Genetic analysis of progeny performances from local and imported boar semen used in the South African pig industry

by

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Declaration

I, Donné Andrea Krüger, hereby declare that this thesis, submitted for the MSc(Agric) Animal Science: Animal Breeding and Genetics degree at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at any other University.

D. A. Krüger
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Abstract

The widespread use of artificial insemination in the pig industry has provided breeders access to genetic material from superior boars from around the world. Selection of parent stock is based on estimated breeding values (EBVs) which are regularly computed in all countries performing genetic evaluations. Application of EBV's, are restricted to the country of estimation for animals part of the genetic evaluation. In dairy cattle, conversion equations, and more recently Multiple Across Country Estimation (MACE), have successfully been applied for comparison of breeding values across countries. The purpose of this study was firstly to investigate estimation of conversion equations for South African, Canadian and USA breeding values of boars based on number born alive (NBA), 21 day litter weight (21DLWT), average daily gain (ADG), feed conversion ratio (FCR) and back fat thickness (BF) for Duroc, Landrace and Large White pigs. The analyses were based on data provided by the South African Stud Book Association. The correlations estimated for these traits highlighted several data restrictions such as differences in measurement of traits between the countries. Insufficient data further resulted in non-significant ($P > 0.05$) correlations and accurate conversion equations could not be developed. The second phase of the study focused on the value of foreign sires in the South African pig industry by comparing the on-farm performances of progeny for average daily gain (ADG), feed conversion ratio (FCR) and back fat thickness (BF) form progeny sired by USA and Canadian born sires to the performance of progeny from local sires and to progeny with paternal USA grandsires (F1-US sires). The progeny analysed included Duroc, Landrace and Large White pigs. Sex differences were highly significant ($P < 0.0001$) for all traits as males outperformed females. Farm differences were highly significant ($P < 0.0001$) for all traits except Duroc BF ($P < 0.05$). Due to large differences seen in progeny performances on farms in similar climatic regions, farm differences were expected to be due to management rather than environmental influences. The effect of country was significant ($P < 0.05$) in all the models. However, although the USA-sired progeny performed better overall, the effect of country, as measured by a stepwise R^2, was the smallest across all models except BF in the Landrace, with farm, sex and year-season contributing larger portions of the variation seen in the on-farm progeny performances. These results indicates limited superiority of imported semen with most of the variation attributed to differences in farm as explained by management.

Contents

List of Abbreviations

21DLWT	21 day litter weight
ADG	Average daily gain
Adj r^2	Adjusted coefficient of determination
AGSA	Alliance Genetics South Africa
AGE	Age to 100 kg
AI	Artificial insemination
ANOVA	Analysis of variance
ARC	Agricultural Research Council
BF	Back fat thickness
BLUP	Best linear unbiased prediction
CA	Canada
CCSI	Canadian Centre for Swine Improvement
COV	Covariance
CSIP	Canadian Swine Improvement Program
CV	Coefficient of variation
CW	Chester White
DAYS	Days to 250 lbs
DNA	Deoxyribonucleic acid
DRC	Democratic Republic of Congo
DUR	Duroc
DYD	Daughter yield deviations
EBV	Estimated breeding value
EPD	Estimated progeny difference
ETA	Estimated transmitting ability
F1-US	First generation AI boar born to a SA dam and sired by a USA sire
FAO	Food and Agriculture Organisation of the United Nations
FCR	Feed conversion ratio
FE	Feed efficiency
g	Grams
GEBV	Genomic estimated breeding value
GxE	Genotype-environment interaction

h^2	Heritability
kg	Kilograms
ICAR	International Committee for Animal Recording
INTERBULL	International Bull Evaluation Service
LAN	Landrace
lbs	Pounds
LSMean	Least square mean
LW	Large White
LWW	Litter weaning weight
MACE	Multiple Across Country Evaluation
MAS	Marker Assisted Selection
mm	Millimetres
MT-MACE	Multiple-Trait Multiple Across Country Evaluation
N	Number
NBA	Number born alive
NB	Number born
NPIRIS	National Pig Recording and Improvement Scheme
NSR	National Swine Registry
PEDv	Porcine Epidemic Diarrhoea virus
pH_u	Ultimate post-mortem pH
PIT	Pietrain
QTL	Quantitative trait loci
r	Correlation coefficient
R^2 or r^2	Coefficient of determination
RVI	Rand value index
SA	South Africa
SAPPO	South African Pork Producers Organisation
SD or σ	Standard deviation
SE	Standard error
SGI	Swine Genetics International
STAGES	Swine Testing and Genetic Evaluation System
ST-MACE	Singe-trait Multiple Across Country Evaluation
USA	United States of America

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Chapter 1: Introduction

1.1 Introduction to the South African pig industry

The South African pig industry is approximately 350 years old, dating back to 1652 when pigs were introduced to the Cape of Good Hope by Jan van Riebeeck (Visser, 2004). According to the 2013 South African Yearbook (Department of Agriculture Forestry and Fisheries, 2013), the South African pig industry makes up 2.15% of the primary agricultural sector, with an average gross value of R1 592 million over the past 10 years (Department of Agriculture Forestry and Fisheries, 2011). The Large White is the most widely used breed, occupying 60% of the market, followed by SA Landrace (30%) and Duroc (5.5%), with the remainder of other breeds (Pietrain, Kolbroek and Chester White) constituting only 4.5% (Kirsten *et al.*, 2009). According to 2014 statistics, the number of pigs in South Africa has remained relatively stable since 2001/02, although the total number has decreased by approximately 7% from 1.678 million in 2000/01 to 1.562 million in 2013/14 (Department of Agriculture Forestry and Fisheries, 2015). The number of commercial farmers, however, have decreased by more than 60% with only 230 commercial pig farms remaining in 2013 from approximately 700 farms in the early 1990s. During the same period, the number of stud breeders also decreased from 36 in 1990 to only nine in 2013 (Streicher, 2013; Visser *et al.*, 2014). Although the number of farms decreased, the total number of pigs and average herd size has increased since 1990. The trend is towards larger farms that encompasses both a breeding and grower/finisher units (Kirsten *et al.*, 2009; Davids *et al.*, 2014).

In comparison to other agricultural industries in South Africa, the South African pig industry remains relatively small. Preliminary beef and veal production and consumption figures for 2013 indicated 855 000 tonnes of red meat produced and a per capita consumption of 17.07 kg per year, while 1 529 000 tonnes of white meat was produced and 36.33 kg was consumed per capita. In contrast, South Africans only consume an average of 4.7 kg of pork per capita per year (Department of Agriculture Forestry and Fisheries, 2014a; FAO, 2015). This seems to be a trend among developing countries, as is seen when comparing Africa to any of the developed countries such as those in the European Union. In part, this is a result of the insignificant role played by pigs as livestock in Africa; a direct consequence of religious taboos, its susceptibility to diseases, it's inadaptability to the tropical environment and because it needed to compete with alternative livestock, such as cattle, that were more suited to a nomadic lifestyle (Swart *et al.*, 2010).

On a global scale, the South African pig industry is also small in comparison to the large pork producing countries and regions such as China, the USA and Europe. In South Africa, out of a total of 1.5 million pigs (Department of Agriculture Forestry and Fisheries, 2014a; FAO, 2015), approximately 110 000 are commercial sows housed on 230 farms (Streicher, 2013), producing 208 200 tonnes of pork per year. The frontrunners in pork production, China, the USA and Germany, produce 53.78 million, 10.5 million and 5.5 million tonnes of pork, respectively. Of the three countries, China has by far the largest numbers, with over 400 million pigs. In second, the USA has 68 million pigs, while Germany has 26 million, shortly behind Brazil with 35 million pigs. The largest consumers of pork, however, is the European Union at 40.38 kg per capita per year, followed closely by Eastern Asia and the USA at 33.91 kg and 30.1 kg, respectively (Figure 1.1)

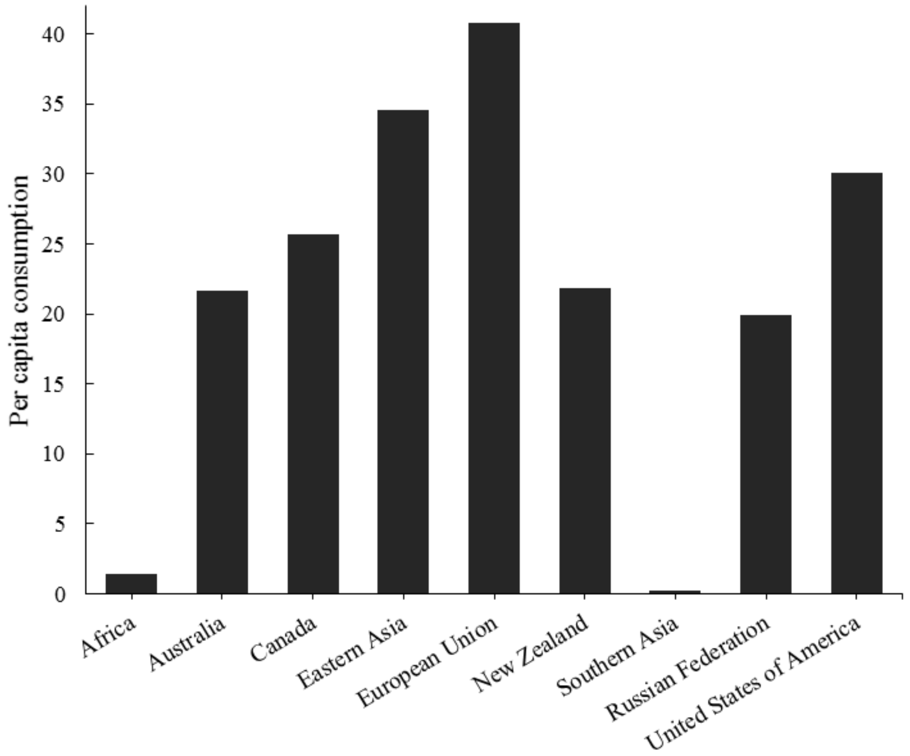

Figure 1.1 Per capita consumption of pork in different countries/regions during 2009 (FAO, 2015).

Eastern Asia = China, Korea, Japan, Mongolia;
European Union = Austria, Belgium, Belgium-Luxembourg, Bulgaria, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, United Kingdom;
Southern Asia = Bangladesh, India, Iran, Maldives, Nepal, Pakistan, Sri Lanka

Although South Africa is self-sufficient in pork production, pork imports still exceeds its exports due to the large requirement of processed products such as ribs. Imports are predominantly from the European Union (Germany, Spain, France and Belgium) and Canada, while exports are made largely to SADC countries (Angola, DRC, Mauritius, Malawi, Mozambique, Seychelles, Tanzania, Zambia and Zimbabwe) (Department of Agriculture Forestry and Fisheries, 2012). However, the South African pig industry is growing with both production and per capita consumption almost doubling over the last decade (Department of Agriculture Forestry and Fisheries, 2014a).

The South African pig industry is broadly divided into two main sectors, a breeding sector and a commercial sector. In the commercial sector there are currently 230 commercial pig farms (Table 1.1), of which the largest numbers are found in Kwazulu-Natal, Western Cape and Free State (Streicher, 2013). Of the total number of pigs in South Africa, 79.85% of all pigs are part of the commercial sector, with an average pig herd size of 535 pigs (Department of Agriculture Forestry and Fisheries, 2011). Furthermore, 60% of the pig farms are considered to be mixed farming enterprises with either crops or cattle/dairy farming. Over 97% of pig farms have both a breeding and grower section (sows, weaners, growers) on one farm, while the remaining 3% are either a breeding or commercial pork unit (Kirsten *et al.*, 2009). The breeding farms are predominantly intensive farming units that still use individual gestation crates. According to a press release by SAPPO (2013), 30% of all pork-producers have already implemented group housing for their sows, with a target set for 2020 where individual sow crates will no longer be used in South Africa. The South African Pork Producers Organisation (SAPPO) acts as the representative for 65% to 70% of South Africa's commercial pig farmers (Visser, 2004). Furthermore, SAPPO focuses on promoting the pork industry, communicates with the government on behalf of the commercial farms, ensures the well-being and health of the pigs, and regularly supports important research in the pig industry (Department of Agriculture Forestry and Fisheries, 2014b).

Table 1.1 The total number of commercial pig farms and producing sows per province in South Africa (Streicher, 2013)

Province	Number of commercial farms	Number of sows	Percentage of sows
Gauteng	18	11 300	10.23
Limpopo	12	12 700	11.50
Mpumalanga	7	14 000	12.68
North West	20	17 800	16.12
KwaZulu-Natal	85	16 600	15.03
Western Cape	45	21 000	19.02
Eastern Cape	7	6 000	5.43
Free State	34	9 000	8.15
Northern Cape	2	2 000	1.81

In the breeding sector, there are only nine independent pig stud breeders in South Africa, jointly contributing 27% to South Africa's pig breeding stock (Streicher, 2013). Of the nine remaining stud breeders, six came together in 2011 to form the breeders company Alliance Genetics South Africa (AGSA), which is also in collaboration with other international companies, such as Alliance Genetics Canada and the University of Guelph. AGSA has access to top quality genetic material and remain updated on research and development in the global community. The AGSA group own 2 000 purebred sows and provide semen, boars and gilts to commercial pig producers in South Africa (AGSA, 2015). The remaining 73% of the breeding stock in South Africa is supplied by two international breeding companies, namely TOPIGS and PIC (Kirsten *et al.*, 2009; Buchanan & Stalder, 2011). TOPIGS SA was established in South Africa in 1995 and currently holds 30% of the market share in pig genetics in South Africa. They have both nucleus and multiplier herds and supply eight producers who jointly own between 8 000 and 9 000 sows. TOPIGS SA supplies semen for insemination of 31 500 sows a year. They mainly supply pork to the processing company Escort, slaughtering approximately 3 500 pigs per week; equating to 10% of all pigs slaughtered in South Africa. PIC is a vertically integrated franchise with their own nucleus herds of dam and sire lines, and hold the largest share of the pig genetics market in South Africa (43%). PIC boast the largest single-ownership sow herd, with 8 500 sows in South Africa. Kanhym supply 70% of their pork to Tiger Brand/Enterprise Foods (Kirsten *et al.*, 2009) with approximately 2 600 carcasses per week (Kanhym, 2013a).

South Africa is following the global trend of using artificial insemination with an estimated 70% to 75% of matings in South Africa done through artificial insemination (AI) (Gerrits *et al.*, 2005; Visser *et al.*, 2014). There are five recognised AI stations across the country with a joined standing capacity of 290 boars, with a potential maximum output of 10 000 doses per week (Department of Agriculture Forestry and Fisheries, 2011). Kanhym is responsible for over 50% of the semen production in South Africa, produced at its own AI station with 116 boars (Kanhym, 2013b). With the use of artificial insemination comes several advantages, one of the most significant being the availability of semen from superior boars across the global community, allowing breeders to choose parents far superior to their own breeding stock (Whittemore, 2006a).

Selection of breeding stock is predominantly based on their estimated breeding values (EBVs). EBVs are calculated using BLUP (best linear unbiased prediction) methodology, which aids breeders by removing environmental influences and indicates an animal's genetic worth as a parent based on the average performance of its offspring (Falconer & Mackay, 1996). BLUP makes use of an animal model, allowing it to conduct simultaneous genetic evaluations for all animals in the evaluation by including all relationships (Wiggans *et al.*, 1988). EBVs however have a limitation in that they are only accurate in the country of estimation (Wilmink *et al.*, 1986).

Due to stringent import requirements, pig semen imports by the local stud breeders have been largely restricted to Canada, and until recently, the USA. Following a recent outbreak of Porcine Epidemic Diarrhoea virus (PEDv), all pig semen imports have been stopped except for individual trade partners that have sufficient health measures in place to prevent the spread of PEDv (DAFF, 2014b; Visser, 2015). When possible, selection of foreign sires is based on available EBVs provided by the country of origin, or when lacking, the boar's own on-farm performance records. As the international EBVs are not directly comparable to South African derived EBVs, progeny testing in the South Africa environment is required for unbiased analyses. Factors such as environmental influences, management practices and their interactions with the animal's particular genome also influences its phenotype. Progeny testing is performed on the semen by the local stud breeders, after which the progeny performance data is sent to SA Stud Book to calculate local EBVs for the imported semen.

The USA and Canada have similar methods for calculating their breeding values. In the USA, a program developed at the Purdue University in 1985, called STAGES (Swine Testing and Genetic Evaluation System), is used. STAGES is an across-herd recording and evaluation program that is used to calculate breeding values for economically important traits of participating nucleus herds, using BLUP (best linear unbiased prediction) methodology. STAGES makes use of a moving genetic base to calculate daily breeding value estimates from submitted on-farm and test-station data (Conatser *et al.*, 2000; NSR, 2013a). The STAGES database currently has 2 million performance records (NSR, 2013a). In Canada, the Canadian Centre for Swine Improvement (CCSI) oversees the Canadian Swine Improvement Program (CSIP). Development of CSIP began in the 1960s and by 1985 it was the first national genetic improvement program that used BLUP (CCSI, 2015a). In 2014, 90 herds were using the CSIP. The Canadian Swine Improvement Program is one of the largest genetic improvement programs in the world, with 91 000 nucleus herd pigs performance tested in 2014. The CSIP calculates EBVs and indices for 18 economically important traits from on-farm, test station and packing plant data. Genetic evaluations are performed bi-weekly, producing breeding values and indexes for 18 traits across seven breeds.

Besides progeny testing, the ideal would be an international across country evaluation of foreign boars used as sires in the South African pig industry without requiring extensive progeny testing first. In other livestock industries, specifically dairy cattle, tools such as conversion equations (Goddard, 1985; Schaeffer, 1985; Wilmink *et al.*, 1986), multiple across-country evaluations (MACE) (Schaeffer & Zhang, 1993; Schaeffer, 1994) and genomic breeding values (GEBVs) (Sullivan & VanRaden, 2009; Sullivan *et al.*, 2011) have been successfully used to aid in the problem of across country evaluations. Conversion equations are the most basic of the three, using boars with breeding values in two countries to estimate genetic correlations between traits in different countries. MACE requires sires to have progeny with performance records in several countries as well as full pedigree information to link all animals within and between countries. Furthermore, genetic correlations between traits in different countries, as well as heritability estimates for the traits in each country is required (Schaeffer & Zhang, 1993; INTERBULL, 2015). GEBVs are obtained using a 3-step process whereby a reference population is first genotyped to find DNA markers, single nucleotide polymorphisms (SNPs), which are in linkage disequilibrium to quantitative trait loci (QTL), after which the effect of each QTL is estimated based on the animals' respective phenotypes. A weighted sum of the markers can then be used in genotyped animals to obtain an individual's genomic breeding value (Meuwissen *et al.*, 2001; Schaeffer, 2006; Goddard & Hayes, 2007; Hayes *et al.*, 2009). The development of GMACE, the incorporation of GEBVs into the International Bull Evaluation Service's (INTERBULL) MACE evaluations for dairy cattle, was accomplished by Sullivan & VanRaden (2009).

Although these sophisticated methods have been developed and are globally used by INTERBULL for international dairy cattle evaluations, no large scale equivalent is available in the pig industry and selection of foreign boars is done only on their foreign breeding values. To assist local South African pig breeders, methods need to be investigated that will improve the selection accuracy of foreign sires, and ultimately improve genetic progress in South Africa.

1.2 Aim

The South African Pork Producers Organisation (SAPPO) requested a research project based on available EBVs and on-farm performance data from the AGSA stud breeders, to investigate methods that will improve selection accuracy of imported boars, thereby supporting an increase in genetic progress in the South African pig industry. Furthermore, an investigation into the role of imported boar semen used in the South African pig industry, in comparison to South African boars was done. The study was conducted in two phases based on the following two objectives:

1. Investigate conversion equations as a tool to estimate local EBV equivalents for foreign breeding sires
2. Evaluate and compare the on-farm performances of locally born progeny from local sires and imported semen

Chapter 2: Literature Review

2.1 Introduction

As technology advanced, pig breeding moved away from only using natural mating, resulting in a substantial increase in artificial insemination. By the end of the 1990s, almost 50% of the world's gilts and sows were inseminated (Gerrits *et al.*, 2005; Roca *et al.*, 2006; Riesenbeck, 2011). Artificial insemination has several advantages, one of the most important being the ability to utilise some of the best boars in the world. Further advantages include the lower cost of semen and insemination compared to housing and keeping costs of several boars, reducing the transmission of sexually transmitted diseases (Maes *et al.*, 2008), maintaining a closed herd (Dekkers *et al.*, 2011; Knox, 2015), and the overall success where low percentage of sows return to oestrus after the first service (Vishwanath, 2003). Artificial insemination allows breeders to increase the selection intensity (Weigel & Powell, 2000) by selecting semen from across the globe and ensure maximum genetic progress. Breeders have the opportunity to practice stricter selection and increase the selection differential due to the availability of a larger group of potential parents to choose from. The increased availability of semen led to expanding the market for potential sires world-wide; today, many countries frequently import and export semen, embryos and live animals (Riesenbeck, 2011).

To ensure accurate and informed mating decisions, breeders use estimated breeding values (EBVs) to evaluate an individual's worth as a parent. However, the limitation of a breeding value is that it is only comparable for a specific breed and only applicable to the country or region in which it was estimated (Wilmink *et al.*, 1986). This incompatibility is as a result of the data being disconnected due to differences in environment (Goddard & Beard, 2005), base year, scale, trait definitions and the units of measurement (Weigel & Powell, 2000). Breeding values are estimated using methodology that was derived by Henderson in 1950 (Robinson, 1991), known as BLUP (best linear unbiased prediction). To overcome the incompatibility of EBVs across countries, tools such as conversion equations (Goddard, 1985; Schaeffer, 1985; Wilmink *et al.*, 1986), and more recently MACE (multiple across country evaluations) (Schaeffer & Zhang, 1993; Schaeffer, 1994) have been used successfully to compare animals across countries (Goddard & Beard, 2005)

The aim of this chapter is to provide a review of available literature on the genetic improvement in pigs by referring to available genetic tools that are applied in the pig industry. Special mention is made of methods to improve the accuracy of prediction of breeding values across countries.

2.2 Breeding strategies and traits of economic importance

The basic structure used in the pig industry is the classic three-tier breeding pyramid (Figure 2.1**)** together with cross-breeding, that consists of a nucleus herd, multiplier herd and commercial production herds (Visschera *et al.*, 2000; Dekkers *et al.*, 2011). In the top tier of the breeding pyramid, the nucleus, or super-nucleus herds are generally closed herds to ensure optimum herd health. Artificial insemination and embryo transfers are used to introduce new genes while preventing the introduction of diseases (Whittemore, 2006a; Maes *et al.*, 2008; Knox, 2015). In the nucleus herd, pure-breeding great-grandparent stocks are intensely selected to produce grandparent stock. Grandparents are then moved to a multiplier herd where planned crossbreeding occurs to multiply the selected stock and produce parent stock, including the F1 gilts and terminal sires. The parent stock are then sold to the commercial farmers to produce the final generation of crossbred pigs to be slaughtered (Visschera *et al.*, 2000; Whittemore, 2006a).

