NEW SOURCES OF INFORMATION IN PIG BREEDING

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INTRODUCTION

Currently pig breeding programmes across the world show many similarities, based on crossbreeding of sire and dam lines, performance testing instead of progeny testing and BLUP animal model, often utilizing PEST (Groeneveld and Kovac, 1990) or PIGBLUP (Long et al., 1990) to estimate breeding values. The design of breeding programmes generally follows methods and general findings as proposed by De Vries (1989) on derivation of breeding goals, size of lines and utilization of test capacity. The organization of the breeding programmes differs between “national” programmes and companies but are expected to become more similar in integrated pork chains (Brascamp, 1994). Common to all these pig breeding programmes is selection for production traits like daily gain, backfat or lean meat % and reproduction traits like litter size.

The last decade the number of traits under selection has increased rapidly due to:

1. further specialization and internationalisation of existing dam and sire lines to meet the various market requirements (Pereira et al., 1998; Knap, 1998);
2. considerations with regard to long term requirements to remain competitive in breeding as well as to obtain public acceptance and balanced breeding (Merks, 2000);
3. the possibilities that computers nowadays provide for breeding value estimation (Bidanel, 1998) and the wider interest of breeding organizations in “secondary traits”. Due to the boost in information and computer technology (ICT), pig breeding programmes have been given the opportunity to obtain more detailed information, both on performance and reproduction. Furthermore, ICT has enabled the collection of pig data from many other herds than only the nucleus herds. Genomic information has opened a fully new area that may be added on the long term to the existing amounts of phenotypic information. The goal of this paper is to review new sources of information and their value for present and future pig breeding programmes.

GROWING AND CARCASS INFORMATION

Especially for performance testing, ICT has given several opportunities for new information sources that may be applied in pig breeding programmes. This includes electronic feeders, 2-D ultrasound scanning, video imaging and health recording systems.

Feed intake and growth data. Electronic feeders installed in central testing of nucleus farms allow for measurement of individual daily feed intake of growing pigs housed in group pens. This form of performance testing reflects the situation in commercial housing systems better than the previously used individual penning of pigs to measure feed intake. Data from these electronic feeding stations have been analysed among others by Labroue et al. (1997), Von Felde (1996), Casey and Dekkers (2001) and Schnyder (2001). They all conclude that these
feeders provide measures of feed intake and additionally feed intake pattern information such as: number of meals taken each day, size of these meals and time spent eating per meal or per day. However, before using this information editing is clearly advised by Eissen et al. (1998) and Casey and Dekkers (2001) to ensure the quality of the information. Although feed intake behaviour is highly heritable, Von Feltz (1996) and Hall et al. (1998), showed that this information added little to genetic progress for production traits like daily gain and feed efficiency. Hall et al. (1998) and Schnyder (2001) reported that changing the shape of feed intake curves by selection to improve the efficiency of lean growth will be very difficult.

In some cases electronic feeders have been combined with a platform to weight the pig while eating (Ramackers et al., 1996) or even cameras to produce a picture of the pig to enable development registration. The combination of daily registration of feed intake and weight with this equipment will enable fitting accurate growth and/or development curves. The application of random regression (Huisman and Van Arendonk, 2001) on this data may help to improve efficiency but perhaps also the shape of the growth curve.

A new and limited tested application of electronic feeders is feed intake registration of individual sows during lactation. This is of interest due to the expected correlated change of weight loss during lactation with single trait selection on growth rate and backfat thickness during the growth period. Feed intake registration of sows during lactation, perhaps in combination with weight and backfat loss, needs further research to point out clearly its value for both production and reproduction traits.

Scanning data. Ultrasound scanners, especially A-mode (single loin and fat depth) have been applied already for several decades in pig breeding to measure backfat thickness ultrasonically on live pigs. Also in this field information technology has enabled more sophisticated measurements. This may be applied during own performance testing but also along progeny information collected at slaughterhouses. Dion et al. (1998) compared an A- and B-mode (2-dimensional scan) ultrasound machine with the slaughterhouse probe and cut-out measures. The A-mode (single backfat measurements) predicted cut-out measures best and little value could be added by the B-mode scanner of which the images were stored on a computer for analysis. Similar findings were reported by Tholen et al. (2001). They compared ultrasonic backfat measurements on central tested pigs with different genotypes with the FOM probe in the slaughterhouse and the AutoFOM which measures backfat and muscle thickness ultrasonically 2-dimensionally at several points across the back of the pig at the beginning the slaughter line. Strong genetic correlations between the different traits are reported, however due to lower heritabilities for AutoFOM traits (especially in Pietrain), selection based on AutoFOM traits only is not preferred. AutoFOM or Dual Energy X-ray absorptiometry (Suster et al., 2001) data may help to direct selection towards optimal weight of relevant carcass cuts.

