The Economic Consequences of Reciprocal Translocations (RTs) in Global Pig Breeding and the Benefits of Using a Novel "Multiprobe" Approach as a Standard Screening Methodology

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Declaration

No part of this thesis has been submitted in support of an application for any degree or qualification of the University of Kent or any other University or institute of learning

Nicole Lewis

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Glossary of Pig Industry Terminology

- **AI**- the medical or veterinary procedure of injecting semen into the vagina or uterus.
- **Boar Effect**- the number of offspring a mating boar has the potential to affect.
- **Boar Stud**- a farm that specifically hold boars and sends doses of collected semen to sow farms.
- **Born Alive**- the number of pigs born alive per farrowing, this excludes stillborn and mummified piglets.
- **Breeding Pyramid**- the structure of the pig industry or a specific business enterprise. Mainly comprises of pure animals in a nucleus, pure animals in multiplication making crossbred sows, and commercial animals creating terminal offspring for animal protein.
- **Commercial**- the stage of production focused on production of pig meat.
- **Dam Line**- A line of pigs primarily focused on female traits.
- **F1 Gilt**- the progeny that results from breeding a male of one breed, to a female of another breed resulting in a gilt with hybrid vigor. These gilts are usually highly prolific.
- **Farrow-** the production of a litter of pigs.
- **Farrowing Rate-** the ratio of the number of sows that farrow to the number of AI services given. (two doses of semen count as 1 service in this case)
- **Finisher**- pigs that have been grown to market weight. This weight can vary with geography.
- **Gene Transfer Centre** (GTC)- Gene Transfer Centre, see boar stud.
- **Gilt-** a female pig intended for breeding but has not yet mated.
- **Grandparent**- a pure breed animal that is crossbred to make parent animals for commercial production.

- **Great-Grandparent**- a pure breed animal that is bred pure to make grandparent animals for multiplication or great-grandparent replacements
- **Integrators**- a commercial enterprise that owns multiple levels of production usually including the live productions, feed manufacture, and slaughter / processing.
- **Litters per sow per year**- the number of litters per year a sow can produce
- Maternal Line- breed/lines of pigs that are focused on maternal traits, such as reproductive success, that are used for the creation of commercial sows.
- **Multiplier**- a farm of pure line sows with the desired goal of generating commercial female animals for use in commercial herds.
- **Nucleus**- a farm of pure line, high merit sows, with the desired goal of generation of genetic gain through own replacement and also the creation of sows for multiplication and boars for use in all other parts of the pyramid.
- **Opportunity Cost**- the potential cost of missing animals
- **Parent**- a commercial female or sire whose offspring are focused on sale for meat.
- **Parity**- the number of litters a sow has farrowed.
- **PCAI**- post cervical artificial insemination: an AI technique where-by semen is deposited beyond the cervix directly into the uterine body.
- **Post-Weaning Mortality**- mortality (death / removal) that happens post wean but before slaughter.
- **Pre-Weaning Mortality**- mortality (death / removal) that happens before the weaning event.
- **Semen Extender-** a liquid dilute added to semen to preserve its fertility so that it can be transported to the sow.

- **Semen Pooling-** the practice of combining the semen of multiple boars to inseminate a sow.
- **Service**- mating a boar to a sow from either natural methods or artificial insemination.
- **Single Sire Mating-** mating a sow with only the semen from one boar.
- **Terminal Mating**- a mating to a sire line that would create offspring intended for sale to meat.
- **Terminal Sire**- a line focused on efficient growth and carcass parameters that will be used in matings to commercial sows there the offspring are intended for sale to meat.
- **Total Born**- the total number of pigs born per farrowing event and this would include all born alive / dead / mummified.
- **Weaned Pigs**- the total number of pigs weaned alive per farrowing event that go into the nursery.

1. Abstract

Pig protein remains the most popular worldwide, representing >30% of all consumed meat; a figure that is expected to rise from 106 to 127 metric kilotons per year in the next 10 years. As the market and demand for pig meat continues to grow across the world, so does the importance of its sustainability and its economic accessibility. With this in mind, great focus and attention is turning to reducing food and protein chain waste as a means of both environmental stability and improving economic growth/productivity (FAO 2020). Food loss at all levels from the level to consumer leads not only economic loss, but also lack of food available to consumers. In order for businesses to combat chain wastage and improve profits, behavioural change among the different levels is necessary, but it can also be prevented through innovation and technology. A major biological issue that causes the pig industry problems is that of chromosomal reciprocal translocations (RTs), which are relatively common and a primary cause of hypoprolificacy in boars (boars that produce a lower number of offspring). They cause significant economic losses due to reduction in litter sizes and many countries have set up screening programs to remove RT affected pigs from the populations. The current standard method for screening is standard banded karyotyping, but this is often inaccurate, requires a specialist, is subjective, and limited for detecting smaller (cryptic) RTs. A potential solution to this problem is a novel device created in the Griffin Lab at the University of Kent. This multiprobe device does not require expertise nor advanced knowledge of the domestic pig karyotype and is able to detect cryptic RTs. Because of its superior accuracy and ease of use, this technology has the potential to replace standard karyotyping as the predominant screening method for RTs. The major pitfall to date is the

relatively expensive cost of the screening, which has kept it from being widely adopted. The main aims of this thesis were to give an empirical assessment of the impact of RTs in modern pig breeding and thence calculate the relative benefit (if any) of the novel multiprobe device compared to karyotyping for RT detection. Specifically, this thesis provides an extensive overview of the structure of the pig industry, gives insight into how an RT can affect different businesses and calculates potential losses incurred from an RT being allowed to persist in a herd. In so doing, the relative benefits of the multiprobe were assessed. The key findings were that, in a "farrow to wean" hypothetical scenario, with one RT boar having performed 335 matings, the costs of an RT were ~£75,921 to ~£100,424. In a "farrow to finish" scenario with the same number of matings, the general costs of an RT were ~£240,719. In a dam line grandparental (GP) boar with a hypothetical RT scenario, in general the cost of an RT is £1,340,686. In a dam line great grandparental (GGP) boar with a hypothetical RT scenario, the cost of an RT is approximately £130,183,215. The study also examined two real world cases where an RT was missed by karyotyping but detected by the FISH multiprobe device, in each case, if FISH multiprobe device had been used initially, it would have saved the companies £17,430.91 and £738,085.16 respectively. The thesis concludes that the costs of mass screening of single sire breeding boars by the FISH multiprobe device far outweighs the potential risks of an RT being undetected (either by using karyotyping, or by not screening at all) and that the multiprobe approach is far more cost-effective in the long run than standard karyotyping.

2. Introduction

Pig meat is currently, and has consistently been, an important source of animal protein around the world for thousands of years (Simm, 2020). Presently, it is the most consumed meat globally, representing >30% (OECD/FAO 2020). It is expected that the current yearly consumption rates for pig meat will rise from 106 metric kilotonnes of carcass weight consumed, to 127 metric kilotonnes by the year 2029 (OECD/FAO 2020). Figure 1 below shows this trend.

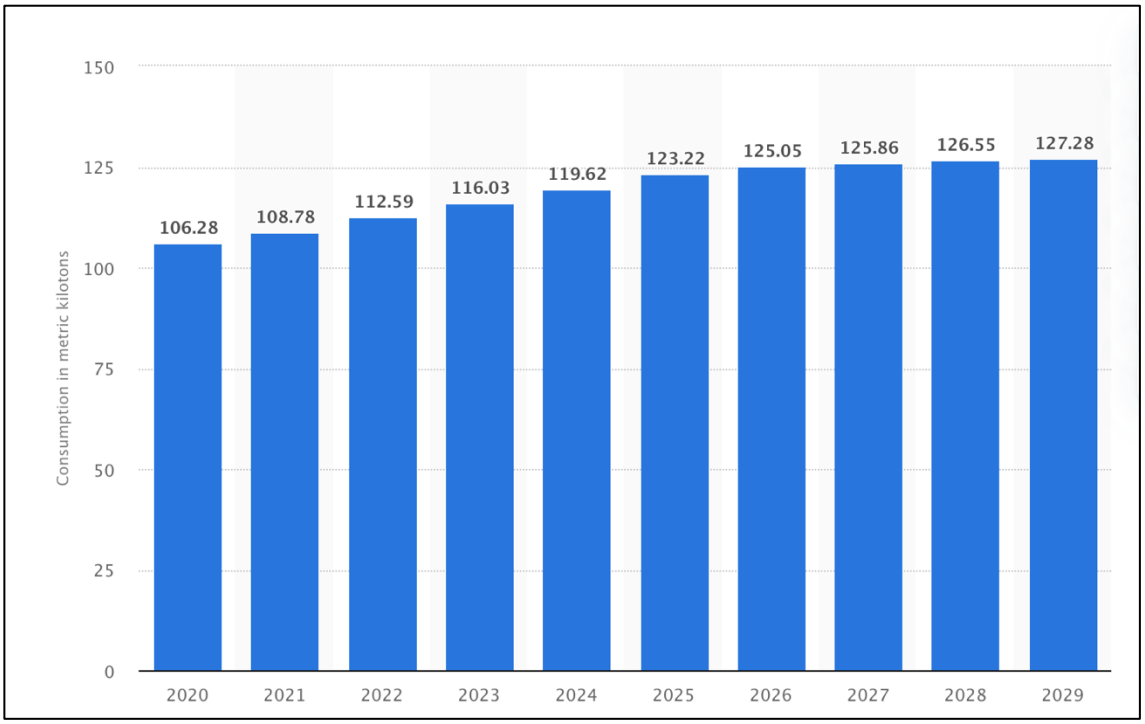

Figure 1: Projected Pig Meat Consumption Worldwide 2020 to 2029 in Metric Kilotons (Shahbandeh, 2020).

As the market and demand for pig meat continues to grow worldwide, so does the importance of its sustainability and its economic accessibility (Riche and Roser, 2019). With these things in mind, great focus and attention is turning to reducing food and protein chain waste as a

means of not only environmental stability but also improving economic growth and productivity (FAO 2020). Food loss can occur in the pig industry at all levels of production from the farm level down to the consumer (FAO, 2020). This causes not only economic loss, but also loss of food available to consumers (FAO, 2020) and, from the business perspective, there is a further motivator for preventing food loss in that it helps to maximise profits (McGlone 2002). In order for businesses to combat wastage and improve profits, change in practice at a range of different levels is necessary, but it can also be prevented through innovation and new technology (FAO, 2020). This can be seen currently as attempts are being made to create a vaccination for African swine fever, which is estimated to have cost the Asian pig industry between 55 and 130 billion US dollars (Linden 2020).

Another biological issue that causes the pig industry problems is that of reciprocal translocations (RTs), which are relatively common (reported incidence 0.47%) in swine (Ducos et al 2007). Reciprocal translocations (RTs) are gross genomic (chromosomal) rearrangements, which are a primary cause of hypoprolificacy (reduced fertility) in boars (Pinton et al 2000). They can cause significant economic losses due to a reduction in litter sizes of anywhere from 10 to 100% (Ducos 2007). Because of this, since the late twentieth century, labs both in Europe and the United States and have set up screening programs to test for RTs and remove the affected boars from the breeding herd (Ducos et al 2008). The current gold-standard for chromosomal screening for reciprocal translocations (RTs) is standard banded karyotyping (discussed later). Briefly, this involves the staining chromosomes to create a karyotype (a representation of how the chromosomes are arranged) and then a visual assessment to check for abnormalities (Gersen and Keagle 2013). Standard karyotyping, while currently a standard practice, is often inaccurate and requires a

specialist. It is also subjective, and limited in its ability to detect smaller or "cryptic" RTs (O'Connor et al 2017). Inaccuracies and missed translocations can cause RTs to disseminate through the breeding population of the pig industry which can have costly economic consequences (Kahn and Line 2010). A potential solution to this problem, is an innovative and novel device created in the Griffin Lab at the University of Kent, which allows for all chromosomes to be tested simultaneously (O'Connor et al 2017). The "multiprobe" device does not require expertise or advanced knowledge of the domestic pig karyotype and is able to detect cryptic translocations inaccessible to karyotyping (O'Connor et al 2017). Because of its superior accuracy, and ease of use, this technology has the potential to replace standard karyotyping as a screening method. However, the potential costs of RTs to the industry and thus the benefits of screening by multiprobe have not been accurately quantified. This is particularly in light of the fact that multiprobe relatively more expensive than karyotyping, a factor that has kept it from being widely adopted.

The main aims of this thesis were therefore to assess the value to the global pig breeding industry of chromosome screening (for RTs) in general, and through using the multiprobe FISH strategy in particular.

2.1. Chromosomes and Chromosome Rearrangements

In all Eukaryotic organisms, genetic material (the genome) is organized into thread-like structures ("chromosomes") that are housed in the nuclei of nearly all cells (Russell 2002). Chromosomes are represented as uncondensed domains of DNA and protein in most nuclei, however, when the cell divides, a specific structure (a metaphase chromosome) forms thus:

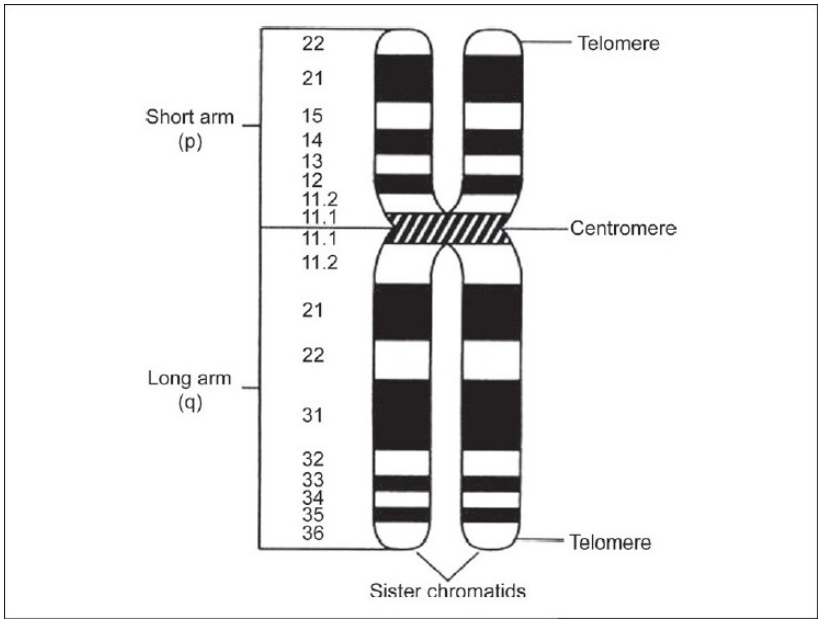

Figure 2. Anatomy of a Metaphase Chromosome

Each metaphase chromosome is comprised of two genetically identical sister chromatids, which each contain a super-condensed linear double stranded DNA molecule and its associated proteins (Gersen and Keagle 2013). Figure 2 (above) shows the anatomy of a chromosome.

Eukaryotic organisms have a diploid (2n) number of chromosomes in each cell, meaning the half the genome comes from the mother and half from the father, with each chromosome having a homologous pair, one donated from each parent. Homologous pairs of chromosomes contain the same set of genes, although they may contain different variants of those genes (alleles). The chromosomes of most organisms can be visualised as apparently identical pairs (the exception being the X and Y sex chromosomes in males), however certain individuals display deviations from the normal species-specific pattern (Snustad 2016). Unbalanced deviations involve net gain and loss of DNA and cause severe disorders (Down

syndrome is the most commonly described in humans). Balanced abnormalities (no net gain or loss) however can lead to reduced fertility. Reciprocal translocations (RTs) are the best know example of balanced abnormalities.

2.1.1. Reciprocal Translocations (RTs)

When two non-homologous chromosomes exchange genetic material, it is referred to a translocation (Russell 2002). This exchange is commonly reciprocal (although not always) in which each chromosome donates and receives chromosomal segments and there is no loss of genetic material (Goodenough 1984). Figure 3 below shows a simplistic diagram of an RT.

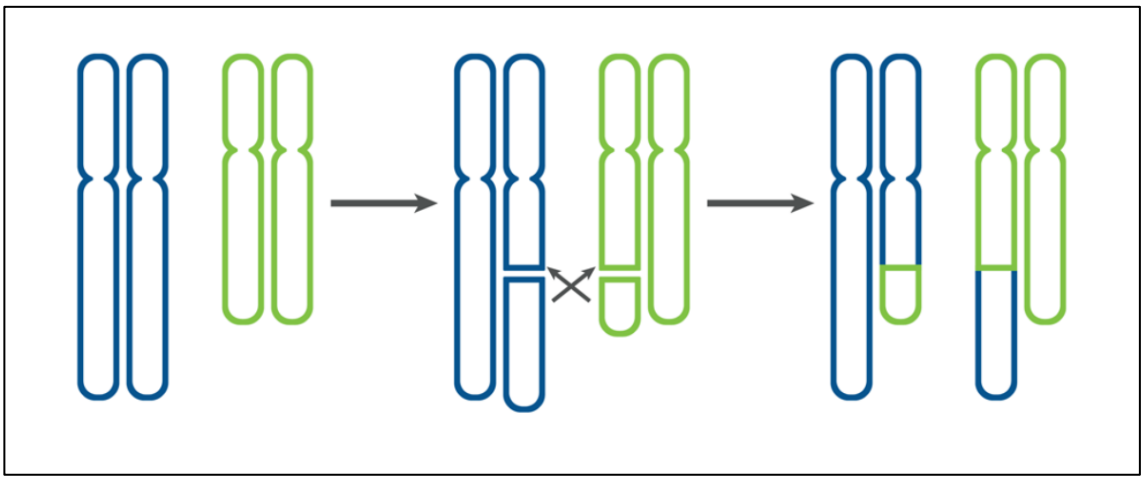

Figure 3. Reciprocal Translocation (RT) (Cooper Genomics 2020).

An RT effectively relocates parts of gene sequences to new locations in the genome (Russell 2002). In organisms that are heterozygous for a translocation (where only one chromosome in a diploid pair contains the translocation), this can greatly affect the process of meiosis where the sperm and egg undergo cell division. This is due to the inability of homologous chromosomes to pair properly, which can result in duplications and/or deletions causing the production of an inviable gamete (Russell 2002). Specifically, when translocation and normal

chromosomes attempt to pair, a cross-like configuration occurs with all four chromosomes involved (Russell 2002).

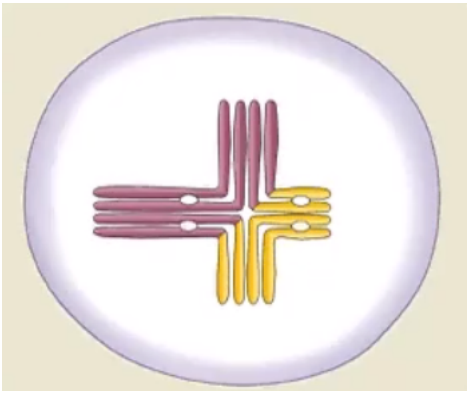

Figure 4. Translocation Chromosomes Forming a Paring Cross at Meiosis

The most favourable outcome at the end of meiosis is so called “alternate segregation”, which leads to normal or balanced gametes. This outcome is positive in that each gamete created is viable and contains a complete set of genes, although half will carry the translocation like the parent (Russell 2002). Another frequent outcome however is called adjacent segregation (Snustad 2016). There are two forms of adjacent disjunction, adjacent 1 and adjacent 2. These occur when adjacent non-homologous centromeres migrate to the same pole, resulting in all of the gametes being chromosomally imbalanced. These gametes are usually inviable as most will contain duplications and/or deletions of genetic material. The third and rare option for segregation is three chromosomes segregate to one gamete and one to the another (3:1 segregation), or four to one and none to the other (4:0 segregation) (Russell 2002). Alternate, adjacent (1 and 2), 3:1 and 4:0 segregations and their consequences are depicted in Figure 5.

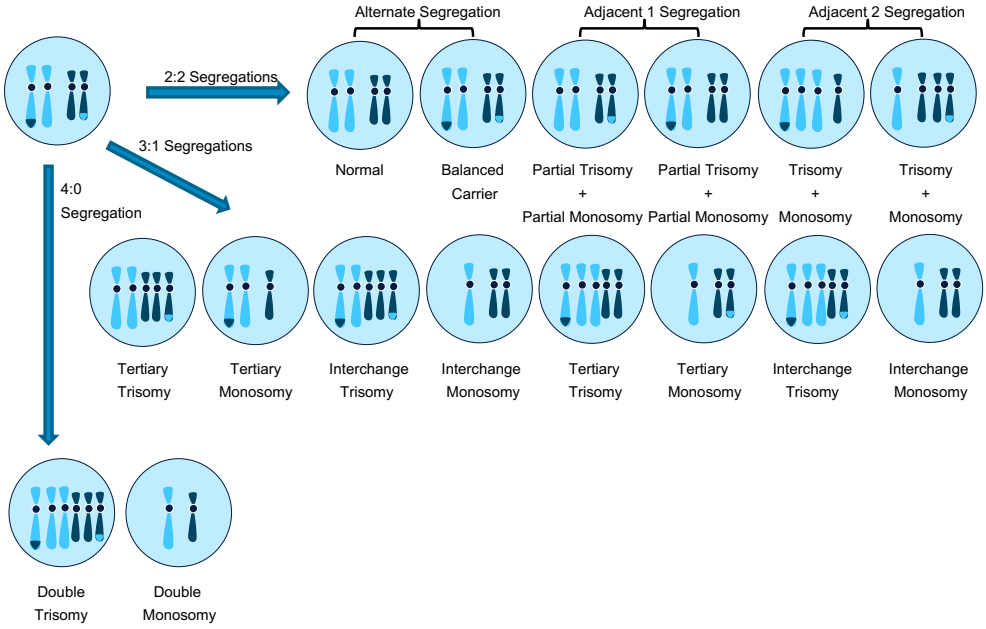

Figure 5. Chromosome Segregations following an RT. Alternate, adjacent (1 and 2), 3:1 and 4:0 segregations are shown (Ogur and Griffin 2020)

Organisms, such as boars, that carry RTs often have reduced fertility therefore. This is partly because formation of the pairing cross impedes meiosis, and partly due to the production of unbalanced gametes, which lead to unbalanced embryos that do not develop (Snustad 2016).