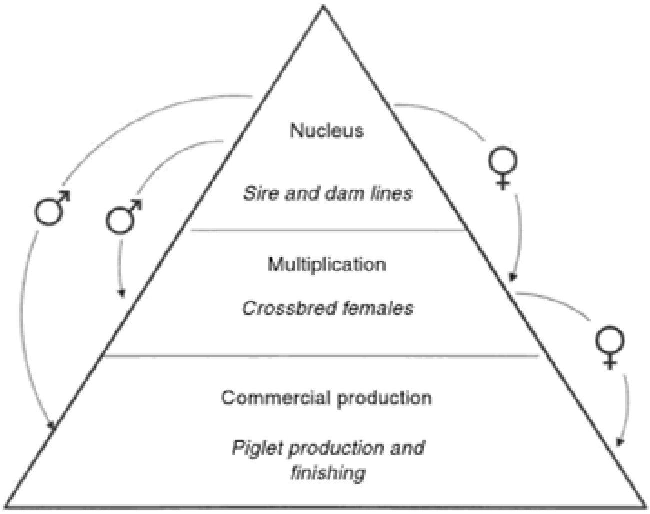

Figure 2.1 The classic three-tier breeding pyramid used in the pig breeding industry (Dekkers *et al.*, 2011)

The pig industry can be divided into two major sectors; a breeding sector that focuses on the nucleus and multiplier herds, using different cross breeding combinations and lines to ensure genetic progress is maintained and produce F1-gilts and terminal boars; and a commercial sector that buys the F1-gilts and terminal boars to produce the weaners that are raised to be slaughtered (Visschera *et al.*, 2000; Whittemore, 2006a). Each sector employs different breeding objectives and favours different traits of importance. The breeding sector's focus is primarily on reproductive traits and secondarily on production traits; while the commercial sector's primary focus is production and quality, while reproduction is a secondary focus (Ollivier, 1998).

Although the breeding sector supplies the commercial farmers and needs to cater for the changing market requirements, it must ensure genetic progress is made (Dickerson & Hazel, 1944). Maximum genetic progress is achieved in four ways; by selecting within populations, importing new genes, utilising hybrid vigour and separating sire and dam lines (Whittemore, 2006a). To ensure genetic progress is maintained, and still cater for the different commercial requirements, several purebred lines, each with their own breeding objective and selection criteria, are developed and later crossed to produce different types of F1 females (Ollivier, 1998). In addition to purebred lines, nucleus herd breeders and breeding companies also develop synthetic lines by crossing two or more breeds and then line breeding the crossbred to ensure the desired characteristics are fixed (Dekkers *et al.*, 2011). Dam lines are selected with a primary emphasis on reproduction traits, such as litter size; while sire lines have their selection emphasis on production traits, such as growth and feed conversion (De Vries *et al.*, 1990; Dekkers *et al.*, 2011). Crossbreeding is predominantly used in pig breeding to utilise the advantageous effects of heterosis and complementarity (Sellier, 1976) and improve maternal and reproductive traits, with a smaller influence on carcass traits (Ciobanu *et al.*, 2011). In a common three-way cross, Landrace and Large White are crossed to produce F1 gilts that are bred to terminal Duroc sires (Dekkers *et al.*, 2011). This is also the system used by the AGSA breeders in South Africa (Visser, 2014; Visser & Hofmeyer, 2014). Hybrid vigour has been shown to enhance both sow reproduction traits (age of puberty, conception and ovulation rate, embryo and foetal survival, litter size at birth and nursing ability), as well as improve piglet survival and performance (Bidanel, 2011). Results from two studies done on the direct effects of heterosis and recombination on reproduction (Cassady *et al.*, 2002a) and growth and carcass traits (Cassady *et al.*, 2002b) indicated a significant increase in both reproduction and performance traits due to the effects of heterosis and recombination in crossbred pigs. Hybrid vigour from crossbreeding can therefore lead to a major improvement at two levels. Firstly, the crossbred litter from two purebred parents can have up to 5% improvement in litter size and 10% improvement in litter weaning weight due to the litter's improved vigour and greater size. The second level of improvement is in the use of the F1 females, where their litters have a further 5% performance improvement due to the sow's improved reproductive ability (Whittemore, 2006a).

The main objective of creating a female line is to increase lifetime reproduction efficiency of the sow by improving prolificacy, mothering ability, sow longevity and shorten the time period to sexual maturity. The sire line, on the other hand, focuses on increasing production through emphasis on growth rate, feed efficiency, decreasing back fat thickness and improving structural soundness (Visser, 2004). The specialised sire or dam lines are created over several generations by focusing on improving specific characteristics. Typically, Landrace and Large White breeds are used to create dam lines and are crossbred to produce F1 gilts in the multiplier herd, while Duroc and Pietrain are used for the sire lines (Dekkers *et al.*, 2011), which are used as terminal sires in the commercial sector. Generally, the traits that are included in the selection program are based on the breeding objective of both the specific breeder and the national pig industry (Visser, 2004). A genetic lag is seen in the breeding sector, where it takes three to five years before the genetic changes in the nucleus herds can be realised in the commercial herds. It is therefore vital that breeders consider the future needs and requirements of the commercial farmers when deciding their breeding objectives (Dekkers *et al.*, 2011). The genetic lag can be reduced to between two and three years by creating a larger nucleus herd and cutting out the pure-bred multiplication of grandparents (Whittemore, 2006a).

Commercial farms produce pork using F1 gilts and terminal boars that originate from breeders and multiplier herds from the breeding sector (Koryazhnov & Lebedev, 1977). Boars can either be purchased from the breeding sector or are home bred. These boars are cross-bred to F1 gilts to produce the weaner pigs that are raised for eventual slaughter (Whittemore, 2006a). World-wide, the role of artificial insemination in the commercial sector has steadily increased, where more than 90% of sows are already bred through artificial insemination in Western Europe (Maes *et al.*, 2008).

2.2.1 Record Keeping

Performance recording has several benefits: it indicates the present status and previous performances of a production unit and its individuals, it provides factual data that allows accurate decision making and provides a basis for production management (Whittemore, 2006b). The purpose of animal recording is therefore to improve animal performances, herd and farm management and the eventual quality of the product produced (Peters & Zumbach, 2002). The characteristics/traits that are recommended to be recorded were listed by Pockley (1979), these include traits of economic importance for inclusion in the breeding plan, traits that can be readily measured objectively (e.g. body weight), those that are not readily measured but are recorded (e.g. number weaned), characteristics that need to be assessed or that can be present or absent (e.g. temperament), and lastly, any characteristics that are unacceptable (e.g. coloured pigment).

According to Whittemore (2006b), management information that should be recorded include farrowing date, prospective weaning date, return to oestrus and insemination date and recurring oestrus. At farrowing, litter size, number born alive and number stillborn needs to be recorded. Litter weight at farrowing and weaning is only important for some litters/breeders. For weaners, weight at weaning and finishing can be used to calculate the average daily gain, while the dates of weaning and exiting the herd are required to estimate the length of stay and growth rate. Other important information includes veterinary treatments, sickness and decrease in food or water intake. One of the most important carcass traits in pigs is back fat thickness as it is related to both meat quality and the efficiency of pork production (Kolstad, 2001). The need to slaughter animals to measure body composition and lean yield has been immensely reduced (Whittemore, 2006b). Back fat was initially measured by visual estimates and linear body measurements, after which an invasive method was later developed whereby a narrow metal ruler was inserted into the pig (Hazel & Kline, 1952). More recently, non-invasive methods, such as ultrasound (Wilson, 1992) and computer tomography, are used that requires the pigs to be immobilized for three minutes (Jopson *et al.*, 1997; Kolstad, 2001) to accurately measure back fat thickness.

Performance recording, identification and evaluation of all farm animals is standardised by a world-wide organization known as the International Committee for Animal Recording (ICAR). Their main role is to formulate and define the standards for measuring and recording economically important traits and establishing guidelines for animal identification and parentage registration (ICAR, 2012). Usually, each country has their own performance scheme to assess the state of their different livestock enterprises. Details of the South Africa national pig recording scheme, known as the National Pig Recording and Improvement Scheme (NPIRIS), were provided by the Department of Agriculture (2007). Phase-D on-farm testing played a vital role in NPIRIS where on-farm testing of boars and gilts include measuring growth rate, feed intake, feed conversion and ultrasonic back fat thickness (Table 2.1). Phase-B central testing, as well as carcass evaluation, was only required for random samples from breeders participating in the scheme.

Table 2.1 Definition and abbreviations for six traits with the highest economic importance in the South African pig industry (Visser & Hofmeyer, 2014; Voordewind, 2014)

Trait	Abbreviation	Definition
Number born alive	NBA	Number of piglets born alive per litter
21 day litter weight	21DLWT	Litter weight at 21 days (kg)
Average daily gain	ADG	Average daily gain (g) during the test period
Feed conversion ratio	FCR	Average feed conversion ratio (kg intake/kg gained) during the test period
Back fat thickness	BF	P_2 back fat thickness (mm) measured ultrasonically at the end of the test period
Rand value index	RVI	Aggregate of the five economically important traits, indicating the bio-economic efficiency

During 2008, central testing fell away, while only on-farm testing is still performed by the AGSA breeders. Today, on-farm testing of growth performances occurs during the test period, which runs for between 11 and 13 weeks, once the pigs leave the weaner house. Pigs are weighed once in the morning and again in the afternoon at the start of the test period, and the average of the measurements used as the starting weight. During this period, some breeders also perform individual testing of feed intake which is used to calculate the average feed conversion rate at the end. At the end of the test period, the pigs’ starting and end age and weight is used to calculate the average daily gain, and P_2 back fat thickness is measured ultrasonically. The test period commonly starts between 20 and 40 kg and ends between 85 and 100 kg, with those weighing less than 80 kg disqualified (Visser, 2015), although the minimum end weight was removed for EBV calculations in April 2015 to accommodate slow growers in the Stud Book database (Voordewind, 2015). Lastly, pigs are evaluated for the following functional traits: testes size and shape, vulva size and shape, teat number and spacing, teat abnormalities, shoulder, back and topline, legs and claws, ham development, movement and breed characteristics (Visser, 2014).

Another important source of information for analyses are records from progeny testing. Bourdon (2000) defined a progeny test as a method used to predict the breeding value of an individual through several matings and evaluating the performance of his offspring. Progeny testing increases the reliability of the breeding value by adding more relatives to the BLUP analysis (Muir, 2007)

2.2.2 Genetic Parameters

It is important to consider not only the heritability estimates of traits, but also the favourable and unfavourable genetic correlations between them. A list of traits that are commonly used as selection criteria are listed in Table 2.2. Female reproduction traits generally have a low to moderate heritability, while the heritability of male reproductive traits are moderate to high (Bidanel, 2011). A large maternal effect is seen in litter traits due to the maternal environment that the piglets are exposed to up until weaning. Production traits tend to be moderately heritable and respond well to selection (Clutter, 2011), while meat and carcass traits exhibit low to moderate and moderate to high heritability, respectively (Ciobanu *et al.*, 2011).

Table 2.2 A summary of heritability estimates for important selection criteria in pigs

Trait		h^2 range	References
Reproduction	Number born alive	0.08 – 0.1	Rothschild, 1996; Hermesch *et al.*, 2000; Chen *et al.*, 2003; Bidanel, 2011; Akanno *et al.*, 2013
	Litter birth weight	0.11 – 0.29	Rothschild, 1996; Hermesch *et al.*, 2000; Bidanel, 2011; Akanno *et al.*, 2013
	Litter size at weaning	0.02 – 0.08	Rothschild, 1996; Chen *et al.*, 2003; Bidanel, 2011; Akanno *et al.*, 2013
	21 day litter weight	0.07 – 0.14	Hermesch *et al.*, 2000; Chen *et al.*, 2003; Bidanel, 2011; Akanno *et al.*, 2013
	Ovulation rate	0.32 – 0.39	Rothschild, 1996; Bidanel, 2011
	Weaning to conception interval	0.08 – 0.23	Rothschild, 1996; Akanno *et al.*, 2013
	Libido	0.15 – 0.2	Rothschild, 1996; Bidanel, 2011
	Sperm quality and quantity	0.19 - 0.3	Rothschild, 1996; Bidanel, 2011
	Efficiency of lactation	0.12	Visser & Hofmeyer, 2014
	Teat number	0.21 – 0.25	Visser & Hofmeyer, 2014
Production Traits	Average daily gain	0.28 – 0.5	Kaplon *et al.*, 1991; Lo *et al.*, 1992; Ducos *et al.*, 1993; Suzuki *et al.*, 2005; Clutter, 2011; Akanno *et al.*, 2013
	Feed intake	0.29 – 0.52	Suzuki *et al.*, 2005; Clutter, 2011; Akanno *et al.*, 2013
	Feed conversion ratio	0.19 – 0.34	Ducos *et al.*, 1993; Bidanel & Ducos, 1996; Suzuki *et al.*, 2005; Clutter, 2011; Akanno *et al.*, 2013
	Lean tissue growth rate	0.34 – 0.39	Clutter, 2011; Visser & Hofmeyer, 2014
	Lean tissue feed conversion	0.31	Clutter, 2011; Visser & Hofmeyer, 2014
	Milk yield	0.15 – 0.25	Visser & Hofmeyer, 2014
	Milk quality	0.30 – 0.5	Visser & Hofmeyer, 2014
	Age to 100kg	0.23 – 0.43	Kaplon *et al.*, 1991; Lo *et al.*, 1992; Bidanel *et al.*, 1994; Bidanel & Ducos, 1996; Akanno *et al.*, 2013

Table 2.2. Continued.

Trait		h^2 range	References
Carcass traits	pH_u	0.07 – 0.39	Lo *et al.*, 1992; Bidanel *et al.*, 1994; Ciobanu *et al.*, 2011; Visser & Hofmeyer, 2014
	Water holding capacity	0.1 – 0.43	Ciobanu *et al.*, 2011; Visser & Hofmeyer, 2014
	Meat colour	0.15 – 0.57	Lo *et al.*, 1992; Ciobanu *et al.*, 2011; Visser & Hofmeyer, 2014
	Tenderness	0.17 – 0.46	Lo *et al.*, 1992; Suzuki *et al.*, 2005; Ciobanu *et al.*, 2011; Visser & Hofmeyer, 2014
	Back fat thickness	0.42 – 0.72	Lo *et al.*, 1992; Ducos *et al.*, 1993; Bidanel *et al.*, 1994; Bidanel & Ducos, 1996; Suzuki *et al.*, 2005; Visser & Hofmeyer, 2014
	Dressing percentage	0.3 – 0.39	Ducos *et al.*, 1993; Visser & Hofmeyer, 2014
	Intra muscular fat	0.46 – 0.61	Suzuki *et al.*, 2005; Visser & Hofmeyer, 2014
	Loin eye area	0.47	Visser & Hofmeyer, 2014

In selection of parents for the next generation, some traits are economically more important. In the South African pig breeding industry, the five traits considered to be of greater economic importance include two fertility traits, number born alive (NBA) and 21 day litter weight (21DLWT), and three growth and production traits, average daily gain (ADG), feed conversion ratio (FCR) and back fat thickness (BF) (Table 2.1). These are often joined to form an aggregate, known as the Rand value index (RVI) (Visser & Hofmeyer, 2014). These traits are regularly measured on-farm and are used to generate EBVs for the AI sires. The same traits are also used during selection in the USA and Canada, with additional traits including number weaned, lean yield (Robinson & Buhr, 2005; NSR, 2013b), loin eye area, piglet perinatal survivability, farrowing interval and number of functional teats (Chesnais & Sullivan, 2002; CCSI, 2012). However, instead of calculating average daily gain, the USA and Canada measure age at 250 lbs and 100 kg, respectively. Several studies have found strong negative genetic and phenotypic correlations between average daily gain and age, ranging from -0.61 to -0.99 and -0.67 to -0.99, respectively (Kaplon *et al.*, 1991; Lo *et al.*, 1992; Bidanel & Ducos, 1996; Akanno *et al.*, 2013; Dube *et al.*, 2013). Although not the same trait, the strong genetic and phenotypic correlation between the two traits allows the one to be an accurate indicator of the other.

The largest and most important consequence for selection of increased litter size is a decrease in piglet survival (Bidanel, 2011). This is reflected in Table 2.3 where an increase in litter size at farrowing has a positive and unfavourable genetic correlation (0.64) to pre-weaning piglet mortality.

This is due to the large negative correlation litter size has with individual birth weight (-0.66), as shown in Table 2.4.

Table 2.3 Genetic (above diagonal) and phenotypic (below diagonal) correlation estimates for reproduction traits in pigs (adapted from Akanno *et al.*, 2013)

	LSF	LS21	LSW	LWF	LW21	LWW	WSI	MOR	PDG	AFF	AFC	GLT	DFI	MA	SRT
LSF		0.8	0.7	0.55	0.55	0.08	0.05	0.64	0.42	0.19	-0.48	-0.17	0.19	-	-
LS21	0.82		0.87	0.69	0.85	0.52	-	-0.21		-	-	-	-	-	-
LSW	0.74	0.92		0.55	0.74	0.52	0.29	-0.35	-	-	-	0.34	0.27	0.62	0.37
LWF	0.73	0.5	0.68		0.65	0.11	0.09	0.19	-	0.14	-	-	-	-0.1	-
LW21	0.59	0.81	0.76	0.62		0.76	-	-0.64	-	-	-	-	-	-	-
LWW	0.54	0.81	0.86	0.46	0.81		0.05	-0.48	-	-	-	-	-	-0.21	0.42
WSI	0.03	-	0	0.01	-	0		-	-	-	-	-	-	-	-
MOR	0.17	-0.59	0.28	-0.28	-0.65	-0.67	-		-	-	0.35	-	-	-	-
PDG	-	-	-	-	-	-	-	-		-	-	-	-0.96	-	-
AFF	-0.03	-	-	0	-	-	-	-	-		-	-	-	-	-
AFC	-	-	-0.05	-	-	-	0.07	-	-	-		-	-	-	-
GLT	-0.06	-	0.05	-	-	-	-	-	-	-	-		0.1	-	-
DFI	0.02	-	0.11	-	-	-	-	-	-	0.33	-	0.02		-	-
MA	-	-	-0.34	-	-0.19	-0.26	-	-	-	-	-	-	-		-
SRT	-	-	0.48	-	-	0.48	-	-	-	-	-	-	-	-	

LSF = Litter size at farrowing; LS21 = Litter size at 21 days, LSW = Litter size at weaning, LWF = Litter weight at farrowing, LW21 = Litter weight at 21 days, LWW = Litter weight at weaning, WSI = Weaning to service interval, MOR = Pre-weaning mortality, PDG = Pre-weaning daily gain, AFF = Age at first farrowing, AFC = Age at first conception, GLT = Gestation length, DFI = Daily feed intake during lactation, MA = Maternal ability, SRT = Survival rate

Genetic correlations for growth traits are influenced by the level of feeding. Under *ad libitum* feeding, genetic correlations are seen to be higher than for *semi-ad libitum*. This is thought to be as a result of incomplete expression of appetite when animals are not fed *ad libitum* (Clutter, 2011). Unfavourable interaction commonly exist between the production and reproduction traits. Traits such as average daily gain and number born alive have a strong negative correlation (Table 2.4), causing the selection of the one to negatively affect the other.

Table 2.4 Genetic correlations between selected reproduction, growth and carcass traits for pigs (adapted from Akanno *et al.*, 2013).

	ADG	IBW	IW21	IWW	BFT	CWT	CLT	LEAN	DPT	LEA	HYD
LSF	-0.4	-0.66	-0.7	-0.53	-0.02						
LS21		-0.25	0.04	-0.55							
LSW		0.45	0.34	-0.24							
LWF		0.31	0.03	-0.36							
LW21		0.11	0.53	0.15							
LWW		0.04	0.58	0.29							
PDG	0.38	0.87	0.85		0.05	0.08	0.35				
SRT				-0.6							
AFC	-0.04				-0.02						
WSI	-0.08				-0.27						
MOR		-0.21		-0.3							
ADG					-0.35	0.57	0.58	0.5	0	0.02	0.14
MWT					0.16		0.43				
D90					0.18						
FCR					0.22		0.06	-0.53		-0.04	-0.7
ADFI					0.49						

LSF = litter size at farrowing; LS21 = litter size at 21 days; LSW = litter size at weaning; LWF = litter weight at farrowing; LW21 = litter weight at 21 days; LWW = litter weight at weaning; PDG = pre-weaning daily gain; SRT = survival rate; AFC = age at first conception; WSI = weaning to service interval; MOR = pre-weaning mortality; ADG = average daily gain; MWT = mature weight; D90 = days to 90kg; FCR = feed conversion ratio; ADFI = average daily feed intake; IBW = individual birth weight; IW21 = individual weight at 21 days; IWW = individual weaning weight; BFT = back fat thickness on carcass; CWT = carcass weight; CLT = carcass length; LEAN = percentage lean meat; DPT = dressing percentage; LEA = loin eye area; HYD = ham yield

2.3 Genetic Evaluation

Modern genetic tools consists of quantitative evaluation and molecular evaluation. Traditional quantitative genetic evaluation is based on phenotypic records of the individual, its progeny and relatives, thereby removing environmental influences to predict its breeding value. Limitations to this method, however, include lowly heritable traits (e.g. reproduction traits) that limit the accuracy of selection, traits that can only be measured later in life (e.g. longevity), traits difficult to measure directly on the individual (e.g. carcass and sex-limited traits) and traits that are expensive to measure (e.g. disease resistance) (Dekkers *et al.*, 2011). More recently, molecular genetic evaluation is being used to more accurately predict an individual's breeding value by including their DNA information, or rather the presence or absence of particular SNPs or major genes, into BLUP analysis to predict a genomic estimated breeding value (GEBV) (Meuwissen *et al.*, 2001; Muir, 2007; Sargolzaei *et al.*, 2009; Dekkers *et al.*, 2011).

Broadly speaking, the expression of an individual's phenotype is influenced by genetic and environmental variances. However, another important factor that needs to be considered is the interaction between the environment and the individual's genotype (GxE). Different genotypes are more or less suited to a particular environment, and will therefore perform differently in different environments. This is an important factor to consider when using EBVs from different countries; which will be discussed later.

