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Understanding genomic selection in poultry breeding

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Genomic selection is a recent paradigm shift for both animal and plant breeding. The availability of hundreds of thousands of markers covering the entire genome has provided an opportunity to increase the accuracy of estimated breeding values, better manage genetic variation and shorten generation intervals. This paper summarises how these new technologies can be applied to poultry breeding programmes to enhance genetic improvement.

Keywords: genomic selection; poultry breeding

Introduction

The development of technology enables more accurate and efficient selection of animals. This is particularly relevant for poultry, where short generation interval and relatively large populations allow rapid genetic progress. Over the last few decades we have seen the implementation of increasingly complex and computationally demanding statistical approaches which aim at assessing genetic value of an individual using phenotypic and pedigree information. With increased sequence availability and the development of SNP chips, further improvements are expected. This review discusses how genomic selection is a natural extension of previously developed methods and how it can be implemented to increase genetic gains in poultry.

Selection in poultry

Over the last 50 years, genetic selection in poultry has proven to be extremely successful resulting in specialised egg laying and fast-growing meat breeds that far exceed the production of their wild ancestors (*Figure 1*).

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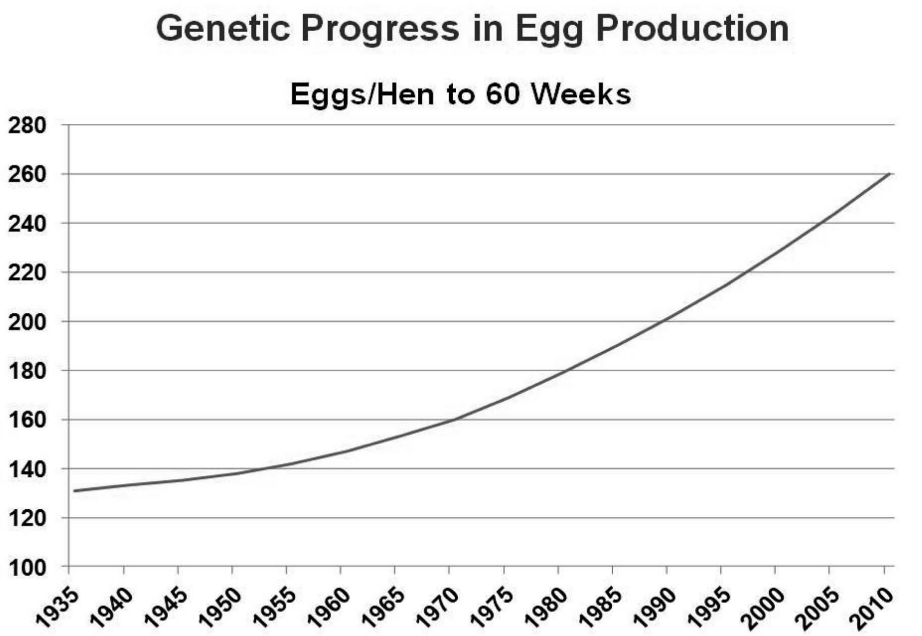


Figure 1 Improvement in average egg production of a brown egg layer line.

This progress has been achieved by selecting and breeding from only the best birds, thus passing favourable alleles on to the next generation. As technology and computing capacity have developed, the methods for determining which animals have superior alleles (or the sum of the allelic effects, known as the breeding value) have also improved. During the early stages of poultry breeding, selection was based on the bird's own performance (phenotypic selection). This method is efficient for traits with high heritability that are measured in all selection candidates (for example, body weight). However this method is not applicable to sex-limited traits (such as egg production and egg quality) and is much less effective for traits with low heritability (for example, disease resistance).

Hazel (1943) proposed a method called the 'Selection Index' which optimally combines information on an individual's own performance with that of groups of relatives (for example, mother, sister or progeny). Seven years later, Henderson (1950) published his mixed model equations which enabled the calculation of breeding values correcting for known non-genetic differences between animals (for example, hatch-week or barn effect). Quaas and Pollak (1980) described a method called the BLUP (Best Linear Unbiased Prediction) Animal Model which combines information coming from all relatives of the selection candidates. Combining all of the information available increases the accuracy in which the breeding value of an individual can be assessed. None of these genetic analysis methods actually used information on the genes themselves, but rather they exploited the information from both phenotypes and pedigree.

