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Perspectives for artificial insemination and genomics to improve global swine populations

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Abstract

Civilizations throughout the world continue to depend on pig meat as an important food source. Approximately 40% of the red meat consumed annually worldwide (94 million metric tons) is pig meat. Pig numbers (940 million) and consumption have increased consistent with the increasing world population (FAO 2002). In the past 50 years, research guided genetic selection and nutrition programs have had a major impact on improving carcass composition and efficiency of production in swine. The use of artificial insemination (AI) in Europe has also had a major impact on pig improvement in the past 35 years and more recently in the USA. Several scientific advances in gamete physiology and/or manipulation have been successfully utilized while others are just beginning to be applied at the production level. Semen extenders that permit the use of fresh semen for more than 5 days post-collection are largely responsible for the success of AI in pigs worldwide. Transfer of the best genetics has been enabled by use of AI with fresh semen, and to some extent, by use of AI with frozen semen over the past 25 years. Sexed semen, now a reality, has the potential for increasing the rate of genetic progress in AI programs when used in conjunction with newly developed low sperm number insemination technology. Embryo cryopreservation provides opportunities for international transport of maternal germplasm worldwide; non-surgical transfer of viable embryos in practice is nearing reality. While production of transgenic animals has been successful, the low level of

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efficiency in producing these animals and lack of information on multigene interactions limit the use of the technology in applied production systems. Technologies based on research in functional genomics, proteomics and cloning have significant potential, but considerable research effort will be required before they can be utilized for AI in pig production. In the past 15 years, there has been a coordinated worldwide scientific effort to develop the genetic linkage map of the pig with the goal of identifying pigs with genetic alleles that result in improved growth rate, carcass quality, and reproductive performance. Molecular genetic tests have been developed to select pigs with improved traits such as removal of the porcine stress (RYR1) syndrome, and selection for specific estrogen receptor (ESR) alleles. Less progress has been made in developing routine tests related to diseases. Major research in genomics is being pursued to improve the efficiency of selection for healthier pigs with disease resistance properties. The sequencing of the genome of the pig to identify new genes and unique regulatory elements holds great promise to provide new information that can be used in pig production. AI, in vitro embryo production and embryo transfer will be the preferred means of implementing these new technologies to enhance efficiency of pig production in the future.
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1. Introduction

Pig meat represents about 40% of all red meat consumed worldwide and continues to be an important part of the human diet throughout the world. In the past 10 years, pork production has increased from 73 to 94 million metric tons according to FAO records (http://apps.fao.org/cgi-bin/nph-db.pl?subset=agriculture) [1]. It is projected that the demand for pork will increase to 125 million metric tons by 2020 (Table 1) [2]. Most of the increase is projected for developing countries.

The improvement in efficiency of pork production, especially in recent years, is the result of implementation of several new biotechnological techniques and production practices. Major research advances have been made in genetics, nutrition, and disease and

Table 1
Past and projected production trends of various meats up to 2020

	1982	1993	2020
Region			
Developed countries			
Beef	32	33	40
Pork	35	37	41
Poultry	17	26	57
Meat	92	100	124
Developing countries			
Beef	17	22	42
Pork	21	39	84
Poultry	9	21	46
Meat	51	88	182

Total production in million metric tons adapted from Delgado et al. [2].

parasite control. Together, these advances have improved the efficiency of pig production. Over the last two decades in the U.S., the feed efficiency ratio per pound of weight gain has improved from 4.25 to 3.75, lean meat in the carcass has increased from 42 to 51% and the pounds of carcass produced per sow per year has almost doubled from 1625 to 3095 pounds (Meisinger, US National Pork Board data, 2000, personal communication). Most of this improvement in efficiency in the U.S. was made without the use of artificial insemination (AI).

Scientists from academia, government and industry are responsible for developing new technologies that producers have rapidly adopted to improve the efficiency of the pig. Although considerable progress has been made to date, many opportunities to improve the biological efficiency of the pig remain. Projected trends in pig production (Table 1) show that there is a continuing need for efficient production of pork.

The use of AI in the pig has had a major impact on pig improvement in the past 35 years, especially in Europe and more recently in the USA. Several new technologies hold promise for further improvements in pig production. The purpose of this paper is to review ongoing and recent biotechnological and genomic advances that have the potential to significantly improve global swine populations when implemented as part of an AI program.

While some of the technologies discussed in this paper are currently associated with ongoing AI programs, some are not; however, they all hold considerable promise. Taking advantage of biotechnological developments and swine genetic improvement is dependent on the use of AI in some form to deliver sperm to the site of fertilization.