2.3.1 Estimated breeding values

The term "breeding value" has not changed much over the years. Already in 1935, Lush described it as the average genetic merit of the offspring produced by mating an individual to a mate that is a true representative of the breed (Lush, 1935). In 1943, Hazel defined a breeding value as the sum of several genotypes weighted according to their relative economic value. A breeding value can also be defined as the sum of the average effects of the genes of an individual (Lush, 1947), an individual's value based on the mean value of its offspring (Falconer & Mackay, 1996), or simply as the value of an individual as a parent (Bourdon, 2000). In simple terms, a breeding value indicates the average expected improvement (or decline) in the level of performance for a trait in the progeny of a specific individual. Breeding values are used by both breeders and commercial farmers as a tool to select the best animals as parents. The definition of the best animal, however, depends on the particular breeding objective of the breeder and shortcomings of his/her herd (Visser, 2004).

Today, BLUP methodology is used to simultaneously estimate fixed effects and produce a breeding value (Falconer & Mackay, 1996). BLUP makes use of an animal model which maximises the use of pedigree information by accommodating and using all information from all known relatives and estimating their individual genetic merits simultaneously (Tavernier, 1988; Wiggans *et al.*, 1988; Robinson, 1991). Through the inclusion of a relationship matrix, which connects an individual to the performances of his relatives based on their relationship, the accuracy of prediction is increased for individuals with few offspring, and individuals can be evaluated earlier by using the performances of their relatives (Henderson, 1975). The accuracy of BLUP to predict the true breeding value, however, is theoretically limited to the number of ancestral and progeny records included in the analysis (Muir, 2007).

BLUP has several advantages; it uses information from all known relatives (Tavernier, 1988; Wiggans *et al.*, 1988; Robinson, 1991), producing a more accurate prediction of the breeding value and allows comparing the genetic merit of performances obtained not only under different management systems, but also for performances over different time periods, between different herds and allows comparison of animals with different amounts of information. Lastly, BLUP separates performances into their genetic and non-genetic components, allowing breeders to evaluate the obtained genetic change (Long *et al.*, 1991).

As was mentioned earlier, breeding values are determined for a specific breed in a particular environment and can only be compared within breeds, countries or regions that are included in the same genetic analysis. The reason for the incompatibility between regions or countries is due to differences in the genetic evaluation; e.g. differences in the base year, scaling and adjustments, differences between countries in the description and measurement of the traits and differences in trait heritability estimated for the different traits (Powell & Wiggans, 1995). These factors could cause the true genetic correlation to be less than 1 for a trait between the two countries (Goddard & Beard, 2005). However, estimated genetic correlations of less than unity can also be attributed to bias in the method used to estimate the genetic correlation, or due to sampling error.

BLUP was first used in a national pig breeding program in Canada in 1985 for on-farm evaluations of back fat and growth (Hudson & Kennedy, 1985). Genetic evaluation in the South African pig industry began in 1956 with a performance testing scheme based on the performance and genetic principles of a Danish System (Visser *et al.*, 2014). In 1993/94, the South African pig industry implemented the use of the Australian within-herd genetic evaluation program, PIG BLUP, to allow breeders to utilise breeding values for selection of their pigs (Visser, 2004; Visser, 2005). PIG BLUP is a computer program that uses multi-trait BLUP model (Long *et al.*, 1991) that simultaneously uses all the measurements of an individual's relatives and of other individuals in the breeding herd to estimate its EBV (Visser, 2005). Although a major step in improving pig selection, limitations were associated with the use of Australian genetic parameters and economic weights (Van der Westhuizen, 2013). In 2012, South Africa adopted its own evaluation program, known as National BLUP, which incorporates South African genetic parameters and economic weights into the evaluation program and estimates breeding values for five economically important traits (Visser *et al.*, 2013). On-farm performance records are sent to either SA Stud Book, a private company, or the Agricultural Research Council (ARC), a government organization, who perform the genetic evaluation (ARC, 2014; SA Stud Book, 2014).

2.4 Improving the accuracy of prediction of breeding values across countries

One of the primary challenges associated with the use of estimated breeding values is the inability to use breeding values across regions/countries (Jorjani *et al.*, 2001). This is especially problematic when importing breeding stock, or rather semen, from a foreign country. An imported animal is considered to be a base animal with no breeding value till enough progeny has been born and performance tested to produce a new breeding value that is significant in the imported country (Van Vleck, 1990). This can, however, take years to do, by which time better breeding stock will be available and different consumer demands must be met.

2.4.1 Conversion equations

To overcome the problem of waiting for a new, relevant breeding value to be developed, conversion equations have been successfully used in the past in the dairy industry to accurately predict the individual's breeding value in the new country. Conversion equations are usually based on simple regression analysis for either single or multiple traits. The most common form for regressions equations is:

$$EBV_{IMP} = a + bEBV_{EXP} + \varepsilon$$

Where EBV_{IMP} is the converted EVB in the importing country, EBV_{EXP} is the EBV in the exporting country, a and b are the intercepts of the regression equation's slope (Jorjani & Fikse, 2004). When using multiple trait regression analysis instead if single trait regression analysis, b is simply expressed as a vector rather than a scalar.

The first conversion equations that were used were those proposed by the International Dairy Federation to assist in comparing foreign and local bulls (Goddard, 1985; Wilmink *et al.*, 1986). A simple formula was produced whereby the converted foreign EBV was predicted by multiplying the foreign EBV with the standard deviation between the transmitting ability in the country of origin and country of import and adding it to the difference between the base years or genetic merit for the two countries (Powell & Sieber, 1992). There were three important disadvantages to using this formula; 1) it did not allow for GxE interaction, which occurs due to different environments or different trait definitions between the two countries, 2) the genetic variance in both countries needed to be known as heritabilities vary between countries, and 3) any inaccuracies in breeding value calculations caused inaccuracies in the converted breeding value. Therefore, if the assumed heritabilities were too high, the individual were consistently overrated, while if the assumed heritabilities were too low, they were consistently underrated (Goddard, 1985; Wilmink *et al.*, 1986).

Conversion equations were proposed by Goddard (1985), based on daughter yield deviations (the average daughters'/offsprings' performances that have been adjusted for fixed and random non-genetic effects for the offspring and the genetic effects of their dams (Liu *et al.*, 2004)), and Wilmink *et al.* (1986), who used EBVs from bulls with progeny in both countries (Weigel, 1997) and adjusted the exported EBV for its reliability in the importing country (Jorjani & Fikse, 2004). Both have been widely used to compare breeding evaluations for individuals between different countries. They were initially used by the International Dairy Bull Evaluation Service to compare the genetic merit of dairy bulls and cows from different countries (Schaeffer & Zhang, 1993; Goddard & Beard, 2005). Fundamentally, the Goddard (1985) and Wilmink *et al.* (1986) methods follow the same form:

$$EBV_1 = b * EBV_2 + a$$

where $$b = b_g = r_g * \frac{\sigma^1}{\sigma^2}$$

where EBV_1 is the breeding value in the country of import, EBV_2 the breeding value in the foreign country, a is the intercept, b is the genetic regression of a trait in country 1 on the trait in country 2, r_g is the genetic correlation between the trait in country 1 and the trait in country 2, and σ^1 and σ^2 are the genetic standard deviations for country 1 and country 2, respectively (Goddard & Beard, 2005).

The main difference between the Goddard and Wilmink method is in the estimation of a and b. For the Wilmink method, b is produced by regressing the exporting country's EBV (EBV_2) on the deviation of the importing country's EBV from its mean, multiplied by the reliability of the EBV in the importing country ($[EBV_1 - \overline{EBV_1}] * REL_1$); while a is calculated as the mean exporting EBV multiplied by b, subtracted from the mean importing EBV ($\overline{EBV_1} - b * \overline{EBV_2}$). Goddard, on the other hand, only regresses the daughter yield deviation of the importing country on the EBV of the exporting country to determine b, while a is merely the intercept obtained from calculating b (Powell & Sieber, 1992).

The Goddard and Wilmink methods have been further compared by Powell *et al.* (1994). Firstly, while the Goddard method is based on daughter yield deviations (DYD), the Wilmink method does not use DYD and is therefore more appropriate to use when DYD are unavailable or if only two countries are being used. The Goddard method, however, has more advantages and remains more accurate (as was shown in a study by Powell (1988)), is easier to understand and explain and is more appropriate when there is incomplete ancestral information in the second country. These methods, in comparison to Schaeffer's linear model (Schaeffer, 1985), are superior as they are based on the relationships between evaluations in two (or more) countries, and therefore automatically account for the effective genetic correlation for the traits in different countries (Powell *et al.*, 1994). Nonetheless, there are still major limitations with using these methods. These include 1) there is often an insufficient number of animals with progeny in more than one country, 2) conversion equations become unstable over time as the group of bulls used to develop the equation changes, 3) bulls can't be re-ranked across countries if a GxE interaction is present, 4) preferential treatment of progeny in the importing country causes bias results when using regression analysis, and lastly, 5) a reduced accuracy of prediction is seen for elite animals as they exceed the data range that is used to develop the conversion equation (Weigel, 1997; Weigel & Powell, 2000).

In order to accurately convert an individual's breeding value from one country to its corresponding breeding value in another, a genetic correlation needs to be found between the performances in the two countries. Calo *et al.* (1973) formulated an equation to estimate the genetic relationship between two traits (beef and milk production) in Holstein-Friesian bulls. The final correlation between beef and milk traits could then be estimated through:

$$r_{GMB} = \ r_{MB}/(\sqrt{b_M}\sqrt{h_B^2}\,)$$

where r_{GMB} is the genetic correlation between the milk and beef traits; r_{MB} is the correlation between the milk and beef EBVs, b_M is the weighting factor for estimating milk production by considering the average repeatability for milk production per sire; and h_B^2 the weighting factor for estimating the beef EBV by using the estimated heritability for beef traits. The correlation between the ETA (estimated transmitting ability) for milk production and the ETA for beef can then be used to estimate the genetic relationship for the traits among the sires; but instead using the average progeny deviation from the contemporary group mean as a weighting factor for beef production.

However, if this formula was to be used to predict the breeding value of a boar in a foreign country, some changes will be required. If performance for a trait is to be considered as separate traits in different countries, the model will be changed so that both traits' weighting factors are estimated in the same manner. Whether repeatabilities are used, as in the case with milk yield, and whether heritabilities are used, as in the case with the beef traits, would depend on the trait in question.

2.4.2 MACE (multiple across-country analysis)

The International Bull Evaluation Service (INTERBULL) was established in 1983 by the International Dairy Federation, European Association for Animal Production and the International Committee for Recording the Productivity of Milk Animals. The main role was to standardise bull evaluations to allow comparison of animals across countries (Powell & Sieber, 1992). From 1985 till 1995, INTERBULL used conversion equations derived from the methods of Goddard (1985) and Wilmink *et al.* (1986) to compare breeding values of bulls between countries by regressing breeding values from the importing country over those of the exporting country (Schaeffer & Zhang, 1993; Weigel & Powell, 2000; Goddard & Beard, 2005). They later adopted MACE (Schaeffer *et al.*, 1993; Goddard & Beard, 2005) that is preferred to conversion equation as all sires that are progeny tested in any of the countries can be included in the analysis (Weigel & Lin, 1999). One of the main reasons MACE is preferred is due to the large amount of traits being recorded and evaluated today, with some countries evaluating more than 50 traits, in comparison to the past where only a few traits were evaluated (Jorjani & Fikse, 2004).

A linear model was initially proposed by Schaeffer (1985) to combine sire breeding evaluation information from two or more countries to produce a single international value that could be used to compare dairy cattle populations. This was achieved by combining data from daughters across countries and uses the male relationships to link the data across countries (Powell *et al.*, 1994). However, several limitations were noted in the model: 1) no genotype-environment interaction are allowed, 2) genetic correlations between performances in different countries are considered to be equal, 3) it is assumed that the genetic evaluation methods of each country remove as much bias information due to non-random mating and preferential treatment of daughters/offspring in foreign countries as possible and 4) that trait heritabilities are considered to be equal across all countries (Schaeffer & Zhang, 1993; Powell *et al.*, 1994). Schaeffer later proposed a multiple-trait linear model that overcame these limitations (Schaeffer & Zhang, 1993; Schaeffer, 1994). The model allows for production in each country to be considered as a different trait, but requires estimation of genetic correlations between the countries. The model was denoted as Multiple-trait Across Country Evaluation (MACE). MACE is essentially an extension of multiple-trait BLUP with a sire-maternal grandsire model.

MACE is preferred over the use of conversion equations as all available sires with progeny can be evaluated simultaneously and any additional data (from any relatives) can be included to increase the accuracy of the evaluation (Weigel & Powell, 2000). The model allows not only for sire and residual components to be different, but also allows a correlation of less than unity for the covariance between sire proofs in different countries, therefore allowing heritabilities to differ and accommodating genotype by environmental (GxE) interactions. Also, the scale in which performances (the daughter yield deviations) were measured do not need to be converted from one scale to another (Schaeffer & Zhang, 1993). Other advantages include the possibility of comparing two countries that share few or no common sires, and the fact that MACE allows reranking of sires even when GxE interactions are present. The only limitations are that preferential treatment of progeny in the importing country is still an issue, and that an accurate estimation of genetic parameters still requires a sufficient amount of genetic ties between the countries (Weigel & Powell, 2000). The use of phantom parent grouping, as initially proposed by Westell *et al.* (1988), allows unknown parents to be assigned to genetic groups based on their progeny's birth year and country of origin (Schaeffer & Zhang, 1993). These phantom parents are given an average value based on their genetic group, thus grouping them helps fill in the gaps where selection data is unavailable (Westell *et al.*, 1988).

Schaeffer (2001) has suggested an improvement to his initial MACE model. Although the initial model evaluated several traits, it combined the EBVs into a single average evaluation to be compared for each country, therefore suggesting that the model should rather be labelled as single trait, multiple country MACE (ST/MT MACE). The improvement is therefore to extend the procedure to accommodate multiple trait evaluations within a country, or multiple trait MACE (MTMACE).

Although MACE is theoretically superior, it is a complex process that may not be appropriate for small scale use. Conversion equations are much simpler to develop and have been shown by Weigel & Powell (2000) to not be significantly less accurate than MACE EBVs, although mainly as a result of a limitation of the data structure, as opposed to the method itself. After a study was done by Maignel *et al.* (2004) to create conversion equations between French and Canadian breeding values for Landrace and Large White boars, conversion equations were successfully used by the Canadian pig industry to accurately estimate the breeding values of hyperprolific boar semen imported from France (Chesnais & Sullivan, 2002). Conversion equations can therefore be a viable method to accurately convert foreign breeding values into local equivalents, allowing breeders to accurately predict the value of the imported semen in the South African pig industry. Being able to select semen from boars who are expected to perform superiorly to our local boars will ensure that maximum genetic progress can be maintained, closing the gap between local and global pig genetics.

Chapter 3: Materials and Methods

3.1 Introduction

Local breeding values for both local and foreign sires, as well as pedigree and performance data for local and foreign sired progeny, was provided by SA Stud Book for the evaluation of foreign sires in the South African pig industry. Only the stud breeders' data was used as neither TOPIGS nor PIC's data was available. The study was divided into two phases were the foreign data for Phase 1 was obtained from the National Swine Registry (NSR) and the Canadian Centre for Swine Improvement (CCSI) for USA and Canadian boars, respectively. As Phase 2 required only local performance data, data was provided by SA Stud Book with the required consent by the Ethics Committee of the University of Pretoria.

3.2 Phase 1: Relationship between foreign and local breeding values of imported semen

Phase one of this study focused on the comparison of foreign and local EBVs for imported Duroc, Landrace and Large White boars. Correlations between South African and foreign EBVs were calculated to assess the viability of producing a conversion equation that can be used with high accuracy. Two groups of boars were used; the first (training) group was used to estimate the correlations and produce conversion equations; it consisted of USA boars whose semen had been used in the South African pig industry and already had accurate South African breeding values. The second (testing) group was to be used to test the conversion equations and consisted of boars recently imported from Canada and whose progeny data was being collected.

3.2.1 Materials

The South African data for the study was provided by SA Stud Book (118 Henry Street, Westdene, Bloemfontein, South Africa) with consent from the South African Pork Producers Organisation (SAPPO). Four sets of data was received from SA Stud Book; namely

- a list of foreign AI boars (AI_Boars),
- litter data entries for the AI boars (Litter_Data),
- a data file with performance information for all AI boars and their families (All_Data),
- a pedigree file linking AI boars, dams, sires and progeny (Pedigree_Data)

The ‘AI_Boars’ dataset included registration number, birth date, breed, country of origin, registered name and number of litters. The AI boars were separated into a training and a testing group. The training group consisting of 74 boars from the USA that had already been used in the South African pig industry, that were born after 2000 and had accurate SA EBVs accompanied by a five generation pedigree. The test group consisted of 10 Canadian boars that were imported to South Africa in 2013 and subjected to progeny testing. The training group data was used to create the conversion equations while the test group was used to test the conversion equations. The majority of the boars in the training group were Large White, followed by Duroc and Landrace. Only four Chester White boars were available (Table 3.1).

Table 3.1 Number of AI boars per breed for the training group of USA boars and the test group of Canadian boars.

Group	Country of Origin	Breed	Number
Training group	United States of America	Chester White	4
		Duroc	23
		Large White	34
		Landrace	13
		Total	74
Testing group	Canada	Duroc	5
		Large White	2
		Landrace	3
		Total	10

The ‘Litter_Data’ included data for sire, dam, farrowing date, sow parity, breeder, number born alive, week three number alive, week three litter weight, week three date for 348 litters. The litter data was combined for all 84 AI boars.

The ‘All_Data’ data set included identification numbers (ID), birthdate, sire ID, dam ID, sex, registration name, breed, breeder and EBVs and accuracy for the five production traits for 1 983 animals. Included in the data set were the 74 USA and 10 Canadian AI boars, 1 495 of their combined offspring, 253 dams, 78 dams of the AI boars and 74 sires of the AI boars, of which six AI boars doubled as sires or grandsire. The traits to be evaluated included number born alive (NBA), 21 day litter weight (21DLWT), average daily gain during the test period (ADG), feed conversion rate (FCR), back fat thickness (BF) and Rand value index (RVI). Additional data was received from SA Stud Book which included data for number of farms using the foreign boar’s semen, number of services, number of farrowing and number of offspring tested per boar per farm, as well as breed averages for the six traits. The final dataset was received on 19 September 2014.

Canadian breeding values, repeatabilities, name and registration numbers for the 10 Canadian boars from the testing group were supplied by CCSI. Traits included number born, litter weight, piglets weaned, age adjusted to 100 kg, feed conversion rate and back fat thickness. The CCSI EBVs were accurate for 18 April 2014. The final South African EBVs for the Canadian boars in the testing group were included in the September 2014 SA Stud Book dataset update.

3.2.2 Method

3.2.2.1 Data editing

Initial data editing required the removal of boars from the training group that did not have breeding values in South Africa. The EBVs for Rand value index was not included in the estimations as it is not comparable to the other countries' indices. Boars were required to have at least one offspring on the SA Stud Book database to be eligible for inclusion in the analyses.

USA breeding values, in the form of EPDs (Estimated Progeny Difference), were required for the USA boars of the training group to allow for a comparison between South Africa and the USA. These were obtained from the NSR's website (NSR, 2013b). Data included registration number of the boar, birth date, registered name, owner, sire, maternal grand sire, number of offspring, number of herds and EPDs and national ranking for back fat thickness, days to 250 pounds, feed efficiency, number born alive and litter weight**.** The EPD report that was generated included only up to date EPDs and rankings for boars born between 1 January 2000 and 27 July 2013. Only 37 of the 74 USA boars had USA EPDs. The boars who had USA breeding values, and were consequently included in the present study, were 15 Duroc, 17 Large White and 5 Landrace boars. A final attempt was made to collect missing original USA EBVs for the training group boars. A list of 33 boars with missing EBVs and 17 with missing registration numbers was sent to Dr Harold Hodson at SGI. Information received by SGI included missing registration numbers and EPDs for 12 boars. The EPDs could however not be used as the boars were no longer in use and the values outdated. SA Stud Book (118 Henry Street, Westdene, Bloemfontein, South Africa) was consulted for original import documentation or old SGI catalogues for information on the USA AI boars; but out of the 41 boars available in the databank, only eight had EPDs that were again outdated values from old SGI catalogues and of no value to the study.

A list of the USA boars was also sent to the CCSI where their original registration numbers were used to locate the boars that had also been used in Canada. The registration numbers included those for the 37 boars from the NSR, as well as 18 boars from Swine Genetics International (SGI) who only had registration numbers. Available data from the CCSI included registered names, breed, birthdate, litters, progeny, EBVs and repeatabilities for number born, litter weight, age, feed conversion rate and back fat for 26 of the USA boars from the training group.

The final number of USA boars used in South Africa that had SA breeding values was 66. Of the 66 boars, only 37 had USA breeding values, in the form of EPDs, which were found on the NSR's website (NSR, 2013b). The boars that had USA breeding values included 15 Duroc, 17 Large White and five Landrace boars. The final number of USA boars with Canadian breeding values, supplied by the CCSI, consisted of 12 Duroc, 11 Large White and three Landrace boars. Common training group boars with breeding values in all three countries included six Duroc, eight Large White and two Landrace boars (Table 3.2).

Table 3.2 The final number of boars with breeding values for each country and per breed

Country	Total	Duroc	Landrace	Large White
South Africa [a]	66	22	12	32
Canada [b]	26	12	3	11
United States of America [c]	37	15	5	17
Common in SA, CA and USA	16	6	2	8

[a] SA EBVs supplied by SA Stud Book
[b] Canadian EBVs supplied by the Canadian Centre for Swine Improvement
[c] USA EPDs supplied by the National Swine Registry (NSR, 2013b)

The statistical software, SAS Enterprise Guide 4.3, which is part of SAS 9.3 (SAS, 2015), was used to perform the statistical analyses. All the South African data was imported into SAS Enterprise Guide, after which a set of queries and filters were used to produce a table with the list of AI boars and their EBV's, called 'SA_EBVs'. The USA EPD's were then imported and duplicated to create the table 'USA_EBVs'. Finally, the Canadian EBVs were imported to create the table 'CA_EBVs' (Figure 3.1).