2.1.2. Robertsonian Translocations and Inversions

Another type of translocation that can occur is a non-reciprocal exchange (Russell 2002). This can occur when, for example, two non-homologous chromosomes become attached at their ends creating a very large chromosome. This is referred to as a Robertsonian translocation (Snustad 2016). Figure 6 below shows an illustration of a Robertsonian translocation.

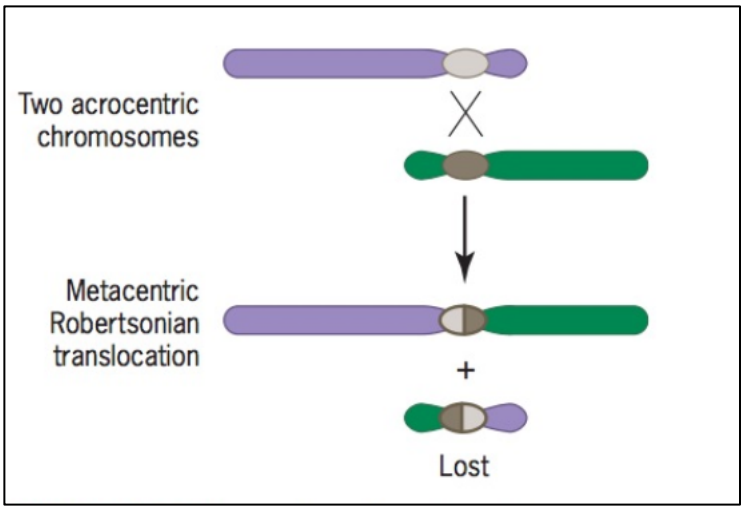

Figure 6. Robertsonian Translocation (Snustad 2016).

The two short arms are usually lost during this process, however since the genetic material is non-essential, a carrier will usually be phenotypically normal. There is a risk however that zygotes produced between a normal gamete and a heterozygous Robertsonian carrier will result in aneuploidy (extra or missing chromosomes). The possible outcomes of this are a normal zygote, a normal phenotype but carries the translocation (carrier), a trisomy, or a monosomy (Russell 2002). This is shown in Figure 7. Robertsonian translocations are a common cause of infertility in cattle.

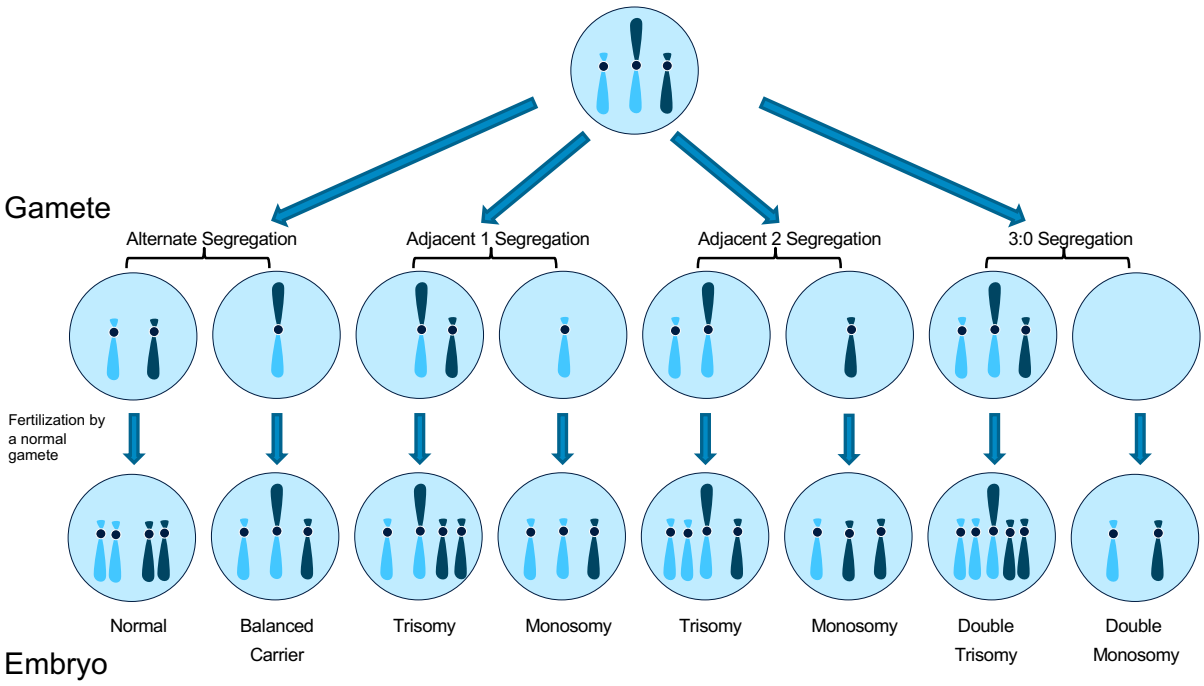

Figure 7. Segregation patterns of a Robertsonian Translocation

Finally, an inversion of part of a chromosome (e.g. to change the gene order from a-b-c-d-e, to a-**d-c-b**-e in one copy of a homologous pair) can also cause infertility. An animal such as a boar with an inversion does not form a pairing cross at meiosis, but a pairing loop. As with RTs, impairment of meiosis and production of unbalanced gametes leads to infertility. Thus, any animal carrying a Robertsonian translocation, an inversion, or an RT is subject to infertility (hypoprolificacy). If that animal is a top-quality breeding male such as a bull or boar then it is a commercial liability to the company that owns it.

2.2. Methods for Detecting Chromosome Rearrangements Including RTs

The preparation of chromosomes for the purposes of detecting abnormalities such as RTs is called “cytogenetics” and, although it has an element of quantitative analysis and data, it is largely a qualitative science, with the morphological characteristics and landmarks of

metaphase chromosomes being described (Gersen and Keagle 2013). Every species has a distinctive “karyotype”, i.e. an agreed convention established by the scientific community by which the chromosomes are arranged for that species (Figure 9). An analyst will thus have to be familiar with the particular karyotype of whatever species is being studied. In order for a karyotype to be easily visualized, it is necessary to have a preparation that is of high quality (Raudsepp and Chowhardary 2016). When studying the chromosomes of any species, the karyotype (Figure 9) is created, which is essentially a picture of arranged chromosomes in their homologous pairs (King 2013). Autosomes (non-sex chromosomes) are given a number based upon their size (usually largest first). Each metaphase chromosome displays a primary constriction (centromere, see Figure 2) and centromere position is also used to help classify chromosomes (Gersen and Keagles 2013). The classifications of centromere positions are metacentric, sub-metacentric, acrocentric and telocentric (Russell 2002). A metacentric chromosome is divided evenly by the centromere, whereas a sub-metacentric has obvious short and long arms as the centromere is not central (Russell 2002). Acrocentric chromosomes have their centromere *near* the end of the chromosome and may or may not display small “satellites” (Campos-Galindo 2020). Telocentric chromosomes have the centromere located at the very tip of the chromosome and thus have only one arm (Russell 2002). This can be seen in Figure 8 below. After a karyotype has been created, a description of it is given using an international system of standard nomenclature ISSN (Gersen and Keagle 2013). This description will include chromosome number, the sex of the subject, and a description of any abnormalities present (Gersen and Keagle 2013).

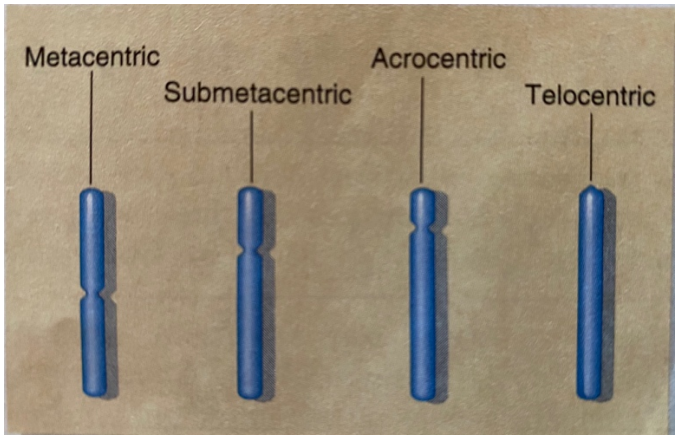

Figure 8. Centromere locations

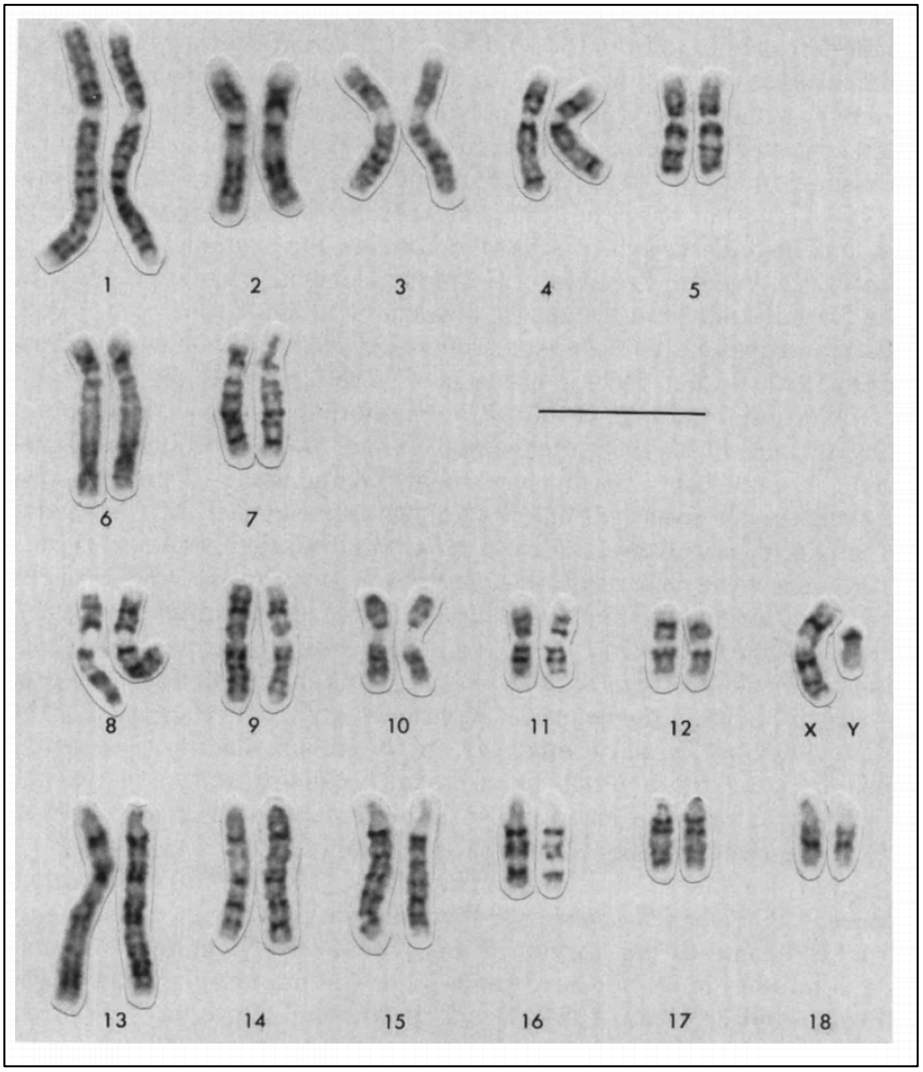

Figure 9. Karyotype of a normal boar (Gustavsson 1990). The technique used to stain the chromosomes is called G-banding (see next section)

2.2.1. Classical "Banding" Techniques

As shown in Figure 9, the chromosomes have distinct stripes or "bands." G-banding, R-banding, C-banding and Q-banding are some of the many techniques available for staining chromosomes, all of which have unique properties and applications (Smeets 2004). Generally speaking, G- banding, or Giemsa banding, is the most common staining technique used in cytogenetics laboratories and the banded chromosomes result forms the basis for published standard reference points (Bickmore 2001, Gersen and Keagle 2013). For most banding techniques to be performed, it is necessary for chromosomes to be harvested during mitosis (regular cell division) (Bickmore 2001). Blood samples are typically prior treated with Phytohemagglutinin (PHA) which is a lectin that stimulates cell division of the lymphocytes (white blood cells) to allow for cells to reach optimum exponential growth approximately 72 hours later (Movafagh 2011). Once in metaphase (the middle stage of cell division, where the chromosomes are most visible), the cells are treated with colchicine (or colcemid), which arrests the cell at this stage, thereby maximising the total proportion of cells in which chromosomes are visible (Smeet 2004). A hypotonic salt solution, typically 75mM KCl, is used to make the cells swell, and then suspended with a fixative such as methanol with acetic acid in a 3:1 ratio (Howe 2014). Finally, the chromosome suspensions are pipetted onto a slide after which the Giemsa stain is applied (Howe 2014). It is important that the cells are not overlapping as this can make arranging the chromosomes difficult, especially if a computer software that recognizes and arranges the chromosomes is being used (Howe 2014). The slide is then treated with a dilute solution of trypsin to maximise the distinctiveness of the bands. Thereafter, the Giemsa staining technique results in light and dark patterns of stain (bands) along the chromosomes giving each a distinct appearance (Spinner 2013). The regions that

stain darkly, tend to be AT-(adenine-thymine) rich DNA, and the lighter regions are GC (guanine-cytosine) -rich DNA (gene rich) (O'Connor 2008). Figure 9 (above) shows a standard G-banded karyotype of a domestic pig.

2.2.2. Fluorescence In-situ Hybridization (FISH)

Fluorescence *in-situ* Hybridization, or FISH, is a cytogenetic method of analysing chromosomes that involves hybridizing fluorescent or labelled probes to specific DNA sequence locations (Gersen and Keagle 2013). It is considered to be one of the most versatile approaches in human and other animal molecular cytogenetics, as it allows "the identification of the location of DNA markers in their original place (in situ) in mitotic and meiotic chromosomes" (Raudsepp 2016). The probes used are created from short sequences of single-stranded DNA, which match the area of genes of interest in the chromosomes (Ratan et al. 2017). It is particularly useful for detecting errors in chromosome structure that are cryptic or too small to be seen in normal karyotyping (Robinson and Spock 2020). For example, a change in structure such as a deletion, that is only a thousand base pairs long would most likely appear normal with normal karyotyping but would be visible easily with FISH (Robinson and Spock 2020). The exact protocol or method of utilizing FISH can be different across laboratories and is largely dependent on what the area of interest is or what the technician is targeting (Ratan et al 2017). In general, the first step in the basic protocol of using FISH is to select a clone that will hybridize or map to the area of interest (Gersen and Keagle 2013). The most common types of probes used can be categorized as, unique sequence probes, repetitive sequence probes and whole chromosome painting probes (Gersen and Keagle 2013). Unique sequence probes contain (as the name suggests) the sequence of a single length of DNA and are often used for gene mapping. Each gene has it specific place on a

chromosome in every cell in the body and this a karyotype can be thought of as a low-resolution map of the genome of that species of interest. Repetitive sequence probes are used to target areas of chromosomes that contain sequences of DNA containing thousands of copies (Kearney 2001). One such example is the targeting of alpha satellite sequences located at the centromeres of chromosomes (Gersen and Keagle 2013). Whole chromosome painting probes involve attempting to “paint” or highlight an entire chromosome (Kearney 2001). All these types of probes can be created from isolating DNA from the chromosome of interest from the genome (Gersen and Keagle 2013). Chromosome painting is often used to study structural aberrations or rearrangements in metaphase chromosomes (Kearney 2001). Unique sequence probes are useful for detecting more cryptic translocations, deletions or inversions and can be used in both interphase and metaphase (Kearney 2001). These probes can be created from cloned regions of the genome such as bacterial artificial chromosomes (BACs), yeast artificial chromosomes (YACs) or cosmids (Gersen and Keagle 2013). The size of unique sequence probes can range from one kilobase to greater than one megabase and can be used to detect chromosomal breakpoints (Gersen and Keagle 2013). Most of these probes such as BAC clones are commercially manufactured and available for purchase (Gersen and Keagle 2013). While other steps may be taken to prepare the probe depending on the type, generally the next step would be to either label the probe with a fluorochrome either directly or indirectly (Gersen and Keagle 2013). Usually, direct labelling involves using a nick translation and a nucleotide that has been modified to contain a fluorophore (O’Connor 2008). Indirect labelling often done by incorporating a hapten into the DNA with a nick translation or using PCR (polymerase chain reaction (Gersen and Keagle 2013). If the probe is labelled indirectly, another step is required at the end to render the probe fluorescent so it can be visualized (O’Connor 2008). This usually involves a reaction using a fluorescently

labelled antibody such as biotin-streptavin or digoxigenin-antidigoxigenin (Gersen and Keagle 2013). The target DNA and the probes must both first be denatured using a high heat incubation before hybridization can occur (O'Connor 2008). The probe is applied and mixed with the target DNA to increase the likelihood of the probe annealing to the target DNA (Gersen and Keagle 2013). The probes will then hybridize to their complementary DNA sequences and can be viewed under a fluorescent microscope (O'Connor 2013). Figure 10 shows a simplified diagram of the FISH process.

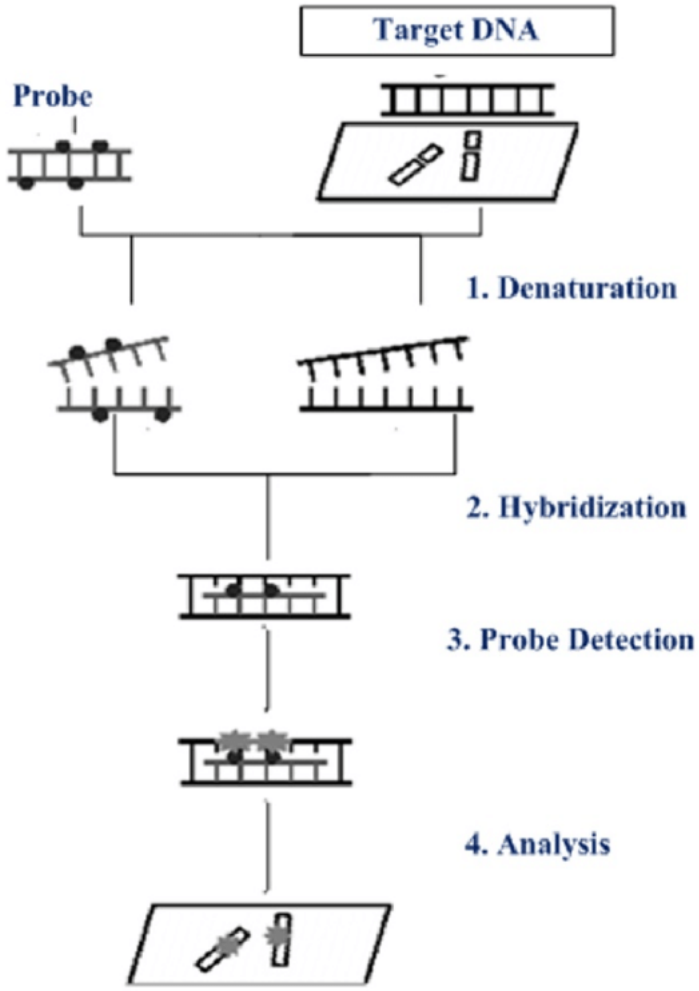

Figure 10. Basic steps for cytogenetics using the FISH Method. (Ratan 2017)

Figure 11 shows an example of the use of FISH (chromosome painting) to detect an RT of chromosomes 5 and 6 in a boar.

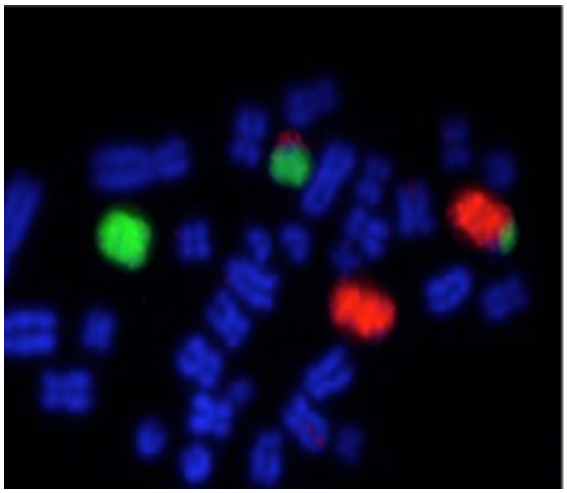

Figure 11. RT detected using chromosome painting (O'Connor et al. 2017). Chromosome 5 is painted in red and chromosome 6 in green. The normal chromosomes are uniformly painted, but the translocation chromosomes have some red and some green

2.2.3. FISH Multiprobe Device

Because of the relatively frequent occurrence of RTs in boars, and the potential economic losses that companies can incur as a result of one being present in a breeding regime, a new technology for screening boars was developed by the Griffin Lab in order to make screening more accurate and efficient (O'Connor et al. 2017). The device utilises the FISH method, however, allows for many individual hybridisations to occur on the same slide (O'Connor et al. 2017). The methodology was based on the work done by Knight and colleagues where 24 individual hybridisations were done on a single slide with human chromosomes (Knight et al., 1997). This methodology was then adapted to make a screening regime specifically for boars where all chromosomes can be tested, although typically excluding the Y chromosome due to

lack of available BAC clones (O'Connor et al. 2017). The probes used are end sequenced BACs from the sub-telomeric region of the terminal ends of each of the porcine chromosomes (O'Connor 2017). The protocol in the Griffin Lab utilises direct labelling of each probe by nick translation with fluroescein-12UTP for the short arm, and Texas Red 12-dUTP for the long arm (O'Connor 2017). Heparinized blood samples from boars are typically provided by genetics companies for RT screening. As outlined above, a heparinised blood culture is cultured for 72 hours at 37^{o} C in a culture medium such as PB Max Karyotyping medium in 5% CO_2 atmosphere (O'Connor et al 2017). The cells are then arrested at metaphase with colcemid at 10 μg/ml concentration for around 35 minutes and then treated with a pre-warmed potassium chloride (75mM KCl) solution before fixation to glass slides using 3:1 absolute methanol:acetic acid freshly prepared (O'Connor 2017).