Genetic and molecular biotechnologies and information generated from research in functional genomics and proteomics will facilitate development of gene knockout and transgenic animals. Marker-assisted selection, when applied pre-conception, will produce pigs with desired production traits, and resistance to parasites and disease. Thus, integration of these technologies with specific sperm manipulation technologies is essential. In this review, we will seek to illustrate the necessity of integrating multiple technologies to improve AI in order to achieve the greatest benefit from individual biotechnologies (Fig. 1).

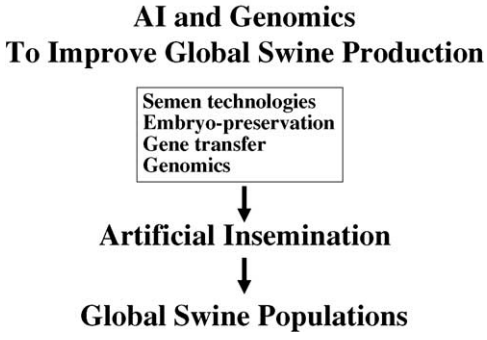

Fig. 1. Artificial insemination (AI) and genomics to improve global swine production. Diagram showing that AI is the crucial intermediate to improve global swine populations using modern biotechnologies.

2. Reproductive biotechnologies with the potential to enhance efficiency of production by AI

2.1. Artificial insemination with liquid stored semen

AI in swine has developed exponentially in the last 35 years for several reasons. This is due to the judicious use of semen and the realization by producers that high-quality genetics is attainable through the application of AI. There is increasing pressure on swine producers to adopt the most economical means of production so as to earn profit. Widespread recognition of this fact was evident in Europe, beginning in the 1970s and followed by significant expansion of AI into the 1990s. The United States, on the other hand, was slow to recognize the benefits from AI and widespread use of AI did not begin until the early 1990s, as reviewed by Weitze [3]. The key to widespread application of AI worldwide is the ability to store semen extended in buffers for up to a week near room temperature. Many extenders have been developed over the years, increasing storage time from 3 days [4] to 5–7 days [5]. There is no doubt that improved extender composition has fueled the growth in AI, particularly in the United States. However, one is unable to document the specific ingredients of 5–10 day extenders because most of the chemical formulas of extenders currently being marketed are proprietary. Even with the advent of longer-term storage technology, the majority of producers are inseminating on the first, second or third day following collection. Levis [5] has provided an excellent review of semen extender technology during the past 20 years.

2.2. Artificial insemination with cryopreserved semen

Cryopreserved boar semen has been commercially available since 1975 [6]. Frozen semen has been used primarily for export and transfer of specific genetics within the domestic market. Some usage of frozen semen for commercial market hog production has been reported [7]. Use of frozen semen in Norway was stimulated by the difficulty of getting liquid semen to outlying regions where standard delivery systems are not economical. Frozen semen is not widely used in the commercial production of swine, simply because it is not economical in comparison to the use of liquid semen [8]). Frozen semen requires two to three times more sperm, the litter size is about one to three piglets per litter less, and the farrowing rate is lower. Nearly 30 years after the introduction of frozen boar semen to the commercial market, it is still considered useable only for specialized genetic transfer applications due to the reduced farrowing rate and impact on litter size. For a more in-depth review of the advances made in hypothermic storage and cryopreservation of boar semen over the past 25 years one should consult the proceedings of the previous four Conferences devoted to the subject [6,9–11].

2.3. Artificial insemination with sexed semen

In contrast to the situation in cattle breeding, sexed sperm is not available for use in commercial swine operations. The technology for sexing swine semen at 95% accuracy and producing piglets with litters exhibiting phenotypic sex at 95% of one sex or the other

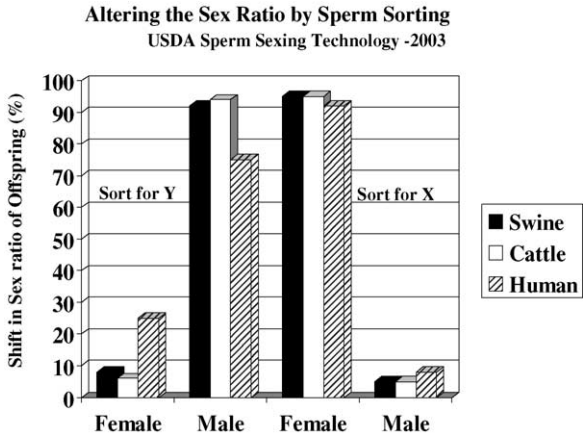

Fig. 2. Altering the sex ratio by sperm sorting using USDA sperm sexing technology. These data show the efficacy of sperm sorting and resultant changes in sex ratios of offspring in swine, cattle and humans under normal sorting conditions; data adapted and modified from that published by Johnson et al. [13].