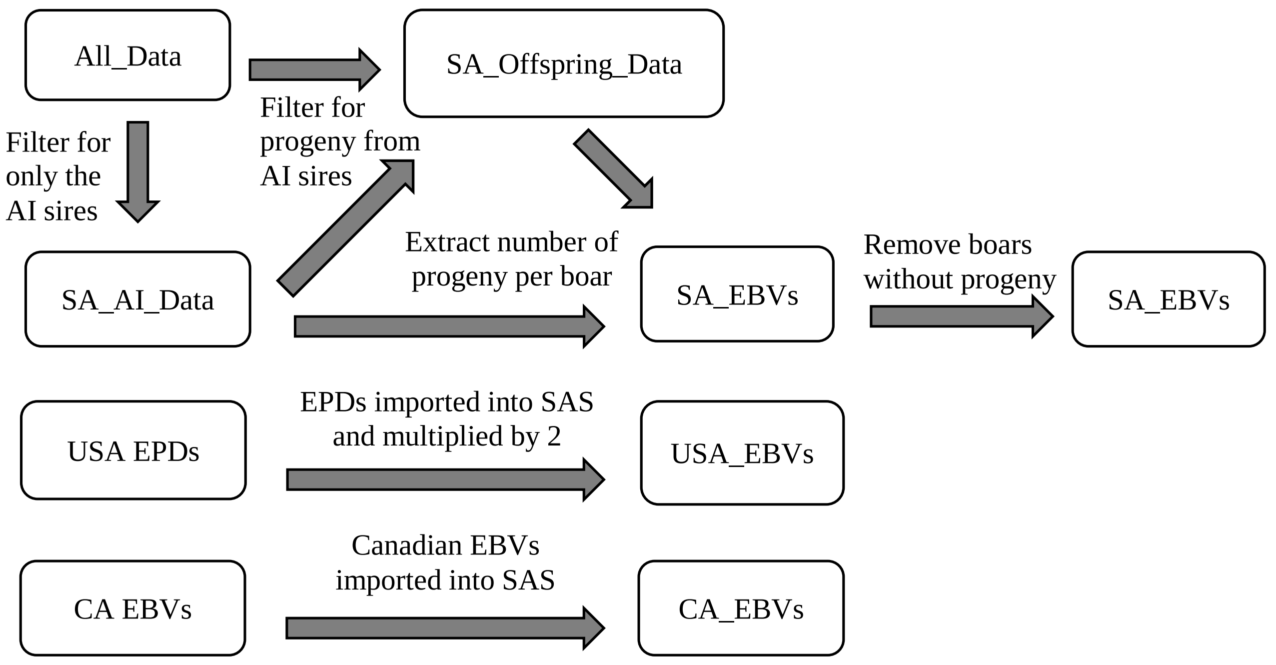

Figure 3.1 Importing and editing process to produce the final input files, labelled 'SA_EBVs', 'USA_EBVs' and 'CA_EBVs'.

3.2.2.2 Statistical analysis

The SAS Enterprise Guide (SAS, 2014) statistical analysis was used for the within- and between-countries analyses. A within-country analysis was done for each trait per breed for each of the three countries. A simple statistics summary was conducted on each of the three tables, 'SA_EBVs', 'USA_EBVs' and 'CAN_EBVs'. The statistics summary produced results for number, mean, standard deviation, standard error, variance (where degrees of freedom was used as the divisor for standard deviation and variance), minimum, maximum and coefficient of variations (where the confidence level was 95%). The traits that were analysed, grouped by breed, included number born/alive, 21 day litter weight/litter weaning weight, average daily gain/age to 100 kg/days to 250 pounds, feed conversion ratio/feed efficiency and back fat thickness (Table 3.2).

Table 3.3 Trait definitions and units for similar traits in South Africa, Canada and the United States

Trait	Abbreviation	County		
		South Africa	Canada	USA
Number born alive	NBA NB	Number of piglets born alive	Number of piglets born per litter	Number of piglets born alive, adjusted for sow parity
21 day litter weight (SA, USA) Litter weaning weight (CA)	21DLWT LWW	21 day litter weight (kg)	Litter weaning weight (kg)	Litter weight (lbs), adjusted to 21 days.
Average daily gain (SA)	ADG	Average daily gain (g) during the test period		
Age to 100 kg (CA) Days to 250 lbs (USA)	AGE DAYS		Number of days to reach 100 kg	Estimated days to reach 250 lbs
Feed conversion ratio (SA, CA), feed efficiency (USA)	FCR FE	Total kg feed / total kg gained during the test period	Feed efficiency, estimated kg of feed per kg of gain	Lbs feed/lbs gain calculated from Days and Pounds of lean. Adjusted for 250 lbs live weight. Calculated from back fat and loin eye area
Back fat thickness	BF	ultrasonically measured at the end of the test period (mm)	Loin fat depth at 100 kg, measured ultrasonically (mm)	Measured ultrasonically in inches, adjusted to 250 lbs live weight

[a] South African trait definitions obtained from SA Stud Book (Voordewind, 2014) and Visser *et al.* (2014)
[b] Canadian trait definitions obtained from the CCSI website (CCSI, 2012) and Robinson & Buhr (2005)
[c] USA trait definitions obtained from NSR glossary (NSR, 2014)

The 'SA_EBVs' table was merged with firstly 'USA_EBVs' and then with 'CAN_EBVs' to produce tables comparing SA with USA and Canadian data, while 'USA_EBVs' and 'CAN_EBVs' were joined to compare Canadian and USA breeding values. Boars available for comparison included 35 boars between SA and the USA, 21 between SA and Canada and 18 between Canada and the USA. The data was merged into tables, namely 'SA_USA', 'SA_CAN' and 'CAN_USA', with the only filter being for boars with at least 1 offspring in the SA Stud Book dataset.

Between-country summary statistics were computed for each of the combined EBV tables. Calculated statistics included mean, standard deviation, standard error, variance, and coefficient of variation. The statistics were calculated for each trait and analyses were grouped by breed. Pearson correlations analyses were performed for each of the three country comparisons, per breed for each trait. Pearson correlations were calculated for EBVs from training group boars with EBVs in both countries. A second high accuracy analysis only included boars with a South African EBV accuracy greater than or equal to 60% for the trait being analysed. The second approach was only applied to correlations between South Africa and the USA and South Africa and Canada. Linear regression analyses was also conducted on each of the three tables, for each of the traits and grouped per breed.

Table 3.4 The numbers of boars available for between-country correlation analyses.

Boars Included	Country Comparison	Breed	NBA/ NB	21DLWT/ LWW	ADG/ AGE/ DAYS	FCR/ FE	BF
At least one local offspring with breeding values	South Africa, USA	Duroc	15	15	15	15	15
		Large White	16	16	16	16	16
		Landrace	4	4	4	4	4
	South Africa, Canada	Duroc	13	13	13	13	13
		Large White	11	11	11	11	11
		Landrace	2	2	2	2	2
	Canada, USA	Duroc	8	8	8	8	8
		Large White	8	8	8	8	8
		Landrace	3	3	3	3	3
≥ 60% accuracy for trait EBV	South Africa, USA	Duroc	12	14	14	13	14
		Large White	15	13	14	16	16
		Landrace	4	3	4	4	3
	South Africa, Canada	Duroc	8	11	11	13	12
		Large White	11	10	9	11	11
		Landrace	2	2	2	2	1

USA = United States of America; NBA = number born alive (Canada); NB = number born; 21DLWT = 21 day litter weight in kg; LWW = litter weaning weight in kg (Canada); ADG = average daily gain during the test period in g (South Africa); DAYS = days to 250lbs (USA); AGE = age to 100kg (days) (Canada); FCR = feed conversion rate (kg feed/kg gained); FE = feed efficiency in lbs (USA); BF = back fat thickness measured in mm (SA and Canada) or inches (USA)

To allow for better comparisons, the breeding values in the three tables, SA_USA’, ‘SA_CAN’ and ‘CAN_USA’, were standardised to a mean of zero and a standard deviation of 1. The standardisation was performed individually for each trait and grouped by breed. Correlation analysis was performed on the standardised tables using Pearson correlations. The correlations were conducted between traits and grouped by breed. Concluding the analyses of Phase 1, EBVs for common boars were plotted per country comparison, per breed and per trait.

3.3 Phase 2: Comparison of progeny performances from foreign and local sires

Phase two of the study analysed the differences in on-farm performances of progeny sired by local boars, foreign boars and first generation local boars that were sired by foreign boars. In addition to the effect of sire country, the influence of farm, sex and year-season on on-farm progeny performances were also evaluated. On-farm progeny performances were compared on the same farm and for the same year-season to reduce environmental variation. Traits that were evaluated included on-farm performances for average daily gain (ADG), feed conversion rate (FCR) and back fat thickness (BF).

3.3.1 Materials

Data for the on-farm performances was supplied by SA Stud Book (118 Henry Street, Westdene, Bloemfontein, South Africa) with consent from the South African Pork Producers Organisation (SAPPO). Four sets of data was received; namely

- a list of all the boars used in South Africa since 2000 (Boars_Data)
- raw data including EBVs and on-farm performances for the resulting offspring (Raw_Data)
- all litter data (Litter_Data)
- a pedigree file linking all the animals to their respective sire and dam. (Pedigree_Data)

The 'Boars_Data' included original registration number (Animal), ID number, birthdate, sex, breed, country of origin, registration name and the total number of litters as of 14 December 2014. The dataset included 407 334 unique entries consisting of AI sires, their own sires and dams and their progeny. Several of the AI boars were also sires to other AI boars, while all the listed dams used were also progeny of the listed AI sires. In total, 3 152 AI boars were listed as well as 400 837 progeny who themselves had no litter data.

The 'Raw_Data' dataset included SA Stud Book ID number, farm code and abbreviation, birthdate, sire ID, dam ID, registered name, sex and breed for 183 495 total entries. In the same dataset, on-farm performances for age at end of test period, average daily gain during the test period, feed conversion ratio during the test period and back fat thickness at end of the test period was available for 87 158 progeny, as well as start and end dates and weights for the test period. EBV's and accuracies for number born alive, 21 day litter weight, average daily gain, feed conversion ratio, back fat thickness and rand value index, as well as the standard deviation for rand value index was available for 87 121 progeny.

The 'Litter_Data' dataset included sire ID, dam ID, farrowing date, farm code and abbreviation/name, number born alive, sow parity, week three date, week three piglet numbers and week three/21 day litter weight for 71 884 litters.

Finally, the 'Pedigree_Data' dataset included the animal ID number, sire ID, dam ID and the animal's birthdate for 415 151 entries (Table 3.5). Of the total list of progeny received in the 'Raw_Data' file, 82 572 had on-farm performance data and were from the sires in the 'Boars_Data' dataset. The progeny were from 3 152 sires and raised across 19 farms.

Table 3.5 Table showing list of data sets, their fields and number of records

Data set	Fields	Number of animals
Boars_Data	Animal, dbanimal, birthdate, sex, breed, country, name, no_litters	407 334 entries 400 837 AI progeny 3 152 AI boars 1 096 sires of AI boars 1 316 dams of AI boars
Raw_Data	dbanimal, partner, birthdate, dbsire, dbdam, name, sex, breed, extpartner, age, ADG, FCR, BF, beg_date, beg_weight, end_date, end_weight NBA, a_NBA, 21DLWT, a_21DLWT, ADG, a_ADG, FCR, a_FCR, BF, a_BF, RVI, a_RVI, sd_RVI	183 495 entries, 96 375 unique progeny 87 158 with on-farm performances 87 121 with EBVs 9 216 with no records
Litter_Data	dbsire, dbdam, birthdate, partner, birthdate, NBA, parity, w3dt, w3no, w3wt, extpartner	71 884 litters
Pedigree_Data	dbanimal, dbsire, dbdam, birthdate	415 151 pedigree records

Boars data: Animal = original registration number/code; dbanimal = SA Stud Book database number for animal; dbsire = SA Stud Book database number for sire; dbdam = SA Stud Book database number for dam; partner = SA Stud Book breeder number; extpartner = breeder name or code

On-farm performances: age = age at end of test period (days), ADG = average daily gain during test period (g), FCR = feed conversion rate measured as total feed consumed/total kg gained during the test period; BF = ultrasonic measure of back fat thickness at the end of the test period (mm); beg_date = date at the beginning of the test period; beg_weight = weight at the beginning of the test period (kg); end_date = date at the end of the test period; end_weight = weight at the end of the test period (kg)

Estimated breeding values: NBA = number born alive; a_NBA = EBV accuracy for NBA; 21DLWT = 21 day litter weight; a_21DLWT = EBV accuracy for 21DLWT; ADG = average daily gain during test period; a_ADG, EBV accuracy for ADG; FCR = feed conversion rate during test period; a_FCR = EBV accuracy for FCR; BF = back fat thickness at the end of the test period; a_fat = EBV accuracy for BF; RVI = weighted sum of EBVs expressed as a rand value index; a_RVI = EBV accuracy for RVI; sd_RVI = standard deviation for RVI

Litter data: PARITY = sow parity; W3DT = week 3 date; W3NO = number of piglets left in week 3, W3WT = 3 week litter weight

The boars included in the dataset were Chester White, Duroc, Landrace, L06 and L65 lines, Large White and Pietrain. The majority of boars were South African, followed by imports from

Canada and the United States of America (Table 3.6). The final datasets were received on, and is therefore accurate for 10 December 2014.

Table 3.6 The number of AI boars and litters, as well as number and sex of progeny per country per breed available for the study conducted in Phase 2

Sire's country of origin	Breed	Boars		Progeny		
		Number	Litters	Number	Female	Male
Canada	DUR	5	19	79	40	39
	L08	16	130	148	87	61
	L65	83	716	2172	1059	1113
	LAN	10	31	135	69	66
	LW	30	180	206	110	96
	PIT	15	75	144	72	72
	Total	159	1151	2884	1437	1447
United States of America	CW	4	10	17	5	12
	DUR	23	105	358	159	199
	LAN	13	45	194	91	103
	LW	33	129	554	240	314
	Total	73	289	1123	495	628
South Africa	CW	35	359	62	26	36
	DUR	569	7263	14865	7220	7645
	LAN	775	29450	15403	8479	6924
	LW	1531	32886	48009	23822	24187
	PIT	10	72	1	0	1
	Total	2920	70030	78340	39547	38793

CW = Chester White, DUR = Duroc, L08 and L65 = L08 and L65 lines respectively, LAN = Landrace, LW = Large White, PIT = Pietrain

3.3.2 Method

The data was processed and analysed using a combination of Microsoft Excel 2013 and the statistical software SAS Enterprise Guide 4.3. The data was first edited to link the progeny data to the different sires. Progeny were then grouped by year, birth month and season and filtered to only include progeny where both foreign and local boars of the same breed had offspring during the same time period on the same farm. Once all the data editing was completed, statistical analyses was conducted to derive trends between on-farm progeny performances from South African and foreign boars.

3.3.2.1 Data editing

Data entries were limited to only include Duroc, Landrace and Large White breeds as these were the only foreign breeds used in South Africa between 2000 and 2014. Data was only available for four Chester White boars used during the time period, resulting in insufficient number of records for the analyses. The boar data was further filtered to only include those who had at least one litter in South Africa for which the progeny performances were available. The number of boars were reduced from 3 179 boars used in South Africa, to 3 010 boars with at least one recorded litter (Table 3.7).

Table 3.7 Number of AI boars with litters in South Africa since 2000.

Breed	Country of origin			Breed Total
	Canada	United States	South Africa	
Duroc	5	23	575	603
Landrace	10	13	782	805
Large White	30	33	1 539	1 602
Country Total	45	69	2 896	3 010

Using Microsoft Excel, the South African boars were further split into SA boars and first generation SA boars were the local boars’ sire is of foreign origin. First generation boars were labelled F1-US or F1-CA, dependant on whether the sire was of US or Canadian origin, respectively. To accomplish this, a duplicate copy of ‘Boars_Data’ was created to allow a ‘=VLOOKUP()’ function to be performed in Microsoft Excel between the reduced list of boars and the complete ‘Boars_Data’ dataset which included all sires and offspring. An additional column was added to indicate the sire’s country of origin. Using a combination of an ‘=IF()’ and ‘=CONCATENATE()’ function, a second column was added to indicate whether the boar was an F1 progeny or not, and if so, whether it was a F1-CA or F1-US.

The filtered and edited ‘Boars_Data’, as well as the ‘Raw_Data’ files were imported into SAS Enterprise Guide 4.3. In SAS, progeny data was filtered to only progeny from the selected list of boars and only those with on-farm performance records. From 86 933 progeny with on-farm performance data, only 84 382 remained after breed and sire filtering. The progeny were split into three spreadsheets, namely Duroc (15 302 progeny), Landrace (15 732 progeny) and Large White (48 769 progeny), to allow for easier data editing.

In Microsoft Excel, the progeny were firstly assigned a country based on their sire's country. This was done using the '=VLOOKUP()" function to return the sire's country based on the value in the 'F1 Status' column. Once progeny were assigned a country, filters were created to allow comparing only progeny where both foreign (including progeny from first generation sires) and local progeny were born during the same time period and on the same farm. Progeny birthdates were used to group progeny into months, seasons (where 'Summer' was used for January and February and 'Summer_2' for December) and then in Summer/Winter (where 'Summer' was grouped with 'Summer_2' of the previous year). Birth year was extracted using the Microsoft Excel function '=YEAR()', and birth month using Microsoft Excel function '=MONTH()". Birthdates were then grouped by season; namely Summer (months 1 and 2), Autumn (months 3 – 5), Winter (months 6 – 8), Spring (months 9 – 11) and finally Summer_2 (month 12). The seasons were then reduced to Summer_1 (renamed from 'Summer'), Winter ('Autumn' and 'Winter' combined) and Summer (Spring and Summer_2 combined) using an extended '=IF()' function. Finally, the years and seasons were joined and "Summer_1" was grouped with "Summer" from the previous year, using an '=IF()' and two embedded "=CONCATENATE()" functions.

Once the time periods were completed, the filters were created using a "=COUNTIFS()" function to count the number of progeny from the same farm, born during the same period (month, season, or summer/winter) and from a specific country. The formula was repeated four times per progeny to account for each country. Thereafter, an extended "=IF()" was used to indicate either a '0' if the value for either local progeny or the sum of the foreign progeny was 0, or a '1' if there were both local and foreign sired progeny. Three filters were created to account for the differences in month, season, and summer/winter time period groupings.

Final data editing was done in SAS Enterprise Guide 4.3. The three spreadsheets, 'Duroc', 'Landrace' and 'Large White' were imported into SAS were the Summer/Winter filters were applied. Furthermore, farms with too few progeny for comparison were removed; this included two farms for Duroc and one farm for Large White. The list of farms with progeny data were extracted for each of the three breeds, resulting in seven farms with progeny across the three breeds. The farms names were renamed alphabetically from A to G. The farms were then plotted on a map indicate the biome that they are situated in (Rutherford *et al.*, 2006).

3.3.2.2 Statistical analyses

All the statistical analyses were conducted in SAS Enterprise Guide 4.3 (SAS, 2014). Analyses were performed separately on each of the three breeds; 'Duroc', 'Landrace' and 'Large White'. The initial analysis performed in SAS Enterprise Guide was a statistics summary which included the numbefr of observations and number of missing observations, as well as the mean, standard deviation, standard error, variance, minimum and maximum. Summary statistics were calculated separately for each sex and farm-country combination for each of the three traits, namely ADG (average daily gain during the test period), FCR (feed conversion ratio) and BF (back fat thickness).

Statistical analysis comparing the influence of known variables on the different traits for each breed was accomplished through the general linear method (GLM) procedure in SAS Enterprise Guide 4.3. A linear model analysis of variance (ANOVA) was conducted separately for each of the traits, for each breed. The linear model used for the analyses is described as follows:

$$y_{ij} = \mu + \beta_i + e_{ij}$$

Where y_{ij} = performance record j for fixed effect i

μ = grand population mean

β_i = i^{th} fixed effect contributing to variation,

e_{ij} = random error for performance record j for the i^{th} effect

The fixed effects to be tested across all models included country, farm, sex, year-season, sire, dam, dam parity and dam age. Additionally, start weight and end age were tested in the ADG models, BF and end age were tested in the FCR models, while ADG, end weight and end age were tested in the BF models. Difference between the least square means (LSMean) were determined by the Bonferroni test for Country, Farm and Sex. Differences were considered statistically significant at *P* <0.05, and highly significant at *P* <0.0001. In addition, a step-wise R^2 was recorded for each effect in the ANOVAs to give an indication of its contribution to the overall variation.

Chapter 4: Results

In order to assist South African pig breeders to maintain high levels of genetic progress, the value of foreign boars in the local pig industry needs to be evaluated. The study was divided into two phases; firstly, to assist breeders in selecting foreign boars that are superior to local sires, imported sires' USA and Canadian breeding values were correlated to their breeding values in South Africa. In cases where EBVs for similar traits were found to be significantly correlated ($P < 0.05$), conversion equations could be created to allow breeders to accurately predict the expected progeny performances from USA and Canadian sires under South African management and environmental conditions. The second phase of the study focused on the role that foreign sires play in the South African pig industry by comparing foreign-sired progeny performances to the performances of the local-sired progeny raised on the same farm during the same time period.

4.1 Phase 1: Relationship between foreign and local breeding values of imported semen

Initial data editing required the removal of boars from the training group that did not have breeding values or litters in South Africa; four Chester Whites boars, one Landrace, one Duroc and two Large Whites were therefore excluded. During the data editing, several of the boars from the training group were found to be sires or grandsires of other boars in the same group (Table 4.1).

Table 4.1 Foreign AI boars from the testing group who are also sires or grandsires of other AI boars also in the testing group.

Breed	AI Boar	Sire of	Grandsire of
Duroc	RWG1 Totally Juiced 134-1	RWG3 Totally Unbelievable 130-4	
	WFD3 Bold Stroke 107-3	STN4 Hemi 32-2	
		RGFD5 Bold Adventure 6-1	
Landrace	CRPO Samstorp 39-3		ZMAC5 Samstorp 67-9
Large White	3 Mac A Roo 1365 0-0		CR6 Mac A Roo II 141-1
	JGR2 Supreme Justice 397-8		JGR6 True Masterpiece 7-3

The final number of boars available for each comparison is summarised in Table 4.2. The SA-USA comparison had the largest number of boars available, 35, while the CA-USA comparison had the least, 16. The number of Duroc and Large White boars were similar for each of the comparisons, while few Landrace boars were available for the evaluation. The Landrace boars were completely excluded from the correlations between SA and CA as only two boars with EBVs were available.

Table 4.2 Number of common USA AI boars available for each country comparison, per breed

Country Comparison	N	Number of boars per comparison		
		Duroc	Large White	Landrace
SA, USA	35	15	16	4
SA, CA	21	10	9	2
CA, USA	18	7	8	3
SA, CA, USA	16	6	8	2

N = number; SA = South Africa, CA = Canada, USA = United States of America

Results for the within- and between-country data analyses are attached in Addendum A. The within-country analysis of the SA EBVs indicated that the EBVs in the dataset were poorer compared to the South African breed averages for each of the evaluated traits (Table 4.3 and Table A.1), with the exception of Large White ADG, Landrace ADG and Landrace BF. The poorer EBVs indicated that the dataset was not an accurate representation of the pig population in the South African breeding industry. The descriptive statistics for SA EBVs found that Landrace sires had the largest EBV variation for 21DLWT, FCR and BF, Large White sires had the largest ADG variation and Duroc sires had the largest NBA variation. Analyses of the USA EBVs (Table A.2) found that the Large White sire EBVs had the largest amount of variation for 21DLWT, DAYS, FCR and BF, while Landrace EBVs showed the most variation for NBA. The descriptive statistics for the Canadian EBVs (Table A.3) found that Duroc sires had the most ADG and FCR variation, Large White the most LWT and BF variation, while Landrace had the most NBA variation.

