for vitality and litter traits. A recent study showed that sire line significantly affects the total number of born piglets, the number of born alive and the number of weaned pigs per sow (Elbert et al. 2021). The same study also implies that further selection for litter size in dam lines is not indicated in terms of animal welfare and production efficiency. A more successful strategy is to stabilise litter size at a high level, while at the same time breed for vitality and survivability in sire lines.

Furthermore, a more successful selection strategy is using pooled semen from a few boars. This can help improve the accuracy of predicting maternal and direct effects for litter-related traits while also enhancing the fertility success ratio of insemination (Maiorano et al. 2019).

3.5. Porcine Congenital Splay Leg Syndrome

Considered one of the most frequent developmental defects in piglets (Muirhead and Alexander 2013), the porcine congenital splay leg syndrome (PCS), also known as spraddle leg syndrome or simply splay leg, is characterized by an impaired ability in newly born piglets to stand and walk due to a lateral abduction of the hindlimbs and, in severe cases, the forelimbs as well (Thurley et al. 1967). Piglets with PCS have an increased probability of dying due to starvation and being crushed by the sow, which leads to higher pre weaning mortality rates. Because of that, PCS is considered an important economic factor as well as a matter of animal welfare (Lax 1971). Figure 3 shows a piglet with PCS.

Figure 3 - A 6-days-old piglet with Porcine Congenital Splay Leg Syndrome (Source: Papatsiros 2012).

3.5.1. Epidemiology

PCS is the most observed hereditary birth defect in pigs, representing about 35% of all recorded inherited defects, and it has a general lethality of up to 50% (Partlow et al. 1993). It’s a widespread problem with a prevalence that can range from less than 1% to 8% or more in some farms (Dewey 2006). In a recent study, PCS was the second most common cause of death in piglets, representing around 22% of all causes of preweaning mortality (Abah et al. 2019). The incidence varies depending on several factors (such as breed and farm size), but it is assumed that it affects around 0,4% of all born alive piglets, with 1 to 4 affected piglets per litter, a few litters at a time (Papatsiros 2012).

Heavily muscular breeds like Landrace and Large White seem to be the breeds with higher incidence of this syndrome (Vogt et al. 1984). As for farm size, large scale production facilities have been associated with higher incidence of PCS (Schumacher et al. 2021).

Male progeny seems to be more affected by this syndrome than female progeny, with the number of affected males being around twice as high as the number of affected females. Even though most authors have reached these results in their studies, the results have not been consistent for there has been some authors who did not find any sex-linkage for this syndrome (Van Der Heyde et al. 1989).

Low birth weight and short gestation lengths have been associated with this syndrome but a significant correlation has not been found for birth weight, gestation length or parity in affected litters. Larger litters tend to have more affected piglets but litter size has not been consistently correlated to have higher incidence. There seems to be a sow effect (a litter effect) rather than a litter size effect (a piglet effect) (Van Der Heyde et al. 1989).

3.5.2. Etiology and Pathogenesis

Histomorphological findings indicate that piglets with PCS have an underdeveloped skeletal muscle, described as myofibrillar hypoplasia (Thurley et al. 1967). This myofibrillar hypoplasia (MFH) was initially thought to be the cause of PCS but healthy new-born piglets also present small skeletal myofibers so histopathology, in this case, cannot be used exclusively to diagnose PCS (Ward and Bradley 1980).

Even though MFH is a common feature in slay leg piglets, an impairment of muscle innervation due to incomplete electrical isolation of primary motor neurons was considered most likely to be the cause. A study showed that splay leg piglets present a reduction of axonal diameter and myelin sheath-thickness of the fibers innervating the adductor muscles. Later, there seems to occur a catching up of myelination leading to recovery. The main hypothesis to justify this occurrence is a deficiency in choline and methionine in the sow’s nutrition, both essential to normal myelin production (Szalay et al. 2001). Another study, however, has shown that choline plasma levels and the activity of various choline esterases were not reduced in PCS piglets and that choline insufficiency was unlikely to be the cause of PCS (Tuček et al. 1985). There have also been studies that showed that including choline supplements in pregnant sows’ diet seemed to prevent PCS in piglets and that administration of acetylcholine esterase blockers seemed to make the symptoms of PCS disappear (Cunha 1968; Schnapperelle and Koch 1980). There doesn’t seem to be a consensus on this matter.

Induced farrowing was also considered as a possible cause for PCS, however, significant correlations between induced farrowing and PCS in piglets have not been found (Sellier et al. 1999)

Porcine Reproductive and Respiratory Syndrome (PRRS) is known for reproductive failures in sows so it was also considered as a cause for PCS. Even though vaccination significantly decreases reproductive problems and it was earlier associated to reduce the incidence of PCS (Papatsiros et al. 2006), in a recent study, the number of piglets affected with PCS did not differ significantly between vaccinated and unvaccinated groups (Jeong et al. 2017).

Environmental factors are likely to be involved in PCS frequency but are more likely to be a secondary cause rather than a primary one (Schumacher et al. 2021).

3.5.2.1. Genetic background

Even if the understanding of the etiology and pathogenesis of PCS is still poor, it is accepted that there is a genetic pre disposition for this syndrome. There have been many studies trying to identify the responsible genes and the two most promising candidates are FBXO32 and HOMER1 (Wu et al. 2018; Xu et al. 2018).

FBXO32 is associated with the process of muscle atrophy and is considered an atrophy marker. Overexpression of FBXO32 in PCS piglets has been proved in various studies and it’s being considered as a main cause of PCS (Ooi et al. 2006; Wu et al. 2018).

HOMER1 is involved in muscle differentiation and calcium homeostasis so disturbances in its expression are likely to lead to muscle atrophy or retarded muscle development. In recent studies, HOMER1 has been associated with PCS (Hao et al. 2017; Xu et al. 2018). HOMER1 is also a member of the Homer protein family, which is predominantly found in neural tissues. Homer proteins are involved in the myelination processes so it's plausible that HOMER dysfunctions may affect motor axon myelination. This would explain the previous reported myelination deficiency in PCS piglets (Schumacher et al. 2021).

It’s still most likely that PCS has more than one gene involved in its etiology and further studies need to be conducted to fully understand the causes behind PCS.

3.5.3. Treatment and Prevention

The usual treatment for piglets affected with PCS is tying the affected hindlimbs in the first days after birth. This increases mobility and ensures the piglet gets proper nutrition by facilitating the access to the sow's teats, decreasing the probability of death (Madson et al. 2019).

In milder cases, tying the limbs isn’t necessary but these piglets will need to be fed artificially or assisted to nurse and they will need extra care from the farm workers. Cross-fostering is also advised since it reduces competition. If these piglets survive the first week of life, they will recover completely and they will not differ clinically or histologically from non-affected pigs (Dewey 2006).

Management practices are important and advised to help avoid the occurrence of PCS. Non-slippery floors, the use of anti-mycotoxins products in feed, avoiding induced farrowing before day 113 and PRRS vaccination are all advised measures to help prevent this syndrome (Papatsiros 2012).

4. Materials and Methods

4.1. Farm Characteristics

The dataset used in this study was retrieved from a 200-sow farrow-to-finish commercial pig farm with a three-week farrowing batch system. About 120 dry sows were kept in a dynamic group. Every three weeks a batch of 20 to 30 sows was introduced to the group, four days after the first insemination. Pregnancy diagnosis was made by ultrasound at four weeks post-insemination. If pregnancy diagnosis was positive, sows would stay in the group, if it was negative, they would be drafted out to the service house to be artificially inseminated again. With the same frequency, another batch was relocated to individual farrowing crates one week before the expected date of parturition. After farrowing, the sows were kept in the individual farrowing crates with their respective litters until weaning.

4.2. Genetics

All sows were PIC-Hermitage Hybrid F1 Large White x Landrace and gilts were purchased from the same provider since 2016, when the farm was originally populated, so all sows have the same genetics. These sows are renowned for their prolificacy, longevity and mothering ability (PIC-Hermitage 2017).

The breeding program used by the farm was “Program I – Purchase Replacement Parent F1 Gilts” which consists in breeding a F1 parent gilt with a terminal line boar to birth a slaughter generation. Around 12 gilts were purchased every 7 weeks and all the purchased semen was pooled.

The semen used before the sire line change (old genetic) was the PIC® 800 Duroc which is a semen selected for rapid and robust growth, shorter throughput time, quality meat and high carcass value (PIC-Hermitage 2021). The semen used after the sire line change (new genetic) was the Topigs Norsvin TN Tempo which is a semen selected mainly for robustness, uniformity, vitality, growth rate and resistance to PRRS. It also seems to have some influence in the number of piglets born, with costumers reporting an increase of up to 0,5 liveborn pigs. Weaning weights of the offspring have also been reportedly higher than the ones of competitor boars (Topigs Norsvin 2021).

4.3. Data processing and analysis

Farrowing house data, weaning data and information on the genetics (sire line used for AI) were acquired for the purposes of this study. The data refers to the time period comprehended between May 28th of 2019 to March 26th of 2020 and it was collected using a swine herd management software (PigCHAMP (513) © Copyright PigCHAMP 2006-2010). Hand-written records, made by the farm workers, were also available and were used to complete missing information from the PigCHAMP records. Data management, cleaning and initial analysis were performed in Microsoft Office Excel® while further data visualizations and statistical analysis were conducted in R (VERSION 3.6.1) using RStudio (VERSION 1.2.5001.0) as an interface.

The studied dataset included 14 batches, seven with the old sire line genetic and the other seven with the new sire line genetic. Batches 1 to 7 correspond to the batches where it was used the old sire line genetic (PIC® 800 Duroc) and batches 8 to 14 correspond to the batches where it was used the new sire line genetic (Topigs Norsvin TN Tempo). The first batch using the Topigs Norsvin TN Tempo semen (batch 8) farrowed on the 23rd of October 2019.

Differences between farrowing house performance indicators and the two genetics used were analyzed using Kruskal Wallis tests. A Fisher test was used to test whether there was a statistical difference between the different causes of death across the two genetics. Piglet survival was modelled using logistic regression, while the number of dead piglets before weaning and the number of weaned piglets was modelled using a Poisson regression with offset. Alpha level for significance and tendency were 0.05 and 0.10, respectively.

4.4. Data handling and cleaning

The dataset used in this study had a total of 222 sows with 375 parturitions and a total number of 5446 born piglets. Most sows (n = 155) farrowed twice, once using the old genetic and another using the new genetic. Only 67 sows farrowed once in this period of time, therefore, using only one of the sire line genetics.

The first data analysis and description detected incomplete information such as:

- non-existing records of the weaning weight of piglets born from a few sows in batch 1 (n = 3), batch 8 (n = 1), batch 10 (n = 2) and from all the sows in batch 14 (n = 30);

- Contradicting information regarding the first farrowing of two sows (from batch 2 and 7) and non-existing records from a sow (when there should have been one).

Due to the gap between the information registered in PigCHAMP and the hand-written records available, the two sows with contradicting information were completely excluded from this study. The sows with missing records regarding their piglets' weaning weight were still included. There was also a sow with conflicting data (the time between the registered farrowings was of only two months, which is incompatible with reality) that was also excluded from this study.

Only minor differences were detected in the documents provided for most sows with duplicate records (i.e. PigCHAMP and hand-written records), with the differences being mainly in the number of born alive piglets and the piglets' birthweight. For the purpose of this study, when in the presence of two different records, only the most complete one was taken into account.

Sow parity ranged from 1 (first parity) to 10 (tenth parity), however, since the number of sows of parity 10 was very low, a new parity level called "Parity 9+" was created, grouping parities number 9 and 10. This facilitated analysis of the dataset.