is available [12,13]. Fig. 2 shows the outcome of sex preselected by sex-sorted sperm for swine, cattle, and humans [13]. The Beltsville Sperm Sexing Technology is limited to producing about 15 million sperm per hour [14], thus making it impractical for standard swine AI. However, as intrauterine and low-dose insemination research moves forward, the practical application of sexing will follow and should have a tremendous impact on swine production worldwide. Current research shows that 50 million sperm inseminated deep into the uterus can produce successful pregnancies [15]. Low-dose technology is critical for optimum sexed sperm usage in a practical, though limited, way. At this stage of development, the impact of sexed semen is similar to the practical use of frozen boar semen, i.e., primarily for transfer of select genetics. Martinez et al. [16,17] have developed insemination catheters and found them to be effective with low numbers of frozen or sexed sperm (50–70 million). Recently, Rath et al. [18] reported the successful preselection of sex after intrauterine AI with sex-sorted boar sperm. One litter of all females resulted from the use of a special deep insemination catheter [16,17]. The use of IVF with sexed semen in the pig has also been shown to be effective [11] for producing sexed embryos. Of all the benefits yet to be derived from technological advances in semen manipulation and storage, sexing sperm may well hold the greatest promise for advancing the reproductive efficiency of swine. Genetic progress, market flexibility and herd management will all be impacted positively by the use of AI and will in turn have a large-scale impact on the genomic character of swine production.

2.4. Embryo preservation

Advances, primarily since 1990, in the development of successful methods to preserve swine embryos provide new tools that will have a major impact on swine production throughout the world [19,20]. Implementation of methodologies for long-term embryo preservation and transfer in pigs would provide a foundation for effective utilization of the

world's most valuable genetic resources, on a global basis, while enhancing genetic improvement programs.

Use of cryopreserved embryos in addition to sperm represents a major increase in the global efficiency of transmitting improved genetic potential while minimizing health concerns. The ability to preserve maternal genetics enables improvement of genetic potential in a form other than the live animal, a first for maternal genetics in swine. Recent outbreaks of foot and mouth disease (FMD) in Europe and other countries illustrate the importance of pig embryo preservation technology to maintain disease-free populations worldwide. Attempts to eradicate this disease caused unintentional loss of millions of animals. If embryos had been cryopreserved and held in long-term storage, permanent germplasm losses could have been averted as present lines could be regenerated through embryo transfer once the threat of the disease outbreak subsided. Herd repopulation through genetic rescue from cryopreservation and embryo transfer of stored genetic lines, as well as importation of genetically superior embryos for transfer, would enhance genetic repopulation. Cryopreservation also permits the transport of genetically superior embryos to developing countries.

A few laboratories have utilized vitrification technologies and developed methodologies that can produce high rates of live offspring after cryopreservation and embryo transfer [21,22]. Delipated morulae/early blastocysts survive cryopreservation and develop normally. The USDA Swine Embryo Cryopreservation Technology [23] is a non-invasive method to cryopreserve all stages of preimplantation pig embryos, from zygotes to hatched blastocysts, resulting in live, healthy piglets that grow normally and are of excellent fecundity. There is a need to improve the in vivo development of cryopreserved embryos after transfer. Presently, less than 30% of transferred embryos actually develop to live offspring. Furthermore, a better understanding of the physiology, endocrinology and synchrony of embryo recipient (surrogate) females at the time of embryo transfer is needed.

2.5. Gene transfer methods

2.5.1. Microinjection

Direct microinjection of the transgene into the pronucleus of a zygote has been the primary method used to produce transgenic swine [24], although the method is rather inefficient (Fig. 3). Micromanipulation requires a considerable amount of skill and specialized equipment. Moreover, the methodology has remained virtually unchanged for the past 20 years.

