

# Breeding and Genetics Symposium: Joint Interbull/JAM Session: Use of genomics to improve limited and novel phenotypes in animal breeding

**15 The effect of genomic technologies in the selection of novel phenotypes in dairy crossbreeding programs.** Richard J. Spelman\*, Mathew D. Littlejohn, Ric G. Sherlock, and Steve Davis, *Livestock Improvement Corporation, Hamilton, New Zealand.*

Genomic selection in dairy cattle has been successfully applied for milk production traits in many countries around the world. This has been enabled through the routine collection of phenotypes over several years and the large body of animals that have been genotyped. The application of genomics for non-routinely collected phenotypes has been less successful due to the cost of phenotyping and the smaller number of animals available for genotyping. Genomic estimates for Johne's susceptibility and residual feed intake have been recently commercialized in the New Zealand dairy population. Johne's susceptibility has been estimated in a case control experimental setting. Over 1,500 animals that have been identified to be affected by Johne's have been genotyped and compared with a control derived from the general population of animals that have been genotyped in the LIC genomic selection data set. The accuracy of evaluation for Johne's susceptibility is approximately 30% with a heritability of 18%. Residual feed intake was measured over 2000 growing Holstein-Friesian heifers in New Zealand and Australia, which were phenotyped over 42 d for feed intake and live weight gain. Genomic estimates for residual feed intake have a reliability of 10%.

**Key Words:** dairy, genomics, crossbreeding

**16 Using genomic technologies to improve broiler health and production.** Rachel J. Hawken\*, *Cobb-Vantress, Siloam Springs, AR.*

Health and welfare traits have always been a critical factor toward the genetic improvement of broiler breeding stock. Current trends toward antibiotic free broiler production have emphasized the need to engage new technologies toward the improvement of these traits. Genomic technologies such as genome selection, genome sequencing, and mutation detection all offer great opportunities to advance these traits. For example, with the aid of genomics, genetic information from birds in disease challenged environments (on pure line breeders or crossbred product birds) can be utilized for the selection of superior breeding stock at the pedigree level, in non-diseased environments. Furthermore, the genetic basis of genetic diseases can be identified and deleterious alleles eliminated from breeding programs. This presentation will illustrate various opportunities for improving health and production traits using genomics at Cobb.

**Key Words:** poultry, genomics

**17 Application of genomic technologies to improve feed efficiency traits in swine.** Kent A. Gray\*, *Smithfield Premium Genetics, Rose Hill, NC.*

One challenge that faces the US pork industry is the efficient use of feed resources as feed costs continue to be the largest variable expenditure. Typically, feed efficiency is measured as feed conversion ratio (FCR) or calculated through residual feed intake (RFI). Regardless of the measure defined as feed efficiency, average daily gain (ADG) and average daily feed intake (ADFI) remain the 2 main components for estimating nutrient utilization traits. Several studies demonstrate improvement of feed efficiency through selection programs focused on improving either

FCR or RFI. However, these programs require recording individual feed intake, which is labor intensive, time consuming, and requires specialized equipment. Additionally, data from feed intake recording equipment (FIRE) systems contain several data errors that require careful editing before the data can be used. With the introduction of advanced genomic technologies in livestock species there is an opportunity to improve selection of feed efficiency. Genomic tools have helped us identify genomic regions associated with feed efficiency and other production traits through whole-genome association studies. One region in particular located on SSC1 ranging from 166 to 170 Mb was significantly associated with ADFI, ADG, and backfat (BF), where *SOCS6* and *DOK6* are proposed as the most likely candidate genes. The use of whole-genome selection methodologies can also be used to improve response to selection by increasing accuracy. Variance components were estimated with AIREML and (G)EBV were computed with either BLUP or single-step genomic BLUP (SSGBLUP). Comparisons of reliabilities between traditional BLUP estimates and SSGBLUP estimates indicate that GEV estimates for FCR and component traits BF, ADFI, ADG, and off-test weight (WT) have increased reliabilities by 9% to 60% when compared with traditional EBV estimates. Because of this increased accuracy, we can conclude that application of genomic technologies will help us improve feed efficiency traits in swine.

