

single SNP that was 100% predictive of the phenotype. This SNP is now being used to eliminate the condition from our population.

Similar efforts to identify predictive mutations for broiler phenotypes have not all been successful. Some of these efforts have utilised the same pooling approach as above and some have utilised an individual sequencing approach. The incomplete genome sequence, inaccuracies of phenotype recording and the complex nature of some of these phenotypes impact the successful identification of predictive tests for all traits.

Challenges

There are a variety of challenges that impact the utility of genomic tools in Cobb-Vantress.

- The chicken genome sequence is currently incomplete. In spite of the continual improvement of the chicken sequence, it is estimated that the current build is missing ~20% of the total genome (Warren 2014). Some of these missing sequences are due to missing micro-chromosome sequences (9 completely missing, and one other is poorly covered) and approximately 30,000 gaps in the available sequence (W. Warren *pers. comm.*). More importantly for the success of our genomic selection program, this missing sequence is estimated to contain between 5% and 20% of the expressed genes. This presents a difficult challenge in our ability to completely scan the chicken genome for genetic elements contributing the expressions of phenotypes.

- Current sequencing technologies are unable to sequence the GC-rich micro-chromosomes. Therefore tools such as genotyping-by-sequencing, or low coverage genome sequence for use in genomic selection will also fail at scanning the entire genome for contributions toward trait expression.

- The development of ‘stable’ and multiple-line genotyping tools (like SNP chips) is complicated by the massive allele frequency differences both between pure line populations, and the rapid changes in allele frequencies between generations of the same line.

- Logistics is one of the greatest challenges for the implementation of genomic selection. Examples of obstacles to overcome are:

- The timing of sampling; genomics is simply not cheap enough to sample and process every chick at hatch; therefore, sampling has to be completed strategically.
- Genotype processing time; the available time between sampling and selection age for the calculation of genomic breeding values is very short.
- Sample collection and management; thousands of samples are collected and processed on a weekly basis from a number of pedigree farms both in the US and Europe.

While many challenges exist for implementing genomics, the opportunities and potential gains for a chicken breeding program are large.

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