Since the discovery of DNA, methods of finding genetic variation and the effect of these differences on phenotypes (physical traits) have been of great interest to researchers

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and breeders. These studies, referred to as 'searching for QTL' (quantitative trait loci) led to the discovery of multiple regions in the genome associated with specific phenotypic traits of interest. The hope was that when all important genetic regions that influence a trait have been identified, a marker-assisted selection (MAS) can be performed, thus greatly enhancing genetic improvement. This was successful only to a limited extent and for traits with simple genetic control (for example, B blood group with B_{21} allele conveying resistance to viral diseases discovered by Briles *et al.,* 1977). It was found that only a few traits are controlled by a handful of genes. Most traits are influenced by multiple regions in the genome, each with a small contribution to the variation in traits. Furthermore, the exact position of these small QTL was difficult to map, primarily due to an insufficient number of markers and limited population sizes (see wide confidence intervals in www.animalgenome.org database for QTL from old papers based on studies using few animals and limited numbers of microsatellite markers).

Genomic selection

Decoding the genomic sequence has revealed millions of places in the genome where birds differ from each other at a single nucleotide (SNP-single nucleotide polymorphism). This accomplishment has allowed the development of SNP detection methods, which allows for rapid genotyping of birds in thousands of places simultaneously at much lower cost. Meuwissen *et al.* (2001) suggested that the solution for successful use of genomic information in breeding is not necessarily in finding a few large QTL, but that the information from the whole genome could be used simultaneously to determine breeding values. This approach, 'Genomic Selection', started a revolution in animal breeding. Some of the promise of genomic selection included improved accuracy of breeding values, a slower increase in homozygosity (by accurately detecting genetic differences), the possibility of better selection of sex-limited and hard-to-measure traits and shortening of intervals between generations.

Proof of concept

To verify if these expectations could be fulfilled, a selection experiment was designed by Iowa State University and Hy-Line International (Wolc *et al.,* 2011). A pure brown, egg-laying line of chickens was divided into two groups, and both were subsequently selected for several generations in parallel over a three year period. The selection index contained 16 production and egg quality traits and was applied by using either traditional phenotypic/pedigree data (based on individual and family performance results) or genomic and phenotypic selection using genomic data.

Before beginning the comparison, researchers developed the basic criteria required to perform genomic selection. They collected and compared information on phenotypes and high-volume genotypes (tens of thousands of SNPs) on a large number of individuals. This initial group of animals (training set) was used to determine the effect of every marker which was genotyped (*Figure 2*).

Now the criteria were ready to be applied to the genomic selection group during the experiment.

In this group, selection was done using the genotype information and the estimated marker-effects (as estimated from the training set) as soon as genotypes were determined on the next generation, giving a much shorter generation interval. Based on genomic breeding values, the best animals were selected as parents of the next generation without

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waiting until their phenotype information (*i.e.* performance results) were available. When phenotypes became available they were added to the training set. Birds from the Genomic Selection group were genotyped with 42,000 markers each using a SNP chip.

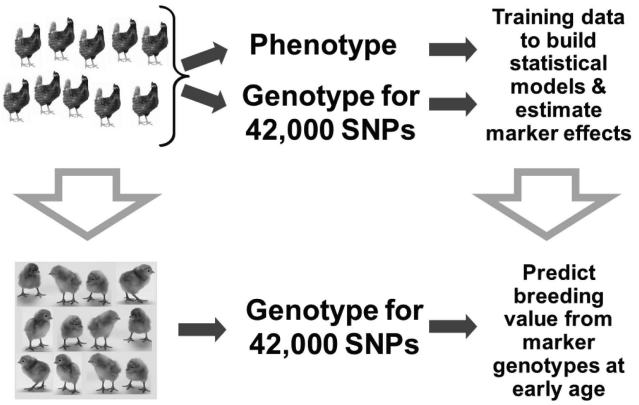


Figure 2 Validating the proof of concept of genomic selection.

A new generation of birds was produced every seven months for the genomic selection group and the active population size was reduced to 50 male and 50 female parents with females mated to multiple sires. At the same time, the traditional phenotype/pedigree group was selected every 13 months with 60 males and 360 females used to produce the next generation. After three years, the last generations of layer progeny from both groups were housed together in the same barn and evaluated for a normal production cycle to allow fair comparison of the achieved progress in trait improvements. Because of the shorter interval between generations, the genomic selection group had six generations of selection in the time required by traditional phenotype group for three generations of selection (*Figure 3*).