Health data. Health traits have been registered poorly in pig breeding programmes until now due to expected low heritabilities and difficulties with objective registration. Mallard et al. (1998) showed in a selection experiment that selection for improved general disease resistance should be preferred above selection for specific disease resistance. Nowadays several slaughterhouses apply veterinary inspection in the line, especially for lung and liver lesions. The information gathered this way is sent back to the farmers to improve their health management. Objective registration in the slaughter line with vision systems to detect skin and
leg problems may open new opportunities for health recording on many pig farms, especially in combination with electronic identification of pigs. Recently both Henryon et al. (2001) and Visscher et al. (2001) reported genetic parameters for health status during life. In both projects, large scale health recordings at the farm and in the slaughterhouse were analysed at the meta level (as 0/1 trait sick/healthy) or according to the clinical symptoms recorded. From both analyses it was concluded that health recordings may contribute to improved disease resistance.

**Meat quality data.** Over the past few years the application of DNA tests for the Halothane and RN (Rendement Napole) genes has improved pork quality to a large extent. Collection of meat quality data on a routine basis is not done as quality information gathered in the slaughter line is not of much value to predict final pork quality. Only information 24 hours post-mortem is seen as informative for selection programmes. The introduction of electronic ID-systems as well as tracking and tracing of pig carcasses will enable the collection of pork quality information on large scale.

**Exterior data.** Exterior appraisal still has a role in most breeding programmes, at least to select boars and gilts before they are sold. From literature it is know that selection for performance has side effects on the exterior of pigs, in particular leg weakness traits have an antagonistic genetic correlation with daily gain. Recently Jorgensen (2000), Yadzi et al. (2000) and Serenius et al. (2001) showed the genetic background of several leg weakness symptoms and their relation with longevity of sows. Clear indications are given for traits to be scored or measured objective, that may contribute to longevity. Vision systems recording these traits objectively on live pigs and image analysis will enable recording and selection for these traits in the near future.

**SOW PRODUCTIVITY**

In current commercial pig breeding programmes, great emphasis is placed on improving reproduction traits in dam lines. In general the breeding goal is to increase the number of piglets weaned per sow per year. Several reports have shown the effectiveness of selection on litter size (Lamberson et al., 1991; Sorensen and Vernersen, 1991). Undesirable correlated responses in other traits such as piglet mortality can decrease the overall effectiveness of selection on litter size, as shown by the selection experiment of Johnson et al. (1999). In addition to litter size, many more traits affecting reproductive performance could be used in a breeding programme. Recently, several studies have reported on the genetics of a large group of fertility traits, among others Sterning et al. (1998), Rydhmer (2000), Hanenberg et al. (2001) and Knol (2001). The information needed for this selection is available in large numbers nowadays since many pig breeders use computerized management systems on their farms to record technical results (especially fertility traits). This includes also repeated sow productivity measurements as data come available for each parity until the sow is culled.

**Oestrus and interval weaning-oestrus.** Onset of oestrus is the first visible sign of reproductive fitness in the gilt. For management of fertility clear symptoms of oestrus and avoidance of silent oestrus cycles, are needed. Rydhmer (2000) clearly showed that genetic variation in oestrus symptoms in gilts is present. Having found a positive genetic correlation
between the ability to show a standing reflex and the intensity of vulvar symptoms, it was concluded that breeding for strong symptoms of oestrus is possible. In addition, it has been shown by Rydhmer (2000) and Hanenberg et al. (2001), that the first pubertal oestrus and the first oestrus after weaning are genetically similar traits in terms of intensity and duration of the symptoms of oestrus. Greatest response for improved interval weaning-oestrus can be expected in the first parity where the heritability of the interval is highest (Ten Napel et al. 1995), as is the occurrence of prolonged intervals of weaning to first insemination.