To prepare the slide for FISH, a probe solution is prepared for each chromosome 1-18 as well as the X chromosome. For each chromosome, 0.15μL of FITC probe is added for the p-arm, 0.15μL of Texas Red probe added for the q-arm, 0.1μL of unlabelled pig DNA added to cut down on signal background, and 0.6μL of water added and mixed together in a tube out of direct sunlight. To ensure correct orientation of the slide, a black mark is added to the back of the slide. This can be seen in Figure 12 below.

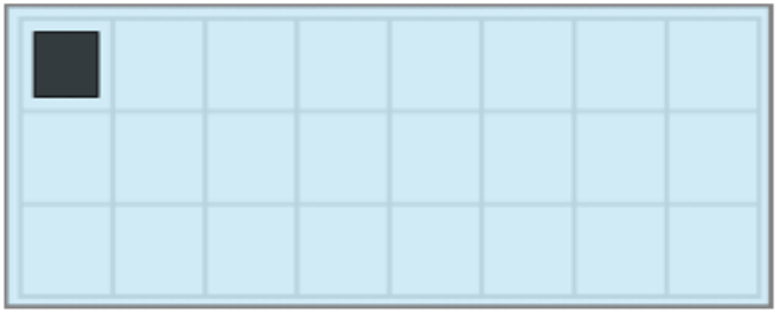

Figure 12. Multiprobe device orientation. (Griffin Lab 2020).

With the etched squares facing upwards, beginning on the black marked square and chromosome 1, 1µL of probe solution for each chromosome is pipetted onto the centre of each square as seen in Figure 13 below.

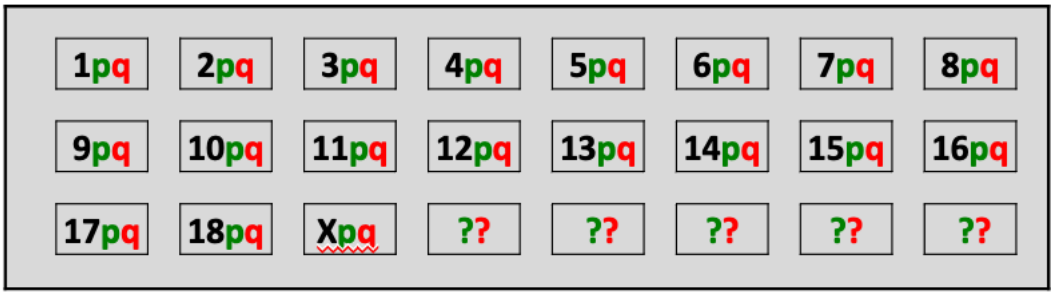

Figure 13. Chromosome orientation on the multiprobe device (Griffin Lab 2020)

The solution must be allowed to dry before the device is then stored in the dark at 4°C. When the metaphase chromosomes are prepared and ready for fluorescence in situ hybridisation, 1µL of hybridization buffer is first pipetted onto the individual squares of the device to resuspend the probes (O'Connor 2017). The two slides are then aligned and pressed together for 10 minutes on a hotplate (O'Connor 2017). The probes and target chromosomes are then denatured at 75°C for five minutes and then left to hybridize overnight (O'Connor 2017). After

hybridisation, slides are then washed and counterstained with DAPI in Vectacshield (a medium to prevent fluorophore fading). Images are then captured using an epifluorescence microscope and the SmartCapture system (Digital Scientific UK). When visualizing the FISHed pig chromosomes on the device, the ends of each chromosome can be easily detected from the bright red and green signals where the probes have hybridised to the chromosomes. This can be seen in Figures 14 and 15 below.

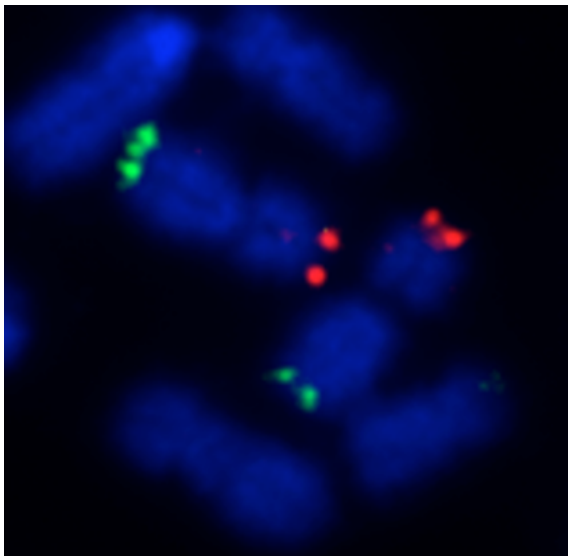

Figure 14. Normal chromosome visualisation (pig chromosome 1) with the multiprobe FISH device (O'Connor et al. 2017). Unique FISH probes near the telomere (subtelomeric) are clearly seen in red and green

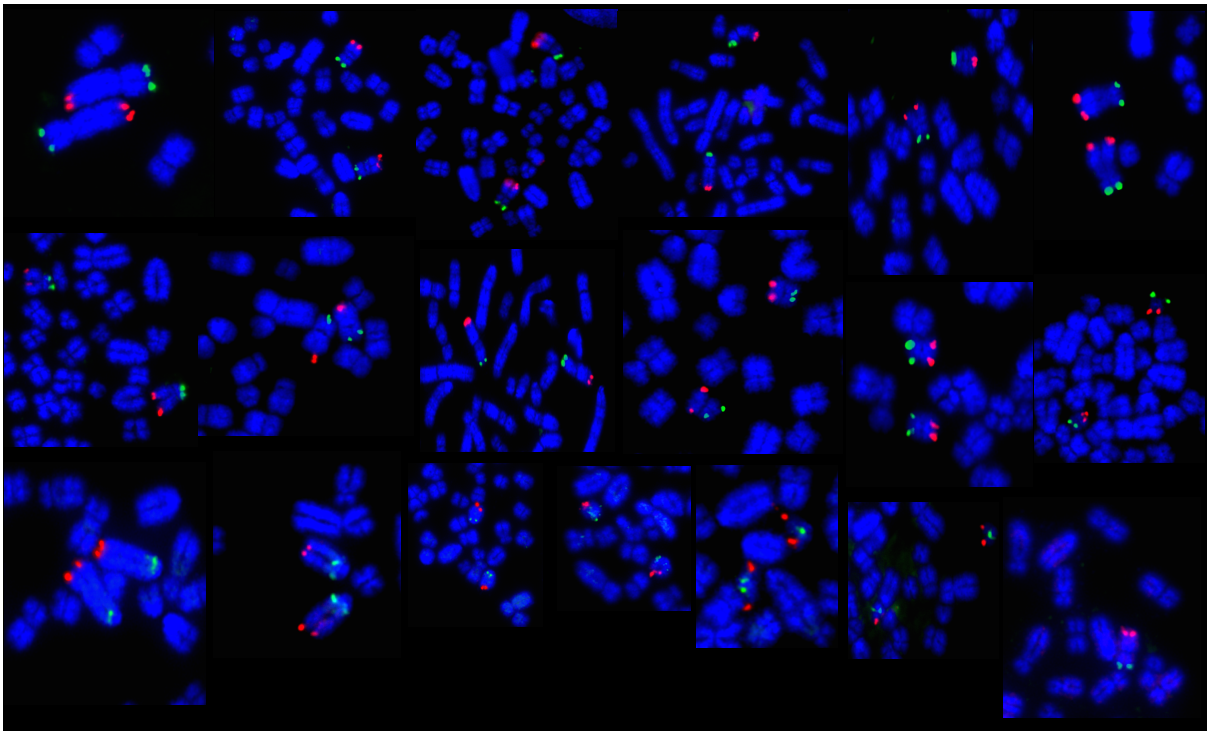

Figure 15. Representative example from each square of the multiprobe device (chromosome 1 top left, X chromosome bottom right). Each pig chromosome stained red and green, top and bottom

Because the probes for each chromosome are from the subtelomeric region, any reciprocal translocation (including cryptic ones) can be visualized, regardless of location. The device allows relatively easy detection of translocations with little training involved. As discussed previously with standard karyotyping, knowledge of the pig karyotype is necessary to identify chromosomal abnormalities, such as reciprocal translocations. However, with the multiprobe device, the user only needs to look for the red and green probe signals in different locations. In Figure 16 below, an RT is visualised by virtue of the fact that the red and green signals are together on one chromosome, and apart on the others.

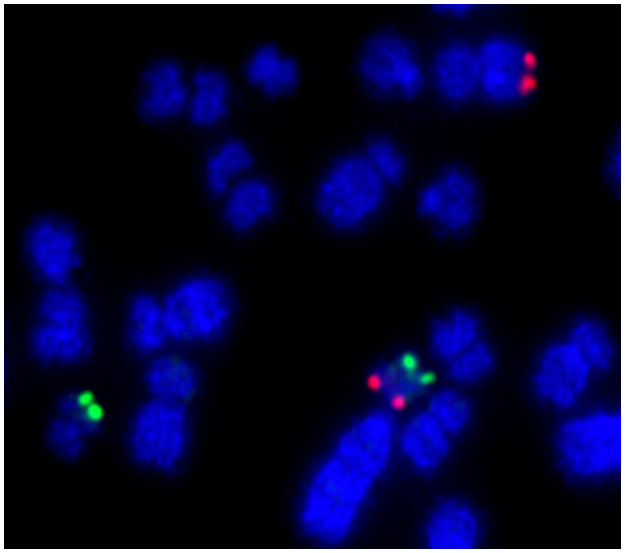

Figure 16. An RT visualized with the multiprobe device

2.3. The Application of Pig Cytogenetics

Interest in animal cytogenetics has developed slowly over time, evolving through various stages, methods, and techniques (Raudsepp 2016). The 1990s saw a peak of publications and discoveries which developed standard nomenclature and conventions for cytogenetics (Raudsepp 2016). The pig karyotype is one that has been extensively studied, mostly due to it having a relatively low number of chromosomes compared to other species, and it being a good model for comparing chromosome aberrations to humans (Rothschild 2011). The karyotype of a normal domestic pig contains 38 chromosomes (see Figure 9 above), which was described in the 1930s and accepted widely in the 1950s (reviewed in Gustavsson 1988). The advent of banding techniques in the 1970s allowed for the individual chromosomes and morphological traits to be identified (Gustavsson 1988). As mentioned above, the most common banding technique used in classical karyotyping of the domestic pig has been G-banding (also Figure 9), however depending on what is specifically being studied, many of the aforementioned techniques can also be applied (Rothschild 2011). As mentioned previously,

due to the costly nature RTs can have on the pig industry, and the frequency with which they occur, many companies and even whole countries have adopted screening measures (Rodriguez 2010). Screening of pigs in various countries began with screening only hypoprolific boars in an effort to discover if an RT was the cause (Ducos et al 2008). Now most purebred boars at the selection level are screened for RTs in France (Ducos et al 2008). Today, most breeding companies regardless of country or region have adopted a screening program for RTs as a means of reducing the risk of allowing an RT to persist within a breeding program (Danielak-Czech 2020). Young boars are usually screened prior to their placement in a breeding program with standard banded karyotyping (Ducos et al 2008). This is not a perfect system however, as the success of standard karyotyping is largely user-dependent and it is possible for a karyotype to appear normal yet still have an abnormality.

2.3.1. Translocations in the Domestic Pig

Chromosomal rearrangements have been extensively studied and well documented in the domestic pig (*Sus scrofa domesticus*) (Rothschild 2011), usually by G-banding and occasionally confirmed by FISH. Structural chromosomal rearrangements in the domestic pig are a relatively common occurrence, with constitutional RTs being the most frequent aberration observed (Rothschild 2011). Over 130 different types of RT have been identified and studied, with all chromosomes being involved with the exception of the Y chromosome (Rothschild 2011, Pinton 1998). There are certain RTs that occur more than more frequently than others, likely due to “some chromosomal bands being more prone to breakage” (Rothschild 2011). For example, chromosomes 1, 7, 14 and 15 participate in rearrangements frequently (Rothschild 2011). A list of frequently occurring translocations can be seen in the appendix. RTs may appear *de novo* in an individual pig, or may be inherited from one or both parents

(Ducos 2007). The typical consequence of an RT in pigs is a reduced reproductive functionality (Ducos 2007) for the reasons outlined above. The percentage of unbalanced gametes that can occur depends on several factors including: the chromosomes involved, the breakpoints, and the length of the segments involved in the RT (Benet et al 2005).

Because RTs have been extensively studied in pigs, the incidence rate is widely accepted to be around 0.47% (Ducos 2007). More recent studies have shown however that this incidence may be 1.5-2x higher when more accurate technologies such as the multiprobe device are used (O'Connor et al. 2021). In hypoprolific boars that are phenotypically normal with normal semen profiles, it has been observed that around 50% are carriers of an RT (Rodriquez 2010). Reduction in litter size from an RT can range from around 10%-100% depending on the nature of the RT; however, the average reduction in litter size observed in pigs is around a 40%-50% loss (Ducos 2007).

Furthermore, approximately half of the offspring of RT carriers may then pass the translocation on to their offspring (Ducos 2007). This can have severe economic consequences in the pork production industry due to the leverage of individual animals because of modern reproductive technologies (Rodriguez et al 2010). One such technology, artificial insemination (AI), is extensively used in the pig industry with a single boar siring multiple litters per year (Rodriguez et al 2010). Different structures and regulations, such as pooling semen doses, can alter how much an RT carrier can affect the industry, however these aspects will be discussed later in the chapter (Rodriguez et al 2010). The potential for such economic losses, however, has caused many production companies, and even countries, to adopt cytological screening for chromosomal abnormalities (Rodriguez et al 2010).

2.4. Pig Industry Overview and Business Structures

In order to understand fully the economic impact that an RT can have on the pig industry, it important to understand the various structures of pork businesses with special attention to semen distribution and structure. There is a myriad of business structures within the pig industry, which can vary regionally and geographically (Ginder 1995). The end goal for most businesses regardless of place or structure within the pig industry is to achieve a high profit by maximizing the number of pigs produced per year (McGlone 2003). There are many different stages of pig production, from the deciding the right genetics for a breeding system, all the way to the grocery store shelves (King n.d.). A general overview of the pig industry can be visualized and represented through a standard breeding pyramid. A graphical representation of this pyramid can be seen in Figure 17.

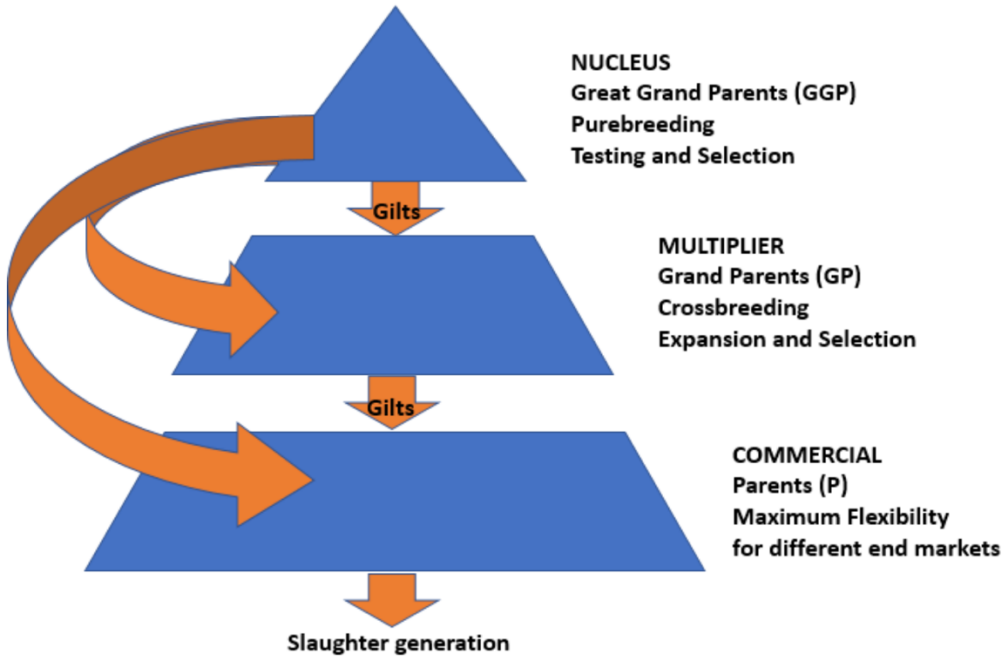

Figure 17. Standard Breeding Pyramid (Meerburg 2014).

The top of the pyramid represents a genetic nucleus of purebred animals, followed by multiplication herds, commercial herds, and finally kilograms of pork sold (Hardy 1998). In some cases, one single company will encompass the entirety of the pyramid; from generating and owning the genetic improvement in the nucleus, all the way down to the slaughter plant and processing. Some companies even have their own retail brands of products such as Smithfield, who sell several different brands of pork products such as Eckrich and Farmland (Smithfield Website n.d.). This is referred to as full integration. Other companies might own their own multipliers, commercial farms, and slaughter plants, but might rely on an external genetics provider for their genetic improvement and boars. In other systems, companies might focus on a single stratum of the pyramid; such as a commercial company purchasing F1 gilts and selling finished pigs. There are even segments of the market that work between, or in subsections of the strata. An example of this would be a gene transfer centre (GTC) who distribute semen to different levels of the pyramid. Another example would be a commercial sow farm that purchases gilts but sells weaned pigs to external finishing companies. Each of these different businesses will be affected by RTs economically different.

The top section of the pyramid is the “nucleus” or purebred breeding herd where animals (boars or sows) are selected for particular characteristics for genetic improvement (Gibson 1996). These characteristics are often traits such as backfat, growth rate, carcass quality, and litter size (Gibson 1996). The pigs in these nucleus herds are referred to as GGPs, or Great-grandparents, and are purebred animals that only operate with single boar mating (Jacques 2020). The primary role of a genetic nucleus within most breeding structures and regions is to supply genetic material through to the other layers of the pyramid (Moeller 2010). At the GGP level, aside from replenishing the GGP population, there are three primary products

produced at a nucleus farm. The first of these is to create GP, or grandparent, females to supply down to the multiplication level of the pyramid. The second is to supply GP maternal line boars to mate to GP sows. Maternal line GP boars are used to mate to the GP sows in multiplication with the end goal of creating parent sows. The third is to provide terminal sires for commercial matings at the parent level. Commercial matings result in piglets going into the protein chain. The next level in the pyramid, often referred to as multiplication, is focused on the creation of F1 parent females for use in commercial production. An F1 parent female is a first cross between two different maternal lines. An example would be crossing a Landrace with a Large White pig. The reason that the commercial pig industry utilizes F1 females is to take advantage of the effect of heterosis, or hybrid vigour, which yields a boost in performance. Generally speaking, the multiplication section represents somewhere between 10-12% of commercial sows. The role of multiplication, in regard to sows, is to place productive females into the commercial sector (Gibson 1996). Optimal genetic management is required at the multiplication level so genetic lag is not accumulated prior to being expressed at the commercial level (Moeller 2010). The section of the pyramid that represent the most animals is the commercial level. Traditionally, maternally selected F1 females are required for the generation of weaned pigs by being mated to a terminal boar. This results in fast growing pigs that produce a quality carcass with good meat-eating quality. For commercial production, the economic goal is to generate margin over cost base. This can be achieved by producing either more kilograms of pork or reducing fixed costs per kilo (McGlone 2002).

2.4.1. Genetics Companies

Genetics providers can range from multinational corporations to local farmer cooperatives, however due to a consolidating global pig industry, and the use of the technologies and genomic selection is leading to a smaller pool of genetic providers (Gura 2007). This can be seen in the marketplace very recently from bankruptcies, acquisitions and mergers between companies (Gura 2007). Genetics companies typically occupy the top of the pyramid, and also work at the multiplication level (Simm 2020). The main role of the genetics company is to create genetic improvement to disseminate through the pyramid (Simm 2020). Genetics companies can generate income from selling elite boars, doses of semen, and often royalty payments from customer output and herd size (Personal communication Craig Lewis 2020). As genetic companies provide boars at all levels of the pyramid, they are susceptible to the effects of an RT. In some cases, this could be a financial liability, but can also result in the loss of customer confidence or business.