5. Results

5.1. Data description

After gathering the data, the number of sows, the number of born piglets, the average number of piglets born per sow, the average birthweight, the average weaning weight, the average weaning age, the number of piglet deaths and mortality rate per batch, parity and genetic was analysed. The summary of the results can be observed in Tables 1, 2 and 3.

Table 1 – Batch description and summary of results during the study period (March 2019 to March 2020). For each batch, the number of sows, number of piglets born alive, average number of piglets born per sow, average piglet birthweight (in kilograms), average weight at weaning (in kilograms), total number of weaned pigs, total number of piglet pre-weaning deaths and pre-weaning mortality rate per batch are described.

Batch	Sows	No of Piglets	Piglets per Sow	Birth Weight (kg)	Weaning Weight (kg)	Weaned	Deaths	Mortality (%)
1	27	373	13.8 ±3.51	1.42 ±0.425	8.59 ±1.790	339	34	9.12
2	23	339	14.7 ±3.37	1.43 ±0.328	8.03 ±0.759	298	41	12.09
3	25	375	15.0 ±2.40	1.40 ±0.356	7.34 ±0.787	330	45	12.00
4	35	539	15.4 ±1.94	1.36 ±0.308	7.58 ±1.364	452	87	16.14
5	24	332	13.8 ±3.32	1.32 ±0.359	7.94 ±1.230	297	35	10.54
6	25	332	13.3 ±3.84	1.37 ±0.408	9.14 ±1.473	288	44	13.25
7	29	414	14.3 ±4.10	1.37 ±0.381	8.61 ±1.315	371	43	10.39
8	26	352	13.5 ±4.59	1.40 ±0.365	8.57 ±1.142	287	65	18.47
9	27	417	15.4 ±4.21	1.39 ±0.372	9.22 ±3.159	362	55	13.19
10	28	453	16.2 ±3.29	1.32 ±0.409	9.07 ±4.325	378	75	16.56
11	20	274	13.7 ±4.12	1.47 ±0.411	8.32 ±2.010	232	42	15.33
12	29	412	14.2 ±4.36	1.35 ±0.379	9.11 ±0.974	331	81	19.66
13	27	395	14.6 ±3.08	1.40 ±0.343	8.62 ±1.094	324	71	17.97
14	30	439	14.6 ±3.52	1.43 ±0.385	NA	374	65	14.81

The number of sows per batch ranged from 20 (batch 11) to 35 (batch 4), with a mean of 26.79 ± 3.556 sows and a median of 27 sows, while the number of piglets born alive ranged from 274 (batch 11) to 539 (batch 4), with a mean of 389 ± 65.1 piglets and a median of 385 piglets. This led to an average number of 14.5 ± 0.83 piglets per sow per batch. The lowest average number of piglets per sow was registered on batch 6 with a mean of 13.3 ± 3.84 piglets while the highest average number of piglets per sow was registered at batch 10 with 16.2 ± 3.29 piglets.

The average body weight at birth ranged from 1.32 ±0.409 kg (batch 10) to 1.47 ± 0.411 kg (batch 11), with a mean of 1.39 ± 0.043 kg and a median of 1.395 kg. At weaning, average body weight ranged from 7.34 ± 0.787 kg (batch 3) to 9.22 ± 3.159 kg (batch 9), with a mean of 8.47 ± 0.606 kg and a median of 8.59 kg. These values do not include batch 14 since the records for the weaning weight of the batch were not available. Average weaning age ranged from 26 ± 1.3 to 28 ± 1.9 days, with a mean of 27.07 ± 0.730 days and a median of 27 days.

The number of piglet deaths before weaning ranged from 34 (batch 1, corresponding to a mortality rate of 9.12%) to 87 deaths (batch 4, corresponding to a mortality rate of 16.14%). The highest mortality rate was registered on batch 12 (mortality rate of 19.66% with a total number of 81 deaths) and the lowest mortality rate was registered on batch 1 (mortality rate of 9.12% with a total number of 34 deaths). The mean number of dead piglets before weaning was 55.93 ± 17.791 deaths, with a median of 50 deaths, while the mean mortality rate was 14.25 ± 3.260%, with a median of 14.03%.

The number of weaned piglets ranged from 232 (batch 11, weaning rate of 84.67%) to 452 piglets (batch 4, weaning rate of 83.86%). The highest weaning rate was registered on batch 1 (weaning rate of 90.88% with a total of 339 weaned piglets) and the lowest weaning rate was registered on batch 12 (weaning rate of 80.24% with a total of 331 weaned piglets). The mean number of weaned piglets was 333.07 ± 53.454 piglets, with a median of 330.5 piglets, while the mean weaning rate was 87.75 ± 3.260%, with a median of 85.97%.

Table 2 – Description of results by sow parity with number of sows, total number of piglets born alive, average number of piglets born per sow, average birthweight (in kilograms), average weight at weaning (in kilograms), total number of weaned pigs, total number of piglet pre-weaning deaths and pre-weaning mortality rate.

Parity	Sows	No of Piglets	Piglets per Sow	Birth Weight (kg)	Weaning Weight (kg)	Weaned	Deaths	Mortality (%)
1	68	964	14.2 ±3.35	1.33 ±0.300	8.15 ±1.157	863	101	10.48
2	47	687	14.6 ±3.99	1.43 ±0.357	8.70 ±2.632	632	55	8.01
3	43	653	15.2 ±2.62	1.39 ±0.347	8.36 ±1.191	583	70	10.72
4	40	616	15.4 ±4.08	1.33 ±0.396	8.84 ±1.242	523	93	15.10
5	44	677	15.4 ±2.32	1.42 ±0.371	8.08 ±1.833	565	112	16.54
6	34	515	15.2 ±3.77	1.37 ±0.396	8.55 ±1.738	402	113	21.94
7	31	432	13.9 ±3.51	1.42 ±0.398	8.41 ±1.452	360	72	16.67
8	48	641	13.4 ±4.66	1.38 ±0.441	8.96 ±3.824	518	123	19.19
9+	17	261	15.3 ±6.48	1.45 ±0.396	7.84 ±1.263	217	44	16.86

The number of sows per parity ranged from 17 (parity 9+) to 68 (parity 1), with a mean of 41.33 ± 13.928 sows and a median of 43 sows, while the number of piglets born alive ranged from 261 (parity 9+) to 964 (parity 1), with a mean of 605.11 ± 193.931 piglets and a median of 641 piglets. This led to an average number of 14.73 ± 0.750 piglets per sow per parity. The lowest average number of piglets born per sow was registered on parity 8 with a mean of 13.4 ± 4.66 piglets while the highest average number of piglets per sow was registered on parity 4 with 15.4 ± 4.08 piglets.

Average body weight at birth ranged from 1.33 ± 0.396 kg (parity 4) to 1.45 ± 0.396 kg (parity 9+), with a mean of 1.39 ± 0.043 kg and a median of 1.39 kg. At weaning, average body weight ranged from 7.84 ± 1.263 kg (parity 9+) to 8.96 ± 3.824 kg (parity 8), with a mean of 8.43 ± 0.369 kg and a median of 8.41 kg. Average weaning age was 27 days in all parities and it did not vary.

The number of piglet deaths before weaning ranged from 44 (parity 9+, corresponding to a mortality rate of 16.86%) to 123 deaths (parity 8, corresponding to a mortality rate of 19.19%). The highest mortality rate was registered on parity 6 (mortality rate of 21.94% with a total number of 113 deaths) and the lowest mortality rate was registered on parity 2 (mortality rate of 8.01% with a total number of 55 deaths). The mean number of dead piglets before weaning was 87 ± 27.9 deaths, with a median of 93 deaths, while the mean mortality rate was 15.06 ± 4.499%, with a median of 16.54%.

The number of weaned piglets ranged from 217 (parity 9+, weaning rate of 83.14%) to 863 piglets (parity 1, weaning rate of 89.52%). The highest weaning rate was registered on parity 2 (weaning rate of 91.99% with a total of 632 weaned piglets) and the lowest weaning rate was registered on parity 6 (weaning rate of 78.06% with a total of 402 weaned piglets). The mean number of weaned piglets was 518.11 ± 182.86 piglets, with a median of 523 piglets, while the mean weaning rate was 84.94 ± 4.499%, with a median of 83.46%.

Table 3 – Description of results by sire line genetics with number of sows, number of piglets born alive, average number of piglets born per sow, average birthweight (in kilograms), average weight at weaning (in kilograms), number of weaned pigs, number of piglet pre-weaning deaths and pre-weaning mortality rate. Batch 1 to 7 used the old sire line genetic while batches 8 to 14 used the new sire line genetic.

Genetic	Sows	No of Piglets	Piglets per Sow	Birth Weight (kg)	Weaning Weight (kg)	Weaned	Deaths	Mortality (%)
Old	188	2704	14.4 ±3.28	1.38 ±0.367	8.14 ±1.416	2375	329	12.17
New	187	2742	14.7 ±3.93	1.39 ±0.383	8.86 ±2.569	2288	454	16.56

When comparing the two genetics, the number of sows ranged from 187 to 188, with a mean of 187.5 ± 0.71 sows and a median of 187,5 sows, while the number of piglets born alive ranged from 2704 to 2742, with a mean of 2723 ± 26.9 piglets and a median of 2723 piglets. This led to an average number of 14.52 ± 0.198 piglets per sow per batch. The lowest average number of piglets per sow was registered on the old genetic with a mean of 14.4 ± 3.28 piglets while the highest average number of piglets per sow was registered on the new genetic with 14.7 ± 3.93 piglets.

Average body weight at birth ranged from 1.38 ± 0.367 kg to 1.39 ± 0.383 kg, with a mean of 1.385 ± 0.007 kg and a median of 1.385 kg. At weaning, average body weight ranged from 8.14 ± 1.416 kg to 8.86 ± 2.569 kg, with a mean of 8.5 ± 0.51 kg and a median of 8.5 kg. Average weaning age was 27 days in both genetics and it did not vary.

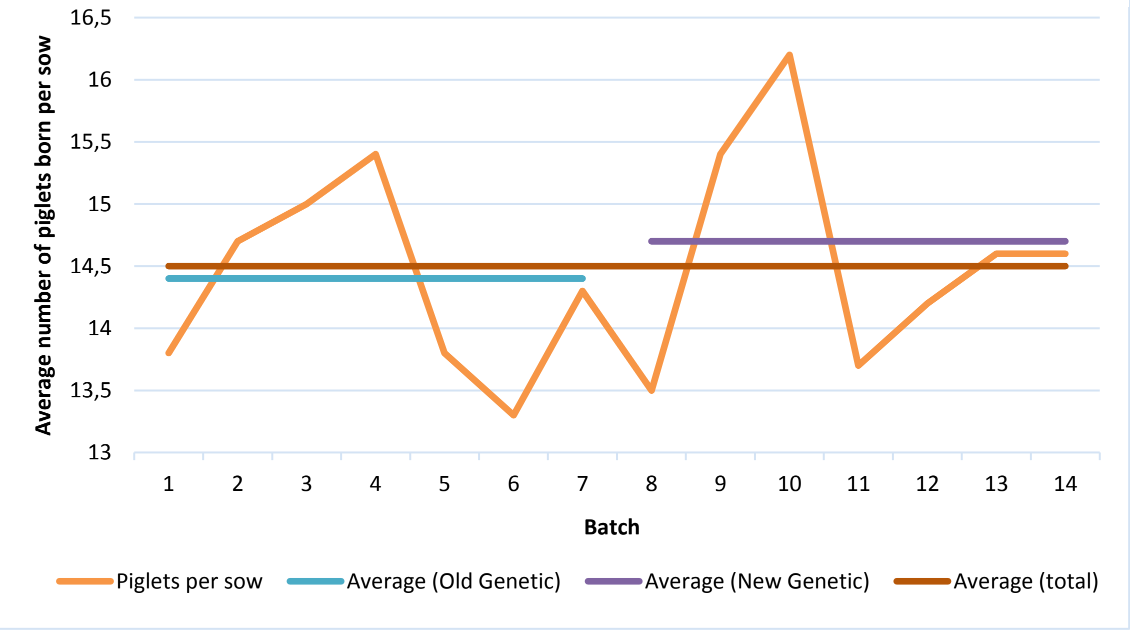
The number of piglet deaths before weaning ranged from 329 (corresponding to a mortality rate of 12.17%) to 454 deaths (corresponding to a mortality rate of 16.56%). The mean number of dead piglets before weaning was 391.5 ± 88.39 deaths, with a median of 391.5 deaths, while the mean mortality rate was 14.36 ± 3.104%, with a median of 14.365%.

