Future Uses of Genomics in the Poultry Industry

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Introduction to Genomics

Genomics in the context of this presentation concerns the use of information on a bird's DNA make-up and how this can be used in the selective breeding program to deliver improvements in performance.

Breeding companies are principally interested in genetic variation as this is what can be exploited to deliver improvements in performance to be passed onto customers. One of the main sources of natural genetic variation between individuals at the DNA-level is single base-pair differences called Single Nucleotide Polymorphisms (SNPs). SNPs can be readily detected in the laboratory using blood samples by a process called genotyping.

Single nucleotide polymorphism (SNP)

Bird 1 - ...GATGGCTCTTTGGAAGA**A**GATGACTATCATGCCACAACCGAG...

Bird 2 - ...GATGGCTCTTTGGAAGA**G**GATGACTATCATGCCACAACCGAG...

Poultry breeders are interested in how these SNPs are related to traits of economical interest and how they can be used to develop novel selection tools. The combination of genomics information with currently available pedigree and phenotypic information will further improve rates of progress in product performance.

The potential of genomics

Improved accuracy

In traditional selective breeding programs, selections are based on direct measurements (phenotypes) of birds which consist of a genetic (inherited) component and an environmental (non-inherited) component. Therefore the better we can predict the genetic component of performance, the more efficiently progress can be delivered through the breeding program.

In situations where we are unable to measure performance directly on selection candidates (e.g. processing characteristics, survival characteristics, performance in commercial environments) breeders need to rely on information from family members. Selection based on family information alone limits selection accuracy as it is not possible to distinguish between offspring of the same sire and dam families (full-sibs) as they share the same amount of information. Use of genetic markers such as SNPs offers the potential to distinguish between full-sibs hence identifying high merit individuals with greater accuracy.

Management of Genetic Variation

The estimation of genetic variation and effective population sizes using genomics provides information to characterise gene pools and manage genetic variation within and between different lines. This is in addition to the ongoing careful management of effective population sizes which is essential to allow the delivery long-term continuous genetic improvement to the industry.

Development of Genomics Technologies in Commercial Poultry Breeding Operations

Chicken genome sequence and SNPs

The publication by the International Chicken Genome Sequencing Consortium (2004) of the DNA sequence of the chicken (genome) and, perhaps more importantly for breeders, the publication by the International Chicken Polymorphism Map Consortium (2004) of some 2.8m SNPs crystallised the possibility of using DNA based selection methods in poultry breeding programs.

Whilst these publications marked the pinnacle of achievement for the molecular biologists who deciphered the code, it was just the start of the development process for the geneticists in breeding organisations. Here the focus was on how best to utilise this information in commercial breeding operations.

Using genetic markers in breeding

Until 2004, sparse coverage of the genome with markers required detailed studies to understand the linkage of potentially useful markers to traits of interest. There are many examples of these markers although few are routinely used in commercial poultry breeding operations (de Koning and Hocking 2007). In addition to the marker trait association study costs, breeders need to understand the potential impact of the markers on other performance characteristics and make significant investments in labour and capital to exploit their potential in a high throughput breeding programme. Poultry breeding is already highly successful using existing breeding techniques. This raises the economic threshold at which the application of marker assisted selection becomes attractive.

With the publication of the 2.8m SNPs in 2004, it suddenly became possible for chicken breeders to run genome wide marker association studies. Here, thousands of SNPs across the genome are typed and marker-trait associations identified for a large number of traits using DNA from pedigree birds with known performance. The result is a panel of SNPs that can be routinely used for selection purposes. However, experience from broiler breeders found the identification of robust SNPs validated across generations to be extremely challenging (summarised by Avendano et al., 2010).

An alternative approach of using markers in breeding programs, genomic selection, proposed by Meuwissen et al., (2001), involves typing birds using a large panel of densely spaced markers across the genome to predict the genetic merit of an individual. The key challenge to adopting this methodology is the high density genotyping cost (around $150-$250 USD per bird, Avendano et al., 2010). In 2005, an industry funded project involving Aviagen, Iowa State University, University of Wisconsin and the Roslin Institute set out investigate the feasibility of genomic selection in a commercial poultry breeding operation.

Evaluation of genomic selection in this project is at an advanced state. Several generations have now been typed using the expensive high density panel. Methods have been developed which enables a cheaper low density panel to impute high density genotypes thus making the prospect of genomic selection an economic possibility (Avendano et al., 2010). In chickens, the combination of a low density panel in selection candidates and a high density panel in parents has allowed improvements in accuracy of selection for body weight and egg production of about 60% (from 0.4 to 0.6) over the standard genetic evaluation when no phenotype was available in selection candidates (Wang et al., 2011).

Application of Genomics in Turkey Breeding

Development of genomics technologies is advancing fast. In 2010, the turkey genome and identification of some 600,000 SNPs was published (Dalloul et al., 2010). The sequencing of the turkey genome cost less than $250,000, a fraction of the $10million+ cost of sequencing the chicken genome. The turkey genome project is the first example in animals where the cost of sequencing was less than the cost of analysis and interpretation of the results (Dalloul et al., 2010).

More recently, Aslam et al., (2012), has reported the identification of 5.49 million SNPs by evaluating 11 lines of turkeys including 7 lines from commercial breeders. It is clear that the background resources chicken breeders needed to progress genomics technologies is fast becoming a reality for turkey breeders.

It is eight years since the Nature publication of the chicken genome (International Chicken Genome Sequencing Consortium 2004) and the commercial application of genomic selection in chicken breeding programs is tantalisingly close. The complexities of integrating genomics based technologies in turkey breeding will be no less challenging than in chicken breeding operations. However, the delivery timescale will be considerably shorter as much of the groundwork has already been done by the chicken breeders. If successfully delivered in chicken breeding (tangible benefits which can be economically and practically delivered), the technology could be available in turkeys very quickly.

Aviagen Turkeys is in the position to capitalise on the progress made in its sister chicken breeding operations. Many of the processes, databases, algorithms, expertise in the construction of SNP chips, genotyping facilities, protocols and practical experience are readily adapted to the similarly structured turkey breeding operation. Moreover, the industry-academic project team of leading scientists in this area means Aviagen Turkeys is well placed to weather any unexpected complexities the turkey genome may produce. It is anticipated that application of genomics in turkey breeding will enhance improvements in low heritability and difficult to measure traits such as disease resistance immuno-competence, robustness and welfare related traits.

Genomics research in turkeys opens the possibility of examining case-control approaches where samples from affected and unaffected birds can be compared to identify markers for use in selection. These are potentially useful for low frequency traits or issues only seen by customers. Techniques to make this particularly cost effective have been developed by the Aviagen led genomics project described above (Peiris et al., 2010).

The extent to which genomics is ultimately applied to turkey breeding depends on whether it can truly deliver cost-effective benefits to the industry. At the end of the day, the success of the breeding operation will be judged by how the breed performs in the hands of the customer, not the sophistication of the breeding process. Therefore, prior to any implementation, there will be an exhaustive validation of the expected improvements alongside a detailed cost-benefit analysis in the context of what is already a highly successful breeding program based on classical selective breeding techniques.

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