Piglet vitality. Given an undesirable correlation with the number of stillborn piglets and mothering ability, selection on only litter size will increase piglet mortality. Including birth weight, number of stillborn piglets, pre-weaning survival and/or mothering ability in the breeding goal can improve piglet survival (Rohe and Kalm, 2000; Hanenberg et al., 2001; Knol, 2001), despite that these traits (except for birth weight) have low heritabilities and an undesirable correlation with litter size. Selection on gestation length, a trait with a high heritability and a high genetic correlation with mothering ability, gives opportunities for an effective indirect selection on mothering abilities. Other methods to select for improved mothering ability are proposed by Edwards (2001).

COMMERCIAL INFORMATION
A pig breeding programme generally consists of different levels in a pyramidal structure, indicated as nucleus, multiplication or crossbreeding and commercial level. Selection takes place at all levels, but improvements generated in the nucleus determine eventually the rate of annual genetic change. This genetic change is economically of importance at all levels, but especially at the commercial level because of its relatively large number of animals. Changes in rank order for genotypes between these environments may occur and decrease the efficiency of pig breeding programmes in terms of genetic progress at the commercial level (Brascamp et al. 1985). During the last decade several studies reported on the genetic correlation with “commercial environment”. The differences with “commercial environment” considered may be separated in the following items:

1. Large differences in environment, which are studied in detail ranging from manageable differences like feeding level and feed composition to substantial differences like health level and climate. Results of Mote (2000) and Bergsma et al. (2001) showed poor genetic correlations (r_g = 0.7) for backfat thickness while correlations for other traits were not significant different from 1 between herds with large climate (tropical versus temperate climate) and health (SPF versus conventional) differences.

2. Purebred versus crossbred performance (commercial level uses crossbreds). Studies of Merks and Hanenberg (1998) and Van Steenbergen and Merks (1998) showed genetic correlations for daily gain and backfat thickness that were lower than one, especially for backfat thickness (r_g= 0.5 to 0.8). Taubert et al. (1998) and Boesch et al. (1998) showed for litter size r_g ranging from 0.7 to 0.9, however, most estimates differed not significantly from 1.

Nowadays information from the commercial level is rather easy to collect and consequently needs careful consideration as an important source of information for pig breeding. For improved genetic progress at the commercial level a satellite nucleus system across
environments and application of Combined Crossbred and Purebred Selection (CCPS) may be applied. The combined crossbred and pure line selection (CCPS) method showed to be superior to pure line selection in many different situations (Bijma and Van Arendonk, 1998). Next to a contribution to CCPS, commercial information is valuable to register genetic quality of the program continuously on large scale. Such a system is of interest to identify undesired side effects of the selection program in an early phase and to help optimise management procedures for use of the improved genetics.

GENOMIC INFORMATION
Most agricultural traits like daily gain, backfat thickness, litter size and meat quality are quantitative in nature with a continuum between high and low performing animals. Thus the regions of the genome that control such traits are called quantitative trait loci (QTL). Variation at mapped QTL can be exploited through marker assisted selection (MAS) in which information from DNA markers flanking the QTL are used to select animals with the desired QTL. However, experience with the halothane gene illustrated the added value of a direct molecular test in contrast to limitations of indirect selection using flanking markers. Until now only a few pig breeding organizations try to exploit the new information emerging from genomics projects. The choice of the traits, however, is critical for successful implementation of genomics technology in the genetic improvement of pigs. Most QTL mapping studies have been on growth and carcass composition traits. Selective breeding for these traits is relatively straightforward and consequently MAS for these traits has little added value. Meat quality and especially disease resistance represent the greatest challenge (Meuwissen and Goddard, 1996), but also the greatest opportunity for genome research.

The list of potential useful markers in pig breeding is impressive and growing continuously (Rothschild, 1998). For the future the amount of cheap genomic information on pigs is likely to grow increasingly and it will be a challenge to utilize the abundance of information. Firstly to select the markers across species along comparative genomics and secondly to use the information from markers in pig breeding programmes. Visscher and Haley (1998) discussed the potential strategies for MAS and they foresee application especially in combination with embryo technologies.

SYSTEMS TO MANAGE INFORMATION FOR PIG BREEDING PROGRAMMES
Phenotypic information. The new sources of information identified that are already available or will come available have clearly one common description: large numbers. However, large numbers are not synonym to quality with regard to pig breeding programmes. The huge amount of data collected by the electronic feeders during performance testing of pigs needs editing and consolidation. A similar approach is needed for the data of ultrasound scanners or vision systems applied on live or slaughtered pigs to ‘measure’ body composition or anatomical disorders (e.g. leg weakness). To handle this information specific software is needed and should be applied shortly after of data collection.