There were a total of 2375 weaned piglets in the old genetic, with a weaning rate of 87,83%, and a total of 2288 weaned piglets in the new genetic, with a weaning rate of 83,44%. The mean number of weaned piglets was 331.05 ± 61.518 piglets, with a median of 331.5 piglets, while the mean weaning rate was 85.63 ± 3.104%, with a median of 85.635%.

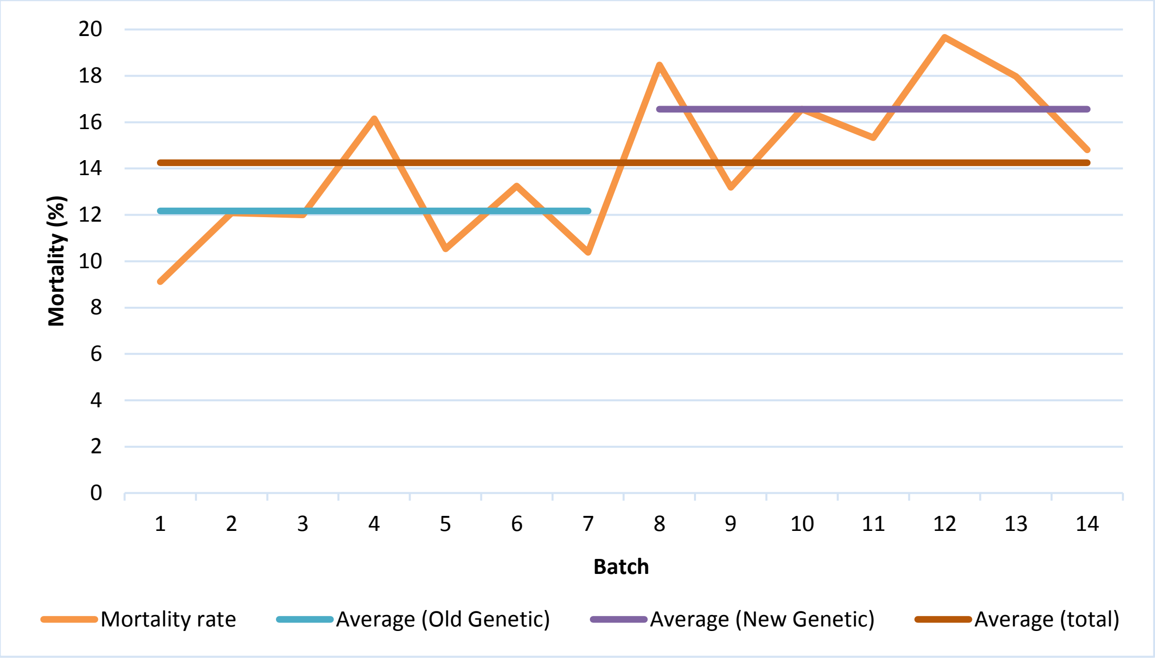
There were no statistical differences across the two sire lines regarding the number of sows, total number of piglets born alive, average number of piglets born per sow, average birth weight, average weaning weight, average weaning days, total number of weaned pigs or total number of deaths (P > 0.05). However, pre-weaning mortality rate and weaning rate were statistically different between genetics (P = 0.009).

Average number of piglets born per sow, mortality rate and average birthweight per batch and per parity are presented in graphs 1 to 6. Graphs for total number of born alive and total number of preweaning deaths per batch and parity can be found in Annexes 1 to 4.

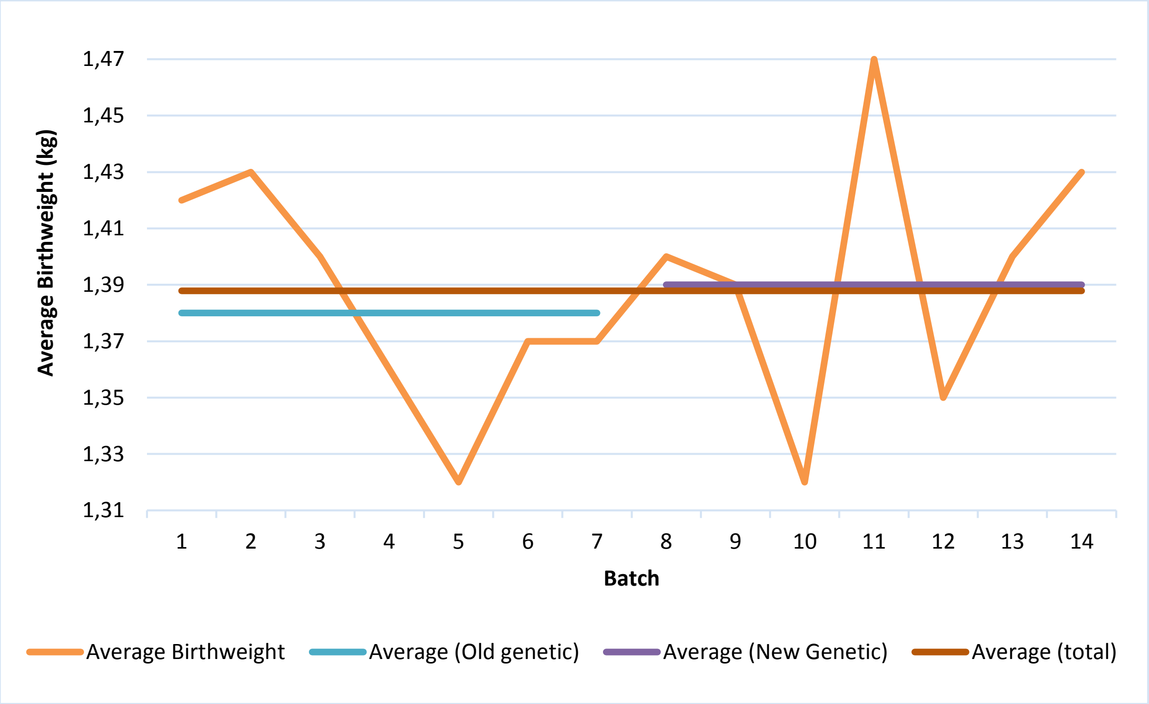
Graph 1 - Average number of piglets born per sow (litter size) per batch.



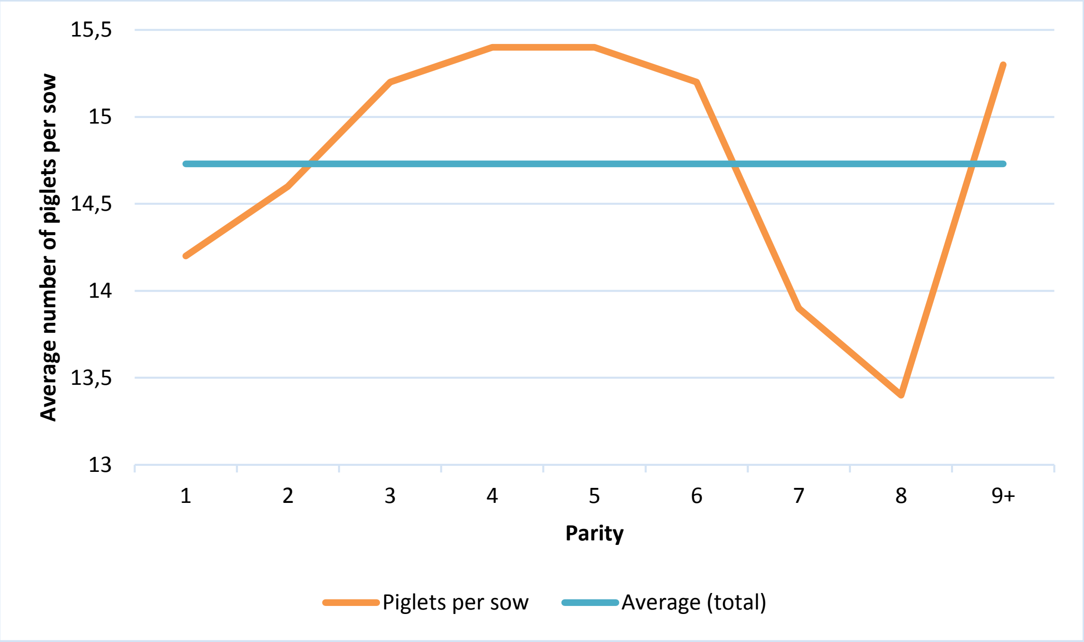
Graph 2 – Pre-weaning mortality rate (%) per batch.



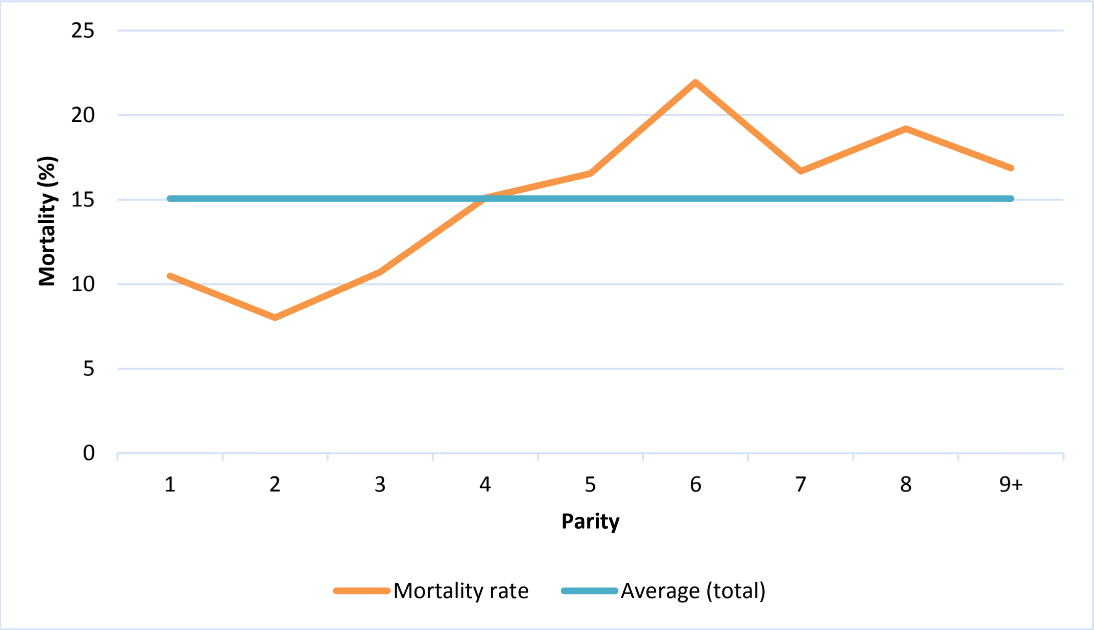
Graph 3 - Average birthweight (kg) per batch.