2.4.2. Integrated Pig Production Businesses

Large scale integrators are typically multinational corporations that are focused on the production of animal protein to consumers. At the most extreme level, an integrator can operate at every level of the pyramid described above. They will own everything from the genetics company, all the way through to meat processing and in some cases retail protein sales (Busse 2014). An example of this is Smithfield Foods, which own Smithfield Premium Genetics, feed mills, farms, slaughter plants, processing, and also have retail brands of pork (Smithfield foods 2020). Some integrators can operate a just a few levels of the pyramid such as multiplication through to processing and sales. An example of this would be the Costa Food Group in Spain. They own and operate their own feed mills, farms, slaughter plants,

processing and retail, however, do not supply their own genetics (Costa Food Group 2020). In this situation, an integrator would partner with a genetics company to supply their genetics. This model is rapidly increasing in prevalence globally as can be seen by the map in Figure 18 that there are currently thirty-four mega producers which own over eleven million sows (Hess 2020).

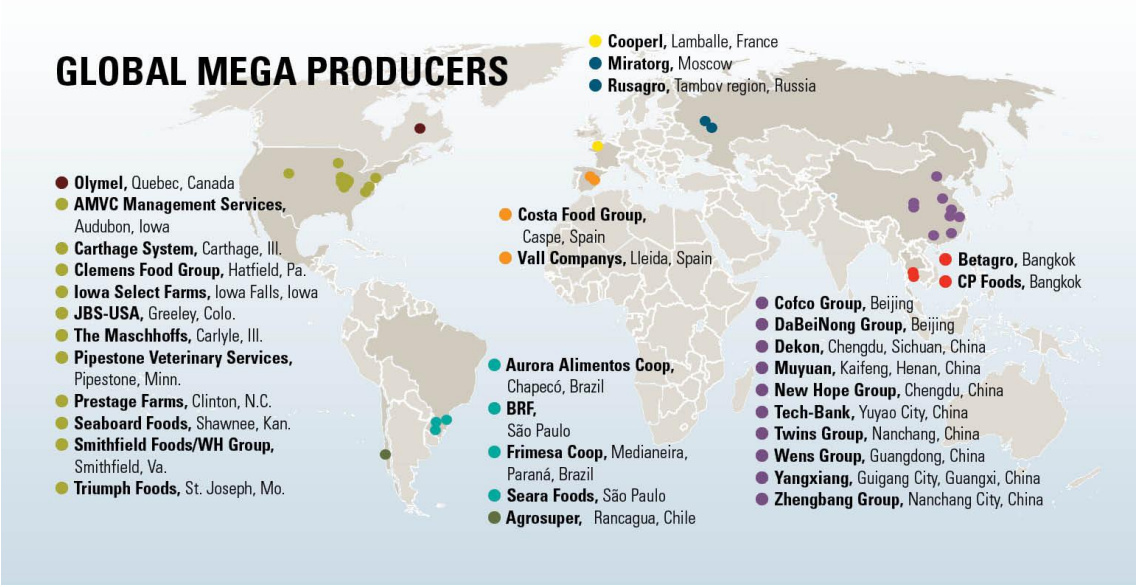

Figure 18. Global Mega-Producers (Hess 2020)

Integrators make their profits mostly from selling kilograms of either raw or processed meat. With to regards to RT in the sense of integrators, full integrators would be susceptible to the effects of an RT at the GGP level as would a genetics company, however, would also be susceptible to losses in production later in the pyramid. For example, an RT carrying boar in the integrator's boar stud can directly impact the reproductive performance and financial performance of the company.

2.4.3. Semen Retail/ Boar Studs

Very few farms currently contain natural breeding practices (Patsche 2015). Advancements in semen preservation have led to the extensive use of Artificial Insemination (AI) being the dominant form for reproduction in the pig industry (Knox 2015). These advancements have led to AI centres, or boar studs, becoming independent businesses with the aim of managing boars and distributing semen (Knox 2015). Boar studs have become quite specialised centres focusing on boar management, health and welfare, housing and feeding which allows for a focus on quality and quantity of semen production (Knox 2015). Separating the boar stud as a separate business allows for importance to be placed on biosecurity and disease prevention, which helps to maintain healthy breeding stocks (Althouse 2007). Boar studs can partner with a single genetics company to manage semen collection as well as a focus on their genetic improvement programs (Knox 2015). An example of this is the Birchwood gene transfer centre in the United States who partner solely with PIC America (Turley 2007). This is one of over 20 gene transfer centres (GTC) that PIC operate exclusively in the United States (Turley 2007). These centres manage the distribution of semen doses to customers as well as their genetic improvement programs (Turley 2007). Another example of this is AIM worldwide, which is a sister company of Topigs Norsvin (AIM website 2020). AIM worldwide manage and house the genetic nucleus of Topigs Norsvin as well as distribute semen to customers (AIM website 2020). Large scale integrator businesses such as Seaboard Foods in the United States, Cherkizovo Group in Russia, and Vall companys in Spain operate their own boar studs (personal communication, Sergio Barrabas, PIC, 2020). These boars are purchased from genetics companies and used in their own studs to distribute semen within their own systems (personal communication, Sergio Barrabas, 2020). There are also retail semen companies that manage, collect and distribute semen for multiple genetics companies (personal

communication, Sergio Barrabas, 2020). This is primarily a European phenomenon and is not very common in other parts of the world (personal communication Sergio Barrabas, PIC 2020). These companies operate as a type of “semen supermarket” and offer the different products from different genetics companies (Personal communication Ian Bond, PIC, 2020). Semen Retailers generate income based on volume of doses sold to customers and therefore health and quality are of great importance to them (Personal communication Ian Bond, PIC, 2020). With regard to an RT, the producer who purchased the semen from the retailer would most likely report hypo-prolificacy back to the retailer, who would then report back to the genetics company (Personal communication Ian Bond, 2020). Examples of semen retailers in Europe are: Genes diffusion in France, GFS in Germany, and Semen Cardona in Spain.

2.4.4. Farrow to Wean / Finish

Farrow to finish farms are more traditional types of farms as people tend to view them. While, in reality, these businesses can be split into two smaller businesses (farrow to wean and farrow to finish). In the breeding pyramid mentioned earlier in the thesis, farrow to wean or finish farms operate at the commercial level. Farrow to wean businesses will typically purchase semen or boars from a retailer or genetics company, and then raise pigs until weaning to sell (Farms.com 2020). Weaner prices can vary from week to week and regionally (agridata.ec 2021). The weaned pigs are typically sold to farms that specialise raising pigs from the weaning stage until they reach market weight (Farms.com 2020). Farrow to finish farms operate in a similar manner, except instead of selling the pigs at the weaned stage, they manage them until they have reached the finished stage and are at market weight (Farms.com 2020). Market weight, like weaner prices, varies regionally. The desirable market weight in the United States is around 130 kg (farms.com 2020). These types of businesses will notice

the effects of an RT when they notice lower total born numbers and will often bear the brunt of economic losses (Personal communication Craig Lewis 2020).

2.4.5. AI

Artificial insemination (AI) is a technology that has been around since the 1930s and most pig production systems both large and small will use it for breeding (Patsche 2015). For the last twenty years >90% of all sows were bred in Western Europe via artificial insemination (Gerrits 2005). The advent of semen extender which allows fresh semen to be used for up to five days has helped to advance the use of AI in the world (Gerrits 2005). AI is used in lieu of natural breeding techniques for a number of reasons including preventing over-use of the boar resulting in lower semen counts, higher conception rates, and higher semen quality (Patsche 2015). In addition to these, most relevant to the topic of RT in pigs, producers have adopted the use of AI as it allows them to utilise high quality genetics in an economical and profitable way (Maes et al 2011). By utilizing conventional AI techniques, a standard ejaculate from a healthy boar can be diluted to inseminate anywhere from 15-25 sows (Maes et al 2011). AI centres may dilute the sperm even further to maximise semen doses and profitability (Maes et al 2011). The use of AI also allows for many tests to be run on the sperm before insemination to check for correct concentration, and that the morphology and motility of the spermatozoa is normal which ensure good herd fertility rates (Althouse 2007). Clearly no company wants semen from an AI boar with an RT.

2.4.6. Semen Pooling and Single Sire Matings

Within the breeding pyramid, whenever parentage needs to be recorded, single sire mating will always be utilised. For example, in a genetic nucleus only single sire matings would occur.

This can also be a legal requirement in certain situations as in the Netherlands, where semen pooling has been banned by the government (Feitsma 2009). Semen pooling in general is utilised in one of two different ways. The first method is where the sow is inseminated by a different boar at each mating event. The semen on each respective event would be only from that specific boar. The other method is to create a single dose for insemination that contains the semen of several boars mixed together (Maiorano 2019). In the context of an RT in both situations, semen pooling can mask the effects of an RT as the chances of it affecting the litter become less with multiple sperm donors. As mentioned previously, some governments in Europe have banned its use after several disease outbreaks in the early nineties (Broekhuijse 2012). It is however still a common practice in the United Kingdom and the United States (Miller 2010). While the advantage of pooling semen can help to mask a hypo-prolific boar, there are disadvantages to not knowing the full genetic information about offspring (Miller 2010). If there is a hypoprolific boar, or a boar carrying a disease it is difficult to locate which sows have reproduced with the defective boar's genetics (Miller 2010). Countries that utilise only single sire matings, as well as the pure-bred genetic nucleus animals would have a higher risk of being affected by an RT.

2.5. New Technologies

As AI continues to increase in usage, the technologies associated with it are also continuing to develop. The ultimate goal when it comes to improving AI technology is to increase the number of AI doses per ejaculate which can be done by reducing the number of sperm cells required per dose or reducing the required number of doses (Bortolozzo, 2015). The current and most widely used standard procedure is intracervical insemination (CAI), which involves a semen dose being deposited into the cervical canal posteriorly (Bortolozzo 2015). Usually,

this procedure requires that the sow be inseminated two or three times depending on the farm, thus using 2 or 3 doses per sow (Knox 2017).

2.5.1. PCAI

One technology that has been in existence for many years now is post-cervical artificial insemination (PCAI). Although this technology allows for less sperm cells used per dose, due to certain limitations, it is not as widely used on farm. PCAI allows for sperm to be deposited past the cervix directly into the uterine body before the bifurcation using a specially designed catheter (Llamas-Lopez et al 2019). In Figure 19 below it can be seen the difference in semen deposit locations between traditional AI and PCAI. The advantages of this type of artificial insemination are that it does not require any more specialist training than standard AI, therefore can easily be implemented on commercial farms (Watson and Behan 2002). The most important factor is that PCAI uses half to two thirds less the amount of sperm cells with a success rate of 75-95% (Llamas-Lopez 2019). The main limiting factor, and most likely why it is not used more routinely in commercial farms, is that the success rates are far lower in younger nulliparous females (Llamas-Lopez 2019). The success rates have been seen as low as 20-60% in young females with PCAI, likely due to the reproductive tract not being fully physically developed and the cervix being less relaxed (Llamas-Lopez 2019). Commercial farms could employ both methods by keeping both types of doses on farm both for traditional AI and PCAI. This would allow purchased semen to go further and save the farmers money. On the other hand, if the semen being used is from a boar that has a reciprocal translocation, it could inseminate more sows than with traditional AI. For example, a boar in a stud can sire around 11,000 piglets per year (boar impact formula) with traditional AI, using PCAI, a boar

can sire over 14,000 piglets. In that boar is carrying an RT then the potential losses to the company could therefore be significant.

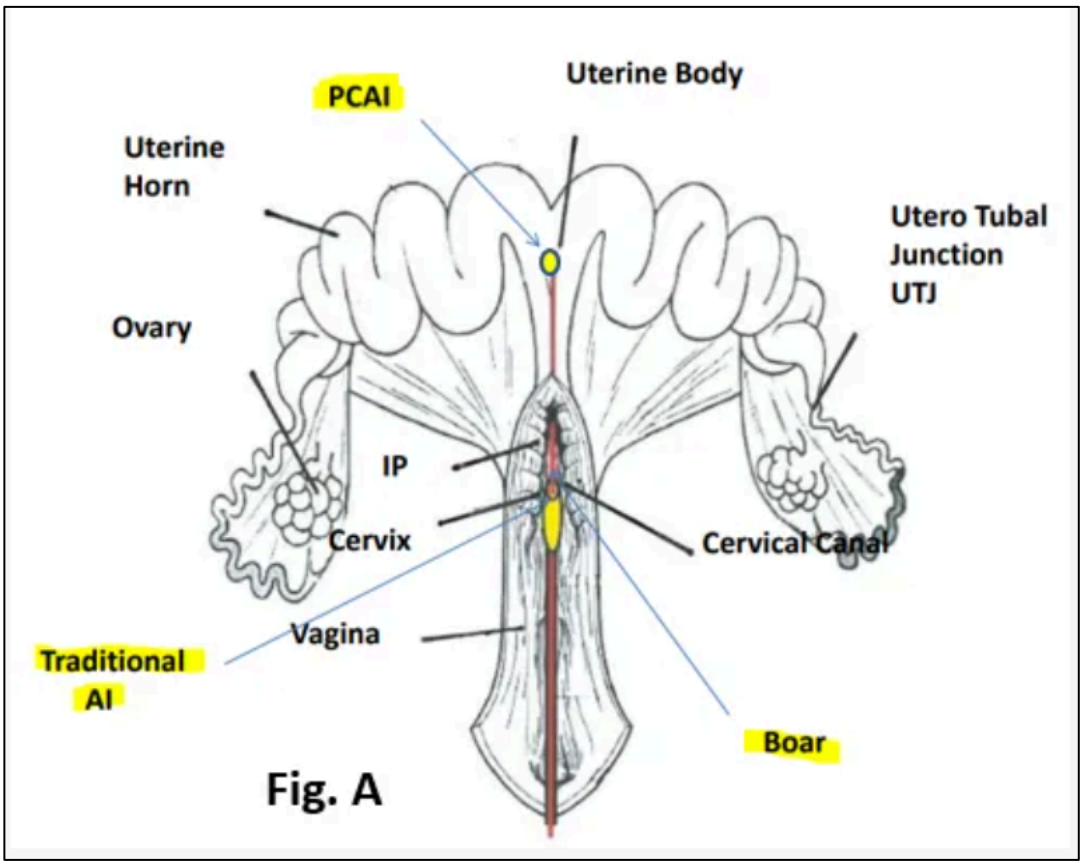

Figure 19. Depth of Catheter of AI and PCAI (Braun 2018).

2.5.2. Fixed Time Artificial Insemination (FTAI)

As mentioned previously, because the ovulation time is variable during the oestrus of a female pig, it is necessary for them to be inseminated two or three times (Quirino 2019). The timing of ovulation can be synchronized using various hormones such as gonadotropin-releasing hormone (GnRH) and porcine luteinizing hormone (pLH) (Bortolozzo 2015). An example of a commonly used GnRH is triptorelin which aids in inducing ovulation, by stimulating the release of luteinizing hormone, (Quirino, 2019). This type of hormone can be used in gel form

and administered intravaginally around 96 hours after weaning (Quirino, 2019). The sows can then be treated with a one-time insemination around forty hours after administration of the triptorelin (Knox et al., 2017). Another GnRH used for FTAI is buserelin (Quirino, 2019). Buserelin provides similar effects but is administered intramuscularly (Driancourt et al, 2013). Using FTAI in the pig industry is potentially beneficial for businesses, as it can reduce the number of doses of semen required, and or the number of boars required, and additionally it would save costs for labour as only one dose is required (Quirino 2019). Like many new technologies, the costs are often higher in the earlier stages, and the cost of these hormones used in FTAI can be expensive which is one of the reasons why it is not as widely used as traditional AI (Quirino, 2019). However, as more farmers adopt the new practices and costs come down, it could become more widely used. This technology can also be combined with PCAI, which would require then only one dose of semen, with a reduced number of spermatozoa per dose (Ulguim et al 2018). With this in mind therefore, screening for RTs may also become a possibility in breeding sows also.

2.6. Rationale and Objectives of the Thesis

As pointed out in section 2.3.1 the presence of an RT in a breeding herd can have dire consequences for the company. To the best of my knowledge however, this has not been accurately quantified, particularly in terms of where the boar sits in the breeding pyramid. The overall aim of this this thesis was therefore to provide an extensive and contemporary overview at the structure of the pig industry in order to give insight as to how an RT can affect different part of the businesses involved. The purpose is to provide a comprehensive overview of current screening methods to compare the relative advantages of using the with the multiprobe approach compared to standard karyotyping. This thesis thus comprises an

economic analysis to show actual and potential losses incurred from an RT being allowed to persist in a herd. While this is only a small part of the overall losses in the pig industry food chain, small technologies such as this can have a cumulative effect on reduction of waste and increases in sustainability in the pig industry (FAO 2020) and this is assessed.

2.6.1. Specific Aims

Specifically, therefore, the aims of the thesis were:

a. To calculate, in a hypothetical model (a theoretical situation) the financial impact of an RT affecting a farm in a *farrow to wean* scenario
b. To perform a similar calculation of the financial impact of an RT affecting a farm in a *farrow to finish* scenario
c. To examine the financial impact of a scenario where a dam line boar at the grandparent (GP) level is used to create females for production use and thus the possible detrimental effects of an RT
d. To examine a scenario at the GGP (great grandparental) level involving a pure line in a commercial breeding company that is used to make pure line, terminal boars and the effect an RT can have in this situation
e. To examine a combined GP and GGP scenario where the GP model (involving a dam line boar) however, in this case, located at the nucleus of the pyramid at the GGP (great grandparental) level
f. To take a “real world” scenario in which a boar was reported as chromosomally normal by karyotyping but a 5:6 RT identified by the multiprobe approach and financial effect that this had on the company involved (case study 1)

g. To take a second “real world” scenario in which a German Pietrain at the GGP level, located in a multi-genetic German retail semen boar stud was reported as chromosomally normal by karyotyping and the financial impact of a 9:18 discovered by the multiprobe approach (case study 2)
h. To calculate cost and benefit as well as the return on investment for karyotyping compared to the FISH Multiprobe Screening approach

3. Materials and Methods

A series of formulae and assumptions were devised, based on conversations with relevant managers and stakeholders within the global pig breeding industry and from basic pig industry parameters derived from published literature.

3.1. Variables Involved in the Economic Model

When calculating the economic damage from an RT in a boar, whether hypothetical (prospective) or for an actual case (retrospective), there are many additional factors outside the direct impact of the RT itself that need to be considered in the calculations. Firstly, the situation (context) and structure of the business in question must be considered as this can vary not only from system to system, but also regionally. These differing scenarios will require different variables and inputs. In this thesis example values were used to calculate the economic impact of the models. In real situations producers should enter into the models data that represents their own specific situation using the last 6-12 months of achieved production as the baseline parameters.

3.1.1. Boar Effect

The first factor that was considered is that of the effect of the boar. This is essentially a calculation of how many pigs a boar at any level in the breeding pyramid can feasibly affect. It also takes into consideration any AI technology being used. This factor is significant with regards to dealing with an RT in a boar as it can help determine how many pigs are affected or could be affected in real and hypothetical situations. The following formula was created

based on conversations and interviews with high level boar stud managers. The formula begins with the number of sperm cells that can be produced per week from a boar. This is on average around 80 billion cells per week from a mature boar. From this, only around 90% would pass as quality ejaculates. On an average boar stud the boar would be used around 39 weeks of the year due to training and rest needed. Each dose created from this boar would contain around 2 billion cells, which gives around 1,404 doses produced from this boar per year. A boar stud would keep a boar around 1.25 years and around 92% of these doses would be used for actual breeding. This is a conservative estimate based on possible issues in supply chain, surplus of supply etc. This formula leads to a figure of approximately 1,614.6 doses available for breeding. Each sow would require around 2.1 doses while in heat, and with a farrowing rate of 0.86 and a weaned average of 12.5, this means that one boar can affect approximately 8,265 pigs in his breeding lifetime. If AI technologies are used, such as PCAI, this figure rises to around 14,694 pigs that this boar can affect. The formulas used for these calculations can be seen below:

Standard AI:

$$(80(\ billion\ cells) \times 0.9\ quality\ \times\ 52\ weeks) \div 2\ billion\ cells\ per\ dose$$

$$= 1{,}872\ doses\ per\ year$$

$$1{,}872\ doses\ \times 1.25\ years\ of\ usage\ \times\ 0.92\ breeding\ doses\ = 2{,}152.8\ doses$$

$$2{,}152.8\ doses\ \div 2.1\ doses\ per\ sow\ \times\ 0.86\ fr\ \times\ 12.5\ weaned\ pigs$$

$$= 11{,}020\ weaned\ pigs$$

PCAI:

$$(80(\ billion\ cells) \times 0.9\ quality\ \times\ 52\ weeks) \div 1.5\ billion\ cells\ per\ dose$$

$$= 2{,}496\ doses\ per\ year$$

$$2{,}496\ doses\ \times 1.25\ years\ of\ usage\ \times\ 0.92\ breeding\ doses\ = 2{,}870.4\ doses$$

$$2{,}870.4\ doses\ \div 2.1\ doses\ per\ sow\ \times\ 0.86\ fr\ \times\ 12.5\ weaned\ pigs$$

$$= 14{,}694\ weaned\ pigs$$

3.1.2. Situation and Breeding Level

The next factor that must be considered is the situation in which the boar is placed, which determines the number of sows he can inseminate, and therefore the number of pigs that he can affect. This is not a variable as such, but rather a factor that determines what level of the economic model for RT that is used for calculating the cost. Many of the variables that will be discussed below are further calculations that are undertaken by the individual farms and companies. For each calculation, situation and breeding level was factored in.

3.1.3. Number of Matings

The number of matings that are performed on single or several farms by a single boar is an important variable to consider as it directly impacts the number of pigs affected by an RT, by inheritance or by loss of litter size. The number of matings that can be performed by a single boar also depends on many factors. The situation that the boar is being used will affect the number of matings that will be performed. For example, if a boar is placed on a farm with a certain number of sows, the mating number will be based on the sow count for that farm.