2.5.2. Sperm-mediated transfer

Recently, numerous researchers have turned their attention toward a second method, sperm-mediated transfer, because of the obvious simplicity (Fig. 3). Although still controversial, sperm-mediated gene transfer involves merely mixing a transgene with spermatozoa and using the mixture to fertilize oocytes, either in vitro or by oviductal AI. Use of sperm-mediated transfer in mice [25] was initially discounted as unrepeatable by many investigators. During the past decade, research on this procedure has persisted and many investigators report successful gene transfers by this technique. Unfortunately, only a

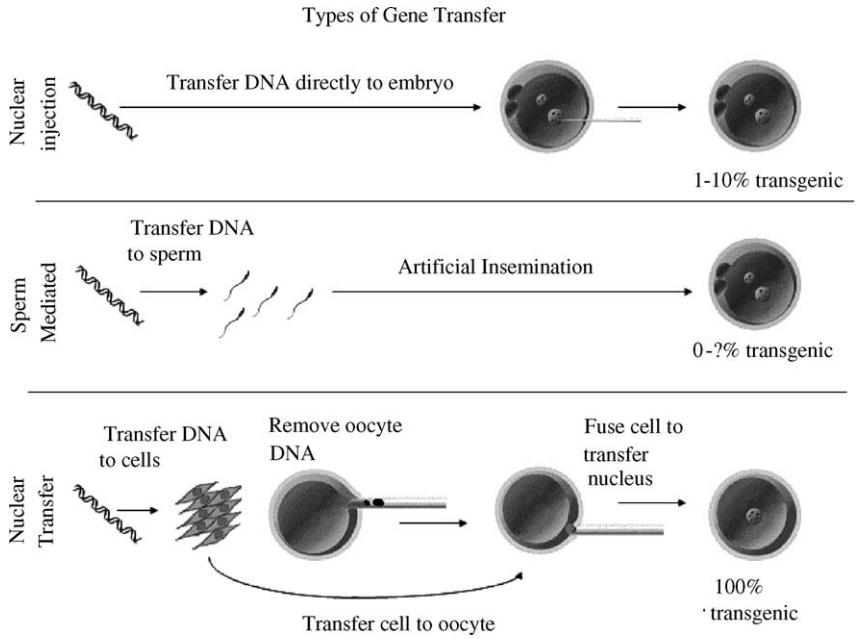

Fig. 3. Gene transfer methods. Adapted from Pursel and Wells (personal communication).

few studies have provided convincing evidence that the transgene was unaltered before or during the integration process and remained capable of appropriate expression in the resulting transgenic animals [24].

2.5.3. Somatic cell nuclear transfer

Somatic cell nuclear transfer (SCNT), also known as cloning, is the third method of introducing genes into the germ line and has recently been developed for swine [26]. This is a two-step process involving, first, transfection of a transgene into somatic cells (primarily fetal fibroblasts) during in vitro culture, and then, inserting the transgenic cell's nucleus into an enucleated oocyte by nuclear transfer (NT). The advantage of this procedure is that a particular genotype can be selected during in vitro culture before NT. In addition, this technique results in site-specific insertion of a transgene by homologous recombination, which will permit one to do gene knockouts or gene replacements. Consequently, SCNT may become the method of choice for gene transfer in this species because the method provides a greater array of possible genetic modifications (Fig. 3). As cloning methodology is improved, far fewer recipient hosts will be required to produce transgenic founder animals than for zygote microinjection.

3. Transgenic pigs to improve production

During the past few years, several research projects have amply demonstrated that transgenesis effectively enhances productivity in swine without adversely affecting animal

health or decreasing their welfare. At present, none of these transgenic pigs have been approved for dissemination to swine producers. However, when transgenic swine are approved by regulatory agencies for general production and consumption by the public, there is little doubt that AI will be used almost exclusively to distribute this valuable germplasm.

3.1. Carcass composition

Pursel et al. [27] produced pigs with a transgene that directed expression of human insulin-like growth factor-I (hIGF-I) specifically to striated muscle. In the 12 founder transgenic pigs that were investigated, muscle IGF-I concentrations varied from 20 to 1702 ng/g muscle compared to less than 10 ng/g muscle in non-transgenic control pigs. Subsequently, one of the transgenic founder boars with a hybrid damline background was mated to 12 non-transgenic gilts from two hybrid sire-lines [28]. Carcass composition was evaluated on 33 transgenic and 42 sibling control pigs at 120 kg body weight. Transgenic gilts and barrows, respectively, had 36 and 29% larger loin eye areas, 9 and 12% more carcass lean tissue, and 18 and 23% less total carcass fat than non-transgenic siblings ($p < 0.001$ for each). In marked contrast to previous experiences with transgenic pigs expressing growth hormone transgenes, definitive phenotypes for the IGF-I transgenic pigs were not detected, and no gross abnormalities, pathologies, or health-related problems were encountered.

