We are delighted that the International Pig Veterinary Society Congress 2004, decided to select South Africa as the host country for the 20th IPVS Congress. The Pig Veterinarians of South Africa will ensure that this congress lives up to the best traditions of previous congresses; incorporating an interesting and topical scientific programme, fascinating accompanying persons tours and an excellent social programme, allowing delegates the opportunity to network with their overseas colleagues.

This, the first IPVS congress on the African continent, will undoubtedly be of enormous benefit in generating solutions to the emerging pig veterinary challenges, especially those related to exotic and changing viral diseases, decreased use of antimicrobials and nutritional advances. The congress is important to further pig veterinary science in South Africa, to encourage younger veterinarians to join the pig industry, as a vehicle to generate funds for research and to improve the pig industry in Southern Africa.

South Africa is a magnificent and beautiful country, and offers tourists value for money. Thus, pre and post congress tours will be a major attraction for delegates to come to South Africa. Durban, in KwaZulu Natal, is a vibrant multi-cultural city with magnificent beaches, easily accessible game parks, theme villages and a moderate winter climate making it an ideal tourist destination. We urge our colleagues throughout the world to use this opportunity to get a glimpse of the continent’s rich and fascinating wonders and to enjoy the hospitality of their African friends.

Dr Peter Evans
Chairman: Local Organising Committee: IPVS 2008
GENETIC IMPROVEMENT OF PORCINE HEALTH

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Introduction

Selection within domestic animal populations has taken place for centuries. However, the first initiatives to exploit performance testing in pigs were not initiated until around the beginning of the last century. The purpose of artificial selection is to obtain genetic improvement for important traits. In respect to choice of breeding goals the economic importance of a given trait is of great significance, furthermore, possibilities for measuring the trait of interest directly or indirectly is a requirement. In the period from 1945 to around 1970 the primary breeding goal in the Danish breeding system was meat content. The development of more sophisticated computational and statistical methods has had a great impact on the efficiency of the selection programs used in animal breeding. In modern breeding programmes a number of breeding goals, separately assigned with an economic weight, are combined for selection in the individual breeds. The most important selection objectives are production traits such as growth rate, food conversion, lean weight and litter size. However, during the latest years the incentives for also considering health related traits has been increased. Thus, in many breeding programs for instance conformation has been included in the breeding objectives.

Traditional selective breeding has produced enormous improvements largely through selection on phenotype. That is, identification of genetically superior animals through their own performance and physical characteristics and those of their relatives. However, the growing understanding of the genome and accompanying technological innovations has opened up possibilities for direct identification and selection of animals carrying the best genes. Thus, selection on genotype has become a possibility.

In the following traditional selection and genomic selection will be discussed together with examples and prospects for genome research.

Complex versus simple traits

Most traits of agricultural importance in livestock are influenced by variation of several or many different genes. The effects of these genes combine to produce continuous (or quantitative) variation between animals in traits such as growth rate, litter size and susceptibility to disease. For traits that are difficult or costly to measure, such as disease resistance, it is difficult to identify which animals carry the best alleles simply from their performance. In such cases, the ability to directly identify animals carrying valuable alleles using DNA-based tests will provide a much improved means of selecting superior animals.

Selection for aspects of lean growth has been associated with high frequency of stress susceptibility (1; 2). Stress susceptibility as defined by halothane sensitivity caused by the HAL mutation (n), is an interesting example of a gene with both positive and negative effects also having an impact on both a complex (quantitative) and a simple (qualitative) trait. Pigs that are homozygous for the mutation (i.e. carry two copies of the Hal mutation) have a high frequency of death caused by stress, produce meat of low quality but are leaner. Thus, using traditional phenotypic selection, it has not been possible to eliminate the deleterious allele. In 1991, however, Fujii and his colleagues (3) showed that the gene responsible for stress susceptibility is the ryanodine receptor gene and they identified the point mutation. This discovery allowed a direct DNA test to be developed to discriminate accurately between all three genotypes (nn, Nn, and NN) and this has subsequently been widely adopted by pig breeding companies. It has been estimated that the removal of the HALn allele from a breeding line has reduced the death through porcine stress syndrome from between 4 to 16 per 1,000 head to zero and at the same time substantially improved meat quality (Max Rothschild and Graham Plastow, personal communication).

In general identification of genes underlying quantitative traits requires a lot of efforts and is much more time consuming and costly compared to identification of genes underlying simple traits. In both cases, however, the general approach is to perform a whole genome scan aiming at scanning the entire genome for regions which are associated with variation in the traits of interest. This approach relies on the phenomenon of genetic linkage that allows individual markers to be used to follow the inheritance of a segment of a chromosome. The segregation of markers spaced at intervals through the genome is studied together with the segregation of the traits of interest. Such studies results in the identification of quantitative trait loci (QTL), i.e. regions of the genome in which genes influencing the traits of interest is located. The results from all genome scans performed in the pig has been collected in the Pig Quantitative Trait Loci Database (PigQTLdb) (4). The database reports on 1,263 QTL representing 236 different traits. Only six of these are listed under the trait description “disease resistance” and specific knowledge leading to the establishment of DNA tests has only been obtained with respect to two disease traits. These traits will be discussed later.
Examples of genome scans
To illustrate how genome scans are conducted two ongoing projects in the research group at Genetics and Bioinformatics, IBHV, KVL will be described in the following.