Table 4.3 South African EBV breed averages for the three most popular breeds for the Rand value index and five economically important traits

Breed	NBA	21DLWT	ADG	FCR	BF	RVI
Duroc	0.022	-0.266	34.04	-0.082	-0.65	21.39
Landrace	0.460	2.132	6.91	0.016	-0.26	116.42
Large White	0.428	1.496	6.21	0.006	0.15	89.26

NBA = number born alive; 21DLWT = 21 day litter weight (kg); ADG = average daily gain (g); FCR = feed conversion rate (kg feed/kg gained), BF = ultrasonically measured back fat thickness (mm); RVI = Rand value index

For the between-country analyses, similarities were seen between average EBVs of similar traits, where average breed EBVs were similarly favourable or unfavourable for selection of the trait. The descriptive statistics between SA and USA EBVs (Table A.4) indicated similar trends between Duroc and Landrace EBVs. For the analyses between SA and CA EBVs (Table A.5), five trait pairs were found to have similar EBVs, namely Duroc 21DLWT, Large White FCR, Landrace NBA, Landrace ADG/AGE and Landrace BF. The descriptive statistics between CA and USA EBVs (Table A.6) also found five trait pairs with similar EBVs, namely Duroc NBA, Landrace NBA, Landrace

FCR/FE, Large White NBA and Large White AGE/DAYS. The between-country comparisons found differences in standard deviations between the trait pairs within a breed for all three country comparisons. The only exceptions, where standard deviations were similar, were SA-USA Duroc 21DLWT (σ = 1.982 and σ = 1.976, respectively), SA-CA Duroc FCR (σ = 0.074 and σ = 1.976, respectively) and CA-USA Landrace FCR/FE (σ = 0.015 and σ = 0.020, respectively).

Analyses between SA and USA EBVs revealed only three traits with significant correlations (*P* <0.05) (Table 4.4). Duroc FCR/FE was strongly correlated (*P* <0.05) in both the full and high accuracy analyses, accompanied by a moderate adjusted r^2 of 0.336. Duroc ADG/DAYS was moderately correlated (*P* <0.05) in the high accuracy analysis, accompanied by a weak adjusted r^2. For Landrace, ADG/DAYS was significant (*P* <0.05) in both Pearson correlations, accompanied by a strong adjusted r^2. However, the high r^2 was misleading as there were only four records available.

Table 4.4 Summary of the between-country correlation analysis of South African and USA EBVs of the AI boars from the training group

Breed	Trait	N	Pearson Correlation (all data)			Pearson Correlation (≥ 60% accuracy for SA EBVs)				Linear Regression	
			r	p-value	COV	N	r	p-value	COV	r^2	Adj r^2
Duroc	NBA	15	0.255	0.360	0.054	12	0.265	0.404	0.061	0.064	-0.007
	21DLWT	15	0.162	0.565	0.596	14	0.147	0.617	0.610	0.023	-0.052
	ADG/DAYS *	15	-0.463	0.082	-39.674	14	-0.534	0.040	-39.674	0.285	0.230
	FCR/FE *	15	0.619	0.014	0.001	13	0.645	0.017	0.001	0.384	0.336
	BF	15	-0.063	0.824	-0.001	14	-0.086	0.771	-0.001	0.004	-0.073
Large White	NBA	16	0.473	0.064	0.130	14	0.501	0.068	0.143	0.224	0.168
	21DLWT	16	-0.365	0.164	8.305	12	0.512	0.089	10.472	0.211	0.155
	ADG/DAYS *	16	0.027	0.921	3.302	15	0.052	0.853	7.610	0.001	-0.071
	FCR/FE *	16	-0.398	0.127	-0.001	16	-0.398	0.127	-0.001	0.159	0.098
	BF	16	0.434	0.093	0.010	15	0.433	0.107	0.011	0.189	0.131
Landrace	NBA	4	-0.872	0.128	-0.195	4	-0.872	0.128	-0.195	0.761	0.641
	21DLWT	4	-0.578	0.422	11.109	3	-0.940	0.222	-2.072	0.551	0.326
	ADG/DAYS *	4	-0.973	0.027	-34.705	4	-0.973	0.027	-34.705	0.947	0.920
	FCR/FE *	4	-0.690	0.310	-0.002	4	-0.690	0.310	-0.002	0.476	0.214
	BF	4	0.317	0.683	0.006	3	-0.091	0.942	-0.002	0.100	-0.349

* South African and USA traits, respectively

N = number of observations; r = Pearson correlation coefficient; COV = covariance; r^2 = coefficient of determination; Adj r^2 = adjusted coefficient of determination; NBA = number born alive; 21DLWT = 21 day litter weight; ADG = average daily gain (g); DAYS = days to 250 lbs; FCR = feed conversion rate (kg); FE = feed efficiency (lbs); BF = back fat thickness

Analyses between SA and CA EBVs are shown in Table 4.5. Only Large White BF was found to be strongly significant (*P* <0.05), under both the normal and high accuracy analyses, with a correlation of 0.710. In the linear analysis, Large White BF had a moderate adjusted r^2 of 0.442. None of the Landrace traits could be analysed as there were only two boars available with EBVs in both SA and CA.

Table 4.5 Summary of the between-country correlation analysis of South African and Canadian EBVs of the AI boars from the training group

Breed	Trait	N	Pearson Correlation (all data)			Pearson Correlation ($\geq$ 60% accuracy for SA EBVs)				Linear Regression	
			r	p-value	COV	N	r	p-value	COV	r^2	Adj r^2
Duroc	NBA/NB [*]	10	0.194	0.592	0.028	5	0.381	0.527	0.071	0.038	-0.083
	21DLWT/LWW [*]	10	-0.081	0.823	-0.140	9	-0.238	0.537	-0.396	0.007	-0.118
	ADG/AGE [*]	10	-0.276	0.440	-42.107	10	-0.276	0.440	-42.107	0.076	-0.039
	FCR	10	0.321	0.366	0.002	10	0.321	0.366	0.002	0.103	-0.009
	BF	10	0.229	0.524	0.122	9	0.201	0.604	0.115	0.053	-0.066
Large White	NBA/NB [*]	10	-0.405	0.245	-0.157	10	-0.405	0.245	-0.157	0.164	0.060
	21DLWT/LWW [*]	10	0.155	0.670	2.145	10	0.155	0.670	2.145	0.024	-0.098
	ADG/AGE [*]	10	-0.582	0.077	-111.432	9	-0.577	0.104	-113.258	0.339	0.257
	FCR	10	-0.563	0.090	-0.002	10	-0.563	0.090	-0.002	0.318	0.232
	BF	10	0.710	0.022	0.552	9	0.732	0.025	0.571	0.504	0.442

[*] South African and Canadian traits, respectively

N = number of observations; r = Pearson correlation coefficient; COV = covariance; r^2 = coefficient of determination; Adj r^2 = adjusted coefficient of determination; NBA = number born alive; NB = number born; 21DLWT = 21 day litter weight (kg); LWW = litter weaning weight (kg); ADG = average daily gain (g); AGE = age at 100 kg (days); FCR = feed conversion rate; BF = back fat thickness (mm)

The analyses between CA and USA EBVs (Table 4.6) also only showed one significant Pearson correlation (*P* <0.05). Large White LWW/21DLWT had a strong Pearson correlation (*P* <0.05), accompanied by a strong adjusted r^2 of 0.635. None of the Duroc or Landrace traits were shown to be significantly correlated.

Table 4.6 Summary of the between-country correlation analysis of Canadian and USA EBVs of the AI boars from the training group

Breed	Trait	N	Pearson Correlation			Linear Regression	
			r	p-value	COV	r^2	Adj r^2
Duroc	NB/NBA *	7	0.133	0.777	0.010	0.020	-0.176
	LWW/21DLWT *	7	-0.215	0.643	-0.652	0.003	-0.197
	AGE/DAYS *	7	0.097	0.836	3.268	0.010	-0.188
	FCR *	7	0.333	0.466	0.002	0.107	-0.072
	BF	7	0.389	0.388	0.010	0.151	-0.019
Large White	NBA/NB *	8	-0.368	0.370	-0.125	0.135	-0.009
	LWW/21DLWT *	8	0.829	0.011	22.694	0.687	0.635
	AGE/DAYS *	8	-0.058	0.892	-1.707	0.003	-0.163
	FCR/FE *	8	0.223	0.596	0.001	0.041	-0.119
	BF	8	0.463	0.249	0.056	0.214	0.083
Landrace	NB/NBA *	3	0.801	0.409	0.684	0.641	0.283
	LWW/21DLWT *	3	-0.452	0.702	-0.637	0.204	-0.592
	AGE/DAYS *	3	-0.554	0.626	-3.712	0.307	-0.386
	FCR/FE *	3	-0.655	0.546	0.000	0.645	0.290
	BF	3	-0.231	0.851	-0.012	0.054	-0.893

* Canadian and USA trait, respectively

N = number of observations; r =correlation coefficient; COV = covariance; r^2 = coefficient of determination; Adj r^2 = adjusted coefficient of determination; NB = number born; NBA = number born alive; LWW = litter weaning weight (kg); 21DLWT = 21 day litter weight (lbs); AGE = age to 100kg; DAYS = days to 250 lbs; FCR = feed conversion ratio (kg); FE = feed efficiency (lbs); BF = back fat thickness

Results for the Pearson correlation analyses of the standardised data is summarised in Table 4.7. Pearson correlations for standardised EBVs between South Africa and the USA showed only one change where Duroc ADG/DAYS was found to be moderately correlated ($P < 0.05$). No changes in significance were observed between the normal and standardised EBV correlations between South Africa and Canada, or for the standardised EBV correlations between Canada and the USA.

Table 4.7 Summary of the between-country Pearson correlations for the standardised EBVs

Breed	Trait	SA vs USA				SA vs CA				CA vs USA			
		N	r	p-value	COV	N	R	p-value	COV	N	r	p-value	COV
Duroc	NBA/NB	14	0.255	0.360	0.255	10	0.194	0.592	0.108	7	0.133	0.777	0.141
	D21LWT/LWW	14	0.152	0.588	0.152	10	-0.081	0.823	-0.081	7	-0.215	0.643	0.067
	ADG/AGE/DAYS	14	-0.534	0.040	-0.534	10	-0.276	0.440	-0.003	7	0.097	0.836	0.099
	FCR/FE	14	0.619	0.014	0.619	10	0.321	0.366	0.293	7	0.333	0.466	0.326
	BF	14	-0.063	0.824	-0.063	10	0.229	0.524	0.186	7	0.389	0.388	0.388
Large White	NBA	16	0.473	0.064	0.473	9	-0.405	0.245	-0.405	8	-0.368	0.370	-0.368
	D21LWT	16	0.460	0.073	0.460	9	0.155	0.670	0.155	8	0.829	0.011	0.477
	ADG/AGE/DAYS	16	0.023	0.932	0.023	9	-0.582	0.077	-0.582	8	-0.058	0.892	-0.058
	FCR	16	-0.398	0.127	-0.398	9	-0.563	0.090	-0.563	8	0.223	0.596	0.202
	BF	16	0.434	0.093	0.434	9	0.710	0.022	0.710	8	0.463	0.249	0.463
Landrace	NBA/NB	4	-0.872	0.128	-0.872					3	0.801	0.409	0.801
	D21LWT/LWT	4	0.742	0.258	0.742					3	-0.452	0.702	-0.529
	ADG/AGE/DAYS	4	-0.973	0.027	-0.973					3	-0.554	0.626	-0.554
	FCR/FE	4	-0.690	0.310	-0.690					3	-0.655	0.546	-0.803
	BF	4	0.317	0.683	0.317					3	-0.231	0.851	-0.231

SA = South Africa; CA = Canada; USA = United States of America; N = number of observations; r = correlation coefficient; COV = covariance; NBA = number born alive (SA and USA); NB = number born (CA); LWW = litter weaning weight (kg) (CA); 21DLWT = 21 day litter weight (kg in SA, lbs in USA); ADG = average daily gain (g) (SA) AGE = age to 100kg (CA); DAYS = days to 250 lbs (USA); FCR = feed conversion ratio (kg) (SA and CA); FE = feed efficiency (lbs) (USA); BF = back fat thickness (mm in SA and CA, inch in USA)

4.2 Phase 2: Comparison of progeny performances from foreign and local sires

On-farm progeny performances, collected before, during and after the test period, were used to evaluate differences between local and foreign sired progeny. Performance records for 25 491 progeny, from three breeds raised on seven different farms across South Africa, were used in the final evaluation. The location of the seven farms, labelled A to G, are displayed in Figure 4.1. The farms were located in the Savanna, Grassland and Fynbos biomes. Each biome can be divided into bioregions that have similar climates. Farm C, E and G were located in the Central Bushveld, a moderate summer rainfall area with high minimum temperatures. Farm A and F were located in high summer rainfall areas, the Messic Highveld Grassland and Sub-Escarpment Grassland bioregions, respectively, where the former has lower temperatures and a higher frost incidence. Farms B and D were situated in the Fynbos region with moderate winter rainfall; located in the West Coast Renosterveld and Southwest Fynbos bioregions, respectively. (Rutherford *et al.*, 2006).

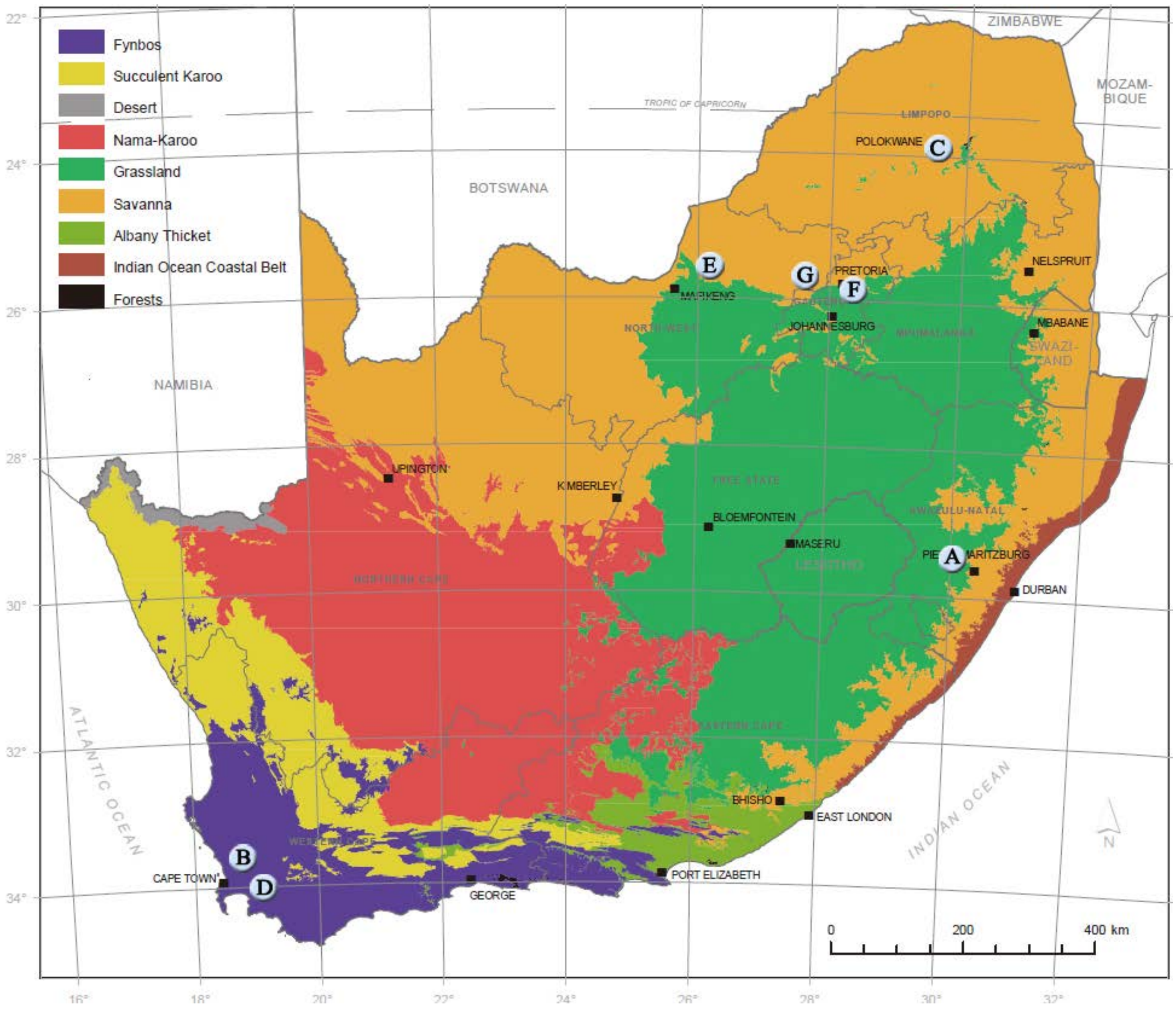

Figure 4.1 Location of each of the farms, labelled A to G (adapted from Rutherford *et al.* (2006)).

The descriptive statistics for on-farm performance of Duroc, Landrace and Large White progeny can be found in Addendum B. Two farms had progeny records from all three breeds, with farm C contributing the largest number of progeny records (Table 4.8). Two farms, farm B and E, only had records for one breed, while F and G had on-farm performance records for both Landrace and Large White progeny.

Table 4.8 Summary of the total number of progeny records available per farm, per breed

Farm	Number of progeny			Farm Total
	Duroc	Landrace	Large White	
A	1 005	634	1 918	3 557
B			315	315
C	7 392	2 161	3 142	12 695
D	492	498	280	1 270
E		137		137
F		5 784	52	5 836
G		82	1 599	1 681

Across all three breeds FCR was not recorded as frequently as ADG and BF. No FCR records were available for any Canadian-sired progeny. Duroc progeny had 8 810 ADG and BF records available, while only 955 records were available for FCR (Table B.1). F1-US progeny had the lowest individual on-farm performance for ADG (638.1 g/day), the lowest average on-farm performance for ADG (860.71 g/day) and BF (9.49 mm), and the highest average on-farm performance for FCR (2.38 kg feed/kg gain). South African sired progeny had the highest individual on-farm performance for ADG (1 902.86 g/day) and BF (27mm), as well as the lowest and highest individual FCR performances (1.59 kg feed/kg gain and 3.73 kg feed/kg gain). The SA progeny also had the highest average on-farm BF performance (10.46 mm). The USA-sired progeny had the highest average on-farm ADG record (1 058.38 g/day), as well as the lowest average on-farm performance for FCR (1.90 kg feed/kg gain).

Landrace progeny had 7 306 ADG and BF records and 1 289 FCR records available (Table B.2). South African sired progeny had both the lowest and highest individual performance for BF (6 mm and 24mm) and FCR (1.54 kg feed/kg gained and 3.37 kg feed/kg gained), as well as the highest individual ADG (1 742.86 g/day). USA-sired progeny had the lowest and highest average on-farm ADG (830.98 g/day and 1051.37 g/day) and BF performance (8.5mm and 11.95mm), as well as the highest average on-farm FCR performance (2.37 kg feed/kg gain). The lowest average on-farm FCR performance was observed for F1-US sired progeny (1.95 kg feed/kg gain).

The largest number of on-farm performance records were available for Large White progeny, with 11 140 recorded performances for ADG and BF, and 847 FCR performances (Table B.3). South African sired progeny had the highest individual on-farm performances for ADG (1 914.29 g/day), BF (28 mm) and FCR (3.25 kg feed/kg gain), the lowest individual FCR performance (1.61 kg feed/kg gain), and the highest average on-farm performance for FCR (2.27kg feed/kg gain) and BF (10.79 m). USA sired progeny had the lowest and highest average on-farm performances for FCR (2.07 kg feed/kg gain on farm A and 2.42 kg feed/kg gain), the lowest average on-farm BF performance (8.19 mm) and the highest average on-farm performance for ADG (1 084.05 g/day). Canadian sired progeny had the lowest average on-farm ADG performance (808.67 g/day).

The significant variables (*P* <0.05) for each of the ANOVAs are shown in Table 4.9. While the influence of sire, dam, dam parity and dam age were tested, none were found to be significant for any of the models. Across all nine ANOVAs, farm, country, sex and the year-season interaction were found to be significant (*P* <0.05). In all the ADG models, additional significant effects included ‘end age’ and ‘end age^2’, while starting weight was significant in the Duroc and Large White ADG models. Across all three FCR models, the effect of BF was significant. In the BF models, ADG and ‘end weight’ were significant across all breeds, while ‘end age’ and ‘end age^2’ were only significant in the Large White analyses.

Table 4.9 Summary of the statistically significant (*P* <0.05) variables and model R-square for each of the nine ANOVAs

Trait	Breed	Significant effects	R-sq
ADG	Duroc	country, farm, sex, year-season, start weight, end age, end age^2	0.5880
	Landrace	country, farm, sex, year-season, end age, end age ^{2}	0.6113
	Large White	country, farm, sex, year-season, start weight, end age, end age ^{2}	0.5308
FCR	Duroc	country, farm, sex, year-season, BF, end age	0.5347
	Landrace	country, farm, sex, year-season, BF, end age, end age^2	0.5512
	Large White	country, farm, sex, year-season, BF, end age	0.5508
BF	Duroc	country, farm, sex, year-season, ADG, end weight	0.3601
	Landrace	country, farm, sex, year-season, ADG, end weight,	0.1713
	Large White	country, farm, sex, year-season, ADG, end weight, end age, end age ^{2}	0.2836

ADG = average daily gain (g); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); R-sq = coefficient of determination

Results for the stepwise R-square contributions was summarised in Table 4.10 for the four main significant effects; country, farm, sex and year-season. Country contributed the lowest average percentage of variation (0.78%) and the least amount of variation in all the models except Landrace

BF, where sex was the lowest contributors. Stepwise R-square for country never exceeded 2.15%, with its lowest contribution in the Duroc FCR model (0.20%). The farm effect contributed a moderate amount of the variation to the on-farm performances, ranging from 1.92% to 18.96%, with an average contribution of 8.08%. The largest contribution of farm was in the Duroc FCR model (18.96%). Sex and year-season were both large contributors of variation, contributing an average of 12.36% and 9.84%, respectively. Sex contributed the highest overall amount of variation in the FCR models for Landrace and Large White, while year-season had the highest contribution in the BF models for Duroc and Landrace. Sex and farm jointly contributed the most variation in the Large White BF model. End age was the only other significant effect with large variation, with the largest contribution across all ADG models, with 30.34%, 28.14% and 24.14% of the variation in the Duroc, Landrace and Large White ADG models, respectively.

