A Genomic Future
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ABSTRACT
Animal breeding has had a large impact on the improvement of livestock production. With the sequencing of the genomes of the various species, the subsequent description of DNA markers and the cheap technology to map these markers, we are entering a new era of animal breeding. This technology enables animal breeders to select animals with a lot more precision at a younger age, i.e. it increases accuracy and decreases generation interval, key components in the rate of genetic gain that can be achieved. Besides accelerating the rate of genetic gain, this new technology also offers better solutions for traits that, up until today, have been proved difficult to measure, for example traits that are only measureable post-mortem e.g. meat quality.

INTRODUCTION
Mankind’s association with domesticated animals goes back more than 10,000 years. During this period a variety of animal species has been adapted to suit our needs. The animals that best fitted our needs were used as parents for the next generation of animals. In the beginning the best animals were probably the animals that were most docile and easy to manage. This led to the formation of a number of different breeds and all these different breeds were adapted to the local circumstances. More recently, as farming became less for subsistence and increasingly a business/economic endeavour, the more specialized breeds were used for selective breeding with the focus being more on traits that maximized production (hence more income for the farmer). In the beginning this was done through phenotypic selection, i.e. the animals with the best performance were selected as parents for the next generation. Improvements were mainly made on traits that were easily observed and with a reasonable heritability. Later on statistical models (BLUP models) were developed that made it possible to include information from relatives (animal models). This made it plausible to also make significant improvements for traits that are less heritable, e.g. number born piglets, which hitherto had proved slow to improve.

GENOMIC SELECTION
On the whole the science and practice of animal breeding has been a major contributing factor to the improvement made in livestock production. For example, between the 1950s and 2005 the number of weaned piglets per sow per year increased by 50% and feed conversion was halved through breeding (Hume et al., 2011). As a rule of thumb improvements of 1-3% per annum are achieved for traits under selection. These results illustrate what can be achieved through traditional breeding methods. The efficiency of these methods reduces substantially when traits are either difficult to measure, cannot be measured on the animal itself, or when traits have a low heritability. There are traits that exhibit these problems that could be potentially very important, for example feed conversion efficiency, meat quality and disease resistance.
Rate of genetic progress is determined by four factors: 1) accuracy of the breeding values; 2) selection intensity—how big is the group of potential selection candidates and how many do I select?; 3) genetic variability of the trait; and 4) the generation interval—how long does it take before I can use the selected animals as parents. Genomic selection potentially impacts three of those, and certainly has an impact on accuracy (1) and generation interval (4).

**Genomic selection, the principle**

Today, animal breeders have a new tool in their toolkit, namely genomic selection. Genomic selection was first described by Meuwissen et al. (2001) and is based on the notion that breeding values can be estimated from the information generated by a large number of DNA (genetic) markers. With a large number of genetic markers spread across the entire genome there will always be a genetic marker close to the gene(s) of interest. Nowadays we have the full genome sequence of many species; more than 20 bird and mammalian species, including the human. The pig was added to this list in late 2009, and hundreds of thousands of SNPs (Single Nucleotide Polymorphisms) are now available. With genome sequencing—the laboratory process that determines the complete DNA sequence of an organism’s genome—the whole library of base pairs of a pig is mapped. Pigs have billions of base pairs. A small part of these (still millions) can be classified as Single Nucleotide Polymorphisms (SNPs); a situation where the nucleic bases in a certain location of the genome are of different types in some of the individuals within a species. These SNPs can be used as easily identifiable markers for locations on the genome of the pig. There are several millions of SNPs discovered in the pig’s genome. These SNPs are the basis of Genomic Selection. Through this technology a large number of SNPs are selected across the genome to serve as an information source for breeding value estimation.

The first, and key, step in genomic selection is the selection of a large group of animals with very precise (known) phenotypes. This is referred to as the reference population. This reference population is genotyped (defining the markers/SNPs each individual carries) and the genotypes are then associated with the accurate phenotypes to develop a statistical model that then provides estimates of the effect of each SNP for the trait of interest. Since from years past it has already been shown that most traits are influenced by a large number of genes each with a small effect, these SNP markers provide a more accurate and reliable measurement of the genetic merit of an individual. In order to make genomic selection work, a large number of breeding boars and sows with a known performance record have been gathered in combination with accurate phenotypes to estimate all the SNP marker effects. The marker effects are then used to predict the genetic merit of animals that do not have measured phenotypes but have only been genotyped for SNP markers, i.e. young animals without a performance record or for a trait that cannot be measured on the animal itself (Figure 1). The accuracy/reliability of the genomic breeding values depends on the size of the reference population, the heritability of the trait and the quality of the phenotypes used.
Figure 1. Principle of genomic selection.