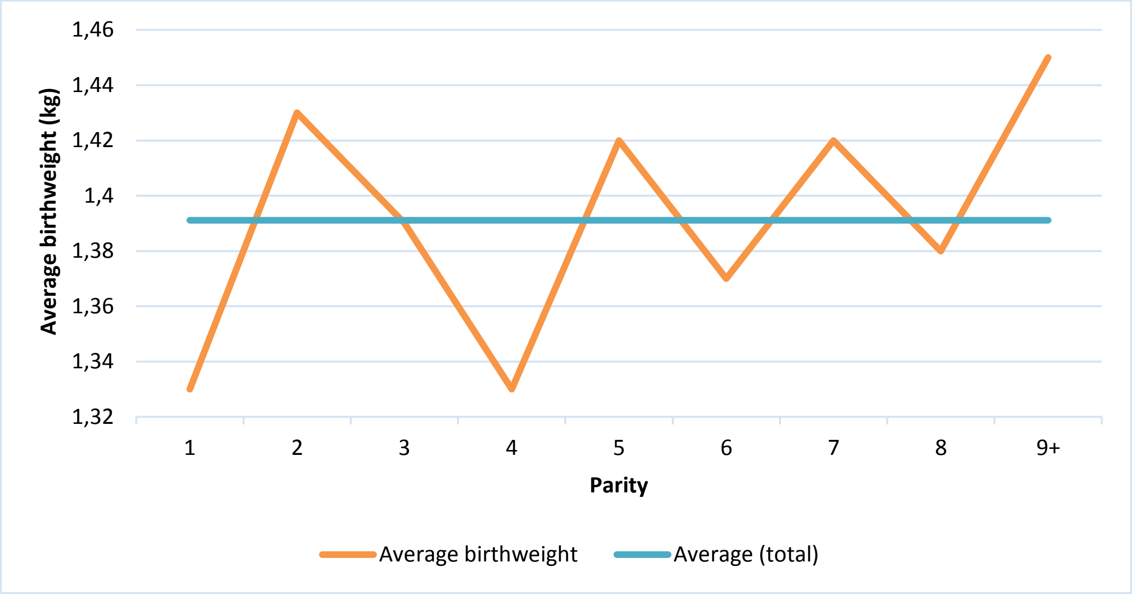
Graph 4 - Average number of piglets born per sow (litter size) per parity.



Graph 5 – Pre-weaning mortality rate (%) per parity.

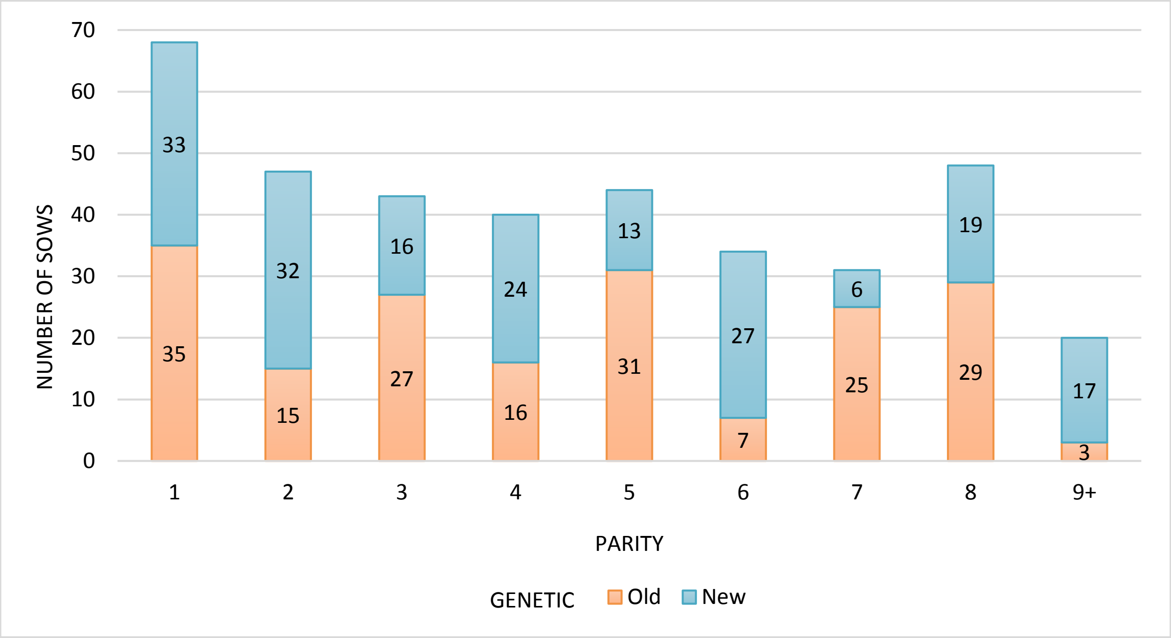


Graph 6 - Average birthweight (kg) per parity.



The number of sows per parity and per genetic is presented in graph 7.

Graph 7 - Distribution of the number of sows per parity and per genetic.



Both genetics registered the highest number of sows in parity 1. The old genetic registered a total of 77 sows in the first three parities, while the new genetic registered a total number of 81 sows. The total number of mid parity sows (parities 4, 5 and 6) was 54 in the old genetic and 64 in the new genetic. The total number of older sows (parities 7, 8 and 9+) was 57 in the old genetic and 42 in the new genetic. The new genetic had more low and mid parity sows, while the old genetic had more high parity sows.

The causes of death across the two different sire line genetics used on farm are presented in Table 4.

Table 4 - Summary of causes of death (pre-weaning mortality) across the two genetics with Fisher test results (p values).

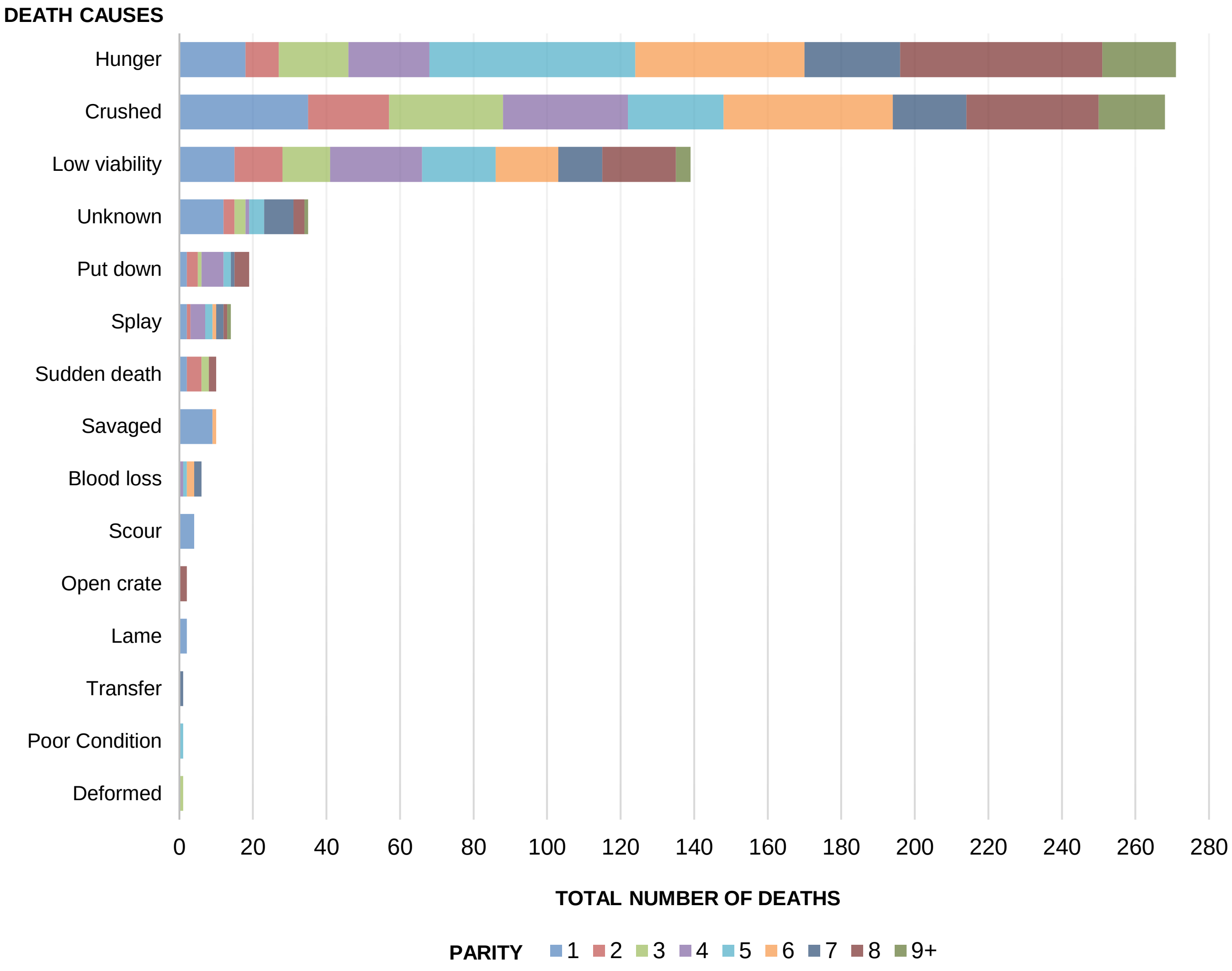
Causes	Genetic				p values
	Old		New		
	No	%	No	%	
Blood loss	4	1.22	2	0.44	0.245
Crushed	96	29.18	172	37.89	0.012 *
Deformation	0	0	1	0.22	1
Hunger	138	41.95	133	29.30	<0.001 ***
Lame	2	0.61	0	0	0.176
Low viability	61	18.54	78	17.18	0.637
Open crate	0	0	2	0.44	0.512
Poor Condition	1	0.30	0	0	0.420
Put down	9	2.74	10	2.20	0.645
Savaged	1	0.30	9	1.98	0.051 .
Scour	0	0	4	0.88	0.143
Splay leg	4	1.22	10	2.20	0.416
Sudden death	4	1.22	6	1.32	1
Transfer	0	0	1	0.22	1
Unknown	9	2.74	26	5.73	0.054 .
Total	**329**	**100**	**454**	**100**	**-**

Significance levels: <0.001 '***', 0.01 '**', 0.05 '*', 0.1 '.'

Most deaths in both the old and the new genetic occurred due to hunger/starvation, low viability and being crushed. When compared to the old genetic, the new genetic had more deaths due to being crushed, deformation, open crates, savaging, scour, splay leg, sudden death, transfers and unknown causes. However, less deaths occurred due to blood loss, hunger, lameness, low viability, poor condition and being put down. Crushing and hunger were the only causes of death that varied significantly when the sire line genetic changed (P = 0.012 and P <0.001, respectively), and there was a tendency for savaging and unknown to be statistically significant (P = 0.051 and P = 0.054, respectively).

The total number of preweaning deaths per cause of mortality and per parity is presented in graph 8.

Graph 8 – Total number of preweaning deaths per cause of death and per parity.