**Key Words:** feed efficiency, swine, genomic selection

**18 The role of genomics in the development of novel phenotype-based products in the beef industry.** Matthew A. Cleveland\*, *Genus plc, DeForest, WI.*

The use of genomics in beef cattle evaluation has experienced relatively widespread adoption. Breed associations and improvement programs have used genomic information to varying degrees, particularly for well-characterized traits. The opportunity for transformational change from genomics, however, lies with novel traits that are typically more difficult to capture or describe during normal production processes. Genomic associations have been reported for novel traits such as those related to feed efficiency, animal health, meat quality and consumer preference, reproduction, healthfulness of beef and effects on human health, the environment and animal welfare. While several interesting genomic regions have been identified across traits, there is scant evidence of application in structured breeding programs for beef cattle. The collection of phenotypes for some novel traits can have near-term direct genetic and economic impact. For example, improvements in individual feed intake or even disease resistance can generate measurable increases in beef system profitability. Other novel traits of interest, such as fatty acid composition or methane production, have large perceived consumer impact, but remain aspirational in terms of providing a direct economic benefit or even a logical selection objective. Regardless of the trait, the optimal use of genomics in a beef improvement program requires a structured data collection system, or large project-based phenotyping efforts, to realize the benefits and deliver a truly differentiated product. Ultimately, the value derived from genomics-enabled differentiation must at a minimum cover the cost of the investment. The value of genomics in the beef industry is difficult to elucidate without some measure of actual or "virtual" integration of the value chain, which is often lacking. Commercial breeding programs, such as Genus ABS, have developed the structure to deliver well-defined genetically improved products to

the beef supply chain. At the core of this improvement is the ability to make rapid progress for economically relevant traits, which is often optimally achieved with the aid of genomic information.

**Key Words:** beef cattle, genomics, novel phenotype

### 19 Using genomics to enhance selection of novel traits in North

**American dairy cattle.** Jacques P. Chesnais\*<sup>1</sup>, Mehdi Sargolzaei<sup>1,3</sup>, Filippo Miglior<sup>2,3</sup>, and Jennie E. Pryce<sup>4</sup>, <sup>1</sup>*The Semex Alliance, Guelph, Ontario, Canada*, <sup>2</sup>*Canadian Dairy Network, Guelph, Ontario, Canada*, <sup>3</sup>*CGIL, University of Guelph, Guelph, Ontario, Canada*, <sup>4</sup>*Department of Economic Development, Jobs, Transport and Resources, Bundoora, Victoria, Australia.*

Genomics offers new opportunities for the effective selection of novel traits. For traits such as mastitis resistance, hoof health, or milk composition records based on medium infrared (MIR) data, for example, enough records are usually available to carry out genomic evaluations based on sire genotypes and the phenotypes of their daughters. For traits that are more novel or expensive to collect, such as individual feed intake or immune response, the development of a cow reference population is the most effective approach. The reliability of the resulting genomic

predictions depends primarily on the size of the reference population and on trait heritability, as shown by Daetwyler et al. (2008). To provide an empirical check of these theoretical estimates of reliability, the reliability of genomic selection was estimated for various traits using a reference population of 1,000 to 10,000 Canadian-born Holstein cows that had been genotyped with a panel of 6,000 SNP or more. All genotypes were imputed to 50K. The effects of SNP were estimated from cow records only, after excluding the dams of validation bulls. Bulls first proven in 2013 and 2014 were then used to carry out a validation and estimate the accuracy of genomic selection based on these SNP effects. Differences between accuracies obtained this way and using the Daetwyler formula are reported for traits of varying heritability and degree of indirect selection. Results confirm that large reference populations are usually required to achieve adequate accuracy. In many instances, the accuracy of genomic selection for novel traits can be increased through the use of indicator traits. Cow size and MIR data are used as examples to show how they can increase the accuracy of genomic selection for feed efficiency. Expected rates of genetic progress are calculated for each scenario, using the selection intensities and generation intervals currently realized in North American dairy cattle.

**Key Words:** novel trait, genomic evaluation, dairy cattle