Enhanced carcass characteristics provided by the IGF-I transgene serves as an excellent prototype for a transgene that might be economically advantageous to the swine industry. Because society in general will not embrace use of a human gene for food products destined for consumption, a pig IGF-I gene should replace the human IGF-I gene used in this study. In addition, use of a gene switch that would enable IGF-I expression to decline to endogenous levels in striated muscle prior to harvest may be essential to overcome regulatory roadblocks that will accompany any transgenic animal that is destined for the marketplace.

3.2. Milk production

Wheeler and coworkers at the University of Illinois [29] have produced transgenic pigs that express bovine α-lactalbumin (α-lac) in their milk, resulting in a higher milk lactose content in early lactation and a 20–50% greater milk yield on days 3–9 of lactation than was found for non-transgenic sows. Weight gain of suckling piglets from α-lac first-parity sows was greater at days 7 and 21 after parturition than that of control piglets. Thus, over-expression of α-lac milk protein provides a means for improving the lactation performance of pigs.

3.3. Phosphorus utilization and decreased excretion

Forsberg and coworkers at the University of Guelph [30] constructed a transgene to provide expression of phytase in the salivary glands of pigs. The saliva of these pigs contains the phytase that allows pigs to digest the phosphorus in phytate, which is the

most abundant source of phosphorus in the pig diet. Without this enzyme, phosphorus in phytate passes undigested into the feces to become the single most important pollutant of swine manure. Their research showed that salivary phytase essentially provides complete digestion of dietary phytate phosphorus, relieves the requirement for inorganic phosphate supplements, and reduces fecal phosphorus output by up to 75%. These pigs offer a unique biological approach to the management of phosphorus nutrition and reduction of one of the major environmental pollutants generated on swine farms.

4. Genomic biotechnologies with the potential to enhance AI

4.1. Swine map update

Swine genetic maps were developed rapidly in the early 1990s due to the discovery of microsatellite markers [31] and a worldwide emphasis on map development. By 1994, there were approximately 500 genetic markers mapped [32–34]. However, only the map produced by the US Meat Animal Research Center has been continually developed. This map contained over 1000 markers in 1996 [35] and now has over 3000 loci (http://www.marc.usda.gov/genome/genome.html). Half of these loci are microsatellite markers and the other half are single nucleotide polymorphism (SNP) markers associated with genes (Table 2). Another type of swine map that has developed rapidly is the radiation hybrid (RH) map. The RH map, first published by Hawken et al. [36], had over 700 markers but at last report over 7000 loci had been mapped. These maps can be accessed on: http://www.genome.iastate.edu/pig.

The swine genomics community is preparing for a whole genome sequencing project by developing a bacterial artificial chromosome (BAC) fingerprint map of the entire genome through a collaborative project with USDA Agricultural Research Service, the British Biotechnology and Biological Sciences Research Council, and the University of Illinois. The anticipated completion date for the BAC map is early 2005. The BAC map will be essential for the efficient sequencing of the swine genome. A white-paper to sequence the swine genome was submitted to the National Institute of Health and received a high scientific priority (http://www.genome.gov/10002154) in 2002. Funding to complete the sequencing project still needs to be identified.

Table 2
Swine linkage map update

Type of marker	MARC map
Microsatellite	1546
Single nucleotide polymorphisms (SNPs)	1759
Other (RFLP)	91
Total	3396
Total number of genes represented	>1200

Data from USDA MARC Swine genome database, 2003.

4.2. Swine genetic markers for production

Literally, hundreds of associations between performance traits and genetic marker information have been published. A comprehensive review of this research is summarized in a recent review article by Bidanel and Rothschild [37]. The association of a performance trait with a genetic maker or region of a chromosome is termed a quantitative trait locus (QTL). QTL have been detected for virtually every important performance trait ranging from growth and body composition to reproduction, pork quality and immune function. Fig. 4 shows the QTL mapping for several important production and reproduction traits [38,39]. A QTL affecting serum follicle-stimulating hormone (FSH) maps near the position 70 cM with a distinct peak due to a large number of records (>400) and a large effect of the QTL on reproduction. The lower peak for backfat (BF) is likely due to a smaller effect of the QTL and the flat peak for testes weight (testes) is due to the low number of measured animals (<100). Detailed genome mapping has helped delineate the chromosomal locations for some of these QTLs [38,39]. More information has been gained by comparative genome mapping using the human and mouse genome maps to help identify candidate genes (Fig. 5) [40]. However, few of these QTL have been transferred to the swine industry. Some of these associations are not real (false-positives) or may not be useful to commercial swine production as the variant alleles are only present in the research population studied (most populations contained Meishan germplasm). For others, a useful assay for the industry has not been developed.

