DISSECTING THE BOVINE GENOME: IT'S ALL IN THEIR GENES

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Genomic selection has become routine. Genotyping promising young animals using SNP-Chips is standard practice on many farms. Current developments allow analysis of the entire hereditary material of an animal.

FIGURE 1: Overview from an LD-Chip to sequence information

Each base of the genetic alphabet is coloured differently (A = blue, C = red, G = light blue and T = grey). The figure shows the different SNP densities, from the small Low Density (LD) chip, which contains only a few SNPs, all the way up to Sequence, which contains all the SNPs in an animal. For example, animal 1 and 3 are blue at position 1,804 (letter "G"), whereby all other animals are red. This variation is not visible on the 50K or LD SNPs. If the key ancestors of the population are sequenced, the missing positions (white boxes) on 50K or LD Chip can be imputed.

THERE ARE AROUND 22,000 GENES in each cell of a cow. These genes control the composition and function of the body. The "alphabet" of genes consists of only four letters (A, C, G, and T), which occur in a very specific order (called "sequence"). A specific portion of the sequence may be associated with a specific function – this is called a "gene". The entire sequence of the bovine genome was decoded in 2009. It contains approximately 3 billion letters (bases).

   It is extraordinary that most of the letters in different animals of a population are identical – on average, only every 300th base is different. For example, where *Monument Impression-ET* might have an "A", *Marbri Facebook* might have a "T". These differences in single bases are called "SNP", and they are the simplest kind of variation between animals. Today, approximately 13 million SNP in the Holstein cattle genome are known. A few of them are included on Chips (High Density, 50K, or Low Density), which can be used for genomic breeding value estimation.

Sequencing: What's the advantage?

Instead of using only 50,000 or 800,000 SNP, sequence information contains all existing 13 million SNP (Figure 1). The sequence can therefore be thought of as "the ultimate SNP chip". Estimating breeding values with all of these SNPs, however, doesn't really make sense, because only a precious few of them affect fitness or performance traits. It is therefore important to understand and identify the most important SNP, and to take these into special consideration. This will eventually allow even more accurate estimation of genomic breeding values. The current goal of a lot of research is to analyze SNP function in order to identify the most important regions of the DNA. Here, the main focus is on traits with low heritability, because the gains are most difficult to achieve with traditional breeding.

Sequencing: What are the challenges?

Sequencing is still an evolving area of research. Universities and breeding organizations all over the world are trying to use this information to better understand the heredity of economically important traits and, ultimately, to further improve genomic breeding value estimation. Massive amounts of data and computing power can be limiting factors, as well as the technical know-how of dealing with this new and sometimes tricky information. International collaborations are essential in order to keep up with the incredible speed of development in this area.

Summary:

In the age of genomics, constant adjustment of routine procedures to account for new developments and information are important. The use of sequence information in routine breeding value estimation is not yet ready for practical application, however the Canadian dairy industry is involved in various research projects which will help to move this area forward.

   Genetic regions with significant influence on traits of economic interest are being identified, and it will likely become possible to eventually increase the reliability of genomic breeding values. This will ultimately lead to higher genetic gain – especially for traits with low heritability.

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