



## Summary of papers relevant to pig genetics presented at 7<sup>th</sup> World Congress Applied to Livestock production

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### *Introduction*

The 7<sup>th</sup> World Congress Applied to Livestock Production (7WCGALP) was held in France (Montpellier) from the 19<sup>th</sup> to 23<sup>rd</sup> of August 2002. The conference is held every four years and covers a wide range of topics relevant to animal breeding. More than 1000 papers were presented in 29 sessions during this conference. No attempt is made in this summary to provide a full cover of the whole program but rather to present a selective summary of papers that provide an overview of the research topics that are currently underway worldwide in pig breeding. Please contact me, if you are interested in further information (e-mail: [Susanne.Hermesch@pobox.une.edu.au](mailto:Susanne.Hermesch@pobox.une.edu.au) or phone: (02 6773 3787).

### *Invited reviews*

***New sources of information in pig breeding*** by Jan Merks and Aflred de Vries (The Netherlands). This review summarised the data available to pig breeders covering growth, carcass, sow productivity, and genomic information. The fast amount of data requires sophisticated systems for data management which have been or are in development by a number of breeding organizations. The authors conclude that breeding organisations will use information from two sources: 1). Nucleus (and multiplier) herds in which relatively small number of purebred pigs are followed intensively for a wide range of information (including molecular information). This information is the main basis for genetic evaluation. 2). Commercial herds in which huge numbers of pigs (sows as well as slaughter) are followed for specific information to improve and/or monitor the breeding program. This information is used for breeding value estimation as well as for monitoring the indirect/side effects of selection decisions to ensure a balanced breeding program.

***Simultaneous improvement of meat quality and growth-and-carcass traits in pigs*** was discussed by Pieter Knap and co-authors (Germany). The paper covers the practice of selection for meat quality in the early nineties, followed by a description of developments during the past 10 years. Various breeding objectives and selection procedures used by different breeding companies are outlined. Links to web pages of various companies and organizations are included. The efforts of various research groups to explore opportunities of marker-assisted selection are outlined.

Pieter Knap proposes that future developments will include sophisticated process control techniques to evaluate the interaction between environment and genetics to reduce end-product variability. A breeding organisation must then: 1). establish breeding objectives, selection criteria and molecular genetic technology which includes results from research into muscle differentiation and protein deposition, and functional genomics and proteomics. 2). implement guidelines for on-farm management of production and pre-slaughter stress; 3). work with customers on statistical process control procedures; 4).

implement procedures to electronically identify groups of carcasses which are evaluated for weight, leanness and meat quality. This information will then be used in quality assurance procedures to monitor and minimise variation in meat quality. Finally, the payment for slaughter pigs should reflect the value of leanness and meat quality.

***The additional genetic gain that can be achieved by using molecular data in breeding programs*** was reviewed by Mike Goddard and Ben Hayes (Australia). The authors outlined four main factors which determine the additional gain achievable: 1). The accuracy of the existing Estimated Breeding Value (EBV) for the breeding objective. Using additional marker/molecular data for traits with high accuracies provides little additional genetic gain. High accuracies for traits could result from high heritabilities and/or large amount of data,. 2). The proportion of variation in the \$EBV that is explained by marked QTL (Quantitative Trait Loci). It is intuitively obvious that the additional gain using information from markers increases if the marker/QTL explains a large proportion of the genetic variance. 3). The accuracy with which the QTL allele effects are estimated. Direct tests for the QTL allele are more accurate. 4). The costs of genotyping.

The proportion of variance explained by molecular data increases as more data are used, however, the optimum amount of data can be low because the high costs of genotyping cannot be repaid by QTL of small effect. Please note, that this review summarised results from simulation studies. Information on the commercial use of marker information in breeding programs is not readily available.

***Issues and opportunities of breeding for disease resistance*** were discussed by Steve Bishop et al. (United Kingdom). The need to develop sustainable production systems places pressure on breeders to select for disease resistance. Breeding programs, which consider disease resistance have to be regarded as a component of an integrated approach to control disease. Bishop and co-authors outline the mechanisms of disease resistance and the epidemiological context. Steve Bishop argues that many unexploited opportunities exist to breed for disease resistance. Examples include the neonatal E. Coli diarrhea in pigs where markers closely linked to the causal mutation are known (Edfors-Lilja and Wallgren, 2000). In addition, the Danish study by Henryon and co-workers (Henryon et al., 2001; 2002 and comments below) indicates that well-designed breeding programs have opportunities to select for decreased disease incidence. In practice, however, it is necessary to priorities diseases, which may not always be straightforward. Bishop et al. (2002) predict that breeding for disease resistance will gain focus of breeders and emphasise that an integrated multi-disciplinary approach is required which considers the disease biology, the epidemiological context of the disease and the underlying immune mechanisms of resistance.

### ***Health, disease resistance and animal welfare***

***Genetic parameters for reproduction and performance traits were estimated for different health conditions*** by Rob Bergsma and Egbert Knol (The Netherlands). Estimates of genetic parameters were similar between both health environments (conventional and SPF) for reproduction traits. However, observed performance in production and carcass traits differed substantially between both health environments. For example, feed intake increased from 2.457 kg/day in the conventional environment to 2.875 kg/day in the SPF environment. The optimum feed intake, which is defined as the minimum feed intake required to meet the maximum protein deposition, was similar in both health environments. Therefore, the extra feed intake in the SPF environment was

directed to extra lipid deposition, which increased from 181 g/day (conventional) to 293 g/day (SPF). Variance components also differed between the two health environments and breeding program need to consider heterogeneous variances when evaluating pigs from different health environments.