Most deaths, in all parities, were due to hunger/starvation, being crushed or low viability. Most deaths due to savaging, scour, lameness and unknown causes occurred in the first parity, with deaths by scour and lameness occurring exclusively in this parity. Savaging occurred almost exclusively in parity 1. Death due to hunger was higher in parities 5 and 8 and lower in parity 2. Death due to crushing was higher in parity 6 and lower in parity 9+. Death by unknown causes and splay leg occurred in all parities except parity 6 and parity 3, respectively. Most deaths due to low viability, splay leg and being put down occurred in parity 4. Death by blood loss only occurred in parities 4, 5, 6 and 7 and sudden deaths only occurred in parities 1, 2, 3 and 8. Deaths by open crate, poor condition, being transferred and being deformed exclusively occurred in parities 8, 5, 7 and 3, respectively. Annex 5 shows the distribution of causes of death per parity in percentage.

5.2. Data analysis

The relationships between the number of preweaning dead piglets and parity, genetic and birth weight are presented in tables 5 and 6.

Table 5 - Logistic regression and odds ratio (alpha = 0.05) estimates of the occurrence of preweaning death depending on parity, genetic and individual birth weight (kg).

	Estimate	SE	Odds Ratio [95%]	p
Intercept	1.593	0.234	0.077	<0.001 ***
Parity	0.151	0.031	1.163	<0.001 ***
Genetic				
Old	-	-	-	-
New	0.319	0.071	1.376	<0.001 ***
Birth Weight (kg)	-3.406	0.153	0.033	<0.001 ***

Significance levels: <0.001 '***', 0.01 '**', 0.05 '*', 0.1 '.'

Preweaning mortality varied significantly with parity, genetic and individual birth weight (P <0.001). The higher the parity, the higher was the probability of preweaning death. Each increased unit in parity corresponded to an increase of 16,3% in the probability of dying before weaning. When the sire line changed, the probability of preweaning death also increased. The change for the new sire line genetic led to an increase of 37,6% in the probability of dying before weaning. On the other hand, the higher the individual birth weight, the lower was the probability of preweaning death. Increasing 1 kilogram in individual birth weight would lead to a decrease of 96,7% in the probability of dying before weaning.

Table 6 - Poisson modelling estimates with offset (litter size) of the number of preweaning dead piglets depending on parity, genetic and average birth weight (kg).

	Estimate	SE	p
Intercept	-0.680	0.328	0.038 *
Parity	0.105	0.020	<0.001 ***
Genetic			
Old	-	-	-
New	0.227	0.055	<0.001 ***
Average Birth Weight (kg)	-1.392	0.233	<0.001 ***

Significance levels: <0.001 '***', 0.01 '**', 0.05 '*', 0.1 '.'

Preweaning mortality varied significantly with parity, genetic and average birth weight (P <0.001). The higher the parity, the higher was the number of preweaning dead piglets. Each increased unit in parity corresponded to an increase in the number of preweaning dead piglets by 0.105 units. When the sire line changed, the number of preweaning dead piglets also increased. The change for the new sire line genetic increased the number of preweaning dead piglets by 0.227 units. On the other hand, the average birth weight decreased the number of preweaning dead piglets. With each unit increased in average birth weight, there was a decrease in the number of preweaning dead piglets by 1.392 units.

The relationships between weaned pigs and parity, genetic and average birth weight are presented in table 7.

Table 7 - Poisson modelling estimates with offset (litter size) of the number of weaned pigs depending on parity, genetic and average birth weight (kg).

	Estimate	SE	p
Intercept	-0.394	0.0980	<0.001 ***
Parity	-0.018	0.006	0.002 **
Genetic			
Old	-	-	-
New	-0.038	0.021	0.064 .
Average Birth Weight (kg)	0.229	0.069	<0.001 ***

Significance levels: <0.001 '***', 0.01 '**', 0.05 '*', 0.1 '.'

Weaning rate varied significantly with parity and average birth weight (P = 0.002 and P <0.001, respectively), and there was a tendency for genetic to be statistically significant (P = 0.064). The higher the parity, the lower was the number of weaned dead pigs. Each increased unit in parity corresponded to a decrease in the number of weaned pigs by 0.018 units. When the sire line changed, the number of weaned pigs also decreased. The change for the new sire line genetic decreased the number of weaned pigs by 0.038 units. On the other hand, the average birth weight increased the number of weaned pigs. With each unit increased in average birth weight, there was an increasement in the number of weaned pigs by 0.229 units.

6. Discussion

In this work, farm data from a 200-sow farrow-to-finish farm was described and analysed, along with the possible differences in the reproductive and productive performances of two sire line genetics. A total of 375 parturitions were studied and the relationships between total number of sows, total number of born alive piglets, average litter size, average birthweight, average weaning weight, total number of preweaning deaths, total weaned pigs and parity were investigated.

In the farm used in this study, the average number of piglets born alive per sow lines up with the common scenario, reported by Quesnel et al. (2015), of sows farrowing 14 to 16 piglets per batch. The average number of piglets born per sow per batch (14.5 ± 0.83), per parity (14.73 ± 0.750) and per genetic (14.52 ± 0.198) were all slightly above national average (14.12 in 2019 and 14.26 in 2020), reported by Teagasc (2021). The parities with the highest average number of piglets born alive per sow were registered in parities 4 and 5, which is consistent with previous findings claiming that litter size peaks at mid-parity sows (Milligan et al. 2002).

The lowest average birth weight was registered in the same batch and parity than the highest average number of piglets born per sow (batch 10 and parity 4). Moreover, the highest average birth weight was registered in same batch and parity than the lowest number of piglets born alive (batch 11 and parity 9+). These findings line up with the already reviewed relationship between litter size and birth weight: when the maximum uterine capacity is reached, an increase in either total number of piglets born or average litter birth weight will lead to a decrease in the respective other trait (Kapell et al. 2011). Batch 10 and parity 4 also had one of the highest birth weight variations between individuals (SD = 0.409 and SD = 0.396, respectively), which is in concordance with findings by Milligan et al. (2002), that suggest that increased litter sizes have a higher within-litter birth weight variation. The first parity had the second lowest average birth weight and parity 9+ had the highest. This is also consistent with previous findings claiming that birth weight is lower in gilts and higher in older sows (Milligan et al. 2002). As for the relationships between birth weight and survival, number of preweaning dead piglets and number of weaned pigs, increasing individual birth weight improved the probability of survival (P <0.001), while an increasement in average birth weight decreased the number of preweaning dead piglets (P <0.001) and increased the number of weaned pigs (P <0.001). These findings are all in concordance with the literature (Roehe and Kalm 2000; Milligan et al. 2002; Fix et al. 2010; Kapell et al. 2011; Muns et al. 2016).

Although the records for the weaning weight of batch 14 were missing, the data from other batches could confirm that the average weaning weight in the new genetic was higher when compared with the old genetic, which coincides with previous reports from the genetic company (Topigs Norsvin 2021).

Preweaning mortality rate was higher than national average (11%) in most batches and parities, but it was within the usual range of preweaning mortality rates registered in most commercial farms around the world (10% to 20%), except for parity 6, that registered a preweaning mortality rate of 21.94%. Parity 2 registered the lowest preweaning mortality rate (8.01%) and the highest average birthweight, which may have a correlation with previous reports by Devillers et al. (2007), claiming that colostrum yield is higher in second and third parity sows. As for the relationships between parity and survival, number of preweaning dead piglets and number weaned pigs, increasement in parity decreased the probability of survival (P <0.001) and the number of weaned pigs (P = 0.002) and increased the number of preweaning dead piglets (P <0.001). These findings are in concordance with Milligan et al. (2002), that reported that piglets with low birth weight and from sows of sixth parity or older have significantly lower chances of survival.

As for the two genetic lines, the new genetic had a higher total number of born alive piglets, higher average number of piglets born per sow, higher average birth weight and higher average weaning weight, but it had also higher variations between individuals in the average number of piglets born per sow (SD = 3.93), average birth weight (SD = 0.383) and average weaning weight (SD = 2.569). Moreover, the new genetic also registered less weaned pigs and more preweaning deaths, as well as, a lower weaning rate and a higher preweaning mortality rate, with these last two being statistically different when compared with the old genetic (P = 0.009). These findings are in concordance with Grandison et al. (2002) and Su et al. (2008), who reported that increased birth weight will not, necessarily, result in higher overall survival rate. As for the relationships between the genetic lines and survival, number of preweaning dead piglets and number weaned pigs, the change for the new sire line genetic decreased the probability of survival (P <0.001) and the number of weaned pigs (P = 0.064) and increased the number of preweaning dead piglets (P <0.001). These findings are also in concordance with Elbert et al. (2021), who reported that sire line has an effect on vitality, litter traits, number of born alive piglets and number of weaned pigs per sow.

The higher mortality rate in the new genetic could have been caused by the increasement in total number of born alive piglets and larger litters, since these two parameters have been associated with higher preweaning mortality, as reported by Varona et al. (2020). The semen used in the new sire line genetic is a semen selected for vitality, growth and increased litter sizes, while the dam line used was a line selected for prolificacy and mothering abilities. As suggested by Elbert et al. (2021), further selection for litter size is not a good strategy in terms of animal welfare and production efficiency. A more successful strategy would be to maintain litter size at a high level and select for survivability in the sire line. Furthermore, using a Duroc terminal sire line genetic, like the one used before the change in sire lines, might be beneficial to improve piglet's survival, as suggested by Pedersen et al. 2019.

Another possible reason for the increased preweaning mortality in the new genetic is that the farm used in this study is considered a small farm (<570 sows) and smaller farms usually have less workers so when litter size increases, it becomes harder for this type of farms to control preweaning mortality, as suggested by Koketsu et al. (2021).

Most preweaning deaths occurred due to being crushed by the sow, hunger/starvation and low viability, but only crushing and hunger were statistically different between genetics (P = 0.012 and P <0.001, respectively), with crushing being higher in the new genetic line and hunger being higher in the old genetic line. A possible explanation for the increase in deaths by crushing in the new genetic could be the registered increase in litter size, which is a known risk factor for death by crushing, as reported by Muns et al. (2016). As for death by hunger being higher in the old genetic, that could be explained by the fact that there was a higher number of older sows in the old genetic when compared to the new genetic. As reported by Vasdal and Andersen (2012), older sows have reduced and more variable function and accessibility of teats, which can lead to insufficient colostrum intake and, consequently, death by starvation.

As for death by low viability, the difference between genetic lines was not statistically significant, albeit there were more registered deaths by low viability in the new genetic and in mid parity sows. According to Rutherford et al. (2013), prolonged farrowings and large litter sizes are associated with perinatal asphyxia and are known risk factors for low viability. Prolonged farrowing is more common in higher parity sows (Zaleski and Hacker 1993; Alonso-Spilsbury et al. 2005) and larger litter sizes were registered in the new genetic, so these are possible explanations for the increase in deaths by low viability in these two subgroups.

There was a tendency for savaging and unknown to be causes of death statistically higher in the new genetic (P = 0.051 and P = 0.054, respectively). Savaging usually occurs in gilts that are aggressive or fearful of humans and piglets. The results confirmed this, since savaging occurred almost exclusively in parity 1. However, the dam line did not change and the number of gilts in both genetics was about the same so these results could be a consequence of poor stockmanship skills. As for the unknown causes, it can reflect poor stockmanship skills or insufficient number of stockhandlers. It is recommended that stockhandlers are more attentive to the animals around farrowing to prevent both of these causes of death (Baxter et al. 2013; Jääskeläinen et al. 2014). It is also recommended the culling of savaging sows, since this a behavior that tends to persist across parities (Harris et al. 2003; Harris and Gonyou 2003).