Table 4.10 Summary of stepwise R-sq contributions for the four main significant (*P* <0.05) effects in the different ANOVA models

Trait	Breed	Country	Farm	Sex	Year-Season
ADG	Duroc	0.22%	1.92% *	13.80% *	9.99% *
	Landrace	0.13% *	8.69% *	18.07% *	4.14% *
	Large White	0.12% *	8.39% *	7.96%	10.32% *
FCR	Duroc	0.20%	18.96% *	15.3%7 *	6.18% *
	Landrace	2.15%	9.39% *	21.35% *	9.35% *
	Large White	1.27%	10.82% *	19.14% *	12.11% *
BF	Duroc	0.91%	0.82%	5.81% *	24.88% *
	Landrace	1.79% *	5.34% *	1.30% *	6.07% *
	Large White	0.25% *	8.42% *	8.48% *	5.52% *

* indicates the effect was highly significant (P < 0.0001)

ANOVA results for Duroc progeny performances are summarised in Table 4.11. Country differences were significant (*P* <0.05) for ADG, FCR and BF. Canadian sired progeny performed statistically no different to the other progeny for both ADG and BF. The ADG and FCR performances of US sired progeny were significantly superior (*P* < 0.05) to both F1-US and SA sired progeny performances, while SA sired progeny's BF performances were significantly higher (*P* <0.05) to both F1 US and US sired progeny's performances. Farm differences were highly significant (*P* <0.0001) for ADG and FCR and significant for BF (*P* <0.05). Farm A had the highest ADG (*P* <0.0001), farm C the lowest FCR (*P* <0.05), while farm A and D had the lowest BF. Sex differences in Duroc performances were highly significant (*P* <0.0001) with males outperforming females in all three models.

Table 4.11 ANOVA summaries for Duroc progeny performances for ADG, FCR and BF

Effect		N	ADG (g)		FCR (kg)		BF (mm)	
			LSMean	N	LSMean	N	LSMean	N
Country	CA	79	944.032 $^{a, b}$				10.001 $^{a, b}$	
	F1 US	1 895	946.474 ^{a}		2.042 ^{b}		9.779 ^{a}	
	USA	339	964.299 ^{b}		1.903 ^{a}		9.655 ^{a}	
	SA	6 576	949.565 ^{a}		2.048 ^{b}		9.900 ^{b}	
Farm	A	1 005	994.835 ^{c}	8 875	2.010 ^{b}	955	9.713 ^{a}	8 875
	C	7 392	922.458 ^{a}		1.605 ^{a}		9.902 ^{b}	
	D	492	935.985 ^{b}		2.378 ^{c}		9.886 $^{a, b}$	
Sex	F	4 266	929.905 ^{a}		2.082 ^{b}		10.391 ^{b}	
	M	4 623	972.280 ^{b}		1.914 ^{a}		9.277 ^{a}	

$^{a, b, c,}$ LSMeans with different superscripts in the same column for the same effect are significantly different (*P* <0.05)
N = number of records, ADG = average daily gain (g), FCR = feed conversion ratio (kg feed/kg gain), BF = back fat thickness (mm), CA = progeny sired by Canadian boars, F1 US = SA sired progeny with a USA grandsire; USA = progeny sired by a USA boar, SA = progeny sired by a South African boar; Sex F = female; Sex M = Male

Landrace ANOVA results are summarised in Table 4.12. Country differences were highly significant (*P* <0.0001) for ADG and BF, and significant (*P* <0.05) for FCR. Canadian progeny performed significantly worse (*P* <0.05) in ADG, although statistically no different in the BF model. Although highest, the South African ADG performance were not significantly higher than the performances of both F1-US and USA sired progeny. The F1-US and USA sired progeny had the lowest FCR performances (*P* <0.05), while no significant differences were found between the lower USA and high SA BF performances. Farm differences were highly significant (*P* <0.0001) for all three models. Farm F had the highest ADG performance, although not significant higher than farm A. Farm A had the lowest FCR and BF performance, although the BF performances were not significantly lower than those of farm B and F. The influence of sex on Landrace performances was highly significant (*P* <0.0001) in all three models, where males outperformed the females.

Table 4.12 ANOVA summary for Landrace progeny performances for ADG, FCR and BF

Effect		N	ADG (g)		FCR (kg)		BF (mm)	
			LSMean	N	LSMean	N	LSMean	N
Country	CA	119	856.705 ^{a}	7 299		1 289	10.498 $^{a, b}$	7 306
	F1 US	1 304	898.096 ^{b}		2.287 $^{a, b}$		10.383 ^{a}	
	USA	193	888.359 ^{b}		2.196 ^{a}		10.312 $^{a, b}$	
	SA	5 690	901.702 ^{b}		2.314 ^{b}		10.667 ^{b}	
Farm	A	1 918	909.876 ^{c}		2.124 ^{a}		10.125 ^{a}	
	B	315	887.869 ^{b}		2.257 ^{b}		9.907 ^{a}	
	C	3 142	857.825 ^{a}				11.519 ^{c}	
	D	280	866.469 ^{a}		2.446 ^{c}		10.551 ^{b}	
	F	52	914.150 ^{c}				10.111 $^{a, b}$	
	G	1 599	882.105 ^{b}		2.234 ^{b}		10.576 ^{b}	
Sex	F	3 987	864.659 ^{a}		2.379 ^{b}		10.820 ^{b}	
	M	3 319	908.325 ^{b}		2.152 ^{a}		10.109 ^{a}	

$^{a, b, c, d,}$ LSMeans with different superscripts in the same column for the same effect are significantly different (*P* <0.05)
N = number of records; ADG = average daily gain (g); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); CA = progeny sired by a Canadian boar; F1 US = SA sired progeny with a USA grandsire; USA = progeny sired by a USA boar; SA = progeny sired by a South African boar; Sex F = female; Sex M = Male

The Large White ANOVA results are summarised in Table 4.13. The influence of sire country was highly significant (*P* <0.0001) for ADG and BF, and significant (*P* <0.05) for FCR. Although no differences were observed between SA and USA progeny performances for ADG, they were significantly higher (*P* <0.0001) than the CA progeny performances. The USA sired progeny performance were superior in the FCR (*P* <0.05) and BF (*P* <0.0001) models. Farm differences were highly significant (*P* <0.0001) in all three models. The ADG performances of Farm E and A were the highest (*P* <0.0001), farm E and G had the lower FCR (*P* <0.0001), while farm E and G had the lowest BF (*P* <0.05) performances. Sex differences were highly significant (*P* <0.0001) for all traits as male progeny performed superior to female progeny.

Table 4.13 ANOVA summary for Large White progeny performances for ADG, FCR and BF

Effect		N	ADG (g)		FCR (kg)		BF (mm)	
			LSMean	N	LSMean	N	LSMean	N
Country	CA	91	833.918 ^{a}	11 139		847	10.757 ^{c}	11 139
	USA	521	899.299 ^{b}		2.138 ^{a}		9.460 ^{a}	
	SA	10 528	907.841 ^{b}		2.194 ^{b}		10.174 ^{b}	
Farm	A	634	906.060 ^{d}		2.144 ^{b}		10.547 ^{b}	
	C	2 161	853.588 ^{a}				11.090 ^{c}	
	D	498	868.207 $^{b, c}$		2.398 ^{c}		10.197 ^{b}	
	E	137	910.174 ^{d}		1.953 ^{a}		9.468 ^{a}	
	F	5 784	879.626 ^{c}		2.263 $^{b, c}$		8.982 ^{a}	
	G	1 926	864.462 ^{b}		2.070 $^{a, b}$		10.498 ^{b}	
Sex	F	5 229	878.637 ^{a}		2.271 ^{b}		10.698 ^{b}	
	M	5 911	882.069 ^{b}		2.060 ^{a}		9.562 ^{a}	

$^{a, b, c, d}$, LSMeans with different superscripts in the same column for the same effect are significantly different (*P* <0.05)
N = number of records; ADG = average daily gain (g); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); CA = progeny sired by a Canadian boar; USA = progeny sired by a USA boar; SA = progeny sired by a South African boar; Sex F = female; Sex M = male

Chapter 5: Discussion

The South African pig industry is a relatively small sector compared to the other livestock sectors in South Africa (Department of Agriculture Forestry and Fisheries, 2014a; Visser, Kirsten *et al.*, 2014; FAO, 2015). To remain relevant, the South African pig breeders need to improve the genetic progress in the local herds to close the gap between the South African genetics and that of the global market. The tool central to the genetic advancement of livestock, especially in dairy cattle, and more recently in pigs, was the use of artificial insemination. The role of artificial insemination has grown tremendously since the early development of swine AI in the early 1900s (Foote, 2002; Knox, 2015). In South Africa, semen from proven boars is regularly imported from the USA and Canada to assist local breeders to improve the genetic potential of their herds. Foreign sires are largely selected based on their breeding values in their country of origin, however, these are seldom an accurate prediction of how the sire will perform under South African systems (Wilmink *et al.*, 1986; Goddard & Beard, 1994; Powell & Wiggans, 1995). In dairy cattle, the disassociation of breeding values across countries was overcome firstly through conversion equations, and more recently through the implementation of MACE (Jorjani *et al.*, 2001; Goddard & Beard, 2005). The aim of this study was to investigate methods that will improve the selection accuracy of foreign boars to be used in the South African pig industry, as well as assess the value of these foreign sires in comparison to local sires. The results for the two phases will be discussed separately in the following two sections.

5.1 Phase 1: Relationship between foreign and local breeding values of imported semen

The aim of the first phase of this study was to evaluate the correlations between the South African, Canadian and USA breeding values of foreign boars used in South African pig herds. Breeding values were compared for foreign boars, used in South Africa between 2000 and 2013, for the traits number born alive (NBA), 21 day litter weight (21DLWT), average daily gain (ADG), feed conversion ratio (FCR) and back fat thickness (BF).

To successfully convert breeding values from one country to another, countries are required to be connected through common sires with progeny and breeding values, accompanied by an indicator of its accuracy or reliability, for each of the traits in both countries (Schaeffer, 1985; Wickham & Philipsson, 1990). The genetic correlations between the trait pairs are then estimated using a correlation analysis method such as the one proposed by Calo *et al.* (1973). In the absence of MACE, conversion equations can then be developed for strongly correlated traits to allow breeders to accurately select foreign boars based on their converted breeding values.

Due to data limitations, only five of the traits that were analysed showed significant Pearson correlations ($P < 0.05$). The most important limitation was few and incomplete data records, and consequently a reduction in the size of the dataset. Only 37 out of the 67 USA boars used in South Africa had breeding values in the USA, while the remaining EBV's for these boars were either missing or incomplete. The lack of breeding values were a consequence of semen being imported from either breeders who weren't part of the STAGES program at the time, or from boars who did not have enough progeny from herds that do participate. Furthermore, a large percentage of boars born in the USA in 2000 never had breeding values estimated (Dr Harold Hodson, Export director at SGI, boars@swinegenetics.com, 2014). Consulting import documentation at SA Stud Book further revealed that of the 67 USA AI boars in the SA Stud Book database, only 41 had import documentation available. In cases where import documentation was available, the documentation mostly lacked supporting information providing any reason for selection or importation of semen from these boars. Unfortunately, the import documentation and EBVs that were available from old Swine Genetics International catalogues were outdated and of no use to the study.

In addition to the dataset restrictions, average daily gain, as measured in South Africa, was not regularly measured or used in Canada or the USA. In South Africa, average daily gain is measured during the test period and applied in EBV estimation, while in the USA and Canada breeding values are instead estimated for the time period taken to reach 250 lbs (100 kg). However, performances for ADG and DAYS/AGE have been reported in other studies to have strong negative correlations (Kaplon *et al.*, 1991; Lo *et al.*, 1992; Bidanel & Ducos, 1996; Akanno *et al.*, 2013; Dube *et al.*, 2013), where genetic correlations ranged between -0.65 to -0.99, while phenotypic correlations ranged between -0.70 to -0.99. In this study, significant ($P < 0.05$) negative Pearson correlations of -0.463 and -0.534 were found between the Duroc breeding values for SA ADG and USA DAYS, for the normal and high accuracy analyses, respectively.

The correlations between local and foreign EBVs were disappointing as only four out of the 40 analyses delivered significant ($P < 0.05$) Pearson correlations, namely Duroc ADG and DAYS (SA vs USA), Duroc FCR and FE (SA vs USA), Large White BF (SA vs CA) and Large White LWW and 21DLWT (CA vs USA). Although several of the Landrace Pearson correlations were moderate to strong, and the correlation between SA ADG and USA DAYS significant ($P < 0.05$), no valid conclusions could be drawn for any of the Landrace correlations as too few boars with EBVs were available for the comparisons. Five Landrace boars had original USA breeding values while three had Canadian breeding values. As one of the boars did not have a South African EBV as of yet, only four USA and two Canadian boars were available for the South Africa-USA and South Africa-Canada comparisons, respectively.

Due to the reduced dataset and lack of significant correlations, it was not possible to develop accurate conversion equations for breeding values across countries. For conversion equations to be reliable, there needs to be a large number of breeding values to estimate the regression coefficient, the genetic correlations between the traits needs to be high and the EBV’s must have a high accuracy (Goddard, 1985). When INTERBULL implemented conversion equations, to increase the accuracy of the formulae, they recommended that the data used not be more than 10 years apart, that a minimum of 20 bulls be included in each analysis, each with daughters in at least 20 herds, that the animals have a minimum EBV accuracy of 75% and that the traits have a genetic correlation of no less than 0.75 (Wickham & Philipsson, 1990; Powell & Sieber, 1992; Robinson & Chesnais, 1993; Weigel & Lin, 1999). Although the high accuracy analysis did filter the breeding values for an accuracy above 60%, the boars only had progeny on an average of two farms in South Africa and an average of six farms in the USA. Furthermore, the significantly correlated traits lacked consistency as different traits were significant for each of the breeds and country comparisons. Conversion equations were therefore no longer a viable next step and the development and testing of conversion equations was not done.

To ensure genetic progress in the long run, the methods that breeders are using to select foreign boars must be investigated. A temporary alternative to conversion equations is to implement a ranking system that converts foreign EBVs into the scale of the local evaluation. This method was briefly described in a study by Pabiou *et al.* (2007) where an attempt was made to develop conversion equations between French and Irish beef cattle EBVs. This non-genetic approach is done by applying the scale of the local trait to the standard deviation of the mean of the imported trait. Foreign boars can then be ranked alongside local boars to judge their level of superiority.

Nonetheless, the use of conversion equations as a tool to select foreign boars would be an invaluable asset to the breeders. Although conversion equations were not possible, it remains an option for future studies. Many studies have been published by INTERBULL on converting dairy and beef cattle breeding values across countries (Weller *et al.*, 1992; Banos, 1994; Beard *et al.*, 1994; Miglior & Lohuis, 1994; Mönig & Pogačar, 1995; Pabiou *et al.*, 2007), though the subject has not received much attention in other livestock industries. However, two similar studies have been done on sport horses and pigs, resulting in the successful development and implementation of accurate conversion equations.

A study on Belgium show jumper horses integrated breeding values from French and Dutch Warmblood stallions into the Belgian evaluation systems (Vandenplas & Gengler, 2012). Pre-corrections of the foreign EBVs were required to ensure the same scale using the regression method detailed by Goddard (1985). Conversion of foreign EBVs were accomplished by using the Goddard (Goddard, 1985), Wilmink (Wilmink *et al.*, 1986) and least squares (Powell, 1988) methods. In the study, improvements were made to the classic conversion methods based on the study by Vandenplas & Gengler (2012) by taking into account double counting which occurred with related individuals. The dataset was much larger compared to this study, where 98 and 67 stallions were available for French and Dutch Warmbloods, respectively.

In 2003, a similar study was done by Maignel *et al.* (2004) to convert EBVs from French Large White and Landrace boars into the Canadian system. Two simple methods derived from the Goddard (Goddard, 1985) and Wilmink (Wilmink *et al.*, 1986) methods were compared; first a linear equation that assumed the French and Canadian bases were equal, and a second model assuming the French and Canadian bases were not equal. The study was conducted over three years, with new data added annually. No significant differences were found between the two models, and in both the standard errors decreased as more data was added, resulting in more accurate conversion equations. Although the final dataset was slightly smaller than the study by Vandenplas *et al.* (2013), the initial dataset was similar to what was available in Phase 1 of this study. This presents the opportunity for a follow-up study where more boars can be included in the analyses. With additional boars, more EBVs can be included in the comparisons, hopefully resulting in additional significant correlations for most of the traits. If strong, significant correlations can be detected for traits across all the breeds between the two countries, it may be worthwhile to develop conversion equations that will accurately convert foreign breeding values into a local equivalent. In addition, collaboration with Canada and the USA may further assist in access to a larger database and improve communications and data collection.

5.2 Phase 2: Comparison of progeny performances from foreign and local sires

In this phase of the study, the differences in on-farm performances of progeny sired by local boars, foreign boars and local boars with foreign sires were evaluated. In addition to the effect of sire country, the influence of farm, sex and year-season on on-farm progeny performances were included in the analyses. As phase two focused on the on-farm performances of all progeny who had performance records, as opposed to only a handful of foreign sires with EBVs, a much larger dataset was available. The final number of sires evaluated, across all three breeds, was 3 010. Combined, the local and foreign sires had 25 491 progeny with on-farm performance records, across seven farms, that were born on a farm where both local- and foreign-sired progeny were raised during the same time period.

Sex contributed a large portion of the variation accounted for by the model, showing highly significant differences (P <0.0001) between the mean performances of male and female progeny. For Duroc and Landrace progeny, males gained 40 g more per day in comparison to the female pigs, while the margin was much smaller for Large White ADG, with only 3.4 g separating male and female performances. For Duroc and Large White progeny, the female pigs' back fat was on average 1.1 mm thicker, while only 0.7 mm thicker for female Landrace progeny. Males were shown to have a lower FCR, with male Duroc, Landrace and Large White progeny consuming 0.168 kg, 0.227 kg, and 0.211 kg less food per kg gained, respectively. Most studies investigating the effect of sex on growth and performance, compared the performances of gilts and barrows. Two studies found gilts to perform superiorly to barrows for ADG, FCR and BF (Bruininx *et al.*, 2001; Serrano *et al.*, 2008), while another found barrows to perform better than gilts (Latorre *et al.*, 2004). In South Africa, male piglets are rarely castrated as they are marketed at 21 to 22 weeks of age, before the onset of puberty and the presence of a boar taint (Cilliers & Schutte, 2014). A literature review comparing performance differences between sexes found boars to have a higher growth rate, higher feed efficiency and lower back fat in comparison to gilts and barrows (Xue *et al.*, 1988). A single study on the performance differences between boars and gilts contradicts the findings of this study as few significant differences between boars and gilts for ADG and BF were reported (Dunshea *et al.*, 2003). Sex difference in fat deposition are well documented across several species, with males generally appearing leaner than females at the same weight, while females are leaner than castrated males (Leenstra, 1986; Perkins *et al.*, 1992; Nürnberg *et al.*, 1998; Bruininx *et al.*, 2001). Leaner pigs are also found to have a lower FCR, explained in part by the higher energy cost of fat deposition compared to lean yield (Serrano *et al.*, 2008). Studies suggest the favourable correlation between BF and FCR is as a result of a larger genetic (0.19 to 0.65), rather than phenotypic (0.04 to 0.21) correlation (Bidanel & Ducos, 1996; Hermesch *et al.*, 2000; Kuhlers *et al.*, 2003; Suzuki *et al.*, 2005; Akanno *et al.*, 2013; Dube *et al.*, 2013).

The differences between farms were highly significant (*P* <0.0001) for all traits except Duroc BF (*P* <0.05). Farm differences include differences in feed and management practices, as well as climate differences. Of the 3 010 sires used in the study, 30 were used on more than one farm, of which only six boars had progeny records on three or more farms. For these sires, large differences were seen in the ranges between average progeny performances on different farms. The Duroc farm averages differed from 33.61 to 239.26 g/day for ADG and 0.08 to 1.56 mm for BF (Table B.4). Duroc FCR had one case where a sires progeny had identical FCR performances on two farms, while other farms differed by 0.29 to 0.47 kg feed/kg gain. Landrace performance differences ranged from 5.16 to 254.74 g/day for ADG, 0.14 to 0.41 kg feed/kg gain for FCR, and 0.13 to 1.62 mm for BF (Table B.5). For Large White sires, differences between the average on-farm ADG performances for progeny from the same sire ranged between 16.6 to 294.08 g/day, FCR performances differed by 0.07 to 0.23 kg feed/kg gain, while BF performances differed by 0.14 to 2.06 mm (Table B.6). The farms are spread across South Africa, encompassing a range of bioregions and climates (Figure 4.1). Farms C, G and E were located in the Central Bushveld, consisting of hot summers with moderate rainfall and warm, dry winters. Farm F and A were located in the Messic Highveld and Sub-Escarpment Grasslands, respectively. These regions have warms summers with high rainfall and dry, cool winters. Lastly, farms B and D were located in the West Coast Renosterveld and Southwest Fynbos regions, respectively. Both are winter rainfall areas, although the Southwest Fynbos bioregion has a slightly higher rainfall, both with hot summers and cool winters (Rutherford *et al.*, 2006). However, based on the ANOVA results, farms in the same area still displayed significant performance differences. In the Landrace analyses, farms B and D had significantly different (*P* <0.05) ADG, BF and FCR performances, while differences in on-farm performance on farms C, E and G were highly significant (*P* <0.0001) in all the Landrace and Large White analyses. However, performances for farm A and F were similar in the Landrace analyses and significantly different (*P* <0.0001) in the Large White analyses. Climatic influences on progeny performances seem to have had a limited effect.

Across all of the models, year-season was found to be highly significant (*P* <0.0001) and contributed to most of the variation in on-farm performances, especially for BF in the Duroc and Landrace analyses. The differences in year-season was largely linked to changes in management practices, breeding objectives, nutrition and yearly and seasonal climate change. However, as was mentioned, most of the year-season variation was expected to be due to management and nutritional changes.

