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Genetics of production and product quality: A Minnesota perspective

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The past half-century in American agriculture has witnessed a significant increase in on-farm production and product quality. Major advances in technology have fostered this improvement and, with it, economic power, but the expansion of integrated production systems dedicated to maximize output of a relatively homogeneous product has created new issues related to product quality, bio-security, and food safety. This is no less true for the swine industry. Industry responsiveness to increasing consumer and governmental pressure for product quality assurance or certification is hampered by a lack of information relating to such issues in vertically integrated production schemes that extend from "semen to cellophane." Diverse global management schemes further complicate the flow of information regarding those products during and post-production. Adapting or altering current management systems to address these issues and improve overall product quality clearly depends on how well we are able to integrate a series of biological disciplines, informatics, industrial developments, health and environmental promotion, and social expectation. Economic reality also dictates that new approaches to selection for improved product quality and safety be implemented. The potential for emerging DNA-based technologies and bioinformatics in enhancing swine production efficiency and product quality through selection appears to be significant and may play a crucial role.

Current swine production schemes address four traits of major economic significance to the producer and ultimately to the consumer:

- product quality,
- reproductive performance,
- production efficiency (e.g., lean growth), and
- disease resistance or susceptibility.

In general, management programs have not taken into account the issues of biosecurity, food-borne pathogens, and product certification or 'branding', and it is only recently that they have begun to be discussed and attempts made to incorporate them into production and monitoring schemes. Subscription to an international quality assurance system for production is a first step, but does not provide a guarantee that an individual product is of high quality, merely that the producer has adhered to a particular quality assurance scheme.

Creating certifiable high quality pork product(s) requires a multifaceted strategy that facilitates genetic selection for improved product quality and production efficiency and tracks those products through to the consumer. It should also take into account the use of molecular diagnostics to monitor current and emerging infectious, production-related, zoonotic, and food-borne pathogens. A molecular epidemiologic component that incorporates such diagnostic tools for pre- and post-harvest surveillance of specific pathogens on a local, regional, national, and global basis could significantly reduce industry loss as well as improve product safety.

One feature of such a strategy might be the use of emerging DNA based technologies that identify traits of economic interest. Genetic markers derived from the swine genetic map can be used to identify chromosomal regions that influence economically important traits (ETLs), improve selection accuracy by augmenting current breeding practices, and assist in the development of trademarked products (e.g., unique to a particular source). Markers on a genetic map, simply, give us an idea of what they are near when we seek to identify the locations of genes associated with specific traits. When sufficiently close to the gene or genes responsible for the trait of interest they segregate with that phenotype and identify specific animals whose germplasm can be used in current programs of genetic selection.

Identification of chromosomal locations (loci) of economically important traits within and between commercial breeds currently under production is already underway. For example, markers are being used to focus on specific chromosomal regions already identified with back fat accretion and rapid early growth in commercial populations. Simultaneous development of genetic markers unique to commercial breeds, herds and individual animals potentially provides a hitherto unavailable means to identify the value-added products of each animal through each phase of swine development including growth finish, packing, and retail to the consumer. Identification of ETLs can improve selection accuracy and decrease the cost of progeny testing by allowing selection at a young age. Markers closely flanking the ETL can be used to select

progeny that have received superior alleles. This process of marker-assisted selection, or MAS, can be implemented immediately after detection of an ETL when markers flanking an ETL are sufficiently close (tightly linked) to permit following the trait indefinitely in a selection scheme. Construction of marker panels specific for breed, herd, and so on could immediately and significantly impact the swine production and allied industries. There are several reasons for this. First, genetic improvement of economically important traits, such as production and health, is sustainable because genetic gain is permanent and cumulative. Second, it is clear that genetic markers can identify chromosomal regions that account for significant amounts of variation of an economically important trait in commercial breeding herds. The number of markers needed to implement MAS for individual economic traits in commercial herds and provide positive identification of breed, herd, and individual animals throughout production is currently under active research. Once the transfer of marker technology to commercial populations has been demonstrated for one trait (e.g., growth between weaning and feeder size), there is little reason to think why this strategy cannot be extrapolated to other traits. Significant statistical support for an ETL for early post-weaning growth rate on swine chromosome 1 that explains 25% of the genetic variance in progeny from an experimental population is already available (Paszek et al. 1998). What is the immediate economic impact of such a strategy? Minnesota Agricultural Statistics for 1996 indicate that roughly 55% of every dollar earned from farrowing to feeder size (~$35 x 0.55 = $17) is spent on feed from all sources. If we reduce that figure by only 25% (25% improvement in genetic gain) multiplied by 6.5 million hogs (60 lbs.) produced in 1996, a savings of $4 x 6.5 million pigs or ~$26 million is achieved. The process is easily transferred to genetic improvement in other production traits.