As previously stated, parity 1 had the second lowest birthweight and had the higher number of deaths by crushing and all deaths by scour. According to Herpin et al. (2002), piglets with low birthweight are at a higher risk of suffering from hypothermia, which is rarely recorded as a primary cause of death, but can lead to death by other causes such as crushing and disease, as reported by Edwards (2002).

Although death by splay leg was not statistically different between genetic lines, there was an increase in the number of registered deaths by this cause in the new genetic. Farm workers have also reported that there was an increase in the overall number of splay leg cases in this genetic line. Having only registered deaths in consideration, the incidence of splay leg in the new genetic coincide with the assumed incidence of 0,4% reported by Papatsiros (2012), however, not all affected piglets in the farm used in this study died or were registered. Since splay leg is known to have a genetic predisposition, this increase could be a result of the sire line change. It could also be due to the fact that larger litters have higher incidence of this syndrome, as reported by Van Der Heyde et al. (1989). Moreover, the increase number of splay leg cases could also present an explanation for the increased number of deaths by crushing registered in the new genetic, since splay leg is a known risk factor for death by crushing, as reported by Lax (1971).

There were some limitations to this study. Eventual health impairments of the study group were not accounted for, which is a factor that could have caused an impact on the reproductive and productive performance of this farm. Another limitation is that the raw data collected had some missing and contradicting records so this analysis should be interpreted with caution. The usage of software like PigCHAMP has helped the farm workers to keep more complete and organized records with the possibility of accessing and exporting data more easily, but there was still a divergence in information when compared with hand-written records. As reported by Strange et al. (2013), it is important that raw data is precise for a correct analysis, therefore, a recommendation for this farm would be to improve the precision of their records for a more accurate analysis, which will lead to better decision-making.

Based on the results of this work, the changing in the sire line genetic was not a helpful management strategy for this farm, since it led to higher preweaning mortality and lower total number of weaned pigs. The genetic selection strategy of this farm should focus on selecting against perinatal mortality since it has been reported to have a positive correlation with the number of weaned pigs and overall survival rate at birth (Su et al. 2007; Su et al. 2008). Moreover, there were several undesirable outcomes due to high parity sows, so culling older sows is recommended for a more efficient production and lower preweaning mortality rates.

7. Conclusion

The results in this study were consistent with the literature findings. These include the effect that birthweight, litter size and parity have on preweaning mortality and number of weaned pigs, the importance of adequate management strategies and skilled stockmanship in herd production and the influence of genetic selection in survivability and litter traits. The theory that sire line has an effect on litter traits and piglet’s vitality is supported by this study. Nonetheless, further studies should be conducted to confirm the extent of this relationship.

This work highlights the importance of having robust data for internal benchmarking, monitoring and decision-making and the relevance of having an adequate information system to support both production efficiency and quality standards in commercial swine herds. Data should be collected thoroughly, analysed by professionals and handed to producers, in order to make informative decisions. This will lead to better reproductive and productive performances.

8. Bibliography

Abah K, Itodo J, Ubah S, Shettima I. 2019. Reproductive performance of pigs raised by intensive management system in Abuja, Nigeria. Vet World. 12(2):305–308. doi:10.14202/vetworld.2019.305-308.

Agostini PDS, Manzanilla EG, De Blas C, Fahey AG, Da Silva CA, Gasa J. 2015. Managing variability in decision making in swine growing-finishing units. Ir Vet J. 68(1):20. doi:10.1186/s13620-015-0048-z.

Alonso-Spilsbury M, Mota-Rojas D, Villanueva-García D, Martínez-Burnes J, Orozco H, Ramírez-Necoechea R, Mayagoitia AL, Trujillo ME. 2005. Perinatal asphyxia pathophysiology in pig and human: a review. Anim Reprod Sci. 90:1–30. doi:10.1016/j.anireprosci.2005.01.007.

Andersen HML, Pedersen LJ. 2016. Effect of radiant heat at the birth site in farrowing crates on hypothermia and behaviour in neonatal piglets. Animal. 10(1):128–134. doi:10.1017/S1751731115001913.

Andersen IL, Tajet GM, Haukvik IA, Kongsrud S, Bøe KE. 2007. Relationship between postnatal piglet mortality, environmental factors and management around farrowing in herds with loose-housed, lactating sows. Acta Agric Scand Sect A — Anim Sci. 57(1):38–45. doi:10.1080/09064700601159626.

Baxter EM, Jarvis S, Sherwood L, Robson SK, Ormandy E, Farish M, Smurthwaite KM, Roehe R, Lawrence AB, Edwards SA. 2009. Indicators of piglet survival in an outdoor farrowing system. Livest Sci. 124:266–276. doi:10.1016/j.livsci.2009.02.008.

Baxter EM, Lawrence AB, Edwards SA. 2011. Alternative farrowing systems: design criteria for farrowing systems based on the biological needs of sows and piglets. Animal. 5(4):580–600. doi:10.1017/S1751731110002272.

Baxter EM, Rutherford KMD, D'Eath RB, Arnott G, Turner SP, Sandøe P, Moustsen VA, Thorup F, Edwards SA, Lawrence AB. 2013. The welfare implications of large litter size in the domestic pig II: Management factors. Anim Welf. 22(2):219–238. doi:10.7120/09627286.22.2.219.

Benjamin M, Yik S. 2019. Precision livestock farming in swinewelfare: A review for swine practitioners. Anim. 9(4):133. doi:10.3390/ani9040133.

Cador C, Rose N, Willem L, Andraud M. 2016. Maternally Derived Immunity Extends Swine Influenza A Virus Persistence within Farrow-to-Finish Pig Farms: Insights from a Stochastic Event-Driven Metapopulation Model. PLoS One. 11(9). doi:10.1371/journal.pone.0163672.

Cunha T. 1968. Spraddled hind legs may be a result of a choline deficiency. Feedstuffs. 40:25.

Devillers N, Farmer C, Le Dividich J, Prunier A. 2007. Variability of colostrum yield and colostrum intake in pigs. Animal. 1(7):1033–1041. doi:10.1017/S175173110700016X.

Dewey CE. 2006. Diseases of the Nervous and Locomotor Systems. In: Straw BE, Zimmerman JJ, D'Allaire S, Taylor DJ, editors. Diseases of Swine. 9th ed. Ames, Iowa: Blackwell Publishing. p. 87–111.

Dewey CE, Straw BE. 2006. Herd Examination. In: Straw BE, Zimmerman JJ, D'Allaire S, Taylor DJ, editors. Diseases of Swine. 9th ed. Ames, Iowa: Blackwell Publishing. p. 3–

14.

Dufrasne M, Misztal I, Tsuruta S, Gengler N, Gray KA. 2014. Genetic analysis of pig survival up to commercial weight in a crossbred population. Livest Sci. 167(1):19–24. doi:10.1016/j.livsci.2014.05.001.

Edwards SA. 2002. Perinatal mortality in the pig: environmental or physiological solutions? Livest Prod Sci. 78(1):3–12. doi:10.1016/S0301-6226(02)00180-X.

Elbert K, Matthews N, Wassmuth R, Tettens J. 2021. Vitality in relation to litter size of crossbred pigs and the effect of the terminal sire line. Anim Prod Sci. 61:1519–1525. doi:10.1071/AN20424.

Fangman TJ, Amass SF. 2007. Postpartum Care of the Sow and Neonates. In: Youngquist RS, Therlfall WR, editors. Current Therapy in Large Animal Theriogenology. 2nd ed. W.B. Saunders. p. 784–788.

Ferrari C V, Sbardella PE, Bernardi ML, Coutinho ML, Vaz Jr IS, Wentz I. 2014. Effect of birth weight and colostrum intake on mortality and performance of piglets after cross-fostering in sows of different parities. Prev Vet Med. 114(3–4):259–66. doi:10.1016/j.prevetmed.2014.02.013.

Fix JS, Cassady JP, Holl JW, Herring WO, Culbertson MS, See MT. 2010. Effect of piglet birth weight on survival and quality of commercial market swine. Livest Sci. 132(1–3):98–106. doi:https://doi.org/10.1016/j.livsci.2010.05.007.

Grandinson K, Lund MS, Rydhmer L, Strandberg E. 2002. Genetic Parameters for the Piglet Mortality Traits Crushing, Stillbirth and Total Mortality, and their Relation to Birth Weight. Acta Agric Scand Sect A — Anim Sci. 52(4):167–173. doi:10.1080/090647002762381041.

Hao X, Plastow G, Zhang C, Xu S, Hu Z, Yang T, Wang K, Yang H, Yin X, Liu S, et al. 2017. Genome-wide association study identifies candidate genes for piglet splay leg syndrome in different populations. BMC Genet. 18:64. doi:10.1186/s12863-017-0532-4.

Harris MJ, Gonyou HW. 2003. Savaging behaviour in domestic gilts: A study of seven commercial farms. Can J Anim Sci. 83(3):435–444. doi:10.4141/A02-001.

Harris MJ, Li YZ, Gonyou HW. 2003. Savaging behaviour in gilts and sows. Can J Anim Sci. 83(4):819–821. doi:10.4141/A02-111.

Herpin P, Damon M, Le Dividich J. 2002. Development of thermoregulation and neonatal survival in pigs. Livest Prod Sci. 78(1):25–45. doi:10.1016/S0301-6226(02)00183-5.

Van Der Heyde H, De Mets JP, Porreye L, Henderickx H, Calus A, Bekaert H, Buysee F. 1989. Influence of Season, Litter Size, Parity, Gestation Length, Birth Weight, Sex and Farrowing Pen on Frequency of Congenital Splayleg in Piglets. Livest Prod Sci. 21:143–155. doi:10.1016/0301-6226(89)90045-6.

Hollifield MK, Lourenco D, Tsuruta S, Bermann M, Howard JT, Misztal I. 2021. Impact of including the cause of missing records on genetic evaluations for growth in commercial pigs. J Anim Sci. 99(8). doi:10.1093/jas/skab226.

Ibáñez-Escriche N, Varona L, Quintanilla R, Noguera JL. 2009. Bayesian threshold analysis of direct and maternal genetic parameters for piglet mortality at farrowing in Large

White, Landrace, and Pietrain populations. J Anim Sci. 87(1):80–87. doi:10.2527/jas.2007-0670.

Jääskeläinen T, Kauppinen T, Vesala KM, Valros A. 2014. Relationships between pig welfare, productivity and farmer disposition. Anim Welf. 23(4):435–443. doi:10.7120/09627286.23.4.435.

Jeong J, Kim S, Park KH, Kang I, Park SJ, Park C, Chae C. 2017. Evaluation of the effect of a porcine reproductive and respiratory syndrome (PRRS) modified-live virus vaccine on sow reproductive performance in endemic PRRS farms. Vet Microbiol. 208:47–52. doi:10.1016/j.vetmic.2017.07.016.

Kapell DNRG, Ashworth CJ, Knap PW, Roehe R. 2011. Genetic parameters for piglet survival, litter size and birth weight or its variation within litter in sire and dam lines using Bayesian analysis. Livest Sci. 135:215–224. doi:10.1016/j.livsci.2010.07.005.

Kirkden RD, Broom DM, Andersen IL. 2013. Invited review: Piglet mortality: Management solutions. J Anim Sci. 91(7):3361–3389. doi:10.2527/jas.2012-5637.

Koketsu Y, Iida R, Piñeiro C. 2021. A 10-year trend in piglet pre-weaning mortality in breeding herds associated with sow herd size and number of piglets born alive. Porc Heal Manag. 7:4. doi:10.1186/s40813-020-00182-y.