The most effective method to transfer a QTL to the swine industry is by assaying the actual variation in the DNA sequence that causes the difference in performance. Unfortunately, identifying these variations requires a large amount of resources and time. Trained animal breeders could use QTL information in industry pigs; however, there is a large upfront cost and the current cost of commercial genotyping is too great.

In spite of all of the resources required for transferring information to producers, there are currently several genetic tests commercially available or being used by swine companies. The first and probably most valuable test developed was one that determined an animal's susceptibility to the porcine stress syndrome. The syndrome is caused by a single nucleotide difference in the DNA sequence of the ryanodine receptor [41]. Other genetic tests are currently available that can improve pork quality (RN gene, [42]), growth and leanness (near IGF2, [43,44]) and reproduction (ESR, [45]). The vast amount of research in this area will hopefully produce a large number of genetic tests for swine producers in the near future.

4.3. Swine genetic markers for disease resistance

Sellwood [46] was the first to identify pigs that are fully resistant to a disease, bacterial (*Escherichia coli*) diarrhea, and proved that this resistance was due to lack of expression of the intestinal K88 receptor (F4 receptor). Despite years of research using modern genomic tools, the gene encoding this receptor has been localized to a region on swine chromosome 13 (SSC13), but the exact locus is still not known. Although breeding companies do offer F4-resistant stock, to date there is no publicly available, quick molecular test for this trait.

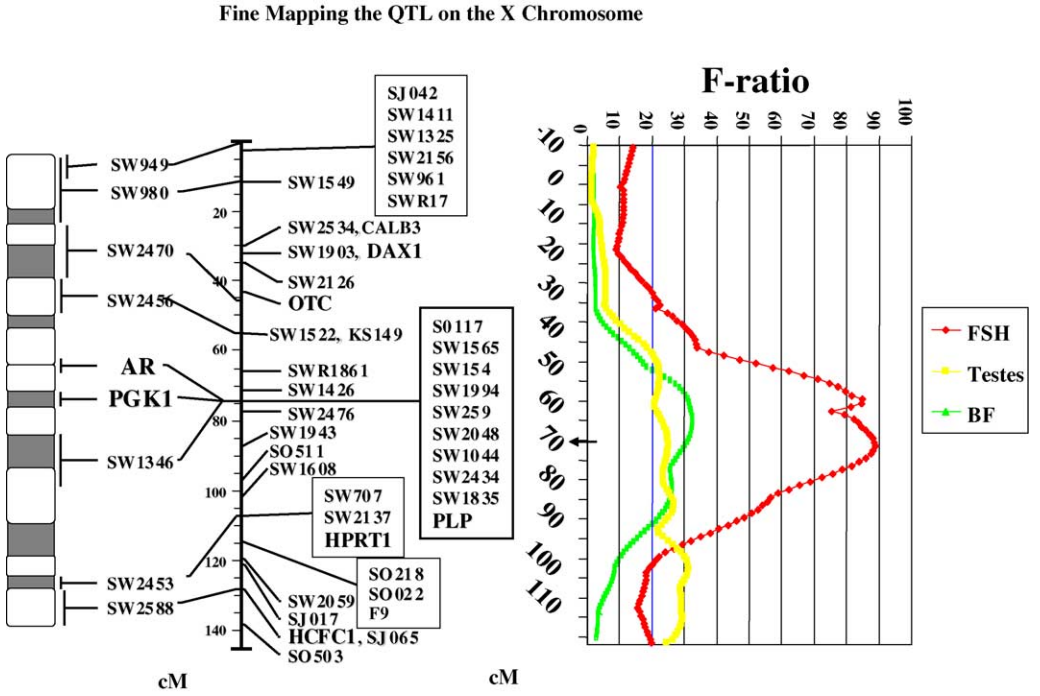

Fig. 4. QTL mapping for several important production (backfat depth, BF) and reproduction traits (testes weight, Testes; serum FSH concentration, FSH). The left-hand side depicts the physical and genetic maps for pig X chromosome where the physical map indicates the position on the banded chromosome (far left) and the genetic map has a stick diagram of the linear alignment of genetic markers with the distance between markers relative to the amount of recombination expressed in centi-morgans (cM). The right-hand side shows the statistical support for the presence of a QTL; an *F*-ratio of approximately 20 is required for genome-wise significance. The statistical support for a QTL affecting serum FSH is greatest near the position 70 cM. The distinct peak for FSH is due to a large number of records (> 400) and a large effect of the QTL. The lower peak for backfat (BF) is likely due to a smaller effect of the QTL. The flat peak for testes weight (testes) is due to very few measured animals (<100). Detailed genome mapping has helped delineate the chromosomal locations for some of these QTLs; adapted from Rohrer et al. [38,39].

