

Symposium: Beef Species: The Evolution of Beef Cattle Genetic Evaluation

4 Milestones in beef cattle genetic evaluation. L. L. Benyshek*, *University of Georgia, Athens.*

The first national beef sire evaluation summary was published in 1971. Since 1971 beef breeds that have serious genetic improvement programs have adopted this genetic evaluation technology. Today it is rare when a bull is offered for sale without Expected Progeny Differences. Initially, application of methodology was limited by hardware and software constraints. The current genetic evaluation summaries show that the industry has taken genetic evaluation seriously with more traits than producers can assimilate into breeding program. This has spawned an effort in decision making software including selection indexes. The advent of DNA technology for beef cattle has begun to blossom with the sequencing of the beef genome. Genetic evaluation began in the 1930's with research in performance testing. In the 1940's large regional research programs were funded leading to state beef cattle improvement associations in the 1950's. In the late 1950's some breed registry associations began to formalize the collection of performance data. In 1968, a major milestone was achieved with the establishment of the Beef Improvement Federation which standardized the collection and analysis of data. In 1972 C. R. Henderson presented an invited ASAS paper that formalized his mixed model procedures providing best linear unbiased predictions (BLUP) of breeding value. Established breeds produced estimated breeding values; however, mixed model procedures were first applied only to designed progeny tests. With the advent of increased artificial insemination the data structure evolved to warrant national sire evaluation using BLUP in the 1970's. In the 1980's animal model procedures began to evolve particularly after the first genetic prediction conference in 1983 where the reduced animal model was elucidated. In 1984 the reduced animal model was applied to field data for four breeds resulting in the first published evaluations using the technology. In the years following, the animal model became the standard for genetic evaluation. Currently, researchers continue to look at improved models leading to across breed evaluations and the incorporation of genomic information in the procedures.

Key Words: Beef, Genetic Evaluation, Mixed Model

5 Producing and using genetic evaluations in today's beef industry. D. Garrick*, *Iowa State University, Ames.*

Genetic change is a straightforward consequence of selection. Genetic improvement is more difficult to achieve because it requires the cumulative value of favorable changes to exceed the costs incurred by unfavorable changes, data collection and recording and infrastructural investments. The principal technology that has been available to assist breeders make informed selection decisions has been the expected progeny difference or EPD. The nature and scope of EPDs has grown enormously over the last few decades, to encompass a large array of easily measured attributes. Breed Associations have acted individually in the production of EPDs, gaining scientific and servicing support from land-grant Universities, principally, Colorado State, Cornell, Georgia and Iowa State Universities. This approach is now structurally, financially and technologically challenged, unable to meet current or future demands of industry. Bull buyers are now demanding across-breed EPDs including crossbred or composite bulls, most commonly Angus derived. The Breed Association data systems are not well structured to unambiguously record crossbred animals or any external pure-bred

parents. The land-grant service providers are keen to pass on their subsidized servicing roles in favor of software licensing and research support. The advent of small panels of molecular test information has created challenges with new kinds of data that have not been able to be harnessed by Breed Associations. This will likely get worse with the adoption of high-density SNP marker panels. Finally, in contrast to other industries, beef cattle EPDs have failed to move to properly reflect economic rather than just productive characteristics of alternative bulls. These challenges must be addressed if the beef industry is to retain its competitiveness, nationally and internationally.

Key Words: Genetic Evaluation, Selection, Beef Cattle

6 DNA technology: Estimation of genetic merit from large DNA marker panels. R. L. Fernando*¹ and C. Stricker², ¹*Iowa State University, Ames,* ²*Applied Genetics Network, Davos, Switzerland.*

Given trait and marker data on a sufficient number of individuals, the effects of all markers can be estimated accurately and used for genetic evaluation of future candidates using only marker genotypes. In practice, however, the number of marker effects in the model is much greater than the number individuals with trait phenotypes. Several strategies have been proposed to overcome this problem. One strategy includes markers in the model as random effects with a constant variance for all markers. We will show that as the number of independent markers increases, this approach converges to pedigree based BLUP, which does not use any marker information. As markers on a chromosome are not independent, even though the accuracy drops with the number of markers included in the model, this approach gets higher accuracies than pedigree based BLUP. Better results are obtained, however, when locus-specific variances are estimated from the data. We used computer simulated data to investigate the relationship between the accuracy of prediction and the number of markers included in the model for a Bayesian method that uses a zero-inflated inverse chi-square prior for the locus-specific variances. A genome of 30 chromosomes, each 1 Morgan in length, was simulated. Random mating in a population with an effective size of 100 for 1000 generations was used to generate linkage disequilibrium. Marker effects were estimated with trait phenotypes and marker genotypes on 2120 animals. The estimated effects were used to predict the breeding value of 2000 animals in the following generation. Accuracy of prediction was quantified by the square of the correlation between the predicted and true breeding values. Accuracies were obtained with 3,000, 30,000 and 60,000 markers in the model from four replications of the simulation. The mean values of the accuracies were 0.82, 0.88, and 0.88 for the three marker densities. This Bayesian method seems to be well suited for estimation of genetic merit from large DNA marker panels.

Key Words: Whole-Genome Analysis, Genomic Selection, Marker Assisted Selection

7 Integrating genetic evaluations with DNA technologies for the ultimate selection tool. R. J. Tempelman*¹ and S. D. Kachman², ¹*Michigan State University, East Lansing,* ²*University of Nebraska, Lincoln.*

Various genomics companies have recognized the value of marker assisted selection for beef cattle improvement by marketing estimated molecular values (EMV) based on genetic markers as determined from tissue samples submitted by participating breeders for animals of interest. These EMV are typically based on dozens or hundreds of markers whose individual effects have been estimated from reference populations as based on extensive records on a large number of phenotypes on thousands of cattle. Only the EMV, as the sum of these estimated effects, and not the marker genotypes themselves, are generally reported back to the breeder. We will address how EMV can be integrated with existing phenotypic and pedigree data, as currently used to provide expected progeny differences (EPD), to enhance the accuracy of national beef cattle genetic evaluation. Attention will be drawn to computational issues, improvements in accuracy of EPD and its concomitant potential

for earlier selection, potential ascertainment bias, and selection for traits that are not extensively recorded. These assessments will be based on various assumptions on how well the EMV correlate with the true genetic merit. The drawbacks from not having individual marker genotype information will be directed towards issues that are particularly relevant for beef cattle production, such as multibreed genetic evaluation, genotype by environment interaction, multiple trait selection, multi-sire pastures, and selection for uniformity. Whole genome selection based on emerging high throughput single nucleotide polymorphism (SNP) chips appears to offer substantial promise in addressing some of these limitations.

Key Words: Genetic Markers, Expected Progeny Differences, Genome Selection