Within the EU project “Control of Porcine Circovirus Diseases (PCVDs): Towards Improved Food Quality and Safety” one of the work packages is focusing on molecular genetic characterization of the host response to PCVD/PMWS infection and aim at identifying the gene(s) responsible for susceptibility/resistance in the pig. The evidence for genetic aetiology of the disease is circumstantial. I.e., both field studies and experimental infection studies have shown that in a given pen/among a given litter only some individual pigs exhibit clinical signs of PCVD/PMWS, and certain boar lines have been reported to produce either a high or a low number of susceptible offspring. We use a range of complementary approaches to work towards identifying the genes potentially responsible for the differences in susceptibility and to pinpoint the molecular mechanisms in the host responsible for development of disease. A total genome scan is conducted in families in which susceptibility is segregating in order to identify regions of the genome harbouring genes influencing susceptibility/resistance towards PCVD. Following the identification of candidate regions expression studies of the genes will be conducted and fine mapping using additional markers will be used to identify potential allelic differences between susceptible and resistant animals.

We are also involved in a study concerning Ascaris suum in collaboration with Parasitology, IVP, KVL. Infections by the nematode A. suum are often present with high prevalence in the pig population (5). An extremely aggregated distribution of Ascaris with a few pigs carrying the large majority of the adult worm population is characteristic for both natural and experimental infections (reviewed in 6) indicating that host genetics is of importance in regard to worm burden. In order to examine the association between host genotype and resistance to parasite infections, 195 piglets have been produced after artificial insemination of 19 Landrace/Yorkshire sows with semen, from 13 Duroc boars (7).

The piglets were reared outdoors and they received infections with Ascaris suum eggs for 14 weeks. Faecal samples have been taken at regular intervals during patency and examined for eggs. The results of the egg count indicate that there are clear differences in parasite load, between litters, which most likely are related to host genotype. Linkage analysis using genetic markers is underway. These analyses will focus on candidate regions identified in the human genome in a study of Ascaris infected humans in Nepal (8).

Genome scan has also been performed in order to shed light on the genetic background for a variety of different inherited defects. For instance anal atresia (9); artrogryposis multiplex congenital (10) and hernia (e.g. 11).

DNA tests for disease traits
As mentioned above, DNA based tests have been established for two disease traits. These traits are susceptibility/resistance towards E.coli F18 and E.coli F4. Both traits are controlled by a single gene. Adhesion of F18 and F4 fimbriated E.coli to small intestinal brush border membranes causes edema disease/post-weaning and neonatal diarrhoea in piglets respectively. These diseases are of considerable economic significance in the pig breeding industry, thus, it is desirable to eliminate genetically susceptible pigs from breeding herds.

The gene potentially controlling expression of the E.coli F18 receptor (a(1,2)fucosyltransferase, FUT1) has been characterized by Meijerink and co-workers (12). A polymorphisms resulting in the amino acid substitution at position 286 (ArgÆGlu) has been shown to segregate together with susceptibility/resistance towards E.coli F18. The DNA test established for discriminating between resistant and susceptible animals have been patented with exclusive rights to “Pig Improvement company” (PIC). No information on the outcome of the selection against the disease has been published as yet.

The gene potentially controlling expression of the E.coli F4 receptor (mucin 4, MUC4) has been characterized by Jørgensen and co-workers (13). A polymorphism in intron 7 has been shown to segregate together with susceptibility/resistance and a DNA test has been established. The test is available through commercial genotyping laboratories. In 2003 the Danish breeding company DanAvl started breeding efforts in order to breed resistant finishers (14). At the start of the program the frequency of resistant animals in the Landrace and Yorkshire population was 1% and 20% respectively. The comparable numbers were 88% in Duroc and 100% in Hampshire. After approximately two years of selection, the frequency of resistant animals in Landrace has increased to approximately 11%. Preliminary data indicate that the breeding program influences the breeding index in a positive manner.

Conclusion
During the latest years a lot of new resources of importance for genetic research have been generated. Sequencing of the porcine genome has been initiated, thus the amount of sequence information is growing rapidly. Through the Sino-Danish pig genome sequencing project approximately 3,84 million shotgun sequences (0,66X coverage) of the pig genome have been generated (15) together with approximately 1 mill sequences from coding regions (16). Furthermore,
high throughput technologies are under development both in regard to genotyping and expression studies. Thus, it is becoming easier to get from the knowledge of the phenotype of a trait of interest to characterization of the genotype behind it.

Knowledge of the genetic and phenotypic relationships between traits will enable evaluation of more efficient selection strategies. Given that it is difficult and costly to measure disease traits it would, of course, be of great advantage if it was possible to identify a genotype that was superior with respect to disease resistance in general. A challenge for breeding is to select superior animals and reduce the genetic variation on one side and to conserve genetic variation at loci that are involved in immunity. Studies both of the innate and cellular immune response indicate that it is of great importance to maintain a high degree of polymorphism in many genes involved in immunity rather than breed for a specific genotype (e.g. 17). More studies of host-pathogen interaction together with more information about the individual components of the immune system will be of benefit to sustainable animals breeding. In addition specific knowledge of host-pathogen interaction will be of immense importance in respect to development of more efficient vaccines.

Although collection of good performance information will remain crucial for the foreseeable future, high-density marker information will certainly complement or even to some extend replace pedigree recording. The future of animal breeding is genomic breeding where all specific information concerning the genetic and phenotypic information is included together with marker information covering the whole genome.

References


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