3.1.4. Farrowing Rate

Farrowing rate is a variable that must be considered in nearly all systems. This is the proportion of sows that are served that go on to farrow. For example, if 100 sows were bred, and only 80 of them farrow, the farrowing rate is 80%. While this seems like a simple

calculation, in real life situations, the calculations for each farm will be different and more complex than this, however. There are many factors that can affect farrowing rate which go beyond the scope of this project; however, geographical location, semen quality, genotype, health status and nutrition are a few examples. A generally accepted and realistic value is around 85-90% (Young et al, 2010). Despite having this accepted value for the farrowing rate, to create a robust model that can be applicable to multiple stakeholders in the industry, farrowing rate should remain a variable and not a fixed value. For example, a farm that is experiencing health issues may have a farrowing rate of only 80%, and a different healthy farm with the same structure may have a farrowing rate of 95%. Changing the farrowing rate effectively changes the number of pigs a single boar will, and could, potentially affect, and thus the number of pigs negatively affected by an RT. This was a crucial factor in the calculations of this thesis.

3.1.5. Total Born, and Total Born Alive

Total born is essentially the number of pigs born in a litter no matter what their condition and sets the baseline for number of actually pigs born alive. The total born number can include born alive, stillborn, mummified or various other situations (McGlone 2003). In order to calculate the average total born for a specific farm, it is usually the total pigs born in a group or on farm, divided by the number of litters in that group. There are numerous factors that can affect this number, including RT. The genetics of a sow play a role in litter size, with some breeds being more prolific than others. For example, maternal Duroc breeds are less prolific than Landrace or Yorkshire breeds (Nowak 2020). Parity number, or number of litters a sow has had, can affect the total born number marginally. Usually, a sow's first litter produces a smaller number of total born, and then this number will peak somewhere around parity three

and four and then decline again (Aherne and Kirkwood 2001). The service management of gilts and sows can also affect the number of total born, with poor timing or management of the semen and insemination can lead to lower numbers. This can include the age of the semen, and days post collection used in the sow or gilt. The underlying health status of the farm can be a contributing factor as well. For example, a disease such as PRRS, which is highly contagious, can cause embryonic death (Aherne and Kirkwood 2001). Total born numbers are variables that will either be supplied by the farms from their records, or, averages based on data from the area and the various factors that can alter this number. While the focus of this thesis is not on total born, nor the various factors that affect this number, it is important to understand the baseline numbers and averages of total born and thus born alive pigs that will flow through to later stages in production. This allowed me to quantify the losses (or potential losses of pigs) that are caused by an RT.

3.1.6. Pre- and Post-weaning Mortality

Following on from the above discussion involving reduction in pig numbers, two more variables that were considered in this thesis were pre-weaning and post-weaning mortality. Pre-weaning mortality is defined as a piglet that is born alive but dies before weaning happens (McGlone 2003). There are various causes of pre-weaning mortality and the rates can run from 5-53%. Most often this is caused by crushing (Mainau 2015). Starvation and hypothermia can contribute to piglets being crushed as they move closer to the sow seeking heat and food (Mainau 2015). Low birthweight is also a contributing factor to pre-weaning mortality as lower birthweights can affect locomotor skills, vitality, thermoregulation, and the ability to nurse (Feldpausch et al, 2019). Post weaning mortality is defined as pigs that die after weaning, but before they are finished or slaughtered (McGlone 2003). The average rate for

post-weaning mortality is 4-8% (Gebhardt et al, 2020). The issue of post-weaning mortality is more complex, with often multiple factors contributing (Gebhardt et al, 2020). The most common cause of post-weaning mortality reported by the USDA is respiratory disease (Gebhardt et al 2020).

3.1.7. Point of Sale Parameters

In order to create an economic model that can predict or demonstrate the economic consequences of an RT in a pig business, it was necessary to create a flexible model to meet the parameters of specific business models as well as the constantly changing variables of the pig market. For example, in the context of a producer that sell weaned pigs, post weaning mortality would not be applicable, and the current market price for weaned pigs needs to be variable as it can change from week to week. In contrast, a “farrow to finish” producer would need to take both the pre and the post weaning mortality into consideration and therefore apply those variables using the records from their business. These parameters were taken into consideration for genetics companies with boars at the GGP and GP level as well.

3.1.8. Calculations of the Impact on the Industry of an RT

Using all of the parameters and factors mentioned above, the models and calculations were designed to show how many pigs or kg of meat were lost /missing or could have been lost / missing due to an RT. From that information and looking at the context parameters such as business type and location of the boar in the breeding pyramid, a financial impact or opportunity cost was calculated for various scenarios.

3.2. Keeping Numbers Within Realistic Bounds

Of course, if you have a boar with an RT in the breeding herd, the outcome is usually seen in terms of a dramatically reduced reproductive performance in terms of total born. As such, a boar with RT is unlikely to be continually used long after the poor outcomes are seen on farm. Therefore, it is important to understand the biology of the pig to arrive at a reasonable timeline at which the impact of the RT is seen at farm level. If you consider that the gestation length of a pig is roughly 116 days or 16.6 weeks, then it is likely that about 3 weeks of production results are required to underline a production issue associated with a specific boar. Then one can consider that it is feasible that 19.6 weeks of production is in the production flow before any boar is stopped from sending doses into commercial farms. This is all also assuming that there is good recording of reproductive performance of the boar at farm level, and that single sire doses are used.

3.3. Economic Models Used

As discussed previously, there are various business structures within the pig industry, the economic model used to calculate the losses, or potential losses in revenue due to an RT will differ slightly depending on the situation. The purpose of this thesis was to consider several of these. As an example, we can take a farrow to finish scenario and then extend this to boars used for parent sow production. These are called GP (grandparent) boars and an example could be a Landrace boar in stud that is producing doses that will be used in Large White sows on farm to make parent sows. To show that the constructed models are based within reality the Griffin lab had two actual examples of RT sires. Interviews were held with different

stakeholders within both scenarios, and these helped with first construction of the economic logic for the results section of the thesis.

3.4. Case study 1

This case study was of a large white boar at the GP level being used to create parent sows for commercial use. The boar was karyotyped with standard banded karyotyping and reported to be normal. However, the boar performed sub-optimally and a blood sample was then sent to the Griffin lab and using the multiprobe device a cryptic translocation (5:6) was discovered. After discussions with Director of Genetics with the company Dr Grant Walling, a basic economic calculation was provided with this specific context which served as basis for the expanded models discussed later in this thesis.

3.5. Case study 2

This case study was of a German Pietrain at the GGP level, but also making terminal commercial matings, located in a multi-genetic retail semen boar stud located in Western Germany. This boar was also karyotyped twice with standard banding karyotyping and reported as normal but was also performing sub-optimally. Like the previous case study, a blood sample from this boar was sent to the Griffin lab and an RT (9:18) was found using the FISH multiprobe device. This case study differs from the previous one in that this boar was being used in multiple situations and therefore multiple models were applied. This case study showed the need for multiple models and that the economic impacts can vary based on the situation of the boar.

4. Results

4.1. Specific Aim a: Impact of an RT in a Farrow to Wean Scenario

This hypothetical model explores a theoretical situation of an RT affecting a farm in a farrow to wean situation. In this scenario, the location is a commercial sow farm producing and selling weaned piglets. This model assumes that the farm is purchasing retail semen from a boar stud without the use of semen pooling. In this case, the semen used on this farm is from a terminal boar containing an RT. As mentioned in the materials and methods, the first variable to mention is the number of matings performed by this boar on the farm. On average, a boar can produce around 1,872 doses of semen per year however this number can vary if other reproductive technologies are being employed.

To arrive at a realistic number of matings for this scenario, I calculated the number of weeks the boar's semen would be in use before a problem was noticed. With an average of 116 days, or approximately 16.5 weeks, for gestation length, another three weeks was added to this time frame to account for a farmer noticing a problem of low litter sizes. This three-week addition is not a precise value, however an estimation on when a farmer might decide to take action and stop the use of the boar, or if the farm in question does not have good record keeping practices, it might take longer for the problem to be noticed. If we assume that the farm is on a weekly insemination routine, and using the maximum possible output from the boar, (1872 doses divided by 52 weeks in a year is 36 maximum doses per week) 19.5 weeks is multiplied by 36 doses per week to equal approximately 704.5 total doses. The total number of theoretical matings is approximately half of this number because each sow would be given on average 2.1 doses, which gives 335.5 total matings.

In order to get an approximate number of farrowings for the calculation, the number of matings was multiplied by the farrowing rate. Farrowing rate can vary from farm to farm with anywhere from 85-90% being an accepted target rate (Young et al 2010). For this example, a farrowing rate of 90% was used thus giving 301.5 total farrowings. This number was then multiplied by the average born alive for the farm. In general, born alive numbers range from 13-16, so in this case 14 was used (Freyer, 2018). From this, we get a total of 4221 total piglets that could potentially be born on this farm. To get a more realistic value for total piglets however pre-weaning mortality should also be considered. Although the normal range of pre-weaning mortality rates is quite large (5-35%) a well-managed farm usually aims for 5-8% (Muirhead 2013). For this example, a 10% pre-weaning mortality was used to give a total piglet number of 3,798.9 piglets. In order to calculate the potential missing revenue from an RT, the effect of the RT must be considered to find out how many piglets would be lost. As discussed previously, this number has quite a range of variation. In reality, a farmer would need to look at his records to determine the average loss in litter size. For the purposes of this theoretical situation, a 50% loss was used giving 1899,45 missing pigs due to the RT. If the farmers are selling at 7kg weaners, the current price as of October 2020 in the United Kingdom was £39.97, and if they are selling at 30kg then the price was around £52.87. Using these prices multiplied by the number of lost piglets gives a loss of £75,921.02 for selling at 7kg, and a loss of £100,423.92 for farmers selling at a 30 kg weaner weight. This is summarised below in a simple equation where nm is the number of matings, “fr” is farrowing rate, “ba” is born alive, “pwm” is pre-weaning mortality, “RT” is the effect of the RT.

Expressed mathematically therefore, the following formula was applied:

$$loss\ of\ revenue\ FtoW = (nm) \times (fr) \times (ba) \times (pwm) \times (RT) \times (Price)$$

$$FtoW = (335 matings) \times (0.9\ fr) \times (14 ba) \times (0.9 pwm) \times (0.5\ RT)$$
$$\times\ (£39.97) or\ (£52.87) = \mathbf{£75,921.02\ or\ £100,423.92}$$

In other words, a company "gains" £75,921.02 (lower end) or £100,423.92 (upper end) each time an RT is detected in a *farrow to wean* scenario.

4.2. Specific Aim b: Impact of an RT in a Farrow to Finish Scenario

Farrow to finish farms are essentially the same model as the farrow to wean scenario, except the pigs are weaned and kept until they are ready to be sold at market. The calculations are essentially the same except post-weaning mortality and must be factored into the equation. This, like pre-weaning mortality, can vary from farm to farm depending on factors such as health and welfare. The average rate for post-weaning mortality is around 4-8% (Gebhardt, 2020). For this example, a post-weaning mortality rate of 5% was used. Using the number of missing weaned piglets from the farrow to wean model above and applying the 5% post weaning mortality rate gives 1804,47 missing piglets. As the pigs are being kept until they are finished and ready for market, the carcass weight and price per kilogram of meat is used instead of the weaner price per pig. The average carcass weight for pigs in the UK for October 2020 was 87.19 kg however this weight can vary depending on the country (Driver 2020). The market price per kilo of meat is perhaps the most variable factor here as it can change from week to week (ahdb.org.uk). This variability can be seen in the chart below with current 2021 figures. In the last week of October 2020, the market price for a pig carcass was approximately

153.42 pence per kilogram (ahdb.org.uk). Applying these market weight and prices from the United Kingdom gives a total value of £240,719.

Week end date	EU spec GB APP (p/kg)	Change on week (p)
27/03/2021	145.49	1.56
20/03/2021	143.93	0.24
13/03/2021	143.69	-0.42
06/03/2021	144.11	1.32
27/02/2021	142.80	0.60
20/02/2021	142.20	-0.92
13/02/2021	143.11	-0.85
06/02/2021	143.97	-0.78
30/01/2021	144.75	0.51
23/01/2021	144.24	-3.56

Figure 20. Variability in Price per Kg of pig meat. (ahdb.org.uk)

Expressed mathematically therefore, this formula was applied:

$$loss\ of\ revenue\ FtoF = (nm) \times (fr) \times (ba) \times (pwm) \times (RT) \times (Pwm) \times (kg) \times (mp)$$

Inputting the numbers from this scenario:

$$FtoF = (335matings) \times (0.9fr) \times (14ba) \times (0.9pwm) \times (0.5RT) \times (0.95Pwm)$$
$$\times (87.19kg) \times (£1.53) = \mathbf{£240,719}$$

In other words, a company “gains” £240,719 each time an RT is detected in this scenario.

4.3. Specific Aim c: Impact of an RT in a GP Boar Scenario

This scenario looks at the case where a dam line boar at the grandparent (GP) level is used to create females for production use. This model not only looks at the physical losses of pigs due to the RT, but also the opportunity cost of the missing offspring's progeny. In order to start with an approximate and realistic number of matings for this scenario, the calculations were repeated as discussed in the Farrow to wean model above, to give 335.51 matings. This accounts for time before the smaller litter sizes due to the RT would be noticed and the boar would stop breeding. A born alive value of 13 is used as that is an average value of born alive for pigs at this level. From this it can be estimated that 6.5 females would result from each litter and factoring in pre- and post-weaning mortality yields around 5.56 finished females per litter. An average selection rate of 0.70 was used which means it could be expected that around 3.89 sows would be selected. If around 90% are cycling and in heat this number is reduced to 3.5 selected sows per litter and when multiplied by the total number of matings gives 1174.69 total selected sows. If the assumed effect of the RT is 50%, this yields 587.34 missing select sows. Each of these missing sows would have been capable of creating around 30 pigs per year with around 5 parities, which adds up to around 65 total piglets produced in each sow's lifetime. Multiplying this by the number of missing pigs equals around 38,305 pigs and at a price of £35 per piglet gives an opportunity cost of around £1,340,686.47. This number does not include the losses of non-selected gilts and male pigs. The full calculation can be seen below, and a spreadsheet for these calculations can be seen in the appendix.

$$(6.5\ BA\ females) \times (0.10\ prewm) \times (0.05 postwm) = 5.56\ finisher\ females$$

$$(5.56\ finisher\ females) \times (0.70\ selection\ rate) \times (0.90\ females\ cycling)$$

$$= 3.50 selected\ sows$$

$$(3.5\ selected\ sows) \times (335.51\ matings) = 1174.69\ total\ selected\ sows$$

$$(1174.69\ selected\ sows) \times (0.50\ effect\ of\ RT) = 587.34\ missing\ sows$$

$$\left[\frac{30\ ppsy}{2.3(litters\ per\ year)}\right] \times (5\ parities) \times (587.34\ missing\ sows)$$

$$= 38{,}305.32\ missing\ piglets$$

$(38{,}305.32\ missing\ piglets) \times (£35) = £1{,}340{,}686.47$ opportunity cost

In other words, a company "gains" over £1.34 milllion each time an RT is detected in this scenario.

4.4. Specific Aim d: Impact of an RT at GGP Nucleus Level Boar Production Level

This model describes a scenario involving a pure line GGP boar in a commercial breeding company that is used to make pure line, terminal boars and the effect an RT can have in this situation. This model explores the scenario where a boar at the GGP level with an RT is being used to make the next generation of pure line parent level terminal boars. In this situation, the nucleus farm, or farms, has around 1,000 nucleus sows each producing around 2.2 litters per sow year. One boar at the nucleus level in this breeding situation will typically only make around 10% of the matings to prevent over representation of any single boar's genetics in the breeding program. This creates around 220 matings from the RT boar and from these resulting litters the genetics company would aim to sell around 1.5 of these boars per litter to customers. The number 1.5 boars sold can vary from line to line and can also vary depending on the genetics company. With 220 matings, this boar would go on to make around 280.5 sold boars. Because of the RT, it can be estimated that around 50% of these boars would not

exist because of the RT, bringing the number down from 280.5 to 140.25. The assumption was also made that half of the boars that were born alive would then carry the RT which is around 70.13 carrying the RT. If each of these boars carrying the RT then went on to have around 335 matings, this results in around 23,527.65 total matings by boars carrying the RT. If this number is then put into the farrow to wean model (see calculations below), the result is 121,490.92 missing weaned piglets due to inherited translocations, and a £4,252,182.15 missing opportunity cost. The above numbers would assume no translocation screening had been done, or perhaps a cryptic translocation that had gone unnoticed in traditional karyotyping. The calculations for this can be seen below and in the appendix for the spreadsheets.

$$(1000\ nucleus\ sows) \times (2.2\ litters\ per\ sow\ per\ year)$$
$$\times (0.1\ percent\ herd\ representation) = 220\ matings$$

$$(1.5\ boars\ per\ litter\ sold) \times (220\ matings) \times (0.85\ fr) = 280.5\ sold\ boars$$

$$(280.5\ sold\ boars) \times (0.5\ effect\ of\ RT) \times (0.5\ carrying\ RT)$$
$$= 70.13\ boars\ carrying\ RT$$

$$(70.13\ boars) \times (335.51\ matings\ per\ boar)$$
$$= 23{,}527.65\ total\ matings\ from\ RT\ boars$$

$$(23{,}527.65\ total\ matings) \times (0.85\ fr) \times (13.5\ ba) \times (0.9)\ pwm) \times (0.5\ rt\ effect)$$
$$= 121{,}490.92\ missing\ weaned\ piglets$$

$$(121{,}490.92\ missing\ piglets) \times (£35\ \text{weaner price})$$
$$= £\mathbf{4,252,182.15}\ opportunity\ cost$$

In other words (based on the input parameters used), a company “gains” over £4.25 million each time an RT is detected in this scenario.

4.5. Specific Aim e: Impact of an RT in a Dam line GGP Boar Scenario

This scenario is similar to the GP model in that it involves a dam line boar, however it is located at the nucleus of the pyramid at the GGP level. This model looks at the physical losses of pigs due to the RT, and also the opportunity cost of the missing GP sows that could have been created and their parent offspring's progeny. As in previous models, the number of matings used is 335.51 as this takes into account time to notice the problem boar. The born alive number for this example is 13 which is representative of pure dam line production within a commercial multiplication farm. The expected reproductive potential of any pure line will be lower than an F1 in the same environment due to the impact of heterosis (Cassady 2002). With this born alive number this would yield approximately 6.5 females; and factoring in pre- and post-weaning mortality gives around 5.55 finished females per litter. At this point only around 70% of the females will be selected on physical traits for breeding. Of these 70%, around 90% will be in heat and can be bred which is around 3.5 females per litter or 1,174.69 females in total. If the effect of the RT is 50% this gives 587.34 missing GGP females. Each of these GGP females would have been expected to deliver 30 pigs each per year, with around 3 parities each. Note that the parity number is lower at the GGP level as the turn-over of breeding stock is higher for genetic diversity. This gives 39.13 total piglets per sow with around 19.56 of them being female and 11,491.59 total missing GP piglets. Because this RT began at the GGP level, it is necessary to look even further at the effects from this point. From these 11,491.59 GP female pigs, around 8044.12 would be selected for breeding, and around 7,239.71 would be cycling and available for breeding at the GP level, which then would result in 57,032.65 missing select parent level piglets. Each of these would then produce 65.21 total lifetime piglets giving a price of £130,183,215 total opportunity cost in this situation. The full calculations can be seen below, and the excel spreadsheet can be seen in the appendix.

$$(335.51\ matings) \times (3.50\ selected\ cycling\ females) \times (0.5\ effect\ of\ RT)$$

$$= 587.35\ potential\ missing\ GGP\ females$$

$$(587.35\ GGP\ females) \times \left(\frac{39.13}{2}\right) = 11{,}491.59\ GP\ female\ pigs$$

$$(11{,}491.59\ GP\ female\ pigs) \times (0.7 selection\ rate)(0.9\ cycling\ rate)$$

$$= 7{,}239.71\ GP\ selects$$

$$(7{,}239.71 selects) \times (7.88\ selects\ per\ year) = 57{,}032.65\ total\ selects\ missing$$

$$(57{,}032.65\ missing\ selects) \times (65.22\ total\ piglets\ missing)$$

$$= 3{,}719{,}520.42 total\ piglets\ missing$$

$$(3{,}719{,}520.42\ missing\ piglets) \times (£35) = \mathbf{£130,183,215}\ \text{opportunity cost}$$

In other words, a company "gains" over £130milllion (!!) each time an RT is detected in this scenario.

4.6. Specific Aim f. Case Study 1 - JSR Boar

As mentioned in the material and methods (section 3.4), this case study was of a large white boar at the GP level being used to create parent sows for commercial use. The boar was karyotyped with standard banding techniques and a result of a normal karyotype was returned. This can be seen in Figure 21. The boar was subsequently put into production. It is important to note that during the time that this boar was in production, the farm was suffering from a PRRS outbreak, which affects farrowing rates and total born numbers. The boar performed 73 matings with a farrowing rate of 68%. The lower farrowing rate is likely due to the PRRS disease that was present on the farm at the time. From the 50 litters that the boar sired, the average litter size was 6.5, compared to the average of 11.3 born alive on the rest of the farm. Because of the noticeable difference in born alive, a blood sample was sent

to the Griffin Lab at Kent University to be tested using the FISH multiprobe device. The results showed a cryptic RT between chromosomes 5 and 6. This can be seen in Figures 22 and 23.