Koketsu Y, Takenobu S, Nakamura R. 2006. Preweaning mortality risks and recorded causes of death associated with production factors in swine breeding herds in Japan. J Vet Med Sci. 68(8):821–826. doi:10.1292/jvms.68.821.

Lantzos T, Koykoyris G, Salampasis M. 2013. FarmManager: An Android Application for the Management of Small Farms. Procedia Technol. 8:587–592. doi:10.1016/j.protcy.2013.11.084.

Lax T. 1971. Hereditary splayleg in pigs. J Hered. 62:250–252. doi:10.1093/oxfordjournals.jhered.a108162.

Linneen SK, Mikesell R, Kime LF, Harper JK. 2005. Swine production. Penn State Ext. [accessed 2022 May 4]. https://extension.psu.edu/swine-production.

Lopez BIM, Seo K. 2019. Genetic parameters for litter traits at different parities in purebred Landrace and Yorkshire pigs. Anim Sci J. 90(12):1497–1502. doi:10.1111/asj.13298.

Lurette A, Belloc C, Touzeau S, Hoch T, Seegers H, Fourichon C. 2008. Modelling batch farrowing management within a farrow-to-finish pig herd: Influence of management on contact structure and pig delivery to the slaughterhouse. Animal. 2(1):105–116. doi:10.1017/S1751731107000997.

Madson DM, Arruda PHE, Arruda BL. 2019. Nervous and Locomotor System. In: Zimmerman JJ, Karriker LA, Ramirez A, Schwartz KJ, Stevenson GW, Zhang J, editors. Diseases of Swine. 11th ed. Hoboken, NJ: John Wiley & Sons. p. 339–372.

Maiorano AM, Assen A, Bijma P, Chen C, Silva JAI V, Herring WO, Tsuruta S, Misztal I, Lourenco DAL. 2019. Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar semen: a simulation study. J Anim Sci. 97(8):3237–3245. doi:10.1093/jas/skz207.

Marchant JN, Rudd AR, Mendl MT, Broom DM, Meredith MJ, Corning S, Simmins PH. 2000. Timing and causes of piglet mortality in alternative and conventional farrowing systems.

Vet Rec. 147(8):209–214. doi:10.1136/vr.147.8.209.

Merks JWM, Mathur PK, Knol EF. 2012. New phenotypes for new breeding goals in pigs. Animal. 6(4):535–543. doi:10.1017/S1751731111002266.

Milligan BN, Fraser D, Kramer DL. 2002. Within-litter birth weight variation in the domestic pig and its relation to pre-weaning survival, weight gain, and variation in weaning weights. Livest Prod Sci. 76(1):181–191. doi:10.1016/S0301-6226(02)00012-X.

Muirhead M, Alexander T. 2013. Managing and treating disease in the farrowing and suckling period. In: Carr J, editor. Managing Pig Health: A Reference for the Farm. 2nd Editio. Sheffield: 5M Publishing. p. 227–82.

Muns R, Nuntapaitoon M, Tummaruk P. 2016. Non-infectious causes of pre-weaning mortality in piglets. Livest Sci. 184:46–57. doi:10.1016/j.livsci.2015.11.025.

Nguyen TQ, Knap PW, Simm G, Edwards SA, Roehe R. 2021. Evaluation of direct and maternal responses in reproduction traits based on different selection strategies for postnatal piglet survival in a selection experiment. Genet Sel Evol. 53(1):28. doi:10.1186/s12711-021-00612-7.

Ooi P, Da Costa N, Edgar J, Chang K. 2006. Porcine Congenital splayleg is characterised by muscle fibre atrophy associated with relative rise in MAFbx and fall in P311 expression. BMC Vet Res. 2:23. doi:10.1186/1746-6148/2/23.

Pandolfi F, Edwards SA, Robert F, Kyriazakis I. 2017. Risk factors associated with the different categories of piglet perinatal mortality in French farms. Prev Vet Med. 137A:1–12. doi:10.1016/j.prevetmed.2016.12.005.

Papatsiros V. 2012. The splay leg syndrome in piglets: a review. Am J Anim Vet Sci. 7(2):80–83. doi:10.3844/ajavsp.2012.80.83.

Papatsiros VG, Alexopoulos C, Kritas SK, Koptopoulos G, Nauwynck HJ, Pensaert MB, Kyriakis SC. 2006. Long-term administration of a commercial porcine reproductive and respiratory syndrome virus (PRRSV)-inactivated vaccine in PRRSV-endemically infected sows. J Vet Med Ser B Infect Dis Vet Public Heal. 53(6):266–272. doi:10.1111/j.1439-0450.2006.00965.x.

Partlow GD, Fisher KRS, Page PD, MacMillan K, Walker AF. 1993. Prevalence and types of birth defects in Ontario swine determined by mail survey. Can J Vet Res. 57(2):67–73.

Pedersen MLM, Velander IH, Nielsen MBF, Lundeheim N, Nielsen B. 2019. Duroc boars have lower progeny mortality and lower fertility than Pietrain boars. Transl Anim Sci. 3(2):885–892. doi:10.1093/tas/txz036.

PIC-Hermitage. 2017. PIC Genetics Hermitage AI Stations. Kilkenny (IE): PIC-Hermitage. https://pichermitage.com/wp-content/uploads/2018/02/IrishHermPICIRL17HRw.pdf.

PIC-Hermitage. 2021. PIC® 800 - Hermitage AI. Kilkenny (IE). [accessed 2021 Nov 18]. https://pichermitage.com/products/terminal-lines/pic-hermitage-top-drawer-duroc/.

PigCHAMP. 2022. PigCHAMP. Aimes (US). [accessed 2022 Feb 1]. https://www.pigchamp.com/.

Piñeiro C, Manso A, Manzanilla EG, Morales J. 2019. Influence of sows' parity on performance and humoral immune response of the offspring. Porc Heal Manag. 5:1.

doi:10.1186/s40813-018-0111-8.

Piñeiro C, Morales J, Rodríguez M, Aparicio M, Manzanilla EG, Koketsu Y. 2019. Big (pig) data and the internet of the swine things: A new paradigm in the industry. Anim Front. 9(2):6–15. doi:10.1093/af/vfz002.

Quesnel H, Farmer C, Theil PK. 2015. Colostrum and milk production. In: Farmer C, editor. The gestating and lactating sow. Wageningen (NL): Wageningen Academic Publishers. p. 173–192.

Roehe R, Kalm E. 2000. Estimation of genetic and environmental risk factors associated with pre-weaning mortality in piglets using generalized linear mixed models. Anim Sci. 70(2):227–240. doi:10.1017/S1357729800054692.

Roehe R, Shrestha NP, Mekkawy W, Baxter EM, Knap PW, Smurthwaite KM, Jarvis S, Lawrence AB, Edwards SA. 2009. Genetic analyses of piglet survival and individual birth weight on first generation data of a selection experiment for piglet survival under outdoor conditions. Livest Sci. 121:173–181. doi:10.1016/j.livsci.2008.06.010.

Rutherford KMD, Baxter EM, D'Eath RB, Turner SP, Arnott G, Roehe R, Ask B, Sandøe P, Moustsen VA, Thorup F, et al. 2013. The welfare implications of large litter size in the domestic pig I: Biologica factors. Anim Welf. 22(2):199–218. doi:10.7120/09627286.22.2.199.

Schnapperelle H, Koch J. 1980. Occurrence and treatment of congenital splayleg in unweaned piglets. Mh Vet Med. 35:858–869.

Schumacher T, Röntgen M, Maak S. 2021. Congenital Splay Leg Syndrome in Piglets—Current Knowledge and a New Approach to Etiology. Front Vet Sci. 8:609883. doi:10.3389/fvets.2021.609883.

Sellier P, Dando É, Dando P. 1999. Induction of parturition in the sow and incidence of splayleg syndrome in the newborn piglet. Ann Zootech. 48(3):153–161. doi:10.1051/animres:19990301.

Sørensen D, Vernersen A, Andersen S. 2000. Bayesian analysis of response to selection: a case study using litter size in Danish Yorkshire pigs. Genetics. 156(1):283–295. doi:10.1093/genetics/156.1.283.

Spicer EM, Driesen SJ, Fahy VA, Horton BJ, Sims LD, Jones RT, Cutler RS, Prime RW. 1986. Causes of preweaning mortality on a large intensive piggery. Aust Vet J. 63(3):71–75. doi:10.1111/j.1751-0813.1986.tb02933.x.

Strange T, Ask B, Nielsen B. 2013. Genetic parameters of the piglet mortality traits stillborn, weak at birth, starvation, crushing, and miscellaneous in crossbred pigs. J Anim Sci. 91(4):1562–1569. doi:10.2527/jas.2012-5584.

Su G, Lund MS, Sorensen D. 2007. Selection for litter size at day five to improve litter size at weaning and piglet survival rate. J Anim Sci. 85(6):1385–92. doi:10.2527/jas.2006-631.

Su G, Sorensen D, Lund MS. 2008. Variance and covariance components for liability of piglet survival during different periods. Animal. 2(2):184–9. doi:10.1017/S1751731107001115.

Szalay F, Zsarnovszky A, Fekete S, Hullár I, Jancsik V, Hajós F. 2001. Retarded myelination in the lumbar spinal cord of piglets born with spread-leg syndrome. Anat Embryol.

203(1):53–9. doi:10.1007/s004290000129.

Taylor J. 2021. Which pig herd management software should I use? AHDB. [accessed 2022 Jan 18]. https://ahdb.org.uk/knowledge-library/which-pig-herd-management-software-should-i-use.

Teagasc - Agriculture and Food Development Authority. 2021. National Pig Herd Performance Report 2020. Carlow (IE). https://www.teagasc.ie/media/website/publications/2021/National-Pig-Herd-Performance-Report-2020.pdf.

Thurley DC, Gilbert FR, Done JT. 1967. Congenital splayleg of piglets: myofibrillar hypoplasia. Vet Rec. 80(9):302–4.

Topigs Norsvin. 2021. TN Tempo. Helvoirt (NL). [accessed 2021 Nov 18]. https://tntempo.com/#tntempo.

Tuček S, Svoboda T, Říčný J, Bass A, Soukup T, Vítek V. 1985. The Concentration of Choline and the Activities of Cholinesterases, Creatine Kinase and Lactate Dehydrogenase in the Blood Plasma of Piglets with the Syndrome of Splayleg (Congenital Myofibrillar Hypoplasia). Zentralbl Veterinaermed. 32:1–10. doi:10.1111/j.1439-0442.1985.tb01908.x.

Tummaruk P, Tantasuparuk W, Techakumphu M, Kunavongkrit A. 2010. Seasonal influences on the litter size at birth of pigs are more pronounced in the gilt than sow litters. J Agric Sci. 148(4):421–432. doi:10.1017/S0021859610000110.

Varona L, Noguera JL, Casellas J, de Hijas MM, Rosas JP, Ibáñez-Escriche N. 2020. A cross-specific multiplicative binomial recursive model for the analysis of perinatal mortality in a diallel cross among three varieties of Iberian pig. Sci Rep. 10(1):21190. doi:10.1038/s41598-020-78346-7.

Vasdal G, Andersen IL. 2012. A note on teat accessibility and sow parity — consequences for newborn piglets. Livest Sci. 146(1):91–94. doi:10.1016/j.livsci.2012.02.005.

Vogt DW, Gipson TA, Akremi B, Dover S, Ellersieck MR. 1984. Associations of sire, breed, birth weight, and sex in pigs with congenital splayleg. Am J Vet Res. 45(11):2408–2409.

