Genomic selection in poultry and pig breeding: a breakthrough technology?

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Introduction Contrary to programs for most other species, breeding and multiplication programs for poultry and pigs are using hybridization to benefit from line specialization and heterosis. The introduction of crossbreeding created a breakthrough in poultry breeding in the 1950's and –later and less markedly so- in pig breeding. A second breakthrough technology in pig breeding –not so much in poultry breeding- was the application of BLUP breeding value estimation procedures. These technological breakthroughs have prompted the extinction of small, pure line and private farm based breeding programs and a consolidation among breeding organisations. Today very few (poultry) or some dozens (pigs) of breeding programs remain and these are exclusively (poultry) or increasingly (pigs) owned by private companies. Genomics is now truly coming of age when it comes to applications in animal breeding and this paper discusses the impact of this new development.

Genomics of poultry and pigs The first decades of genomics research (until 2005) produced very little in terms of tools and technologies that were applicable to animal breeding programs. Applications were mostly limited to genotyping for major genes that were largely discovered on the basis of homology with human and mouse sequences. Only after the genome assemblies of the species were completed (chicken, 2004, pig, 2009, turkey, 2009), large numbers of SNPs had become available (chicken, 2004, pig, 2008) and technologies had developed enough to allow relatively cheap high throughput genotyping, could marker assisted selection approaches really be developed. That is where we are today and we are all wondering if we are or are not at the brink of a new era that is to be heavily influenced by yet another breeding technology.

Major genes and the infinitesimal model Breeding programs deal with only a small number of traits that are determined by single or very few genes and selection for these is dealt with independently. Genetic evaluation for such traits is based on phenotypic testing or DNA based genotyping. Breeding value estimation systems for the far majority of (so called quantitative) traits are based on the infinitesimal model: every trait is assumed to be influenced by an infinite number of genes each of them with a small effect. The success of current breeding programs proves that this assumption cannot be totally wrong.
Indeed marker assisted selection addressing only a small number of genes underlying quantitative traits has not been successful up to now. The possibility to select for many loci combined into a single marker based breeding value may totally change the use of genomics technologies in breeding programs.

Genome wide marker assisted selection (GWMAS) The paper of Meuwissen *et al* (2001) showed the way towards application of GWMAS in breeding programs and this approach is now being applied or tried in its original or modified form in many animal breeding programs. Managers of successful commercial breeding programs can only realistically vary two parameters that influence genetic progress: accuracy of estimated breeding value and generation interval. Breeding programs for layer chickens and pigs may not always have minimum generation intervals e.g. because (crossbred) performance of offspring is used for breeding value estimation of selection candidates. In such cases GWMAS has the potential to cause dramatic increases of genetic progress through shortening of generation interval. Fast track programs such as applied in broilers, turkeys and pigs, which already have minimum generation intervals may suffer from less accurate breeding values at the time of selection. GWMAS has the potential to increase these very significantly. A third use of GWMAS is to increase the accuracy of breeding values for traits that are currently not or poorly measured because phenotyping is very expensive or impractical.

Evaluation and optimization Scientists in academia and industry are currently evaluating various options for use of GWMAS and MAS. At least a couple of generations of Genomic Selection are required to prove its effectiveness and to address many uncertain issues such as persistency of SNP effects. Just as challenging is the issue of optimization of commercial breeding programs: the cost of large scale genotyping is very high and cost of genotyping – with many options for fewer or more markers- of individual selection candidates needs to be balanced against the accuracy of breeding values provided, number of candidates genotyped, either or not after various options of pre-selecting these, to ultimately arrive at a design that yields the best competitive position (=profitability) in the mid to longer term for the company that operates the breeding program.

Breakthrough Our current estimates of additional genetic progress that may be obtained by application of GWMAS in commercial breeding programs for layer chickens and pigs make us believe that these are as large as for the previously introduced technologies of hybridization and BLUP breeding value estimation. Therefore: yes, the landscape of commercial breeding of poultry and pigs will change significantly in the next five years because of genomic selection.

References

Meuwissen, T.H.E., Hayes, B.J. & Goddard, M.E. 2001. Genetica 157, 1819-1829.