The huge amount of commercial growing, carcass and fertility data collected on commercial farms may, in its original size, contribute substantially to genetic progress in pig breeding. Several breeding organizations have developed software to ensure a maximum quality of this kind of information by checking its coherence (identification, parentage, date of events etc.). Programmes have been developed to automate the creation of data and pedigree files to
estimate breeding values and their accuracies. This kind of software was not common with only central performance testing, but introduction of on-farm testing and especially selection for litter size based on family information made this software inevitable. For breeding programmes that have this software running, expansion of the number of fertility traits, meat quality or health traits is relatively simple. Of course the number of traits per pig and the number of pigs with information increases simultaneously and needs adequate relational databases to get this information accessible for breeding value estimation as well management of the breeding programme.

Groeneveld and Spilke (1998) showed that bad data structures rarely make mixed model evaluations impossible. They concluded that no minimum requirements can be set for the data structure. However, use of AI with balanced usage of boars is very desirable to improve the efficiency of information via links across herds or central testing units. Also, putting more pigs into intensive testing programmes will increase the accuracy of candidates to be evaluated.

Genomic information. Genomic information is still a rather new source of information for pig breeding programmes. For collection and editing of genomic information tools like AceDB can be used. AceDB (http://www.AceDB.org) is a genome database system (since 1989) developed specifically for handling scientific data in a flexible way and with a graphical user interface with many specific displays and tools for genomic data. AceDB is used both for managing data within genome projects and for making the genomic data available for a wider scientific community. Since the genomic information can be used across species and as this information is stored in different databases, tools like ISYS (http://www.NCGR.org/ISYS) become very useful for managing this information. ISYS is developed by the National Center for Genome Research and is a dynamic and flexible platform for the integration of bioinformatics software and databases. ISYS allows web based resources to be integrated with programs running on the scientist’s desktop.

To collect genomic information in breeding populations a balanced data structure and correct parentage is vital for the quality of the information. This means that optimal use of genomic information should be based on well designed and edited databases with genomic and phenotypic information. Until now statistical methods for combining genomic and phenotypic information into breeding values is mainly in the research phase. Fernando (1998) showed that genetic evaluation is simplest when genotypes are known at all QTL. However, in the near future it is expected that only genotypes at markers linked to QTL will be available. For this situation, BLUP of genetic differences can be obtained by using mixed linear models that include gametic effects at marked QTL. Further development in this field is needed.

DISCUSSION AND CONCLUSIONS
This overview clearly shows that the amount of information available for pig breeding programmes is increasing enormously. Gradually, pig breeding organisations are building their programme on two different parts:

1. Nucleus (and multiplier) herds in which a relative small number of purebred pigs is followed intensively (including genotypic information) for all kinds of information (with electronic ID). This information is the main source for breeding value estimation to manage the breeding programme.
2. Commercial herds in which huge numbers of pigs (sows as well as slaughter pigs) are followed for specific information to improve and/or monitor the breeding programme. This information is also used for the breeding value estimation procedures, sometimes in a “second” run to find out the value of the several information sources. This source of information will also be used to monitor the indirect/side effects of breeding programmes to ensure balanced breeding. In the near future tracking and tracing of pigs and electronic ID-systems will help in providing this information in large numbers.

Genotypic information is still mainly at research stage, except for the Halothane and RN gene. This is due to both the fact that QTL’s are mainly reported for carcass traits (selective breeding can be done more easily by quantitative methods) as well as to the fact that markers/QTL’s show highly variable effects across lines and populations (e.g. Southwood et al., 1999). The efforts made in humans and other species will help us to find relevant major genes for pigs. For both research and application of these new genes, quality of phenotypic information is needed for successful application of genomic information in pig breeding programmes.

Large numbers and more information of commercial pigs especially for low heritable traits will come available. The quality of this information may be moderate or even low. However, large numbers will counterbalance this quality in terms of the accuracy of breeding values, provided that the data have an adequate genetic structure and are timely available to avoid prolonged generation intervals. The fast computers in combination with multiple trait BLUP will break down this information easily into breeding values for a large number of different traits besides daily gain, backfat thickness (or meat%) and litter size. This means that ICT will provide us with many more new sources of information which enable pig breeders to select for a much wider breeding goal as well as to monitor its impact on the commercial level.

REFERENCES