On-farm performance differences due to sire country were significant (P <0.05) for all of the analyses. Due to the low numbers of CA sired progeny available for the analyses, the differences between performances from CA sired progeny and those from other countries were either not significant (Duroc ADG, Duroc BF and Landrace BF analyses), or were found to be significantly poorer (P <0.05) (Landrace ADG, Large White ADG and Large White BF analyses). Least square means from the ANOVAs indicated only small differences between SA, USA and F1-US sired progeny for ADG, FCR and BF. The models for ADG had the smallest performance differences; Duroc USA-sired progeny performance were significantly higher (P <0.05) to the rest with an ADG of 964.299 g/day; although only 14.734 g/day higher than SA sired progeny and 17.825 g/day higher than F1-US sired progeny. ANOVAs for Landrace and Large White ADG only found performances from CA-sired progeny to be significantly different (P <0.05 and P <0.0001, respectively); in both cases the Canadian ADG performances were the lowest, at 856.7 g/day and 833.92 g/day, respectively. The FCR analyses found USA progeny performing superior (P <0.05) to all SA and Duroc F1-US sired progeny, consuming 0.056 to 0.15 kg less food per kg gained, while performing similar to the Landrace F1-US sired progeny. Overall the USA sired progeny had a lower BF. Results for Duroc BF found that F1-US and USA sired progeny had a significantly (P <0.05) lower BF (9.78 mm and 9.66 mm, respectively) compared to the SA sired progeny (9.91 mm). Landrace BF had small significant differences (P <0.05) between country performances; the low USA sired progeny BF performances of 10.31 mm was not significantly lower compared to any of the other countries. Finally, Large White BF was the only trait with significant differences (P <0.05) between all the countries, where USA BF performances were highly significant (P <0.0001) at 9.46 mm, followed by significant (P <0.05) differences between SA (10.17 mm) and CA sired progeny (10.76 mm).

Although country differences were significant (P <0.05) to highly significant (P <0.0001) for all traits and breeds, the stepwise R^2 revealed that sire country contributed very little to the total variation seen in on-farm progeny performances. Differences in farm, sex, and year-season contributed much larger portions of variation to the on-farm progeny performances. The small differences in performances for ADG, FCR and BF between countries can be explained by pig industries in different countries selecting for similar traits. The trend in livestock production is towards an increased production efficiency and output, as well as improved product quality (Thornton, 2010). In the pig industry, this equates to increased reproduction performance, increased feed efficiency and increased growth performance (Visser & Hofmeyer, 2014). Average on-farm performances in Canada during 2015 were similar to the on-farm performances in South Africa, found in this study. The average age at 100 kg (average for Duroc, Landrace ad Large White) was 153 and 162 days for male and female pigs, respectively, while the average BF thickness was 10.4 and 10.2 mm for males and females, respectively (CCSI, 2015b). Average USA on-farm performances published annually by the National Pork Board reported in the 2014 productivity analysis an average ADG of 839 g/day, and a FCR of 2.70 (units feed/units gain) for conventional finisher productivity (National Pork Board, 2014). It must be kept in mind that the test period ends earlier in South Africa, pigs are only tested between the age of 9 and 23 weeks of age with an average end weight of 90 kg (Visser, 2015), while the performances reported in the USA had an average end weight of 125 kg at 27 weeks (National Pork Board, 2014). The poorer performance seen by the Canadian sired progeny can be explained by the small number of records accompanied by limited variation, as indicated by the smaller standard deviations in comparison to the other progeny. Differences observed can also be attributed to a genotype-country interaction due to large environmental differences between Canada, a cold temperate region, and South Africa, an arid and warm temperate region (Kottek *et al.*, 2006; Peel *et al.*, 2007).

In the first stage of the study, it was discovered that the boars with original USA EPDs had a wide range of rankings in the USA, with some boars ranked in the top 10 for some traits, while others were ranked well in the 1000^{s} (NSR, 2013b). The USA boars that were used in the first phase of the study are the same sires whose progeny were evaluated in the second phase. The relatively small variation contributed by country could be due to imported sires not being significantly superior to our local boars, or that these sires are also not the top performers in their country of origin.

As mentioned, the global trend in pig production is towards increased efficiency and product quality. To maintain genetic improvement, a high selection intensity must be upheld. The response to selection is a direct result of the selection differential and the heritability of the trait being selected (Falconer & Mackay, 1996); larger genetic improvement can therefore be expected in traits with higher heritability when selected parents are superior to the herd average. Three of the traits that were analysed in both the first and second phase of this study, average daily gain (ADG), feed conversion ratio (FCR) and back fat thickness (BF), are classified as production (ADG, FCR) and carcass traits (BF). In addition to these, two reproduction traits, number born alive (NBA) and 21 day litter weight (21DLWT), were also included in the first phase. In South Africa, selection is towards an increase in ADG, reduced FCR and low BF, while maintaining a high NBA and 21DLWT (Dube *et al.*, 2013;

Visser & Hofmeyer, 2014). Literature reported heritability estimates for production and carcass traits range from low to high; BF has the highest heritability, with literature estimates ranging from 0.42 to 0.72 (Lo *et al.*, 1992; Ducos *et al.*, 1993; Bidanel *et al.*, 1994; Bidanel & Ducos, 1996; Suzuki *et al.*, 2005; Visser & Hofmeyer, 2014), ADG has a moderate heritability with a range of 0.28 to 0.50 (Kaplon *et al.*, 1991; Lo *et al.*, 1992; Ducos *et al.*, 1993; Suzuki *et al.*, 2005; Clutter, 2011; Akanno *et al.*, 2013), while FCR has a low to moderate heritability ranging from 0.19 to 0.34 (Suzuki *et al.*, 2005; Clutter, 2011; Akanno *et al.*, 2013). The two reproduction traits both have low heritabilities, ranging from 0.8 - 0.1 for NBA (Rothschild, 1996; Hermesch *et al.*, 2000; Chen *et al.*, 2003; Bidanel, 2011; Akanno *et al.*, 2013) and 0.07 – 0.14 for 21DLWT (Hermesch *et al.*, 2000; Chen *et al.*, 2003; Bidanel, 2011; Akanno *et al.*, 2013). Of the five traits, BF is expected to have the largest response to selection, while ADG and FCR, followed by 21DLWT and NBA will be less responsive as the genetic influence decreases.

When accompanied by reliable breeding values to ascertain its superiority, artificial insemination presents the opportunity for breeders to access superior genetics from across the globe, allowing them to maximise their genetic progress.

With the use of artificial insemination, breeders are presented the opportunity to utilise proven superior genetics from across the globe which can aid in maintaining genetic progress by increasing the selection differential. However, due to strict import requirements in South Africa, semen imports have been largely limited to sires from the USA and Canada (Visser, 2015). After the recent outbreak of Porcine Epidemic Diarrhoea virus (PEDv), semen imports have been further restricted to only a few trade partners that can guarantee semen free from PEDv (DAFF, 2014b; Visser, 2015). This has drastically reduced the available options for breeders in terms of sire choice. However, as seen in the second phase of this study, few differences are observed between progeny performances from local and imported boars from the USA and Canada, indicating that sufficient genetic potential may already be available to South African breeders within the local populations. South African breeders should however put guideline in place with criteria for importation of semen to prevent importation of inferior boars and those without accurate EBVs.

Chapter 6: Conclusions

The purpose of the first phase of the study was to attempt to develop conversion equations to allow foreign EBVs to be accurately converted into South African equivalents without requiring extensive progeny testing. Due to only four significant correlations estimated between EBVs in South Africa and the USA, South Africa and Canada, and Canada and the USA, conversion equations could not be developed. The largest limitations in phase one was the small size of the dataset as a direct result of the lack of USA breeding values for the imported boars. It was found that several of these USA boars never had breeding values in the USA. The question remains; what criteria was used by breeders when selecting boars for semen importation?

The second phase of the study evaluated the value of foreign sires in the South African pig industry by comparing the on-farm performances of foreign-sired progeny to local-sired progeny and progeny from local sires with foreign grandsires. Results from the ANOVAs and the stepwise R^2 indicated that farm, sex and year-season had the largest effect on on-farm performances. Although the influence of year-season differed for each breed, the influence of sex was constant, with male progeny significantly out-performing female progeny in all the analyses.

The effects of farm and country were found to be significant for all traits included in this study. Significant differences existed between countries, with USA sired progeny generally performing significantly better. However, the average on-farm ADG performances for SA-sired Landrace and Large White progeny, as well as Landrace BF, were statistically no different to the USA-sired progeny. As the Canadian-sired progeny were largely outnumbered for most of the analyses, few valid conclusions could be drawn on whether their performances were significantly different to those from other progeny. However, the calculated LSMeans indicated that the Canadian-sired progeny had a significantly lower ADG and higher BF.

The results of the second phase indicate that available genetics in South African was not far behind the quality available in Canada and the USA. However, to improve, more attention needs to be given to the animals that are selected as parent stock to ensure a steady rate of genetic progress is maintained. Superiority of the selected individuals must be based on accurate breeding values, keeping in mind the breeding objectives of the individual farm. Although conversion equations could not yet be developed, it remains a viable option for the future. Until then, alternative methods such as ranking could be implemented to assist selection of foreign sires.

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Addendum A: Phase 1

Table A.1 Summary of the descriptive statistics from within-country analysis for AI boars' EBVs in South Africa

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	NBA	22	-0.620	0.913	0.195	-1.810	0.826
	21DLWT	22	-0.153	1.865	0.398	-4.316	4.689
	ADG	22	16.651	26.940	5.744	-31.985	59.628
	FCR	22	-0.043	0.059	0.013	-0.170	0.097
	BF	22	-0.060	0.592	0.126	-1.421	1.195
Large White	NBA	32	0.014	0.767	0.136	-1.551	1.867
	21DLWT	32	-0.197	4.359	0.771	-11.273	6.475
	ADG	32	9.562	44.482	7.863	-54.630	124.568
	FCR	32	0.040	0.060	0.011	-0.102	0.135
	BF	32	-0.835	0.627	0.111	-2.422	0.580
Landrace	NBA	12	-0.575	0.788	0.227	-1.890	0.370
	21DLWT	12	3.546	5.000	1.443	-3.727	8.842
	ADG	12	26.921	30.129	8.697	-41.595	70.317
	FCR	12	0.014	0.156	0.045	-0.174	0.246
	BF	12	-1.187	0.748	0.216	-2.651	0.114

N = Number of boars; SD = standard deviation; SE = standard error; NBA = number born alive; 21DLWT = 21 day litter weight (kg); ADG = average daily gain (g/day); FCR = feed conversion ratio (kg fed/kg gain); BF = back fat thickness (mm)

Table A.2 Summary of the descriptive statistics from within-country analysis for AI boars' EBVs in the USA

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	NBA	15	-0.169	0.229	0.059	-0.660	0.240
	21DLWT	15	-0.193	1.976	0.510	-4.000	3.330
	DAYS	15	-0.211	2.741	0.708	-3.870	5.810
	FE	15	-0.018	0.033	0.009	-0.060	0.050
	BF	15	-0.025	0.021	0.005	-0.080	0.010
Large White	NBA	17	-0.119	0.319	0.077	-0.570	0.430
	21DLWT	17	0.059	4.090	0.992	-5.610	7.150
	DAYS	17	0.866	3.340	0.810	-4.130	5.750
	FE	17	-0.005	0.036	0.009	-0.060	0.070
	BF	17	-0.023	0.035	0.008	-0.080	0.070
Landrace	NBA	5	0.118	0.422	0.189	-0.520	0.610
	21DLWT	5	1.906	2.748	1.229	-2.080	5.390
	DAYS	5	-1.800	1.981	0.886	-5.080	-0.220
	FE	5	-0.032	0.026	0.012	-0.060	0.000
	BF	5	-0.012	0.025	0.011	-0.030	0.020

N = Number of boars; SD = standard deviation; SE = standard error; NBA= number born alive; 21DLWT = 21 day litter weight (lbs); DAYS = days to 250 lbs, FE = feed efficiency (lbs fed/lbs gain), BF = back fat thickness (inches)

Table A.3 Summary of the descriptive statistics from within-country analysis for AI boars' EBVs in Canada

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	NB	12	-0.558	0.245	0.071	-0.960	-0.110
	LWW	12	-0.967	1.114	0.322	-2.180	1.410
	AGE	12	6.458	5.839	1.685	-4.600	16.600
	FCR	12	0.081	0.073	0.021	-0.064	0.216
	BF	12	1.445	0.754	0.218	-0.010	2.620
Large White	NB	11	-1.579	0.553	0.167	-2.340	-0.370
	LWW	11	-2.309	2.824	0.852	-7.410	1.210
	AGE	11	3.273	4.175	1.259	-2.300	12.300
	FCR	11	0.047	0.042	0.013	-0.010	0.145
	BF	11	0.626	1.506	0.454	-1.450	2.640
Landrace	NB	3	-1.393	1.252	0.723	-2.600	-0.100
	LWW	3	-0.830	0.689	0.398	-1.390	-0.060
	AGE	3	-2.133	1.721	0.994	-4.100	-0.900
	FCR	3	-0.017	0.013	0.008	-0.026	-0.002
	BF	3	1.383	0.874	0.504	0.650	2.350

N = Number of boars; SD = standard deviation; SE = standard error; NB = number born; LWW = litter weaning weight (kg); AGE = age to 100 kg (days); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm)

Table A.4 Summary of descriptive statistics for between-country analysis for common AI boars' EBVs in South Africa and the USA

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	SA NBA	15	-0.829	0.916	0.237	-1.810	0.826
	USA NBA	15	-0.169	0.229	0.059	-0.660	0.240
	SA 21DLWT	15	-0.033	1.982	0.512	-4.316	4.689
	USA 21DLWT	15	-0.193	1.976	0.510	-4.000	3.330
	SA ADG	15	21.625	27.097	6.996	-31.985	59.628
	USA DAYS	15	-0.211	2.741	0.708	-3.870	5.810
	SA FCR	15	-0.049	0.060	0.016	-0.170	0.034
	USA FE	15	-0.018	0.033	0.009	-0.060	0.050
	SA BF	15	-0.213	0.598	0.154	-1.421	0.922
	USA BF	15	-0.025	0.021	0.005	-0.080	0.010
Large White	SA NBA	16	0.229	0.836	0.209	-1.551	1.867
	USA NBA	16	-0.113	0.329	0.082	-0.570	0.430
	SA 21DLWT	16	0.693	4.318	1.079	-11.273	6.475
	USA 21DLWT	16	-0.076	4.185	1.046	-5.610	7.150
	SA ADG	16	8.754	43.768	10.942	-41.669	99.827
	USA DAYS	16	1.142	3.244	0.811	-4.130	5.750
	SA FCR	16	0.055	0.059	0.015	-0.102	0.135
	USA FE	16	-0.002	0.035	0.009	-0.060	0.070
	SA BF	16	-0.655	0.653	0.163	-1.896	0.580
	USA BF	16	-0.024	0.035	0.009	-0.080	0.070
Landrace	SA NBA	4	-0.634	0.857	0.428	-1.890	0.031
	USA NBA	4	0.278	0.261	0.130	0.050	0.610
	SA 21DLWT	4	3.539	4.723	2.361	-3.422	6.628
	USA 21DLWT	4	1.958	3.170	1.585	-2.080	5.390
	SA ADG	4	50.641	15.633	7.817	37.311	70.317
	USA DAYS	4	-1.860	2.282	1.141	-5.080	-0.220
	SA FCR	4	-0.016	0.123	0.062	-0.160	0.128
	USA FE	4	-0.028	0.028	0.014	-0.060	0.000
	SA BF	4	-1.791	0.692	0.346	-2.651	-1.224
	USA BF	4	-0.008	0.026	0.013	-0.030	0.020

SA = South Africa; USA = United States of America; N = number of observations; SD = standard deviation; SE = standard error; SA NBA = SA EBV for number born alive; USA NBA = USA EBV for number born alive; SA 21DLWT = SA EBV for 21 day litter weight (kg); USA 21DLWT = USA EBV for 21 day litter weight (lbs); SA ADG = SA EBV for average daily gain (g/day); USA DAYS = USA EBV for days to 250 lbs; SA FCR = SA EBV for feed conversion rate (kg feed/kg gain); USA FE = USA EBV for feed efficiency (lbs feed/lbs gain); SA BF = SA EBV for back fat thickness (mm); USA BF = USA EBV for back fat thickness (inch)

Table A.5 Summary of descriptive statistics for between-country analysis for common AI boars' EBVs in South Africa and Canada

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	SA NBA	10	0.046	0.638	0.202	-1.174	0.826
	CA NB	10	-0.532	0.229	0.072	-0.890	-0.110
	SA 21DLWT	10	-0.023	1.486	0.470	-1.907	2.852
	CA LWW	10	-0.857	1.157	0.366	-2.100	1.410
	SA ADG	10	18.270	27.737	8.771	-20.088	50.769
	CA AGE	10	5.240	5.496	1.738	-4.600	16.600
	SA FCR	10	-0.054	0.074	0.023	-0.170	0.097
	CA FCR	10	0.067	0.070	0.022	-0.064	0.216
	SA BF	10	-0.041	0.672	0.213	-1.421	1.195
	CA BF	10	1.418	0.790	0.250	-0.010	2.620
Large White	SA NBA	10	0.182	0.965	0.305	-1.551	1.867
	CA NB	10	-1.700	0.401	0.127	-2.340	-1.090
	SA 21DLWT	10	0.001	4.664	1.475	-11.273	4.594
	CA LWW	10	-2.325	2.977	0.941	-7.410	1.210
	SA ADG	10	12.239	48.477	15.330	-41.669	99.827
	CA AGE	10	3.830	3.947	1.248	0.400	12.300
	SA FCR	10	0.050	0.067	0.021	-0.102	0.135
	CA FCR	10	0.050	0.043	0.014	-0.010	0.145
	SA BF	10	-0.661	0.547	0.173	-1.430	0.580
	CA BF	10	0.425	1.422	0.450	-1.450	2.200
Landrace	SA NBA	2	-0.182	0.302	0.213	-0.396	0.031
	CA NB	2	-0.790	0.976	0.690	-1.480	-0.100
	SA 21DLWT	2	6.473	0.219	0.155	6.318	6.628
	CA LWW	2	-0.550	0.693	0.490	-1.040	-0.060
	SA ADG	2	63.197	10.069	7.120	56.077	70.317
	CA AGE	2	-2.500	2.263	1.600	-4.100	-0.900
	SA FCR	2	0.079	0.070	0.050	0.029	0.128
	CA FCR	2	-0.013	0.015	0.011	-0.023	-0.002
	SA BF	2	-1.231	0.009	0.007	-1.237	-1.224
	CA BF	2	1.750	0.849	0.600	1.150	2.350

CA = Canada; SA = South Africa; N = number of observations; SD = standard deviation; SE = standard error;; SA NBA = SA EBV for number born alive; CA NBA = CA EBV for number born; SA 21DLWT = SA EBV for 21 day litter weight (kg); CA LWW = CA EBV for litter weaning weight (kg); SA ADG = SA EBV for average daily gain (g/day); CA AGE = CA EBV for age 100 kg (days); SA FCR = SA EBV for feed conversion rate (kg feed/kg gain); CA FCR = CA EBV for feed conversion rate (kg feed/kg gain); SA BF = SA EBV for back fat thickness (mm); CA BF = CA EBV for back fat thickness (mm)

Table A.6 Summary of descriptive statistics for between-country analysis for common AI boars' EBVs in Canada and the USA

Breed	Variable	N	Mean	SD	SE	Minimum	Maximum
Duroc	CA NB	7	-0.494	0.227	0.086	-0.76	-0.11
	USA NBA	7	-0.246	0.331	0.125	-0.6	0.44
	CA LWW	7	-1.133	0.94	0.355	-2.1	0.81
	USA 21DLWT	7	1.717	3.229	1.22	-2.66	6.66
	CA AGE	7	6.843	7.238	2.736	-4.6	16.6
	USA DAYS	7	-2.326	4.649	1.757	-7.74	4.64
	CA FCR	7	0.081	0.092	0.035	-0.06	0.22
	USA FE	7	-0.051	0.064	0.024	-0.12	0.06
	CA BF	7	1.143	0.844	0.319	-0.01	2.62
	USA BF	7	-0.029	0.03	0.011	-0.08	0.02
Landrace	CA NB	3	-1.393	1.252	0.723	-2.6	-0.1
	USA NBA	3	-0.253	0.682	0.394	-1.04	0.18
	CA LWW	3	-0.83	0.689	0.398	-1.39	-0.06
	USA 21DLWT	3	4.147	2.045	1.181	2.58	6.46
	CA AGE	3	-2.133	1.721	0.994	-4.1	-0.9
	USA DAYS	3	-5.68	3.893	2.248	-10.16	-3.12
	CA FCR	3	-0.017	0.015	0.009	-0.03	0
	USA FE	3	-0.1	0.02	0.012	-0.12	-0.08
	CA BF	3	1.383	0.874	0.504	0.65	2.35
	USA BF	3	-0.027	0.058	0.033	-0.06	0.04
Large White	CA NB	8	-1.714	0.45	0.159	-2.34	-1.09
	USA NBA	8	-0.052	0.756	0.267	-1.14	0.86
	CA LWW	8	-2.006	3.12	1.103	-7.41	1.21
	USA 21DLWT	8	0.788	8.776	3.103	-8.16	13.54
	CA AGE	8	3.2	4.096	1.448	0.4	12.3
	USA DAYS	8	1.525	7.226	2.555	-8.26	10.86
	CA FCR	8	0.048	0.048	0.017	-0.01	0.15
	USA FE	8	-0.005	0.084	0.03	-0.12	0.14
	CA BF	8	0.814	1.31	0.463	-1.45	2.2
	USA BF	8	-0.04	0.093	0.033	-0.16	0.14

CA = Canada; USA = United States of America; N = number of observations; SD = standard deviation; SE = standard error; CA NB = Canadian EBV for number born; USA NBA = USA EBV for number born alive; CA LWW = CA EBV for litter weaning weight (kg); USA 21DLWT = USA EBV for 21 day litter weight (lbs); CA AGE = CA EBV for age at 100 kg (days); USA DAYS = USA EBV for days to 250 lbs; CA FCR = CA EBV for feed conversion rate (kg feed/kg gain); USA FE = USA EBV for feed efficiency (lbs feed/lbs gain); CA BF = CA EBV for back fat thickness (mm); USA BF = USA EBV for back fat thickness (inch)

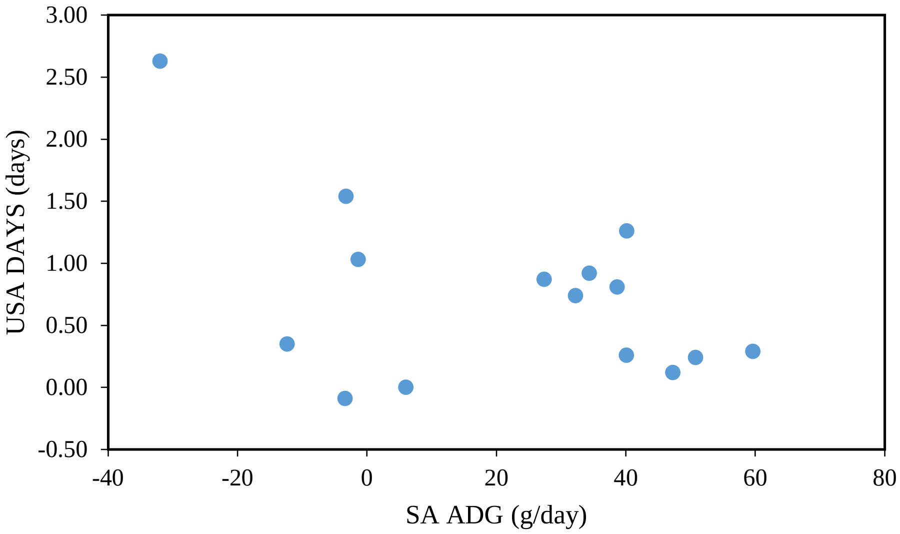

Figure A.1 Scatter plot of South African ADG and USA DAYS EBVs for Duroc AI boars