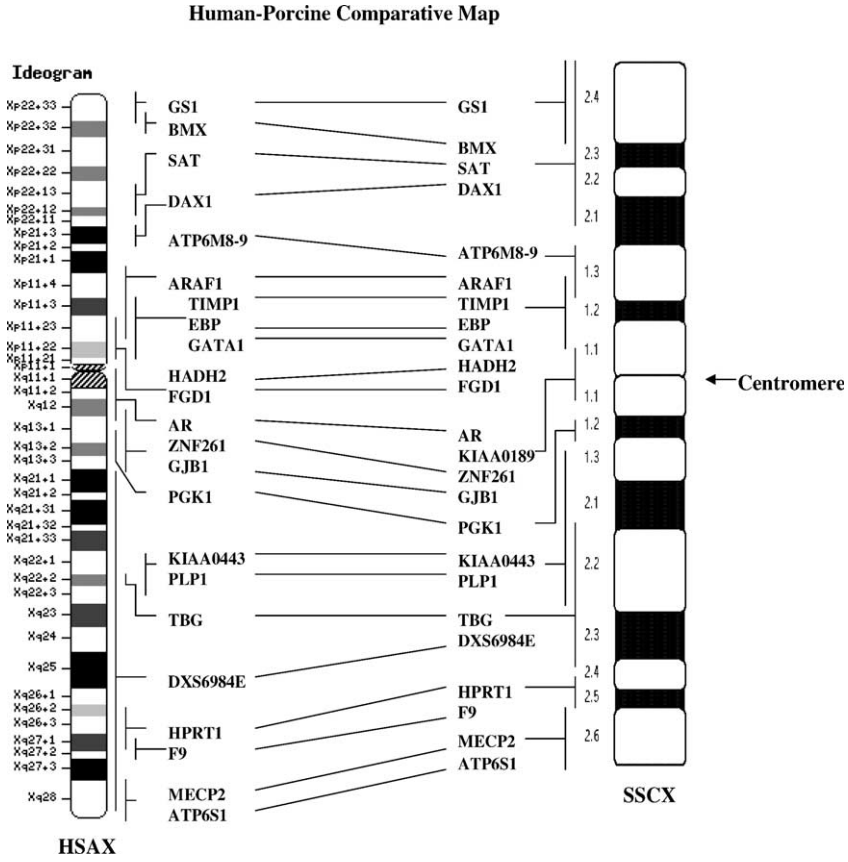

Fig. 5. Comparative genome mapping. Comparative mapping of human and swine X chromosome maps to help identify candidate genes; adapted from McCoard et al. [40]).

Researchers have developed a molecular test for alleles of the FUT1 gene on SSC6 that is associated with post-weaning diarrhea due to *E. coli* F18 infections.

Researchers worldwide have noted the influence of genes in the major histocompatibility complex (MHC), or swine leukocyte antigen (SLA) complex, on SSC7 on protective immune, vaccine and disease responses [47]. These SLA associations rarely encode complete disease resistance, but as with most disease QTL, they alter the time course of infections or the severity of disease symptoms. Reiner et al. [48] identified several potential QTL for resistance/susceptibility to pseudorabies virus in swine. Putative receptors for viral infections, such as for the porcine reproductive and respiratory syndrome virus (PRRSV), have been studied, but genetic alleles associated with PRRSV resistance or susceptibility have not yet been identified, nor is it clear whether single genes would encode resistance to this virus [49]. A recent symposium highlighted the potential for selected pigs with improved health characteristics [50].

4.4. AI and genetics to improve disease resistance

Researchers have taken multiple approaches to identify disease-resistant pigs. Wilkie and Mallard [51] selectively bred pigs for specific immune traits. Edfors-Lilja et al. [52] identified QTL for immune capacity in the pig. Dawson et al. [53] developed functional genomic tools to quantitate immunity. Others are actively working to identify SNPs in immune-related genes. This research will test the hypothesis that variation in ability to respond immunologically correlates with pig health and should help breeders to identify improved stock for AI boars.