***Genetic variations for total and differential numbers of leukocytes exists in growing pigs*** was the title of the paper by Mark Henryon et al. (Denmark). Blood samples of 4204 male piglets taken when pigs were approximately 50 days of age were used to count the total number of leukocytes/ml blood and to measure the proportion of leukocytes that were neutrophils, eosinophils, monocytes and lymphocytes. Heritability estimates for these measurements ranged from 0.22 to 0.29 and positive genetic correlations between measurements were estimated. The study suggests that the total and differential number of leukocytes in pigs offer opportunities for genetic improvement of clinical and sub-clinical disease. Further studies will need to focus on their genetic relationship with resistance and performance traits.

***Incorporating competitive effects in breeding programs*** (Muir and Schinckel, 2002, USA). The actual response to selection using BLUP methodology has often fallen short of expectations. The authors argue that this shortfall of genetic improvement can be caused by an increase in competitiveness of animals selected for higher performance using poultry as an example. The higher competitiveness of an animal then affects the performance of other animals in the group. A selection experiment at Purdue University showed that group selection (selecting a family that was least aggressive) decreased mortality rates from 68% to 8.8% in five generations while eggs per hen housed increased from 91 to 231 (Muir, 1996; Muir and Craig, 1998). Group selection requires that families be grouped together and selected as a group, which may lead to a rapid increase in inbreeding. In this paper, the authors presented a method for incorporating competitive effects into BLUP methodology and showed that response to selection was higher for 6 week weight and mortality rate in Japanese quail.

It is well known that group housed pigs often have lower performance than pigs that were single penned. This reduced performance could be due to associative effects between animals (e.g. Frank et al, 1997; Holck 1997). Therefore, competitive effects of pigs selected for higher performance should be estimated to determine whether these effects are unfavourably related with improved performance.

## ***Reproduction***

***Inbreeding of the litter negatively affects pre-weaning- and piglet-survival*** was the main result presented by Katoele et al., (2002, The Netherlands). The authors used a large commercial data set and found that pre-weaning survival decreased by 2.23% and piglet survival decreased by 2.87% per 10% increase in inbreeding of the litter. In comparison earlier studies by Winter et al. (1947) and Bereskin et al. (1973) reported a decrease in piglet survival of 0.20% and 1.20% per 10% inbreeding increase of the litter.

***Genetic relationships between litter size of primiparous sows and feed intake behaviour of related boars*** were presented by Schulze et al., (2002; Germany). Feeding behaviour traits are available from electronic feeding stations. Usually, studies investigate genetic relationships between feeding behaviour traits and performance traits. This study indicates that feeding behaviour traits measured in boars may provide information for litter size recorded in gilts. Genetic correlations between feeding behaviour traits and

litter size ranged from 0.21 to 0.60. Feeding behaviour traits have higher heritabilities than litter size and genetic correlations between these traits should be estimated in other populations to evaluate the potential use of feeding behaviour traits in breeding programs.

***A better understanding of the genomic regulation of protein and lipid deposition*** is the aim of the project that was introduced by Landgraf et al. (2002, Germany). The first aim was to evaluate the use of indicator cuts (ham traits, fat and loin area) to predict protein and lipid deposition in pigs. These indicator cuts were very variable during the growth period and thus had no value to predict chemical body composition. Protein and lipid depositions can be measured through deuterium dilution technique and magnetic resonance tomography (MRT) on live animals and through serial slaughter trials analyzing the entire body chemically. Landgraf et al. (2002) used chemical analysis and MRT in the current study. Maximum protein deposition of pigs agreed well with estimates presented by Eissen (2000) and this information will be used to optimise feed intake within a biological model. Furthermore, the authors concluded that selection for higher protein mass was required in the given population since it may limit protein deposition during growth.

***These two papers were chosen as examples of studies*** that are underway worldwide with the aim to gain a better understanding of the physiological consequences of selection for improved productivity. Overall, these studies require cooperation of scientists from a number of disciplines to better understand the opportunities and consequences of selection for increased performance.

### ***Miscellaneous***

***Plasma – IGF1 and leptin concentrations*** were measured in pigs at 28 days and 160 days of age (Estany et al., 2002; Spain). In addition, pigs were genotyped for IGF1, IGF2, LEP and LEPR genes. No relationship was observed for IGF1 recorded at 28 days and IGF1 recorded at 160 days which supports results summarized by Kim Bunter in her review (Bunter et al., 2002; Australia). The IGF1 and IGF2 genes were identified by two microsatellites which were highly polymorphic. Five alleles were segregating for the IGF1 gene and eight alleles were segregating for the IGF2 gene. One allele in the IGF1 gene was associated with IGF1 measured at 160 days, killing out% and weight of hams. The authors conclude that the identification of an allelic variant of the IGF1 locus related to plasma IGF1 might help to gain a better understanding of the physiological mechanisms by which IGF1 regulates growth and fatness.

The ***association between Estrogen Receptor Locus (ESR) and growth, carcass and developmental traits*** was the topic of the paper by Leets et al. (USA). It has been shown in the past (e.g. Rothschild et al., 1994, 1996; Short et al., 1995, 1997) that the B allele of the ESR gene is associated with an increase in litter size. The favourable B allele is mainly found in Taihu breeds and domestic Large White and Yorkshire populations. In this study, the B allele had a (unfavourable) dominant effect on backfat with animals having at least one copy of the B allele having 0.155 cm more backfat than homozygous A animals. The B allele of the ESR gene had either a non-significant association with backfat (Rothschild et al., 1996) or a favourable effect on backfat (Short et al., 1997). The authors conclude that this study and previous studies provide evidence for linkage between the ESR gene and a QTL affecting backfat. However, selection for the ESR B allele may be accompanied by an increase or a decrease in backfat depending on the linkage phase that prevails in each herd.