

CANADIAN LIMOUSIN ASSOCIATION'S GENETIC EVALUATION SYSTEM EMPOWERS BREEDING DECISIONS FOR SEEDSTOCK AND COMMERCIAL BREEDERS

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Beef seedstock producers are charged with the development of germplasm to move the industry towards a number of broad goals including improved sustainability, profitability and consumer acceptance of our product—high quality, wholesome beef. This charge is no small undertaking and requires producers of all sizes to utilize the best possible tools to make precise breeding and selection decisions. To that end, your membership in the Canadian Limousin Association (CLA) enables you to access industry leading tools for the genetic improvement of your herd and the genetics your program provides to the broader beef value chain through the sale of animals into the commercial breeding sector. CLA members collectively support two key services to the membership through their herd enrollment, registration, data submission and registry transfer business. The two products are the DigitalBeef portal for data submission and herd management as well as the CLA genetic evaluation powered by the International Genetic Solutions BOLT evaluation.

The DigitalBeef portal plays a key role in the genetic improvement of Limousin cattle by providing a convenient online resource for members to submit pedigree and performance data. The online portal computes adjusted performance records and within herd contemporary group ratios. The platform also provides a data pipeline to the genetic evaluation system. That pipeline returns the genetic predictions in the form Expected Progeny Differences (EPD) back to breeders and others through the lookup features. DigitalBeef provides both members and association staff convenient, 24-7, access to data. The database includes powerful tools to search for animals of defined merit and test mating decisions enabling breeders to make efficient and impactful breeding decisions.

The genetic evaluation system used by CLA is provided through partnership with other breeds in the International Genetic Solutions organization. The state-of-the-art system utilizes both traditional pedigree and performance records combined with genomic data to compute EPD. The evaluation includes over 20 million animals in the pedigree, performance data on more than 12.5 million head and nearly 700,000 animal genotypes

The genetic evaluation methodology employed is a single step process that seamless-

ly combines all data sources for genetic prediction. Genomic data is exploited through a process that adjusts the relationships among related animals based on the genetic material they inherited. Animal's always have one-half of their genetic complement from each their sire and dam. However, due to random assortment of chromosomes to gametes and recombination, animals have relationships that vary between 0 (zero) and 50% with an average of 25%. During egg or sperm cell formation in mammals, haploid cells are formed which have only one of the two copies of each chromosome. During fertilization, diploid chromosome status, where the cell has two copies of each chromosome, is restored. The random selection of one of the two copies of each chromosome results in individuals having a genetic makeup that may not have equal (25%) contribution from each grandparent. The evaluation uses that information to adjust predictions of an animal's genetic merit. It makes sense that if an animal has more genetic content from one particular grandparent, then their genetic merit is also more similar to that grandparent.

The IGS BOLT evaluation utilizes the most advanced analytic model for EPD calculations. In addition to the utilization of genomic data to modify genetic relationships among individuals, it also fits single-nucleotide polymorphism (SNP) marker effects. The BOLT system fits >2,000 markers per trait extracted from the standardized 50,000 marker panel. The included DNA markers have effects that previously have demonstrated an association with the variation in a given trait. These DNA markers are not causal variants but are thought to be nearby the variants that result in changes in animal phenotype. Inclusion of a genotype in a genetic evaluation of young bull that is a selection candidate adds accuracy to the animal's EPDs. The accuracy improvement from genomics is roughly equivalent to collecting phenotypic records and including those in the evaluation for a young sire's entire first calf crop for all traits evaluated. For some traits the equivalent progeny count exceeds 15-20 head.

For replacement heifers, the added value of information from genomic testing now exceeds the information observed from a lifetime of natural calf production. Genomic tools provide a powerful and accurate insight into the genetic merit of an individual breeding candidate. Table 1 provides the estimated progeny equivalents by trait. A progeny equivalent is an estimate of the average number of progeny phenotype records needed to see an equivalent increase in EPD accuracy as compared to the information provided by the genomic test.

Seedstock producers are encouraged to utilize genotyping in their own herd improvement program. Having a genotyped cowherd benefits the seedstock producer in several ways. First, it means that the pedigree of current cows are parent verified. Accurate pedigree is a key step in production and reporting of accurate EPDs. Genotyping of existing cows can identify errors in pedigree improving EPD reliability through correction

of kinship. Typical pedigree error rates, even in very well managed herds, can range from 5-10% due to inadvertent record keeping errors, stray bulls, cows switching calves and even errors in semen selection from the AI tank. Genotyping tests easily find those errors and often provides a path to resolving the error.

Combined, the inclusion of a revised kinship and construction of reliable pedigrees increases the accuracy and reliability of the EPDs produced in the system. Improved EPD accuracies mean more reliable mating decisions can be made for your genotyped cows enabling more rapid genetic improvement.

Investment in genotyping replacement heifer candidates prior to selection provides an effective way for producers to plot out their genetic destiny. Genomics adds more accuracy to female EPDs than their lifetime production of natural calves for many traits. In today's fast moving genetic landscape, time is more valuable than ever. Making investments that help capture genetic information early in an animal's life is essential to remain competitive in the seedstock marketplace.

The incorporation of traditional pedigree and performance data is achieved through the implementation of a mixed animal model in BOLT that accommodates both multi-breed and multi-trait approaches. CLA formally allows percentage cattle into the database and genetic evaluations system. By adjusting animals' performance records to account for differences in breed fraction and both direct and maternal heterosis, the evaluation effectively accommodates genetics from various breed sources. Differences in environment and management are corrected for through establishment of within herd contemporary groups.

Genetic evaluation utilizing phenotypic records depends on analysis of data where animals have had fair competition; in other words, an equal opportunity to perform. The basis of genetic evaluation is the concept that if a group of animals all have the same nutritional and physical environment, then differences observed in their performance is due to genetics. Of course, we have to make sure that the competition is fair, else the genetic predictions include bias from non-genetic sources. Individual performance observations are adjusted for known non-genetic effects. These non-genetic effects include age of calf, age of dam and contemporary group.

The genetic evaluation system leverages the genomic and traditional data to produce genetic predictions across a range of economically important traits. The suite of traits is designed to address the need for improvement in merit across a whole range of traits in value chain. Included in the suite are maternal traits like maternal calving ease and milk. Maternal traits account for the genetic effects in those characteristics exhibited by a cow that affect her calf's performance. One way to think about maternal traits is that they are the heritable components of the environment a cow provides for her

calf. Fertility traits are estimated through both scrotal circumference and stayability EPDs. Direct traits are those exhibited by a calf and influenced by both paternal and maternal genetic contributions. These traits include calving ease, birth, weaning and yearling weights. Additionally, end product traits carcass weight, marbling, ribeye area and fat thickness.

CLA and its members have made sound investments in genetic improvement tools. Now's the time to make sure you are using them to your advantage and positioning your commercial customers for profit and success!