Breeding and Genetics Symposium: Joint ADSA/Interbull Session: Ten Years of Genomic Selection

65   From sequence of Dominette to 10K and 50K SNP chips.
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Genetic markers based on interrogated nucleotide variant sites have been used in cattle genetics since the late 1990s. Owing partly to the excessive cost and labor-intensive means of assessing marker sites, such as microsatellite repeats, their commercial use was relatively limited. Additionally, genotyping accuracy was error-prone and did not cover the cattle genome evenly. In this presentation, we highlight 2 specific improvements that started the modern genomics era. The development of high-resolution DNA sequence maps of the cattle genome and the adaptation of microarrays for high throughput genotyping served as the catalysts for data collection for modern cattle genomic selection. Simultaneously, the development of computational methods for associating animal SNP genotypes with productive trait phenotypes improved the accuracy of animal selective breeding values by providing higher resolution of allelic transmission to offspring. The efficacy of these tandem improvements has generated incredible value for the modern cattle breeder; however, many challenges and questions persist. Linkage between genetic markers and their associated causal genetic mutations can be further improved by genotyping the actual mutation itself. There is additional novel sequence within the cattle pan-genome that is currently not represented in the cattle reference genome assembly, which may not be tracked by current genetic markers. Finally, methods need to be developed that efficiently incorporate whole genome DNA sequence data into genomic selection. Future techniques and technologies that may address these challenges will be discussed.

Key Words: SNP chip, cattle reference, genomics

66   How to implement genomic selection. P. M. VanRaden*, *USDA Animal Genomics and Improvement Laboratory, Beltsville, MD.*

Key features of genomic selection remain essential, and new features continue to be added 10 years after first implementation. Breeding values with higher reliability earlier in life are estimated by combining DNA genotypes for many thousands of loci using existing identification, pedigree, and phenotype databases for millions of animals. Quality control for both new and previous data greatly improves by comparing genomic and pedigree relationships to fix parent-progeny conflicts and discover many additional ancestors. Many quantitative trait loci and gene tests have been added to previous assays that used only evenly spaced, highly polymorphic markers. Imputation now combines genotypes from many assays of differing marker density. Prediction models have gradually advanced from normal or Bayesian distributions within breed and trait to single-step, multitrait, multibreed, or other more complex models. Genomic selection was initially applied to males to predict progeny performance but now is widely applied to females or even embryos to predict their own later performance. The initial focus on additive merit has expanded to include mating programs, genomic inbreeding, and recessive alleles. Many producers now use DNA testing to decide which heifers should be inseminated with elite dairy, beef, or sex-sorted semen; be embryo donors or recipients; or be sold or kept for breeding. Because some of these decisions are expensive to delay, predictions are now provided weekly instead of every few months. International genomic databases and predictions are often more accurate than within-country genetic evaluations previously designed for progeny testing. Obtaining predictions from an international database is usually more effective than computing predictions from only local data unless local breeds, conditions, or traits differ greatly from the large database. Selection indexes include many new traits, often with lower heritability or requiring large initial investments to obtain phenotypes, which provide further incentive to cooperate internationally. The genomic prediction methods developed for dairy cattle are now applied widely to many other animal, human, and plant populations.

Key Words: genomic prediction, DNA testing, dairy cattle

67   The role of Interbull in the successful implementation of genomic selection in breeds other than Holstein. E. C. Santus*, *ANARB, Bussolengo, Italy.*

The use of DNA information in dairy cattle is not a complete novelty as specific markers for interesting genes have been used in selection schemes for specific needs since the late 1980s. As we all know, the breakthrough occurred at the turn of the millennium. First with the envision and later with the practical application of the massive analysis of thousands of markers on cattle genome. Since then, the approach has changed completely passing from the Mendelian identification of desirable alleles to the studies on the associations between markers and phenotypes. At that time, numbers started to matter and the risk of facing the "new opportunities, old inequalities" paradox became a real scenario as the new mechanisms of exploitation of the new technology called for a minimum size population and set a limit for entry into this new market. The Brown Swiss breed is a small breed compared with the Holstein breed, but all breeds are small if you use the Holstein breed as the term of reference. Thus, it is of some relevance to use the Brown Swiss example as a possible model. The greatest advantage of this breed in Europe was the existence of a very active international community. Another advantage was the fact that no single country had alone the size of the population needed for a reliable implementation of genomic selection. Political aspects were not, as always, of secondary importance when the discussion about sharing valuable information started. Since the very beginning, Interbull—recognized by all as an independent, reliable and competent third party—was identified as a natural platform that could solve most of the political issues. The development of an agreement among all parties, called "Intergenomics," was the first necessary step, which was followed by specific agreements between each party and Interbull. Thanks to that approach, genomic selection has become a reality for the Brown Swiss breed and has revolutionized the way the genetic management of the population has been carried out since then. After only a few years, in 2014, Intergenomics evolved into Intergenomics 2.0 and now it has become a routine service provided by Interbull to the member countries that joined the agreement.

Key Words: Interbull, genomics, Brown Swiss

68   Exploiting homozygosity in the era of genomics—Runs of homozygosity, inbreeding, and genomic mating programs. C. Maltecca*[1], C. Baes[2], and F. Tiezza[1], [1]*North Carolina State University, Raleigh, NC,* [2]*University of Guelph, Guelph, ON, Canada.*