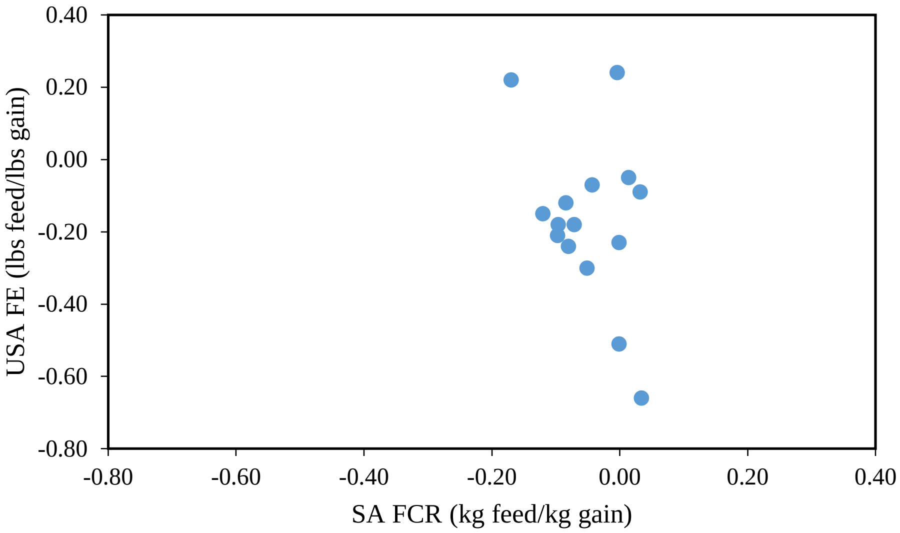

Figure A.2 Scatter plot of South African FCR and USA FE EBVs for Duroc AI boars

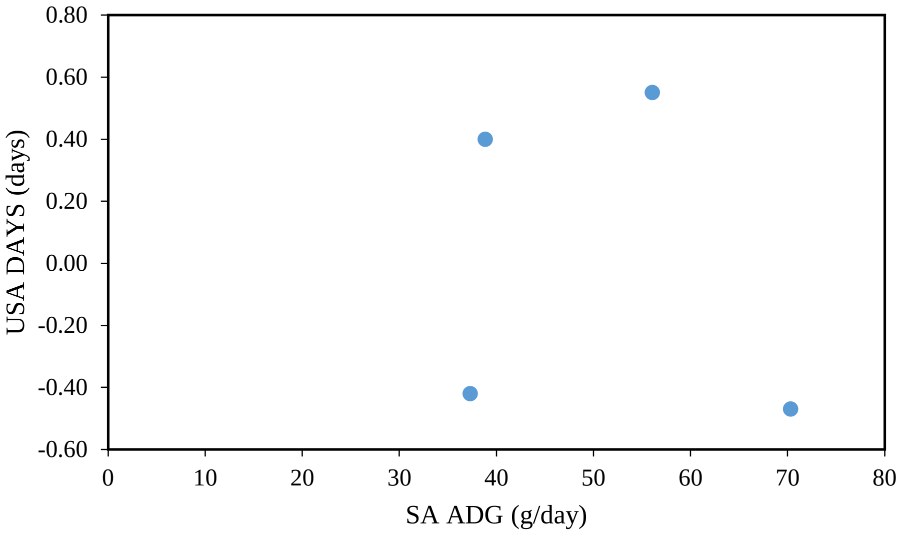

Figure A.3 Scatter plot of South African ADG and USA DAYS EBVs for Landrace AI boars

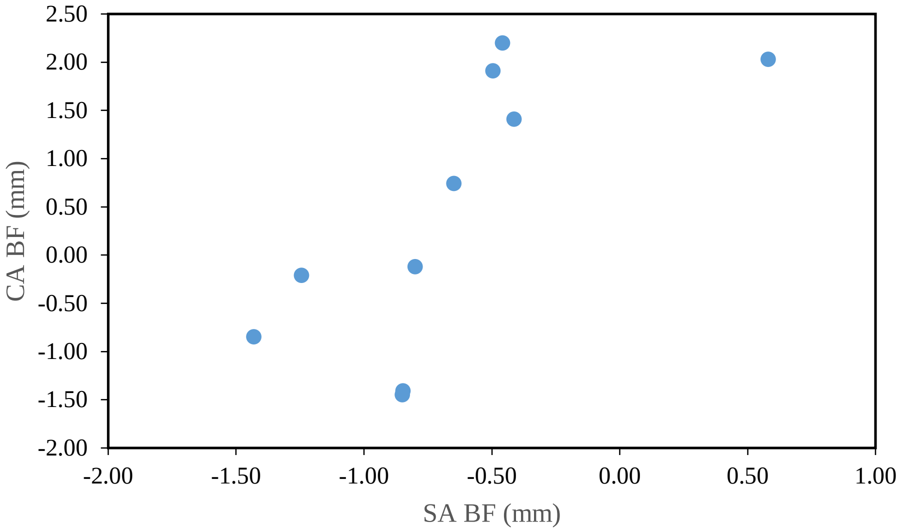

Figure A.4 Scatter plot of South African and Canadian BF EBVs for Large White AI boars

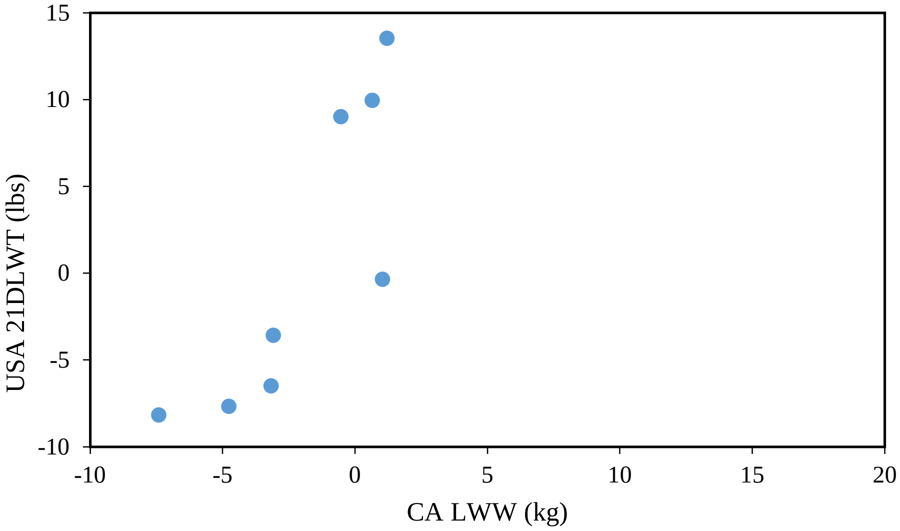

Figure A.5 Scatter plot of Canadian LWW and USA 21DLWT EBVs for Large White AI boars

Addendum B: Phase 2

Table B.1 Summary of descriptive statistics for available on-farm performances of Duroc progeny

Trait	Country	Farm	N	Mean	SD	SE	Minimum	Maximum
ADG	CA	C	79	933.37	90.49	10.18	707.79	1123.21
	F1 US	A	258	955.18	136.99	8.53	714.29	1285.71
		C	1476	922.85	103.00	2.68	638.10	1811.43
		D	161	860.71	132.72	10.46	654.76	1178.57
	SA	A	718	972.02	135.62	5.06	642.86	1333.33
		C	5632	929.66	100.11	1.33	652.38	1902.86
		D	226	907.06	142.20	9.46	666.67	1285.71
	USA	A	29	1058.38	122.14	22.68	738.10	1244.90
		C	205	909.94	81.43	5.69	644.05	1150.79
		D	105	968.55	148.17	14.46	714.29	1428.57
BF	CA	C	79	9.57	1.38	0.16	8	13
	F1 US	A	258	9.98	1.56	0.10	8	22
		C	1476	9.49	1.56	0.04	6	16
		D	161	9.74	0.64	0.05	9	12
	SA	A	718	10.46	2.23	0.08	6	27
		C	5632	9.91	1.83	0.02	6	17
		D	226	9.83	0.63	0.04	9	12
	USA	A	29	9.97	1.94	0.36	8	17
		C	205	10.24	1.63	0.11	6	14
		D	105	10.08	0.68	0.07	9	12
FCR	F1 US	A	145	2.02	0.23	0.02	1.62	2.75
		D	87	2.38	0.26	0.03	1.88	3.19
	SA	A	476	2.07	0.28	0.01	1.59	3.47
		C	2	2.03	0.01	0.01	2.02	2.04
		D	140	2.32	0.24	0.02	1.81	2.93
	USA	A	26	1.9	0.21	0.04	1.63	2.75
		D	79	2.24	0.27	0.03	1.72	3.04

N = number of records; SD = standard deviation; SE = Standard error; CA = Canada; F1 US = SA progeny with USA grandsires; USA = United States of America; SA = South Africa; ADG = average daily gain (g/day); FCR = feed conversion rate (kg feed/kg gain); BF = back fat thickness (mm)

Table B.2 Summary of descriptive statistics for available on-farm performances of Landrace progeny

Trait	Country	Farm	N	Mean	SD	SE	Minimum	Maximum
ADG	CA	C	59	880.05	79.8	10.39	731.17	1080.36
		G	60	840.63	90.43	11.67	702.38	1142.86
	F1 US	A	249	920.66	145.68	9.23	666.67	1265.31
		B	138	985.72	84.79	7.22	690.48	1333.33
		C	411	848.44	85.31	4.21	673.81	1273.47
		D	46	840.41	159.83	23.56	690.48	1224.49
		F	6	901.68	39.85	16.27	828.57	935.06
		G	454	887.87	118.05	5.54	642.86	1685.71
	SA	A	1647	922.68	145.4	3.58	654.76	1742.86
		B	160	952.15	112.02	8.86	642.86	1265.31
		C	2594	851.61	82.4	1.62	645.24	1538.1
		D	197	864.46	159.15	11.34	666.67	1333.33
		F	36	875.79	101.58	16.93	738.1	1265.31
		G	1056	893.98	112.12	3.45	642.86	1742.86
	USA	A	22	991.10	131.07	27.94	766.23	1214.29
		B	17	1051.37	91.04	22.08	920.63	1183.67
		C	78	830.98	76.19	8.63	647.62	1008.57
		D	37	855.35	158.79	26.1	714.29	1179.59
		F	10	842.43	55.5	17.55	773.81	961.04
		G	29	859.01	103.65	19.25	714.29	1204.08
BF	CA	C	59	11.10	1.79	0.23	8	15
		G	60	10.82	1.26	0.16	8	13
	F1 US	A	249	9.97	1.54	0.10	8	22
		B	138	9.49	0.86	0.07	8	12
		C	411	11.01	1.99	0.10	6	19
		D	46	10.24	0.60	0.09	9	12
		F	6	11.17	2.71	1.11	9	15
		G	454	10.52	1.62	0.08	6	16
	SA	A	1647	10.95	2.35	0.06	7	24
		B	160	9.71	0.90	0.07	8	13
		C	2594	11.61	2.07	0.04	6	18
		D	197	10.14	0.60	0.04	8	12
		F	36	11.22	2.03	0.34	7	15
		G	1056	10.81	1.66	0.05	1	18
	USA	A	22	10.50	1.65	0.35	9	16
		B	17	9.47	0.51	0.12	9	10
		C	78	11.95	2.03	0.23	8	17
		D	37	10.22	0.67	0.11	9	12
		F	10	8.50	1.43	0.45	7	11
		G	29	10.79	1.50	0.28	8	14

Table B2. Continued.

Trait	Country	Farm	N	Mean	SD	SE	Minimum	Maximum
FCR	F1 US	A	105	1.95	0.2	0.02	1.61	2.77
		B	21	2.1	0.16	0.04	1.8	2.64
		D	17	2.24	0.2	0.05	1.86	2.58
		G	31	2.25	0.31	0.05	1.79	3.03
	SA	A	769	2.13	0.31	0.01	1.54	3.37
		B	19	2.03	0.12	0.03	1.79	2.3
		D	100	2.32	0.22	0.02	1.87	2.85
		G	176	2.31	0.25	0.02	1.72	3.2
	USA	A	17	1.98	0.26	0.06	1.76	2.64
		B	17	1.97	0.13	0.03	1.82	2.39
		D	17	2.37	0.16	0.04	2.12	2.71

N = number of records; SD = standard deviation; SE = standard error; Country = sire country of origin; CA = Canada; F1 US = SA progeny with USA grandsires; USA = United States of America; SA = South Africa; ADG = average daily gain (g/day); FCR = feed conversion rate (kg feed/kg gain); BF = back fat thickness (mm)

Table B.3 Summary of descriptive statistics for available on-farm performances of Large White progeny

Trait	Country	Farm	N	Mean	SD	SE	Minimum	Maximum
ADG	CA	C	65	906.28	86.41	10.72	714.29	1132.14
		G	26	808.67	81.69	16.02	690.48	1015.87
	SA	A	579	995.66	146.85	6.10	726.19	1476.19
		C	1957	867.81	81.52	1.84	641.67	1169.64
		D	403	890.03	160.65	8.00	690.48	1333.33
		E	115	991.13	175.69	16.38	690.48	1914.29
		F	5630	883.19	99.99	1.33	642.86	1657.14
		G	1844	913.72	113.55	2.64	654.76	1642.86
	USA	A	55	1064.44	122.38	16.5	792.21	1285.71
		C	139	873.68	92.78	7.87	633.33	1178.57
		D	95	985.42	170.09	17.45	690.48	1333.33
		E	22	1084.05	138.05	29.43	855.95	1367.35
		F	154	821.25	84.35	6.80	642.86	1142.86
		G	56	897.34	124.09	16.58	642.86	1244.90
BF	CA	C	65	10.54	1.36	0.17	8	13
		G	26	10.65	1.32	0.26	8	13
	SA	A	579	10.79	2.39	0.1	7	22
		C	1957	10.60	1.83	0.04	6	17
		D	403	9.86	0.65	0.03	8	12
		E	115	10.38	1.35	0.13	7	14
		F	5630	9.23	2.19	0.03	6	28
		G	1844	10.12	1.77	0.04	6	17
	USA	A	55	9.71	1.55	0.21	8	17
		C	139	9.92	1.7	0.14	6	15
		D	95	9.86	0.63	0.06	9	12
		E	22	10.5	1.14	0.24	8	13
		F	154	8.19	1.8	0.14	6	14
		G	56	10.13	1.44	0.19	7	14
FCR	SA	A	372	2.09	0.33	0.02	1.61	3.25
		D	221	2.27	0.23	0.02	1.69	2.93
		E	50	2.04	0.18	0.03	1.64	2.44
		F	19	2.07	0.16	0.04	1.74	2.47
		G	60	2.29	0.33	0.04	1.69	3.09
	USA	A	49	1.9	0.18	0.03	1.67	2.69
		D	69	2.18	0.21	0.03	1.81	2.62
		E	7	2.06	0.23	0.09	1.81	2.4

N = number of records; SD = standard deviation; SE = Standard error; CA = Canada; F1 US = SA progeny with USA grandsires; USA = United States of America; SA = South Africa; ADG = average daily gain (g/day); FCR = feed conversion rate (kg feed/kg gain); BF = back fat thickness (mm)

Table B.4 Average progeny performances per farm for Duroc sires with progeny on more than one farm

Sire Country	Sire ID	Farm	Number		ADG		FCR		BF	
			Female	Male	Mean	SD	Mean	SD	Mean	SD
SA	912506	C	5	4	943.36	56.51			11.56	1.01
		D	3	2	846.75	63.77	2.43	0.12	10.00	
	973031	A	2	2	889.88	122.37	2.34	0.31	11.75	3.20
		D	8	17	950.59	113.62	2.34	0.22	9.52	0.51
	1001508	C	24	31	885.79	60.50			10.95	1.70
		D	8	23	9X19.40	113.80	2.36	0.28	9.45	0.57
	1003575	A	4	9	1050.26	85.32	1.92	0.14	9.54	0.52
		D	1	3	985.97	187.20	2.38	0.07	10.25	0.96
	1004075	A	2	18	1056.8	114.96	1.93	0.11	9.65	0.49
		C	2	1	843.44	85.69			9.00	
		D	8	9	961.67	147.49	2.39	0.15	9.82	0.81
	1072857	A		3	1017.86	17.86	1.95	0.09	9.00	
		D	5	2	868.56	129.44	2.24	0.34	9.86	0.38
USA	1056688	A		4	1086.73	90.02	1.77	0.10	9.50	0.58
		D	14	19	941.99	133.08	2.37	0.29	9.94	0.70
	1056690	A		2	1142.86	25.25	1.67	0.02	10.00	
		D	9	15	1011.64	115.70	2.14	0.19	10.25	0.68
	1056697	A		4	1141.16	126.95	1.86	0.06	9.25	0.96
		C	11	7	901.90	88.30			10.11	1.84
		D	14	15	1037.88	152.89	2.17	0.30	10.03	0.57
	1056726	A		2	1108.42	77.57	1.82	0.04	9.00	
		C	14	11	876.39	60.62			11.00	1.08
	1056731	A	2	1	884.92	224.09	1.95		11.67	2.08
		C	3	2	947.62	41.52			9.40	0.55

Sire ID = SA Stud Book ID; ADG = average daily gain (g/day); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); SD = standard deviation; SA = South Africa; US = United States of America

Table B.5 Average progeny performances per farm for Landrace sires with progeny on more than one farm

Sire County	Sire ID	Farm	Number		ADG		FCR		BF	
			Female	Male	Mean	SD	Mean	SD	Mean	SD
CA	1343375	C	18	19	890.12	83.71			10.22	1.20
		G	7	10	854.54	93.72			10.35	1.46
	1343378	C	11	11	863.11	71.39			12.59	1.62
		G	16	19	821.31	75.77			10.97	1.18
F1 US	1257458	D	.	2	1152.43	101.92	2.08	0.01	10.00	0.00
		G	51	43	897.69	98.13			10.63	1.83
SA	1007093	A	11	7	881.71	120.14	2.14	0.31	11.56	3.01
		G	9	11	940.28	133.57	2.28	0.32	11.80	1.94
	1241019	D	7	2	805.23	143.24	2.25	0.07	10.22	0.67
		G	10	11	908.49	88.67			9.95	2.11
USA	1045305	A	4	4	894.91	115.85	1.85	0.07	9.50	0.76
		G	4	2	889.75	177.82			10.33	0.82
	1190886	C	7	16	829.14	88.89			11.65	1.53
		G	3	4	848.90	65.76			11.14	1.57
	1205037	B	4	4	1009.81	103.95	1.94	0.04	9.50	0.53
		D	7	7	873.99	163.22	2.35	0.14	10.29	0.91
		G	7	6	865.39	81.65			11.15	1.63
	1206165	C	8	9	872.80	48.98			10.53	1.59
		G	2	1	793.51	92.23			9.33	1.15

Sire ID = SA Stud Book ID; ADG = average daily gain (g/day); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); SD = standard deviation; CA = Canada; F1 US = SA sired progeny with USA grandsires; SA = South Africa; US = United States of America

Table B.6 Average progeny performances per farm for Large White sires with progeny on more than one farm

Sire Country	Sire ID	Farm	Number		ADG		FCR		BF	
			Female	Male	Mean	SD	Mean	SD	Mean	SD
CA	1343381	C	17	25	900.29	78.63			10.74	1.34
		G	5	7	806.68	101.59			10.42	1.56
	1343384	C	9	13	912.58	99.80			10.09	1.31
		G	5	9	810.37	63.99			10.86	1.10
USA	942673	F	7	3	802.98	81.43			8.60	1.35
		G		3	1055.56	13.75			10.33	0.58
	942692	C	15	14	897.12	67.88			9.34	1.29
		F	5	21	816.26	64.05			8.65	1.70
		G	3	5	952.63	116.50			10.38	1.19
	1045509	A		16	1117.17	96.38	1.94	0.26	10.56	2.45
		D	7	5	1046.81	80.91	2.22	0.22	10.25	0.62
		F	1	5	833.77	72.48			7.17	0.75
		G	16	7	886.99	97.49			10.22	1.68
	1045514	F	3	4	890.52	90.34			9.00	2.08
		G	2	2	921.83	149.43			10.00	0.82
	1045526	A		3	1080.36	32.19	1.96	0.12	9.67	1.15
		F	3	6	732.80	22.36			8.33	2.29
	1045532	F	3	2	822.73	181.23			9.00	2.83
		G	2	2	913.49	58.56			9.75	0.96
	1056544	A	1	5	1013.65	119.81	1.90	0.07	9.50	0.55
		D	2	8	1111.84	175.20	2.01	0.20	10.20	0.79
	1056564	D	4	4	1001.76	90.57	2.08	0.18	10.38	0.74
		F	6	9	783.30	50.38			7.13	0.92
	1056571	D	5	11	964.65	180.23	2.18	0.20	9.56	0.51
		F	3	6	855.32	50.77			7.22	1.09
	1056592	A		8	1082.53	110.19	1.80	0.06	9.38	0.74
		F	6	3	874.24	96.86			7.44	1.42
	1056606	A		14	1076.84	104.72	1.91	0.15	9.43	0.85
		F	8	10	782.76	73.65			8.67	2.25
	1190873	C	6	12	829.14	115.61			9.94	1.63
		G	1	2	988.38	238.33			12.00	1.00
	1190880	C	8	8	862.42	70.87			9.88	1.26
		D	9	10	915.23	167.39	2.34	0.18	9.74	0.45
		G	7	2	778.02	97.22			9.56	1.33
	1192541	C	12	6	922.12	112.48			9.28	1.07
		E	10	5	1137.26	116.39	2.06	0.23	10.53	0.83

Table B.6 Continued.

Sire Country	Sire ID	Farm	Number		ADG		FCR		BF	
			Female	Male	Mean	SD	Mean	SD	Mean	SD
SA	1020618	A	2	22	1009.31	94.00	1.88	0.10	9.67	0.82
		E	7	9	1063.79	159.96	2.03	0.21	11.13	1.09
	1022337	D	3	11	950.60	173.39	2.30	0.24	9.86	0.77
		E	17	15	1026.72	91.05	2.07	0.16	10.88	0.66
		F	3	7	1010.12	138.12	2.14	0.17	10.10	1.20

Sire ID = SA Stud Book ID; ADG = average daily gain (g/day); FCR = feed conversion ratio (kg feed/kg gain); BF = back fat thickness (mm); SD = standard deviation; CA = Canada; US = United States of America; SA = South Africa