Ward PS, Bradley R. 1980. The light microscopical morphology of the skeletal muscles of normal pigs and pigs with splayleg from birth to one week of age. J Comp Pathol. 90(3):421–431. doi:10.1016/0021-9975(80)90012-2.

Wensley MR, Tokach MD, Woodworth JC, Goodband RD, Gebhardt JT, Derouchey JM, McKilligan D. 2021. Maintaining continuity of nutrient intake after weaning. I. Review of pre-weaning strategies. Transl Anim Sci. 5(1):1–12. doi:10.1093/tas/txab021.

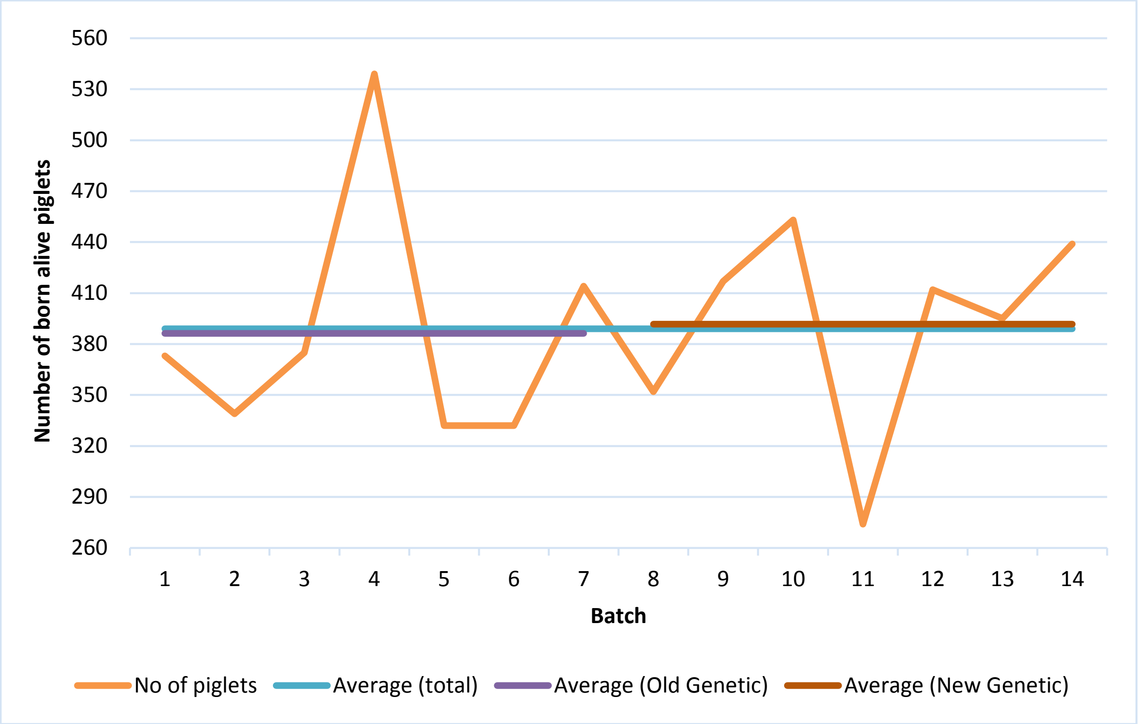
Wu T, Zhang Xu, Tian M, Tao Q, Zhang L, Ding Y, Zhang Xiaodong, Yin Z. 2018. Transcriptome analysis reveals candidate genes involved in splay leg syndrome in piglets. J Appl Genet. 59(4):475–83. doi:10.1007/s13353-018-0454-5.

Xu S, Hao X, Zhang M, Wang K, Li S, Chen X, Yang L, Hu L. 2018. Polymorphisms of HOMER1 gene are associated with piglet splay leg syndrome and one significant SNP can affect its intronic promoter activity in vitro. BMC Genet. 19:110. doi:10.1186/s12863-018-0701-0.

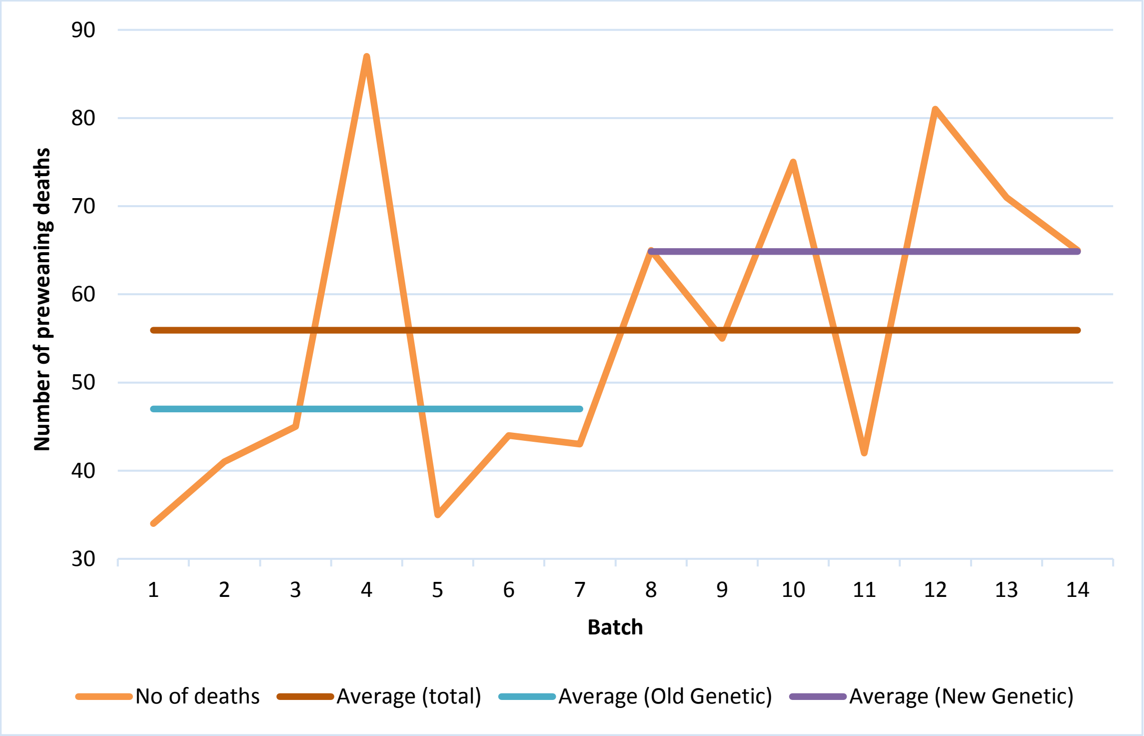
Zaleski HM, Hacker RR. 1993. Variables related to the progress of parturition and probability of stillbirth in swine. Can Vet J. 34(2):109–113.

9. Annexes

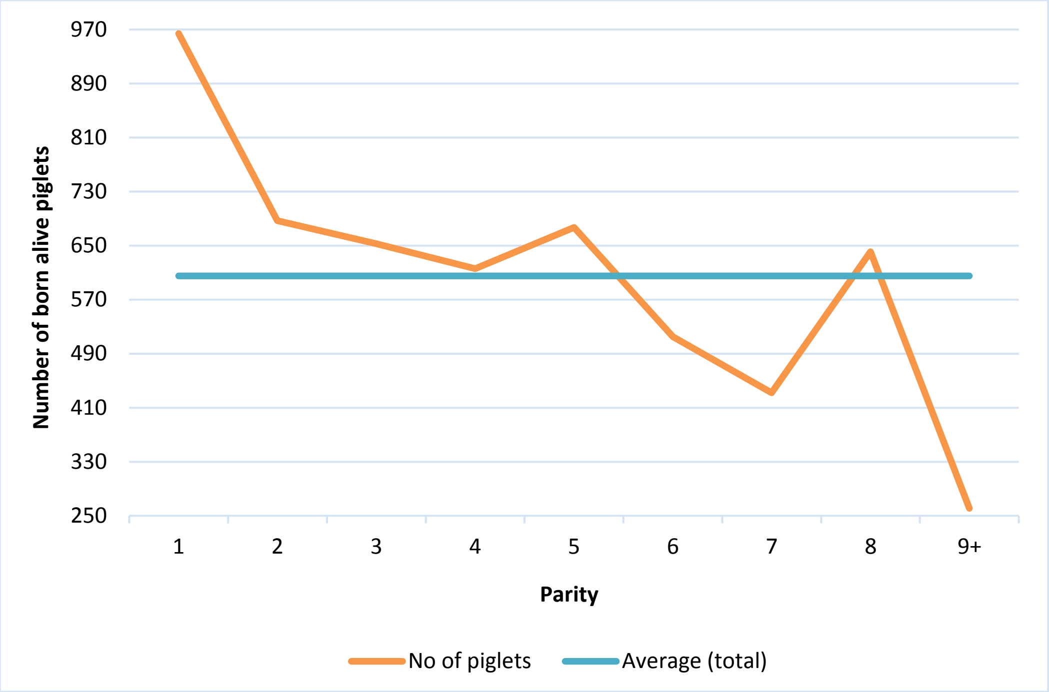
Annex 1 - Total number of born alive piglets per batch.



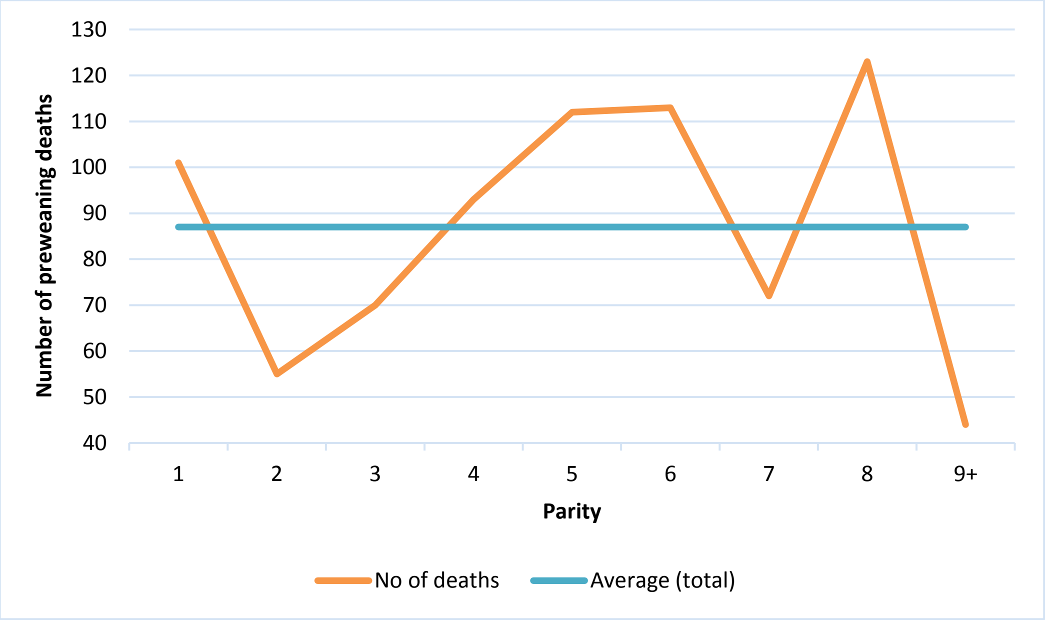
Annex 2 - Total number of preweaning deaths per batch.



Annex 3 - Total number of born alive piglets per parity.



Annex 4 - Total number of preweaning deaths per parity.



Annex 5 - Percentage of causes of death per parity.