Numerous other factors must be considered in planning to breed or select AI boars for disease resistance. Should these studies focus on a single or multiple disease agents? What disease responses (phenotypes) need to be selected: mortality, morbidity, carrier status, transmission in reproductive tissues? Would selection for faster recovery from disease be an advantage? Would identifying highly susceptible animals be useful for removal from breeding stocks? Would disease-resistant breeding stock be useful for repopulation strategies, e.g., for l'Office international des épizooties (OIE) list A diseases (http://www.oie.int), like FMD or African swine fever virus? Which diseases are worth the research investment to identify resistant pigs for future AI boars?

4.5. Biomedical applications for AI

Biomedical uses of pigs change the disease focus substantially. Transgenic pigs are required for many transplant and nutraceutical applications; thus, AI is essential. Such swine are raised under high biosecurity, yet there are still major disease issues to be addressed. Questions about the effects of porcine endogenous retrovirus (PERV) have prohibited xenotransplants. Chardon and his colleagues have used genomic techniques to map and enumerate PERV sequences in the pig genome using BAC libraries [54]. Their recent results suggest that genetic selection can be designed to identify animals lacking a potentially active PERV [55].

5. Genetic and molecular biotechnologies with the potential to increase use of AI

New techniques in functional genomics, transcriptomics and proteomics provide the tools to simultaneously investigate a host of rate-limiting steps regulating economically important multiple gene traits of livestock. The genome is the entire set of genes that is encoded by the DNA of an organism, the transcriptome is the entire complement of mRNA transcripts transcribed from the genome, and the proteome is the entire complement of proteins expressed at a single point in time [56]. Such capabilities will give us a more holistic view of the complex physiological, neurological and endocrinological pathways that control reproduction and growth and the ability to elucidate the function of newly discovered genes. For example, determination of the function of thousands of genes and their protein products simultaneously will reveal the genetic basis, including regulation, of entire biochemical pathways, such as those controlling fat cell replication and differentiation, the neural network of the brain centers that regulate luteinizing hormone

and growth hormone secretion, or the neural circuit by which leptin and other fat cell secretions signal metabolic status to the brain-pituitary unit.

Genome markers, probes, primers, genome libraries, libraries of ''2-D'' protein maps and other biological tools for research and genetic improvement will result. This new knowledge will facilitate the development of gene knockout and transgenic animals and marker-assisted selection. Integration of functional genomics with traditional genetic approaches, along with detailed analysis of the transcriptome and proteome as well as relevant whole animal phenotypes, will make full use of these powerful new tools [57].

6. Application of genetic markers in the industry

The most rapid approach to improve performance and disease resistance using genetic markers in a herd of swine would be to genotype all animals and immediately remove those that have undesirable alleles. However, this is definitely not a practical approach. As the current return on investment in swine production is quite low, producers need a more economical approach.

Fortunately, use of AI has become a common practice in commercial swine production. Now an AI stud can pay to genotype a boar and amortize the cost over hundreds or thousands of units of semen that will be sold from the boar. A producer could reduce the frequency of an undesirable allele in his/her population by 50% each generation by purchasing semen from boars with two good alleles of the gene. This method of transferring desirable alleles from genotyped AI boars would also have a trickle-down effect in pyramid breeding systems. Once an undesirable allele has been eliminated from the elite herd, the multiplier and commercial herds would eventually reap the reward from the use of genetic markers in boars used in the elite herd. Therefore, adoption of one technology, AI, by the swine industry should facilitate adoption of marker-assisted selection.

7. Conclusions

The genetic composition of all living creatures is continually undergoing alteration by mutation, natural selection and genetic drift. Humans have further manipulated the genetic composition of animals to enhance their health and usefulness by selecting for specific phenotypic traits. Development of recombinant DNA technology has enabled scientists to isolate single genes, analyze and modify their nucleotide structures, make copies of these isolated genes, and insert copies of these genes into the genome of animals.

Implementation of methodologies for long-term embryo preservation and transfer in swine would provide a foundation for effective utilization of the world's most valuable genetic resources on a global basis while modernizing production and enhancing genetic improvement programs. It is now time for breeders and producers to adapt pig embryo cryopreservation and transfer into swine production for propagating select genetics and maintaining germplasm resources for the future.

As we look back on genetic improvements in the swine population over the past 40–50 years, it is evident that the swine industry readily adopted technologies that give the

greatest economic advantage for pork production. As we view newer biotechnologies now coming on line, it is clear that a marriage of existing technology (preserved and sexed semen, low-dose insemination, embryo transfer) with genomic, proteomic and disease resistance technology is required to truly impact improvement of the global swine population.

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