Similarly, circumstantial evidence exists for individual susceptibility to bacterial disease. Progress in investigating this possibility has increased dramatically in swine with the availability of probes for a wide variety of "candidate" genes and molecular genetic evidence that accounts for significant variation in the polygenic response to infectious pathogens. Although the exploration of host susceptibility to infectious agents at the molecular genetic level has only just begun, several tantalizing insights are available that provide some indication of the complexity of the mechanisms involved. Initial indications of associations between the incidence and severity of infectious bacterial and viral disease and particular DNA or protein polymorphisms provide impetus for marker/informatics-based whole genome searches for such loci in production herds. However, to date, the list of definite susceptibility loci remains relatively small (Guerin et. al. 1993). Since it is clear that no one gene, or form of a gene, can confer resistance to all pathogens, even marker-based selection for "resistance" may have to be balanced to ensure that a herd or population would have an adequate immune response to a variety of pathogens. Alternatively, susceptibility to a specific pathogen, whose presence is confirmed by DNA-based means, could be selected against, while maintaining marker and allelic heterozygosity for general immune responsiveness and other production traits. As the human genome effort increases our knowledge of the function of genes involved in the complex relationship between host and pathogen, it will allow us to identify new marker traits associated with resistance or susceptibility and produce genetic markers useful for MAS in swine. The economic implications of further research involving host and bacterial or viral genomes and their subsequent transmission for more effective control and management of infectious and zoonotic diseases and foodborne pathogens in swine are significant.

Genetic markers are also useful as a DNA-based diagnostic tool for parentage testing (Heyen et al. 1997). They can also be applied for diagnostic purposes beyond parentage testing such as DNA fingerprinting of a particular inbred line, a cross, or a company product. Consumer, producer, and regulatory concerns over food safety clearly warrant development of means to identify high quality, biosecure products at the production and retail level. The potential for swine producers to use DNA fingerprints to determine the identity of a swine product, or track a swine product from producer to consumer is real and provides the producer with the added value of brand naming or "bar coding" a pork product as to its uniqueness or origin.

A similar scenario can be applied to the use of DNA-based diagnostics for specific pathogens, which—when routinely incorporated into a production scheme that employs DNA-based typing (e.g., for herd or trait identification)—can be used to provide the producer with real-time estimates of production and product quality. This in turn provides the consumer with a high quality product that can be certified as such. The routine incorporation of DNA-based molecular diagnostics for specific pathogens identifies if, when, and where a break in quality assurance has occurred at any point during production or packing, obviates the inconsistencies in clinical diagnosis and inability to diagnose sub-clinical disease, and allows the producer or packer to categorically state "we don't have it."

Most importantly, informatics is an essential feature of any strategy to improve production efficiency, product quality, and safety. Although, to a large extent bioinformatics is currently confined to a drug and gene discovery phase within the pharmaceutical and plant agriculture industries, respectively, this will not continue in the future. Bioinformatics is now permeating every research and production area. With our rapidly increasing knowledge of DNA polymorphisms in swine and depen-

dence on a global export economy, bioinformatics will become the most important tool in the analysis of results from disease monitoring through selection, production, packing, and marketing. As such, bioinformatics has the potential to redesign entire management schemes to affect increases in efficiency, product quality, and biosecurity on a global scale. Obviously, assimilating, warehousing, integrating, and transferring this information between the producer, packer, and public health agencies requires improved, on-site relational (informatics) databases capable of remote access. To maximize efficiency, any informatics platform(s) that incorporates DNA-based monitoring of production, zoonotic, or foodborne pathogens in a production scheme should be incorporated into a state, federal, and global surveillance or epidemiologic approach that incorporates the appropriate health agencies. The information should be available to individual and corporate producers via an appropriate monitoring agency to limit the potential for regional, national, or global spread, particularly with emerging or reemerging pathogens.

The opportunities to establish such platforms are real and should be encouraged as part of an overall industry goal to improve product quality and safety. The issues of how this information will be stored (warehoused), transferred, and used even within a single production system are complex, but not insurmountable. Initially, recording basic events in the production life of individual animals or even on a pen basis (e.g., weights at major points in the growth cycle) would go far towards generating sufficient data to improve animal uniformity. Real-time integration of data streams from nucleus herds and remote multipliers would allow interactive monitoring of performance to reduce variability through appropriate selection. Real-time monitoring of specific pathogens coupled with herd identification could be a first step in product identification, product tracking, and certified biosecure products.

Finally, we must consider the prospect of cloning for economic traits of interest within the context of the new millenium. While pigs have proven a difficult subject, merging the cutting-edge technology developed for cloning in the mouse with that used to create 'Dolly' the sheep, promises to provide a breakthrough in the use of swine organs as xenografts for human transplant. Pigs, genetically engineered to bypass rejection by the human immune response, will certainly provide extensive basic information on the immune system and how pigs respond to pathogen invasion. Extending this technology as a platform for post-selection multiplication once carriers of specific alleles are identified, or as a single platform for selection, is clearly on the horizon. Its potential merits and drawbacks should be considered and discussed as the industry enters the 21st century in the face of increasing global competition and the challenge of increasing production efficiency, product quality, and safety on a global scale.

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