Prepared for:	JSR Genetics
Sample number:	WPWBF579
Collection Date:	29 May 2015
Diagnosis:	38, XY No signs of chromosomal abnormality

Karyotype:

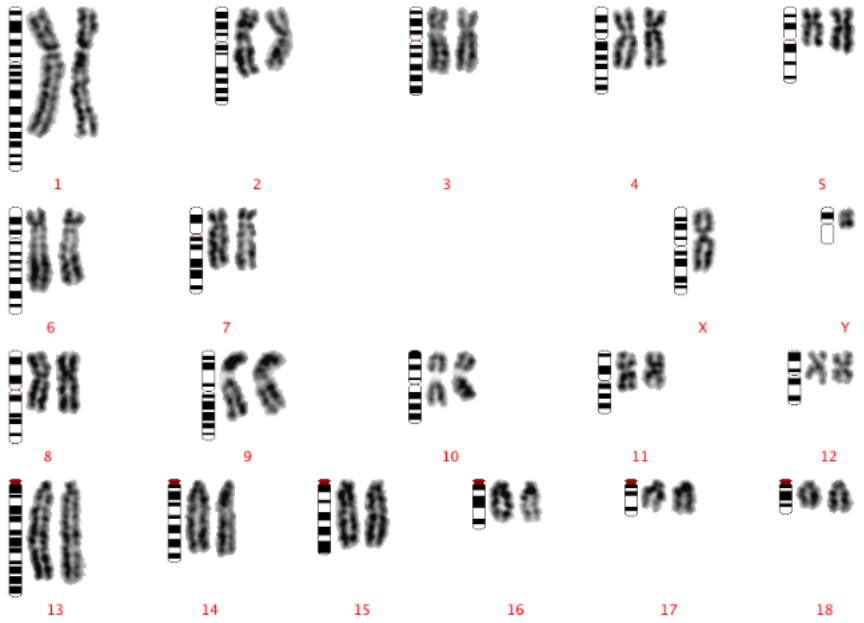

Figure 21 Initial Normal Karyotype Returned

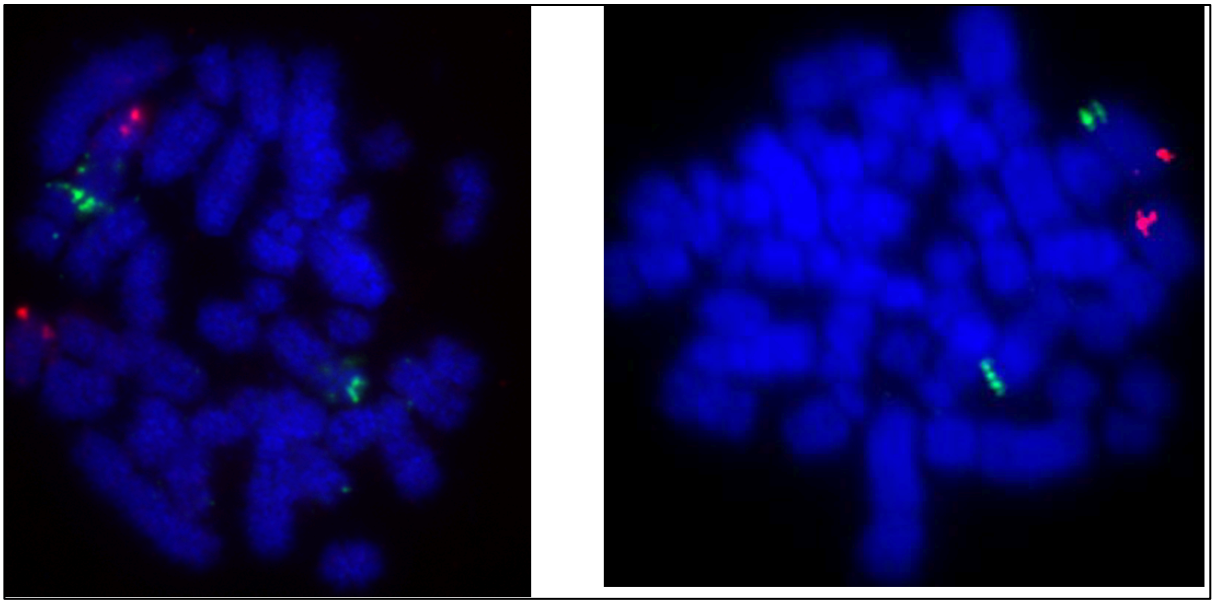

Figure 22. Translocation between chromosome 5 and 6.

A confirmatory chromosome painting experiment was performed in this case to establish what proportion of the chromosomes were translocated and indeed whether the RT was cryptic. Figure 23 shows a tiny proportion of chromatin exchanged, something that would certainly not have been detectable by karyotyping, regardless of the skill of the lab or the length of the chromosomes.

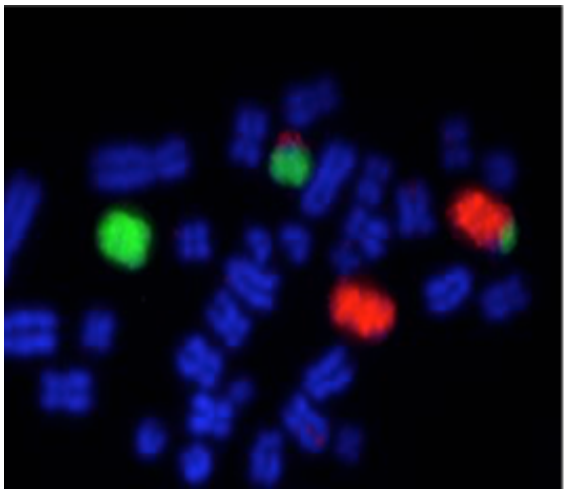

Figure 23. 5:6 translocation in the JSR boar detected by chromosome painting. Chromosome 6 in red, chromosome 6 in green. A tiny proportion is barely detected by chromosome painting but was easily detected by the multi-probe approach. This would not have been detected by karyotyping and was only barely visible by chromosome painting as we already knew what we were looking for.

4.6.1. Financial Analysis

For this example, the genetic provider kindly made available to the University of Kent their financial impact of the RT from this boar. An estimate was calculated of the financial impact the effect of this RT had on the company. To begin, an estimate of missing pigs was calculated

based on the average litter size on the farm. Since the average litter size at the time for this farm was 11.3, if 6.5 litter size for the average of the RT boar is subtracted from this, it equals 4.8 missing pigs due to the RT. From there, the 4.8 missing pigs was multiplied by the number of litters the boar sired, and then multiplied this by the average price of £35 for a weaner pig in the UK to get a loss of £8,400.

$$(11.3\ weaners - 6.5\ weaners) \times (50\ litters)(£35) = 8{,}400.$$

The losses that they incurred due to gilt progeny that could have been sold as breeding stock but were culled as a result of the RT diagnosis where then calculated. It was assumed that they would have three saleable gilts per litter, and multiplied it by the number of litters, as well as a £60 loss of premium from selling the breeding gilts. This gives a loss of £9,000.

$$(3\ gilts) \times (50\ litters)(£60) = £9{,}000$$

These two numbers were then added together to get a total potential revenue loss of £17,400. These general figures were then placed into the economic model for farrow to wean from this thesis (see section 3.1 above), which gave a total loss of £7,948. The difference in losses is due to the inclusion of a pre-weaning mortality of 0.1 in the model which was included as certainly not all of the missing born alive would have converted into weaned pigs. Based on farm practice and statistics, it is necessary to include this figure. An impact of 0.43 for the effect of the RT was used based upon the ratio of 4.8 missing pigs to 11.3 weaned average pigs. Despite the small difference in the estimations of loss, it does provide validation to the model. The full calculation from the model can be seen below:

$$(73\ matings) \times (0.69FR) = 50.37\ total\ farrwowings$$

$$(50.37\ total\ farrowings) \times (11.65\ BA) = 586.8\ potential\ pigs$$

$$(586.8\ pigs) \times (0.43\ RT\ impact) = 252.33\ pigs\ missing$$

$$(252.33\ pigs\ missing) \times (0.1\ pwm) = 227.10\ pigs\ weaned\ missing$$

$$(227.10\ pigs\ weaned\ missing) \times (£35\ weaner\ price) = £\mathbf{7948.34}\ loss\ in\ revenue$$

4.6.2. Select Breeding Gilts Loss

The potential loss from select gilts sold for breeding was also put into the model. The maternal boar model was used to find the number of gilts selected, which includes variables for post weaning mortality, selection rate, and sow cycling rate. It was then adapted for this boar's scenario to find the potential revenue loss. With this model a potential revenue loss of £9,482.56 was calculated. The full calculations can be seen below.

$$(1\ mating) \times \frac{11.65\ BA}{2} = \mathbf{5.83\ BA\ females}$$

$$(5.83\ BA\ females) - [(5.83\ BA\ females) \times (0.1\ pwm)] = \mathbf{5.24\ weaned\ females}$$

$$(5.24\ weaned\ females) - [(5.24\ weaned\ females) \times (0.05\ postwm)]$$

$$= \mathbf{4.98\ finisher\ females}.$$

$$(4.98\ finisher\ females) \times (0.7\ gilt\ selection\ rate) = \mathbf{3.49\ select\ gilts}$$

$$(3.49\ select\ gilts) \times (0.9\ cycling\ females) = \mathbf{3.13\ select\ gilts\ cycling}$$

$$(50.37\ farrowings) \times (3.13\ select\ gilts) \times (£60\ premium) = £\mathbf{9482.56})$$

Combining these two potential revenue losses, a total loss of **£17,430.91** was derived, which is a similar number to what the production company estimated at the time (£17,400 see previous page, section 4.6.1).

It is also interesting to look at this particular situation by eliminating the effect the PRRS disease was having on the farm. If values for born alive and farrowing rate are substituted for values that would be on a healthy farm the loss due to the RT becomes greater. For example, if a farrowing rate of 0.9 and a born alive average of 15 are substituted into the model the loss for farrow to wean changes from £7948.34 to £13,348.60. For the breeding gilt losses, the same figures were substituted to give a value of £15,925.19 loss, and a total combined loss of £29,273.78. In other words, had PRRS not been on the farm, the loss to the company from this RT would have been 1.68x greater.

4.6.3. Closed System Example

This case study can also be used to model a further hypothetical situation where a particular company would have their own multiplication farm, thereby supplying their own commercial gilts. In this scenario, instead of the company selling the gilts as breeding stock to other farms, they are supplying their own farm with breeding stock. This example calculates the loss of progeny from those gilts.

Starting back from the previous model, it can be seen that there were 158.04 select gilts missing. This was calculated earlier from 3.14 selects per litter and then multiplied times 50 litters. As this farm was struggling with PRRS at the time, figures such as pigs per sow per year have been estimated slightly under normal averages. In this case, 25 pigs per sow per year is

estimated and only 4 parities, which is slightly optimistic for a farm with PRRS. Using these parameters yields around 43 piglets in one of these gilt's lifetimes. Multiplying this figure by the 158.04 missing select gilts yields around 6871.42 missing piglets. This figure multiplied by the price of £35 for a weaner pig yields £240,499.82.

These calculations can be seen below:

$$\left[\frac{25ppsy}{2.3\ litters\ per\ year}\right] \times 4\ parities = 43.48\ lifetime\ piglets\ per\ missing\ select\ gilt$$

$$(43.48\ lifetime\ piglets) \times (158.04\ select\ gilts) \times (£35\ weaner\ price) = £240{,}499.82$$

In other words, had a scenario such as this (RT was not spotted by karyotyping but picked up by multiprobe FISH) occurred in a "closed system", then the financial impact could have been 13.8x greater.

4.7. Specific Aim g: Case study 2: German Pietrain at GGP level

As mentioned above (materials and methods section 3.5), this boar, was a German Pietrain at the GGP level, but also making terminal commercial matings, located in a multi-genetic retail semen boar stud located in Western Germany. The recorded mating history of the boar showed both varied conception rates and farrowing rates. This boar was karyotyped prior to its first collection in the GTC with classical standard banded karyotyping as is routinely done for GGP boars by this genetic provider. The karyotype was returned with a normal result, and went on to have matings at the GGP, and Parent levels. At the nucleus level he was mated to pure line Pietrain GGP sows, and the progeny used for either the next generation of Pietrain

GGP boars, for making pure GGP gilts, or for terminal parent boars. While the first results within the pure line production were suboptimal, they were not outside the bounds of normal production variation. This is possibly due to poor reproductive performance in terminal lines (as these lines are selected for terminal and not maternal traits). The first results returned from the Parent level matings within commercial producers demonstrated a significant gap in reproductive success (specifically in terms of total born) compared to other boars within the same contemporary groupings. Upon seeing these initial commercial results, the GTC had the boar karyotyped again with the same standard methods, and a second normal result was returned. This karyotype can be seen in Figure 24, and another version in the appendix.

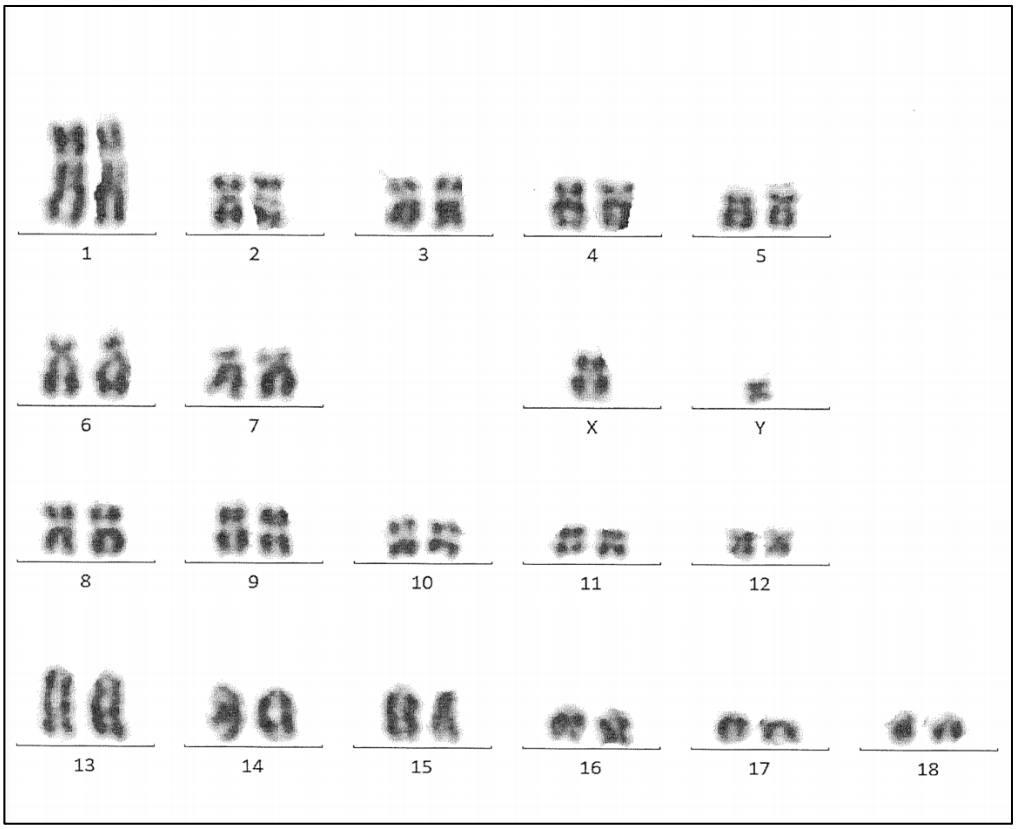

Figure 23. German Pietrain Karyotype Reported as Normal

After additional litter records continued to show suboptimal performance, it was decided that this boar would be screened using the novel multiprobe FISH device technology by the Griffin lab at the University of Kent. The results revealed a translocation of 9:18 which can be seen in Figure 25. Upon confirming the positive result, one last collection of the boar was made and sent for further research, and the boar was subsequently culled. In addition to this positive result, several of the offspring of this boar were sent for FISH testing, and around 50% had also inherited the same 9:18 translocation; they were also were culled.

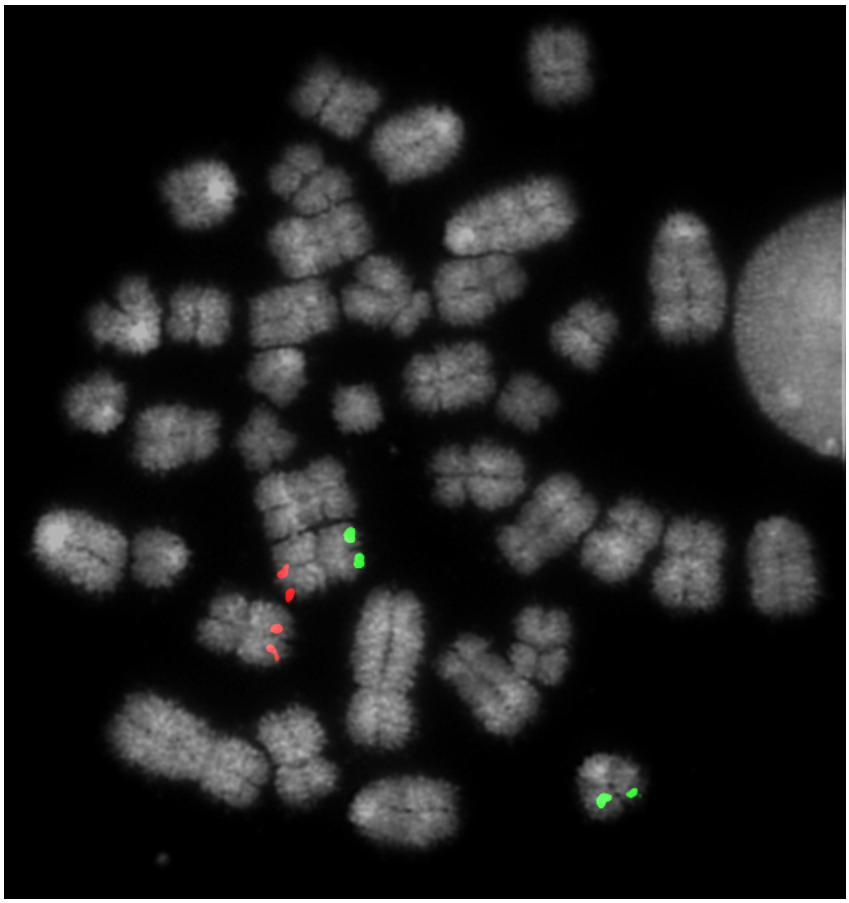

Figure 25. German Pietrain FISH 9:18 Translocation

Because this boar's semen was being used for two separate purposes, two separate calculations were performed to ascertain the full loss of revenue.

4.7.1. Farrow to finish/Farrow to Wean

Unfortunately, complete commercial data on this boar was not available and therefore some assumptions had to be made to make the calculations. The boar was in service in the stud for a total of 288 days, or 41.14 weeks. It is typical or a boar to have settling in time, or training time in a stud, thus two weeks was deducted from that figure to account for this leaving 39.14 weeks. In order to calculate the number of matings that this boar could have made in this time, the boar effect calculator discussed previously was modified and applied to this scenario.

$$(Average\ cells\ produced\ per\ week) \times (\%\ quality\ of\ passing\ ejaculates)$$
$$\times (number\ of\ weeks)$$
$$\div (\ doses\ per\ cell) \times (percentage\ of\ doses\ used\ for\ breeding)$$
$$\div (doses\ per\ sow\ in\ heat)$$
$$80 \times 0.9 \times 39.14 \div 2 \times .92 \div 2.1 = \mathbf{617\ \boldsymbol{total\ matings\ possible}}$$

At the GGP level (the nucleus farms), this boar had already performed 145 matings before he was culled, which leaves 472 potential unaccounted for matings. This number can now be applied using two economic models above (farrow to wean scenario and farrow to finish scenario) to calculate the possible losses in revenue for the customers that were using this boar's semen. As it is unknown exactly what systems the boar was utilised in, both the farrow to wean and farrow to finish situations will be demonstrated.

For the farrow to wean scenario, the farrow to wean model was used inputting 472 matings and assuming a 50% reduction in litter size. The average price of weaner pigs for the year was used as prices are variable on a weekly basis. This gives a revenue loss of around £141,492.80 for one or more of the impacted farmers. Considering the boar's location in Western Germany this would be the most likely scenario for impacted farmers.

For the farrow to finish scenario, which is less likely given the geographical location of the boar, 472 matings was also used, and an average price per kg for the year was used. This gives a revenue loss of around £315,769.56 for either one or more farmers.