Genomic selection, the promise

Several research groups have investigated the potential impact of the use of genomic selection on the rate of genetic gain that can be achieved (Table 1). Estimated improvements vary between 20 and over 100%, where the lower numbers are for species already on a fast track breeding program (pigs, broilers, turkeys) and the higher numbers are for species that are rely a lot on progeny testing (cattle, layer chicken).

Table 1. Potential impact of the use of genomic selection on yearly genetic progress.

<table>
<thead>
<tr>
<th>Species</th>
<th>Additional genetic gain</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dairy cattle</td>
<td>60 – 120%</td>
<td>Pryce, 2011</td>
</tr>
<tr>
<td>Sheep</td>
<td>20 - 40%</td>
<td>Van der Werf, 2009</td>
</tr>
<tr>
<td>Beef cattle</td>
<td>29 – 158%</td>
<td>Van Eckenmaan, 2011</td>
</tr>
<tr>
<td>Swine</td>
<td>20 – 50%</td>
<td>Albers, 2010</td>
</tr>
<tr>
<td>Layers</td>
<td>40 – 100%</td>
<td>Dekkers, 2009; Wolc, 2011</td>
</tr>
<tr>
<td>Broilers</td>
<td>20%</td>
<td>Dekkers, 2009</td>
</tr>
<tr>
<td>Turkeys</td>
<td>15%</td>
<td></td>
</tr>
</tbody>
</table>
Genomic selection, the application

Several breeding companies, in different species, have started with the implementation of this new technology in their routine breeding programs. The cattle breeders were the first to implement this new technology, followed by the layer breeders and later on the pig and broiler breeders. Genomic selection empowers breeding companies to exploit within litter genetic variation in reproductive traits in the selection process. In a departure from the results of BLUP methodology, littermates will no longer have the same expected breeding value at birth; but rather they will each have their own genomic breeding values, based on their own unique pattern of DNA-markers. The genomic breeding values predict, with high accuracy, what the pigs’ genes are worth in the breeding program. Varying market demands require a specific focus on the characteristics and performance of herds on farms. Genomic selection can offer anywhere between 20-50% greater genetic progress in pig breeding programs. This allows producers to tailor existing practices— that are complementary to existing breeding programs on farms.

Genomic selection, the future

Typically, genomic selection has more added value when used for traits with a low heritability, traits that are sex-linked, or the ones that can only be measured at post mortem. In the coming decade many new traits will be added to the breeding goals. We are still at the start of the genomic era; new applications to make most use of this new technology are being developed. Technological developments are helping to rapidly reduce the cost of genotyping and sequencing. For example, 10 years ago the cost of sequencing one animal was millions of dollars, while today the same can be achieved for two to three thousand dollars. This massive reduction in cost of genotyping allows for more and broader applications in commercial breeding programs. Information from further down the chain, e.g. commercial crossbreds and/or slaughter house, can be linked to breeding animals through DNA information. This was not feasible on a large scale before.

The information captured in the genotypes can be used to hunt for specific genes or genomic regions with an (large) impact on traits of interest. An example of this is a study by Boddicker et al. (2012), were a number of pigs were infected with the PRRS virus (not something one would want to do with breeding animals). Then a whole genome analysis was done to identify genomic regions (read SNP markers) associated with the ability to cope with a PRRS infection. These SNP markers can then be used to select the most resilient animals in the breeding herd without having to infect them with the virus.

CONCLUSIONS

Genomic selection caused a revolution in the animal breeding world, it all started in dairy cattle but is also finding its way to the other livestock species. A lot more genetic progress can be expected due the implementation of genomic selection for traits that are measured late in life or are difficult to measure. Especially for the last group of traits, genomics can offer a lot more than the conventional animal breeding technologies.

REFERENCES


Wolc et al.: Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. Genetics Selection Evolution 2011 43:5.