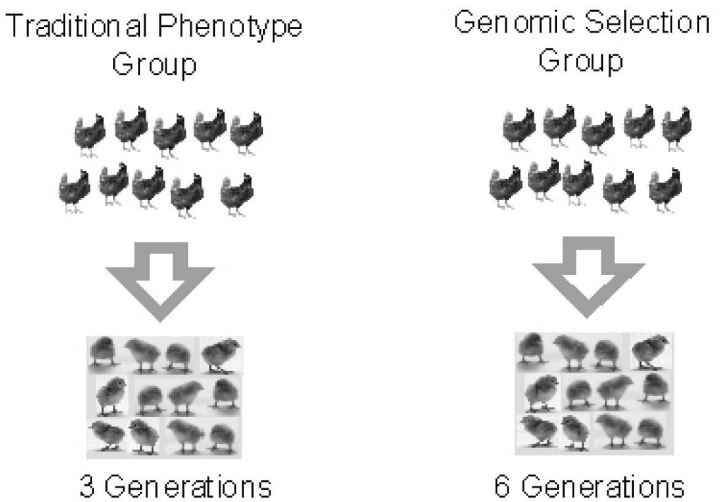


Figure 3 Design of generation comparison trial.

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In 12 out of the 16 traits under selection, the last generation of genomic selection layers outperformed the traditional phenotype selection layers. This progress originated from both better accuracy of breeding values and faster turnover of generations. Data analysis showed that accuracy of genomic breeding values is highest in close relatives, thus phenotyping continues to play an important role to ensure complete information is gathered and validated. It was shown that genomic selection can be successfully applied in poultry breeding to enhance genetic gain.

In addition to the high computing requirements needed to process the hundreds of thousands of data points generated for each bird, the main challenge of Genomic Selection is the cost of genotyping which currently exceeds US$150 per bird. Such investment is justified in the pure lines from which genetic progress is created. The genetic progress that is achieved in the pure lines moves through levels of multiplication in the pyramid-shaped population structure (*Figure 4*).

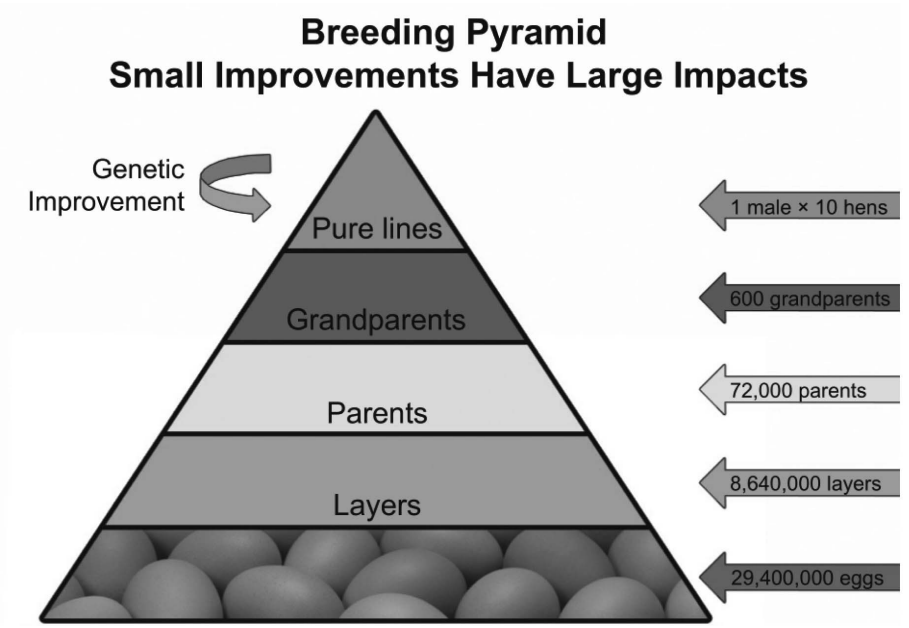


Figure 4 Multiplication of the generations amplifies the progress achieved in the pure lines.

Even small improvements in pure lines can have a large impact on the commercial layers. For example, a one gram change in egg weight may translate into 29 extra tons of eggs at the level of the commercial layers or alternatively achieving the same production of egg mass with fewer hens and less feed, thus reducing environmental footprint.

Conclusions

Genomic selection has been shown to improve accuracy of estimated breeding values and is now being used by all major poultry breeding companies in their product development programmes (Aviagen, 2012; Cobb, 2012; Hy-Line International, 2013; ISA, 2013). Strategic combination of high and low volume genotyping and using genomic

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breeding values for selection seem to be the next big step in the genetic improvement of poultry.

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