4.7.2. GGP Usage Scenario

While data for the boar's usage in the commercial sector was not available, some data for its use within the genetic nucleus was available. Based on a summary for the data collected on two separate sites, this boar's conception rate was quite variable and on average 3.2% lower than normal. Based on the small amount of data received, the impact of the RT appears less than 50% within these nucleus herds, however ascertaining the true effect of the RT is impossible due to an incomplete data set. For simplicity, only the situation of this boar being used for terminal parent boars will be demonstrated as the index of this boar was not high enough to be considered for GGP usage. Because this is a terminal line boar, the litter sizes are typically smaller because they are not bred for multiplication, and an average of eight born alive was used for this calculation. From eight born alive it can be inferred that on average four males will come from each litter. Factoring in pre- and post-weaning mortality gives an average of 3.42 finished boars per litter. At this point, around 60% of the boars will pass physical selection and around 75% of that number will pass index selection. This amounts

to around 3.46 boars sold per year per sow and a total of 251.05 missing boars due to the RT. At a retail cost of 1800 euros per boar, the full price that could have been earned is around £903,777.75. However, with around 50% of the pigs missing, and around 50% of those pigs having inherited the RT and would also have to be culled, the actual profit made would be around £225,944.44 leaving a £677,833.31 opportunity cost. At this point, the offspring were tested using multiprobe FISH which at £240 a test is around £60,251.85 bringing the profit available to earn to around £165,692.59. Thus, the opportunity cost for this boar on the terminal side is around £738,085.16 due to the RT. The calculations can be seen below:

$$(4\ born\ alive\ males) \times (0.9pwm) = 3.6\ weaned\ males$$

$$(3.6\ weaned\ males) \times (0.95pwm = 3.42\ finished\ males)$$

$$(3.42\ finished\ males) \times (0.6\ physical\ selection) \times (0.75\ index\ selection)$$

$$= 1.54\ select\ males$$

$$(1.54\ select\ males) \times (2.25\ litters\ per\ sow\ per\ year)$$

$$= 3.46\ boars\ per\ sow\ per\ year\ sold.$$

$$(3.46\ boars\ per\ sow\ per\ year) \times (145\ total\ matings) = 502.09\ boars$$

$$\frac{[(3.46\ boars\ per\ sow\ per\ year) \times (145\ total\ matings)]}{2}$$

$$= 251.05\ missing\ boars\ due\ to\ RT$$

$$(502.09\ boars) \times (£1800 \text{ retail price})$$

$$= \mathbf{£903,777.75\ profit\ that\ could\ have\ been\ maid}$$

$$\frac{251.05\ boars\ left\ from\ RT}{2(half\ of\ progeny\ carrying\ RT\ are\ culled)} \times (£1800 \text{ retail price})$$

$$= \mathbf{£224,944.44\ profit\ that\ could\ be\ made}$$

$$(£224{,}944.44 \text{ profit}) - (£60{,}251.85 \text{ testing fees}) = £165{,}692.59 \text{ profit after test fees}$$

$$(£903{,}777.75 \text{ possible proft}) - (£165{,}692.59 \text{ actual profit})$$

$$= £\mathbf{738{,}085.16 \text{ opportunity cost}}$$

In other words, the lost to the company of having this RT not detected by karyotyping, but then detected by multiprobe FISH was nearly £740,000.

4.8. Specific Aim h: To calculate the Financial Benefit for FISH Multiprobe Compared to Karyotyping

In order to assess whether FISH or Karyotyping has the greatest financial benefit, calculations to compare the costs and the benefits of doing no screening, karyotyping, and using the FISH multiprobe device were performed for each scenario.

4.8.1. Hypothetical Example

As an illustrative and hypothetical example, imagine a scenario where the impact of an RT was £100,000 (in reality this is not much different to the *farrow to wean* scenario). The reported incidence of RTs following karyotyping is 0.47% but, for the purposes of this example, we will use a rounder figure of 0.5%, i.e. one in 200. In other words, 200 boars would have to be screened in order to incur the financial loss of £100,000. O'Connor et al (2021) suggested (following multiprobe FISH) that the incidence of RTs was much higher than previously appreciated. An incidence of 0.88% (nearly twice as much) was reported, but with the caveat that the error bars were large because of the small sample size. A more conservative estimate (based on karyotypic reanalysis of known RTs) is that, for every two RTs spotted by karyotyping, one was missed that could have been spotted by multiprobe FISH

– a ratio of 1.5 to 1. The Karyotekk https://www.karyotekk.com/ web site quotes a price of £150 for Karyotyping, whereas the price for multiprobe FISH levied by the Griffin lab is £225.

In this scenario of 200 boars being screened by karyotyping, the cost is 200 x £150 i.e. £30,000 but the benefit is £100,000 by virtue of the fact that the impact of a single RT (on average) has been identified. A net benefit of £70,000.

In the same scenario, using multiprobe FISH, the cost is 200 x £225 i.e. £45,000 but an average of 1.5 RTs would have been detected, a benefit of £150,000, and a net benefit of £105,000.

Plugging in the "real" numbers therefore, to get an average of 1 RT from an incidence of 0.47%, 212.7 boars would have to be screened. On average, multiprobe FISH would detect 1.5 RTs as above (i.e. gaining £150,000). Screening 212.7 boars would incur a cost of £31,905 for karyotyping and £47,857 for multiprobe FISH. These numbers were applied in the subsequent calculations.

4.8.2. In the *farrow to wean* scenario (lower end)

No action: Net loss of £75,921

Karyotyping: Net benefit is £75,921 minus the £31,905 screening cost = **£44,016**.

Multiprobe FISH: Net benefit is (£75,921 x 1.5) minus £47,857.50 screening cost **£66,024**.

4.8.3. In the *Farrow to Wean* Scenario (upper end)

No action: Net loss of £100,424

Karyotyping: Net benefit is £100,424 minus the £31,905 screening cost = **£68,519**.

Multiprobe FISH: Net benefit is (£100,424 x 1.5) minus £47,857 screening cost = **£102,779**.

4.8.4. In the *Farrow to Finish* Scenario

No action: Net loss of £240,719

Karyotyping: Net benefit is £240,719 minus the £31,905 screening cost = **£208,814**.

Multiprobe FISH: Net benefit is (£240,719 x 1.5) minus £47,857 screening cost = **£313,221**.

4.8.5. In the GP Scenario

No action: Net loss of £1,340,686

Karyotyping: Net benefit is £1,340,686 minus the £31,905 screening cost = **£1,308,781**.

Multiprobe FISH: Net Benefit is (£1,340,686 x 1.5) minus £47,857 screening cost = **£1,963,172**.

4.8.6. In the GGP (nucleus) Scenario

No action: Net loss of £4,252,182

Karyotyping: Net benefit is £4,252,182 minus the £31,905 screening cost = **£4,220,277**.

Multiprobe FISH: Net benefit is (£4,252,182 x 1.5) minus £47,857 screening cost = **£6,330,415**.

4.8.7. In the GGP (dam line) Scenario

No action: Net loss of £130,183,215

Karyotyping: Net benefit is £130,183,215 minus the £31,905 screening cost = **£130,151,310**.

Multiprobe FISH: Net benefit is (£130,183,215 x 1.5) minus £47,857 screening cost = **£195,226,965**.

5. Discussion

This thesis was largely successful in the fulfilment of its specific aims, namely, to give an overview of current RT screening methods currently used in the pig industry, look at the various structures of the pig industry and how an RT might affect them, and to provide a flexible financial analysis of opportunity cost to businesses that have an RT in a boar. This final point does contain the specific caveat that the goal was to develop the models and show financials based on some standard industry values, specific producers should use their actual data for specific financial analysis.

Specifically:

- The impact of an RT on a *farrow to wean* hypothetical situation was calculated as between approximately £75,921 and £100,424.
- The impact of an RT on a *farrow to finish* hypothetical situation was calculated as approximately £240,719.
- The impact of an RT on a dam line boar at the GP level was calculated as approximately £1,340,686.
- The impact of an RT on a pure line GGP boar in a commercial breeding company being used to make pure line terminal boars was calculated as approximately £4,252,182.
- The impact of an RT on a dam line boar at the GGP level was calculated as approximately £130,183,215.

- In a real-world scenario, the actual loss of an RT previously undetected by karyotyping was £17,431 but could have been 1.68x higher loss if PRRS had not been on the farm and 13.8x in a "closed system."
- In a second real world scenario the actual loss of an RT previously undetected by karyotyping was between £879,578 and £1,053,855.
- Comparisons of the costs of using the multiprobe FISH device and Karyotyping, multiprobe device to give a greater net benefit and a greater ROI for using multiprobe FISH.

There are three options available in the pig industry today when it comes to handling RTs:

- Ignoring the issue and taking the risk
- Standard karyotyping (G-banding)
- Using the multiprobe FISH device

Taken together therefore the results not only indicate that FISH is the more cost-effective option, despite its higher price, but also that there are inherent risks to using karyotyping, through the financial losses and reputational damage that can be incurred if an RT remains undetected by karyotyping. Each of these however is a significantly better option than ignoring the situation completely.

5.1. How Can Companies Handle RTs?

The purpose of this thesis was to understand differing structures and business models that exist in the pig industry and thereby estimate how an RT might affect them.

5.1.1. Farrow to Wean or Farrow to Finish Model

The simplest business model examined was the farrow to wean or farrow to finish model. This model involves a farmer or producer buying either semen from a boar stud or an AI supplier, or buying one or more boars from a genetics company to keep on farm for insemination. An RT in one of these boars or in the semen supplied would result in opportunity cost directly for this producer. This opportunity cost would be the missing piglets from litters that the farmer would have gone on to sell either as weaners or finishers. It is difficult to know if the farmer could recuperate this lost income as it would largely depend on who they got the semen or boars from, and whatever contractual arrangements they had. If the boar came directly from a genetics company, they would likely replace the boar, but the farmer would most likely not recuperate the money lost from missing piglets. If the semen had been provided from a semen retailer or boar stud, most likely some negotiation would take place in order to keep the farmer as a customer and maintain some level of customer satisfaction (Personal Communication in the Industry Anonymous 2020).

In general, semen retailers operate boar studs to collect and sell semen to customers such as farrow to wean or farrow to finish farmers. Most boar studs will have boars from differing genetics companies and will sell their genetics to customers. Because the main aim of semen retailers is to collect and sell semen, it is possible for a boar to have an RT, and the semen of that boar to be sold to customers without knowledge of the existence of the RT. In this case, when the customer had low total born numbers, they would most likely report this back to the semen retailer. The semen retailer would then report this back to the genetics company where the boar originated. Depending on the agreement or contract between the semen retailer and the customer, it is likely that the semen would have been sold with potential

biological risks understood, and the semen retailer would not be obligated to pay for lost income for the farmer. It would be however in the best interest of the semen retailer to give some sort of compensation to the farmer such as a discount on future purchases to keep a positive relationship with the customer. Semen retailers rely on volume of semen sold, so losing a customer would decrease their volume sold, especially if it is a significant customer (Personal Communication, Sergio Barrabas, PIC 2020). Here it can be seen that the RT has affected both parties financially with the farmer having lost piglets, and the semen retailer most likely providing some discount to the farmer.

5.1.2. Genetics companies (GP and GGP)

Genetics companies will experience the negative effects of an RT in a boar in various different situations. The most severe situation would be if an RT established itself in a boar at the nucleus level. This boar would be used for creating the next generation of nucleus animals both gilts and boars. If an RT were left to persist it could potentially be passed to 50% of the offspring which impacts not only the genetics company but also the customers which could be small farms or large-scale integrators (Bouwman et al 2020). It would not only affect the production of the genetics company, but also that of their partners or multipliers, and can also affect the credibility of the genetics company. If the genetics company were to sell a boar with an RT to a boar stud operating as a semen retailer, and it caused problems for the customers of the semen retailer, the genetics company would most likely have to replace the boar, and depending on contractual obligations, might have to give some level of compensation to the semen retailer (Personal Communication in the industry anonymous 2020). This does not always happen; however, it can help to maintain positive customer relationships and confidence.

5.1.3. Integrators

Integrators could potentially experience all of the effects and losses mentioned above depending on how much integration they have. A large-scale integrator might have their own genetics company, boar studs, multipliers, farrow to finish farms, and slaughterhouses in which case the RT would affect the company on multiple levels. An integrator who buys genetics from an outside genetics company would most likely look to the genetics company if they were to experience hypoprolificacy in a boar sold to them. Again, most likely an arrangement would be made between the two companies to continue a positive business relationship (Personal Communication in the industry anonymous 2020).

5.2. Sire or Dam lines?

When looking at what model should be considered the first question that should be answered is if the RT is located in a sire line or a dam line. For clarification, a dam line is a line of pigs focused on maternal traits. A dam line boar, depending on what level it was at, would be used to create a next generation of females for production use. At the GGP level, some of the dam line pure bred females would remain at the GGP level, while others would move down to the GP level depending on their genetic merit. Following this, depending on the parameters of the business, one or more of the models can be used to calculate missing pigs or opportunity cost due to an RT. To illustrate this an example can be used of a large-scale integrator who owns their own genetics company. If an RT was discovered in a terminal boar population used for GGP mating but caught early enough, the model for an RT in a GGP nucleus level terminal boar could be used to calculate the potential losses. However, if the RT was caught after a

period of time, the opportunity cost could be calculated by using the farrow to finish model for each son that made matings.

5.3. Which Model is the Most Appropriate for a Specific Business?

One of the advantages of the models created for these different business scenarios, is the level of flexibility that they have. Previous attempts to calculate the economic impact of RTs have focused largely on single production types or fixed variables or production parameters. An example of this is that in Spain there are a large number of full integrators, while in Germany most farms are farrow to wean and get their semen from retail boar studs. Each of these businesses will have different business structures, but also production parameters that can also vary regionally. These differing production parameters can easily be put into the flexible models. An example would be if there were a disease outbreak such as PRRS on a farm. This type of disease could affect pre- and post-weaning mortality, farrowing rate, and total born. Each of these variables can be put into one of the models to give a more accurate representation of how the RT will affect this farm financially. For example, if we look back at the farrow to wean model and example numbers used, a farrowing rate of 90% was used in the calculations. If this rate was decreased by 5%, instead of a loss of £100,424, there would only be a loss of £94,845. Likewise, if the farm were very healthy with a farrowing rate of 95%, the loss would be higher at £106,003. If a farm had an incredibly high output with a born alive average of 16, this changes the loss to £114,770. Any of the variables can be altered to represent the actual circumstances of an individual business or farm.

5.4. Impact of an RT on Litter Size

The factor in all of these models that is the most variable, and the most difficult to quantify is the actual the impact of the RT itself on litter size. In published literature, this number is often reported as a range in reduction of litter size with some sources citing a reduction of 25-50% (O'Connor et al 2021). Other sources tend to cite around the 50% mark which is why this figure was used as an average in the model (Danielak-Czech 2020). There is really no way of knowing exactly what the impact of an individual RT will be on litter size until a reduction in litter size has been noticed and quantified and the boar will be removed from the breeding program and most likely culled thus limiting data on that particular boar. In order to estimate what the financial impact an RT would have on any pig production business before an RT happens would be to either use an estimate such as 50% or create a range of potential loss for that business. For example, again looking at the farrow to wean model, inputting a 25% reduction of litter size yields a £50,212 opportunity cost. Being conservative it could be said that the opportunity cost for this model could be somewhere between £50,212 and £100,424.

5.5. Boar Effect

Another variable that can affect the financial impact of an RT in a boar is the impact of the boar itself. Under optimal (and often normal) conditions it was discussed previously in this thesis that a healthy boar using normal AI can influence over 8,000 pigs in its breeding lifetime (Personal Communication Michael Kleve-Feld 2020). However, technologies are evolving rapidly to allow the semen of one boar to go further and influence more pigs. While these technologies are ultimately designed to help save money, if an RT is present, they can ultimately cost a producer more. For example, using post cervical artificial insemination

allows a boar to affect many more pigs due needing less doses of semen (Llamas-Lopez et al 2019). In a healthy boar's lifetime, using PCAI that boar can affect over 14,000 pigs which is nearly twice the amount (Personal Communication Michael Kleve-Feld 2020). Looking back again at the farrow to wean model, if that farmer was using a boar with an RT and the PCAI technology, instead of the approximate 335 number of matings before hypoprolificacy was noticed, this boar would be able to make approximately 595 matings. This changes the opportunity cost of an RT from £100,424 with normal AI, to approximately £178,365. Similar figures could be seen if single fixed time insemination was used (such as Ovugel) which require only one dose (Quirino 2019).

5.6. The Consequences of Cryptic RTs Can Be Dire

Banded karyotyping, usually G-banding, requires specialist knowledge and results can vary based on user experience and quality of the sample (Raudsepp 2016). The inconsistency of this type of diagnostic test means that smaller (cryptic) RTs can be missed, and the pig reported as normal (Bouwman et al 2020). This is noted in the two case studies presented in this thesis where both boars were karyotyped twice separately with standard G-banding and reported as normal in both occasions. Nonetheless, both boars were revealed to have cryptic RTs by the multiprobe method and were hypo-prolific. This thesis demonstrates how the multiprobe approach allows for easy visualization of any RT, without the requirement of in-depth knowledge of the pig karyotype. While this type of screening is easier and more effective, it is significantly more expensive than normal banded karyotyping which costs around £150. In both cases however, the loss of business of £17,430 and £738,085 (cases 1 and 2 respectively), not to mention harder to calculate values such as loss of reputation suggest that this alone might be enough to justify the use of multiprobe over FISH.

5.7. Is There a Net Cost Benefit of Using Multiprobe?

When looking at the cost benefit of using the multiprobe FISH device as a regular screening method, the incidence rate of RTs in boars must be considered. From the regular screening done on pig populations in France an incidence rate of 0.47% has generally been accepted (Ducos 2007). It has been established however that this rate is higher based on studies done using the FISH device in the Griffin Lab which showed a higher incidence of 0.88% (O'Connor 2021). In any event, they calculated that at least 50% of RTs were missed by G-banding compared to multiprobe FISH. Although that number likely has some level of bias it is still reasonable to suggest that this rate 0.47% is underestimated due to smaller (cryptic) translocations being missed in standard karyotyping, which was also demonstrated in their study and also even larger translocations being missed by sub-optimally trained staff (O'Connor 2021). While this incidence rate most likely describes the rate of RTs occurring *de-novo* in boars, as shown in the models above, if this RT were to persist within a breeding population, because of inheritance, the rate of appearance of an RT would increase in the subsequent offspring. When looking at a cost benefit for regular screening however, only the rate of *de-novo* translocations is being considered. This is mainly because FISH screening is a preventative measure aimed at discovering RTs before they are allowed to breed and persist within a herd. Based on the current accepted incident rate of 0.47%, one positive RT result would be found using standard G-banded karyotyping for approximately every 212.7 boars tested. As shown by O'Connor et al (2021) the multiprobe device detected a higher incidence rate of 0.88%, which is 1 in every 113.6 boars. To compare the multiprobe device screening method easily against standard karyotyping, a rate of 1 translocation detected per 212.7 boars was used for standard karyotyping, and 1.5 translocations detected per 212.7 boars

was used for multiprobe FISH testing. At £225.00 per test, and with this rate of incidence, approximately £47,857.5 would be spent per 212.7 boars tested with the multiprobe device. Using standard G-banding at £150 per test the cost would be approximately £31,905. For a cost benefit example scenario, the model of the GP maternal boar can be examined in further detail. In this economic model reviewed earlier in the thesis, it was worked out that the potential opportunity cost of an RT in this situation would be around £1,340,686.47. While in the event of an RT this figure is a cost, when using multiprobe FISH or Karyotyping as a preventative measure, this figure is the benefit. By detecting the RT in the population before the boar is put into breeding, the benefit is this figure not being lost due to missing piglets. Using the GP maternal boar scenario, as calculated previously in the thesis, (also shown below) subtracting the screening costs minus this benefit for karyotyping and FISH testing is approximately £1,308,781 and £1,963,172 respectively. These were calculated based on the rates at which each of these methods detect translocations.

Karyotyping: Net benefit is £1,340,686 minus the £31,905 screening cost = **£1,308,781**.

Multiprobe FISH: Net Benefit is (£1,340,686 x 1.5) minus £47,857 screening cost =

£1,963,172.

(taken from section 4.8.5 above)

It should be noted however that the benefit calculated for karyotyping does not take into consideration any losses incurred due to an RT being missed. These losses are quite significant as demonstrated within this thesis. For example, if 227 boars were screened, it is possible that one RT would be found with karyotyping, and one would be missed. The benefits of finding the RT would be cancelled out by the loss incurred from the missed RT. This would

give a negative cost benefit situation for karyotyping. An example calculation can be seen below using the GP maternal boar scenario.

$$(227\ tests) \times (£150\ per\ G-band\ test) = £34{,}050$$

$$(£1{,}340{,}686.47\ \text{benefit}) - (£1{,}340{,}686.47\ \text{loss}) - (£34{,}050\ \text{test cost}) = -£34{,}050$$

The above calculation does not indicate that there is no benefit to standard karyotyping, however it does illustrate the economic risks of using standard karyotyping a regular screening method.

An interesting point of discussion is that of who has the cost and who has the benefit in these different circumstances. Perhaps the most obvious benefactor of this technology is that of full integrators because they are involved in the entire process of pig production. They would put up the cost and receive the benefit from using the FISH device for screening. It becomes more complicated in the other scenarios when the cost and benefit are segregated. In the case of farrow to wean scenario, the cost of screening the boars often fall on the genetics company, however depending on what contract or financial arrangement the genetics company has with the producer, the producer will largely benefit from the boar having been screened. The main benefit for the genetics company in this scenario is customer retention and satisfaction to which it is difficult to assign a monetary value. This becomes an even more complex situation when you have multiple businesses involved, such as a genetics company selling to a boar stud or semen retailer who is then selling to a producer. The disconnect between the genetics companies, the semen retailers, and the production companies when it comes to the losses of an RT and the cost benefit of screening complicates acceptance of this technology

despite the outstanding returns. Hypothetically, the genetics companies could market their RT screened boars as a premium product but would then want to offset this cost by increasing prices. This could make them less competitive in the market, and producers who do not fully understand the risk of not screening might be more inclined to choose a cheaper option. Likewise, boar studs would not want to pay a higher premium because they would then have to offset that cost making them also less competitive. The successful implementation of the multiprobe FISH device as a standard screening method in the pig industry will require dissemination of information at all levels so that the positive value of screening is perceived throughout the industry.

5.8. New Technologies

The next probable step in the advancement of screening for chromosomal abnormalities in pigs is to use DNA sequencing to detect anomalies (Bouwman et al 2020). At present, the cost of any type of sequencing is too high to be used as a regular screening method in the pig industry (Bouwman et al 2020). As costs become reduced and more sequence data on pig livestock becomes available, it is highly likely that sequencing will become routine (Bouwman et al 2020). Several studies have shown that short read sequencing can be successful in the detection of balanced RTs in pigs and that valuable information such as fragile sites and breakpoints can help determine with more certainty common translocation areas (Bouwman et al 2020). In brief, sequencing technology is excellent and used extensively for detecting chromosomal changes that involve net gain or loss of DNA. RTs however do not, and detection by sequencing requires identification of RT breakpoints compared to a standard reference genome. For this reason, costs are currently much higher than FISH and thus not justified at

present. As costs continue to fall however, this may become an option and would not require the bloods arriving “fresh” in the lab (Bouwman et al 2020).

5.9. Is Semen Pooling a Solution?

After reviewing the results obtained from the analyses in this thesis, it seems that screening for boars is highly beneficial at all levels, but particularly the GP and GGP level. Due to the location in the breeding pyramid of GP and GGP boars, there is a high risk of an RT impacting several generations of future pure line boars and gilts. In markets such as the United Kingdom and the United states where semen pooling is utilized with terminal sires, the risk of a sow being inseminated by a boar with an RT is drastically reduced and therefore it would not be seen by the industry as necessary to screen these boars whose semen will be pooled with others. It should be noted however that semen pooling does not completely negate the risk of an RT. Calculating this reduction in risk is a difficult task as it depends on various factors. When semen is pooled, the semen from three to six boars is mixed together and then diluted with extender to create doses (Althouse 2006). Because the semen is mixed, and then diluted with extender all at once, it would be difficult to measure how many sperm cells from a particular boar have ended up in each dose. A rough and simplistic estimation could be made based on how many boars’ semen were pooled. If for example the semen of five boars was pooled, the rough probability of one of them having an RT is 1 in 212.7, and the rough probability of the sow being inseminated by the boar with the RT is 1 in 5. These two events happening together is a rough probability of around 1 in 1,063. So there in still lies some risk. However, as mentioned previously, some markets do not allow for semen pooling, and it is within the best interest of a business to screen any boars who rely on pedigree and single sire matings as the risk of economic loss is higher. An optimal cost benefit solution would be

screening all GGP, GP boars and terminal boars with single sire matings. This would most likely impact the industry effectively and economically.

5.10. Final Practical Considerations

In order to give a more practical example where the costs and benefits are both for the same stakeholder, we can consider an example of a genetics company, that discovers an RT in a GGP boar that has already been in use in the breeding population. In this case the boar will have produced 187 litters. This was calculated based on average number of matings a boar could make until an RT would be noticed, and a farrowing rate of 0.85%. These litters would be at the parent level and the males sold for breeding production. At this point the genetics company would have the option of destroying all of the litters or testing for RT using FISH. Selling the boars without testing could be problematic as customers would then be at risk and thus the customer confidence should something go wrong. Standard karyotyping could be an option, but most likely in this situation the original boar's RT would have been missed using standard karyotyping and using this method to karyotype all of the boars could create additional risk. This example focuses on the company using multiprobe FISH to screen some of the boars and the profit margin that they can still make from the boars. From the 187 litters, it could be assumed that for this sire line around three boars would be tested for each litter making 561 total tests needed. This is deduced as sire lines are typically smaller and only half would be male. The price of FISH testing is currently around £225 per test and at 561 tests this makes a total cost of £126,225 to the genetics company. From these 561 boars tested, it can be assumed that half of these boars would have an RT and have to be culled. This leaves approximately 280.5 boars that could be sold as premium boars. Boars that are selected to be sold are usually selected at a 50% rate. This can be due to physical selection criteria or

index requirements. This leaves 140.25 boars that can be sold at a premium. At a retail price of £1500 per boar (although this price is variable) the genetics company could make £210,375 from selling the boars. After subtracting the cost of the FISH testing this gives a profit of £84,150. Earning this profit is not the only reason for a genetics company to test the boars instead of culling the boars. It may be in the company's best interest to test the stock in order to maintain stock to meet customer needs, to maintain customer confidence and to keep a continuity of supply for the business.

5.11. Conclusions

It has been established for many decades that RTs can cause hypoprolificacy in boars, which can subsequently cost the pig industry significant losses, this thesis quantifies that loss. Boars that have a RT usually present as phenotypically normal, and the effects of this are usually seen after the boar has performed sub-optimally and has produced significantly smaller litters (Rodriguez 2010). Pro-active chromosome screening by karyotyping or multiprobe FISH is a solution. Karyotyping which has been and still is a standard screening method in the pig industry, is largely user dependent and is not always able to detect all reciprocal translocations, especially if they are cryptic (O'Connor et al 2017). An undetected translocation left to persist in a breeding population, depending on what level of the breeding pyramid it is in, can be passed to offspring costing further loss of pigs and a larger economic opportunity cost for producers. It was demonstrated in this thesis that using the FISH multiprobe device is superior to standard karyotyping, not only in the improved detection of RTs but also that as a more financially beneficial screening solution where the benefits outweigh the costs significantly. Importantly this thesis developed the models that multiple stakeholders can utilize to quantify these costs for their specific production system in line

with the aims of this project. What is critical for the uptake of FISH multiprobe screening in the industry as the industry standard screening method, is transparency and understanding through all levels of the industry of the risks and costs associated with RTs. If the necessity of this method of screening is understood and that the perceived extra costs are actually beneficial, the use of FISH multiprobe will become the gold standard.

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7. Appendices

List of chromosomal Rearrangements observed in the domestic pig. (Rothschild 2011)

No.	Rcp translocation	Breed[a]	Reference(s)
1	(1:3)(p;q)	LW, RU	Konovalov *et al.*, 1987
2	(1;4)(q27;q21)	P	Ducos *et al.*, 2007
3	(1;5)(p21;q21)	Polish	Danielak-Czech *et al.*, 1997
4	(1;6)(p11;q11)	LW, SWE	Yang *et al.*, 1992
5	(1;6)(p11;q35)	LW	Locniskar *et al.*, 1976
6	(1;6)(q12;q22)	GA	Ducos *et al.*, 1997a, 1998a
7	(1;7)(q17;q13)	ni	Ducos *et al.*, 2007
8	(1;7)(q2.13;q24)	LR, SWE	Gustavsson *et al.*, 1988
9	(1;8)(p13;q27)	Y, SWE	Gustavsson *et al.*, 1982
10	(1;9)(p;p)	LW	Ducos *et al.*, 1997a, 1998a
11	(1;10)(q2.11;p15)	ni	Ravaoarimanana *et al.*, 1992
12	(1;11)(p23;q15)	LR, FIN, BL	Kuokkanen and Makinen, 1988; Tzocheva, 1994

13	(1;11)(q;q)	LR, SWE	Hansen-Melander and Melander, 1970
14	(1;11)(q11;q11)	P	Ducos *et al.*, 2007
15	(1;11)(q24;p13)	ni	Ducos *et al.*, 2007
16	(1;13)(q27;q41)	DU	Ducos *et al.*, 2007
17	(1;14)(p25;q15)	Y, SWE	Gustavsson, 1984
18	(1;14)(q17;q21)	LW	Tarocco *et al.*, 1987
19	(1;14)(q2.12;q22)	ni	Zhang *et al.*, 1992
20	(1;14)(q23;q21)	SML	Golish *et al.*, 1982
21	(1;15)(p25;q13)	LR, FIN	Kuokkanen and Makinen, 1988
22	(1;15)(q17;q22)	LS	Ducos *et al.*, 2007
23	(1;15)(q27;q26)	LW	Popescu *et al.*, 1988
24	(1;16)(q11;q11)	LR	Förster *et al.*, 1981
25	(1;17)(p11;q11)	P	Ducos *et al.*, 2007
26	(1;17)(q21;q11)	Y, SWE	Gustavsson, 1984
27	(1;18)(q;q)	H	Villagomez *et al.*, 1991
28	(2;4)(p17;q11)	ni	Gustavsson *et al.*, 1982
29	(2;6)(p17;q27)	Y	Ducos *et al.*, 2002
30	(2;8)(p11;p13)	LW	Ducos *et al.*, 2007
31	(2;9)(q13;q24)	LW	Ducos *et al.*, 2007
32	(2;9;14)(q23;q22;q25)	ni	Makinen *et al.*, 1997
33	(2;14)(p14;q23)	ni	Villagomez, 1993
34	(2;14)(p15;q26)	X	Ducos *et al.*, 2007
35	(2;14)(q13;q27)	LF	Ducos *et al.*, 1998b
36	(2;14)(q21;q24)	ni	Ducos *et al.*, 2007
37	(2;15)(p13;q24)	LR, FIN	Makinen *et al.*, 1987
38	(2;15)(q28;q24)	ni	Ducos *et al.*, 2007
39	(2;16)(q28;q21)	SE	Ducos *et al.*, 2007
40	(2;17)(p12;q14)	DU	Ducos *et al.*, 2007
41	(3;5)(p13;q23)	LF	Ducos *et al.*, 1998b
42	(3;6) (p14;q21)	ni	Villagomez *et al.*, 2008
43	(3;7)(p13;q21)	LW	Gabriel-Robez *et al.*, 1988
43	(3;7)(p13;q21)	LW	Gabriel-Robez *et al.*, 1988
44	(3;7)(p;q)	Indian	Ducos *et al.*, 1997a
45	(3;8)(q25;p21)	ni, LS	Ducos *et al.*, 2007
46	(3;11)(q13;p11)	LS	Ducos *et al.*, 2007
47	(3;13)(p15;q31)	LW	Ducos *et al.*, 1998a
48	(3;15)(q27;q13)	LW	Ducos *et al.*, 2002
49	(3;16)(q23;q22)	X	Ducos *et al.*, 2007
50	(4;5)(p13;q21)	X	Ducos *et al.*, 2007
51	(4;6)(q21;p14)	P	Ducos *et al.*, 2002

52	(4;6)(q2l;q28)	LW	Ducos *et al.*, 1998b
53	(4;12)(q21;q13)	X	Ducos *et al.*, 2007
54	(4;13)(p15;q41)	ni	Ducos *et al.*, 2007
55	(4;13)(q25;q41)	LR, FIN	Makinen and Remes, 1986
56	(4;14)(p11;q11)	LW × LF	Popescu *et al.*, 1984
57	(4;14)(q;q)	Indian	Ducos *et al.*, 1997a
58	(4;15)(q;q)	P	Popescu *et al.*, 1988
59	(4;15)(q25;q11)	LF	Ducos *et al.*, 2007
60	(4;16)(q25;q21)	LS	Ducos *et al.*, 2007
61	(5;7)(q23;p11)	SE	Ducos *et al.*, 2007
62	(5;8)(p11;p23)	SE	Ducos *et al.*, 2002
63	(5;8)(p12;q21)	LW	Ducos *et al.*, 2002
64	(5;8)(q12;q27)	Y, SWE	Gustavsson, 1984
65	(5,9)(p11;p24)	LF	Ducos *et al.*, 2007
66	(5;9)(q21;p13)	LF	Ducos *et al.*, 2007
67	(5;14)(q11;q)	H × P	Popescu and Tixier, 1984
68	(5,14)(q21;q12)	DU	Ducos *et al.*, 2007
69	(5;15)(q25;q25)	LR	Parkanyi *et al.*, 1992
70	(5;17)(p12;q13)	Y	Ducos *et al.*, 2002
71	(6;8)(q33;q26)	GA × MS	Bonneau *et al.*, 1991
72	(6;8)(p15;q27) + (10;18)(p11;q24)	P	Ducos *et al.*, 2007
73	(6;13)(p15;q41)	LF	Ducos *et al.*, 1998b
74	(6;13)(p13;q49)	LW	Ducos *et al.*, 2007
75	(6;14)(p11;q11)	LW × Essex	Madan *et al.*, 1978
76	(6;14)(q27;q21)	LW × P	Ducos *et al.*, 1998a
77	(6;15)(p;q)	LR, FIN	Bouters *et al.*, 1974
78	(6;15)(p15;q13)	P × LW	Bonneau *et al.*, 1991
79	(6;16)(q11;q11)	SML	Ducos *et al.*, 1998a
80	(7;8)(q13;q27)	ni	Ravaoarimanana *et al.*, 1992
81	(7;8)(q24;p21)	3/4LF,1/4MS	Ducos *et al.*, 2002
82	(7;9)(q11;q26)	LW	Ducos *et al.*, 2007
83	(7;9)(q15;q15)	LW	Ducos *et al.*, 2007
84	(7;11)(q21;q11)	Y, SWE	Gustavsson *et al.*, 1982
85	(7;12)(q11;p15)	P	Ducos *et al.*, 2007
86	(7;12)(q24;q15)	Y, FIN	Kuokkanen and Makinen, 1987
87	(7;13)(p13;q21)	H	Gustavsson *et al.*, 1988
88	(7;13)(p13;q46)	Polish	Danielak-Czech *et al.*, 1997
89	(7;14)(q15;q27)	X	Ducos *et al.*, 2007
90	(7;14)(q26;q25)	ni	Ducos *et al.*, 2007
91	(7;15)(q24;q12)	LW	Popescu *et al.*, 1984; Konfortova *et al.*, 1995
91	(7;15)(q24;q12)	LW	Popescu *et al.*, 1984; Konfortova *et al.*, 1995
92	(7;15)(q24;q26)	ni	Makinen *et al.*, 1997
93	(7;17)(q26;q11)	H	Villagomez *et al.*, 1995a
94	(8;10)(p11;q13)	ni	Makinen *et al.*, 1999
95	(8;12)(p11;p11)	ni	Ducos *et al.*, 2007
96	(8;13)(q27;q36)	ni	Ravaoarimanana *et al.*, 1992
97	(8;14)(p23;q27)	ni	Ravaoarimanana *et al.*, 1992
98	(8;14)(p21;q25)	Polish	Danielak-Czech *et al.*, 1997
99	(9;11)(p24;q11)	Y, SWE	Gustavsson *et al.*, 1982
100	(9;11)(q14;p13)	MS	Ducos *et al.*, 2007
101	(9;14)(p14;q23)	Polish	Rejduch *et al.*, 2003
102	(9;14)(p24;q15)	LS	Ducos *et al.*, 2007
103	(9;15)(p24;q13)	LW × LF	Ducos *et al.*, 1998a

Continued

104	(9;17) (p24;q23)	X	Ducos *et al.*, 2007
105	(10;11)(q16;q13)	P	Ducos *et al.*, 2007
106	(10;13)(q11;q11)	Polish	Danielak-Czech *et al.*, 1996
107	(10;13)(q13;q22)	LS	Ducos *et al.*, 2007
108	(10;13)(q16;q21)	LW × P × DU × H	Danielak-Czech and Slota, 2007
109	(10;17)(q11;q21)	ni, LW	Ducos *et al.*, 2007
110	(11;13)(q;q)	LW	Ducos *et al.*, 1998a
111	(11;15)(p15;q13)	LR, FIN	Henricson and Backstrom, 1964
112	(11;16)(p14;q14)	LW × P	Ducos *et al.*, 1998a
113	(11;17)(p13;q21)	SE	Ducos *et al.*, 2007
114	(12;13)(q13;q11)	Minisib	Astachova *et al.*, 1988
115	(12,14)(q13;q15)	DU	Ducos *et al.*, 2007
116	(12;14)(q15;q13)	P	Ducos *et al.*, 2007
117	(12;15)(q;q)	LW, RU	Konovalov *et al.*, 1987
118	(13;14)(q21;q27)	Y, SWE	Hageltorn *et al.*, 1976
119	(13;15)(q31;q26)	P	Ducos *et al.*, 2007
120	(13;16)(q41;q21)	ni	Ducos *et al.*, 2007
121	(13;17)(q4l;q11)	LF	Ducos *et al.*, 1998b
122	(14;15)(q28;q13)	SE, ni	Ducos *et al.*, 2007
123	(14;15)(q29;q24)	ni, H	Golish *et al.*, 1982; Gustavsson and Jonsson, 1992
124	(14;16)(q13;q21)	P	Ducos *et al.*, 2007
125	(15;16)(q26;q21)	Y	Gustavsson *et al.*, 1988
126	(15;17)(q13;q21)	LW	Ducos *et al.*, 1998a
127	(15;17)(q24;q21)	LF	Ducos *et al.*, 2002
128	(16;17)(q23;q21)	LR × DU	Popescu and Boscher, 1986; Astachova *et al.*, 1991
129	(17,18)(q21;q11)	P	Ducos *et al.*, 2007
130	(X;13)(q24;q21)	LR × Viet, H	Gustavsson *et al.*, 1989
131	(X:14)(p;q)	ni	Singh *et al.*, 1994; Neal *et al.*, 1998
132	(Y;14)(q10;q11)	DU	Ducos *et al.*, 2007

Economic Model Spreadsheets

Farrow to Wean (Known number of Matings)

Variable	Calculation	Variable Descriptor
Number of Matings	335	Manual Entry
Farrowing Rate	0.9	Manual Entry
Total Born (estimate)	15	Manual Entry
Born Alive (estimate)	14	Manual Entry
Number of Farrowings	301.5	(Number of Matings x Farrowing Rate)
Total Piglets	4221	(Number of Farrowings x Born Alive)
Impact of RT	0.5	Manual Entry
Pigs missing due to RT	2110.5	(Total Piglets x RT impact)
Pre weaning mortality	0.1	Manual Entry
Pigs weaned missing	1899.45	(Pigs missing x 1-PWM)
Price per weaned Piglet	£35	Manual Entry
Total opportunity Cost	£66,480.75	(Pigs Weaned Missing x Price per piglet)

Farrow to Finish (Known number of Matings)

Variable	Calculation	Variable Descriptor
Number of Matings	335	Manual Entry
Farrowing Rate	0.9	Manual Entry
Total Born (estimate)	15	Manual Entry
Born Alive (estimate)	14	Manual Entry
Number of Farrowings	301.5	(Number of Matings x Farrowing Rate)

Total Piglets	4221	(Number of Farrowings x Born Alive)
Impact of RT	0.5	Manual Entry
Pigs Missing due to RT	2110.5	(Total Piglets x RT impact)
Pre-Weaning Mortality	0.1	Manual Entry
Pigs Weaned Missing	1899.45	(Pigs missing x 1-PWM)
Post Weaning Mortality	0.05	Manual Entry
PMW applied	1804.48	(Pigs missing x Post Weaning Mortality)
Sale Weight dead	90kg	Manual Entry
Total Kg missing	£162,402.98	(Sale Weight x Post Weaned Pigs)
Price per Kg	£1.38	Manual Entry
Total Opportunity Cost	£224,116.11	(Price per Kg x Total kg missing)

GP Dam line Boar Situation

Variable	Calculation	Variable Descriptor
Number of matings	335,51	Estimation or Manual Entry
Born Alive	13	Manual Entry
Born Alive Females	6.5	13÷2 or Manual Entry
Weaned Females	5.85	6.5-(6.5 x 0.1)
Post Weaning Mortality	5.56	5.85-(5.85 x 0.05)
Selection Rate	3.89	0.7 x 5.56
Cycling (In heat)	3.50	0.9 x 3.89
Litters per sow per year	2.25	Manual Entry
Select females per year	7.88	3.50 x 2.25

Total Selects	1174.70	335.51 matings x 3.50 select females.
Impact of RT	587.35	0.5 x 1174.70
Pigs per Sow Per Year	30	Manual entry
Parity	5	Manual entry
Total Life-time Piglets	65.22	5 parities x (30 ÷ 2.25)
Total piglets missing	38,305.33	65.22 x 587.35 missing sows
Price per Piglet	£35	Manual Entry
Total Loss	£1,340,686.47	38,305.33 x £35

GGP Dam Line Boar Situation

Variable	Calculation	Variable Descriptor
Number of matings	335,51	Estimation or Manual Entry
Born Alive	13	Manual Entry
Born Alive Females	6.5	13÷2 or Manual Entry
Weaned Females	5.85	6.5-(6.5 x 0.1)
Post Weaning Mortality	5.56	5.85-(5.85 x 0.05)
Selection Rate	3.89	0.7 x 5.56
Cycling (In heat)	3.50	0.9 x 3.89
Litters per sow per year	2.25	Manual Entry
Select females per year	7.88	3.50 x 2.25
Total Selects	1174.70	335.51 matings x 3.50 select females.

Impact of RT	587.35	0.5 x 1174.70
Pigs per Sow Per Year	30	Manual entry
Parity	3	Manual Entry
Total Piglets	39.13	3 parities x (30 ÷ 2.25)
Female piglets	19.57	39.13 ÷ 2
Total missing GPs	11,491.60	587.35 x 19.57
Selects	8044.12	11,491.60 x 0.7
Cycling	7239.71	8044.12 x 0.9
Total Select Parents Missing	57,032.65	7239.71 x 7.88 selects per year
Total Piglets Missing	3,719,520.42	57,032.65 x 65 total lifetime piglets
Total Loss	£130183215	3,719,520.42 x £35

GGP Nucleus Boar Scenario

Variable	Calculation	Variable Descriptor
Nucleus Sows	1000	Manual Entry
Litters per sow per year	2.20	Manual Entry
Total Matings	2200	2.2 litters p year x 1000 sows
RT boar matings	220	2200 x 0.1
Boars sold per litter	1.5	Manual entry
Total Sold Boars	280.50	220 x 1.5 x 0.85 (fr)
Boars lost due to RT	140.25	280.50 ÷ 2

Boars Carrying RT	70.13	140.25 ÷ 2
Number ofl matings	335,51	Manual /estimate
Total matings	23,527.65	335,51 x 70.13
Number of Farrowings	19,998.51	23,527.65 x .85 (fr)
Total piglets	269,979.82	19,998.51 x 13.5 ba
Pigs born alive missing	134,989.91	269,979.82 x (0.5 RT)
Pigs weaned missing	121,490.92	134,989.91 x 0.9 pmw
Total Loss	£4,252,182.15	121,490.92 x £35

German Pietrain Karyotype Reported as Normal