

Gelbvieh National Cattle Evaluation: Improvements Have Been Implemented

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Some major improvements will be implemented for the Gelbvieh genetic evaluation program beginning with the Spring 2003 evaluation. The purpose of this article is to provide some information on the benefits and the possible impact of the new technology that will be incorporated into the Gelbvieh genetic analysis.

The first improvement is the use of a multi-breed model for the analysis of birth, weaning and yearling weight that allows for the incorporation of all animals of every possible breed combination contained in the Gelbvieh data base. In previous analyses, only progeny records from purebred Gelbvieh sires were included; therefore, crossbred sires and animals that had a low percentage of Gelbvieh breeding did not receive an EPD. In the new analysis, animals of any breed combination that are in the Gelbvieh data base and that make it through normal editing criteria are included in the evaluation and receive genetic values. The multi-breed model accounts for heterosis and breed genetic differences between all possible breed combinations, so that all the animals in the evaluation can be fairly compared. The model accomplishes this by using a combination of records and pedigree information provided by AGA and information provided by numerous scientific literature reports on breed differences and heterosis effects involving beef cattle for birth, weaning and yearling weight and milk. Incorporation of literature values allows for the estimation of breed differences and heterosis effects that can not be estimated using the data alone. The use of the multi-breed model should increase the overall accuracy of evaluation because more animals can now be included in the analysis. As a point of clarification, the only traits that were analyzed using a multi-breed model were birth, weaning and yearling weight. Gestation length, calving ease, scrotal circumference and carcass traits were analyzed using traditional approaches.

The second improvement is the use of a multi-trait model that analyzes birth, weaning and yearling weight simultaneously. In previous analyses, birth weight was analyzed using a single trait model and weaning and yearling weight was analyzed together using a two-trait model. Use of the two-trait model involving weaning and yearling weight helps correct any bias that can be caused by the loss of records between weaning and yearling due to culling at weaning. Incorporation of birth weight into a multi-trait model that also includes weaning weight and yearling weight will help to correct potential bias due to possible mistakes or inaccuracies in the reporting of birth weights. Basically, the genetic relationships between the three traits help to provide information that can be used to adjust the EPDs of those traits that have missing or misreported information.

The third improvement involves the use of improved technology to compute accuracies for all traits and models. Accuracy values range between 0 and 1 and provide information on the reliability of an EPD. The higher the accuracy value the more reliable the EPD. Unfortunately, the computation of exact accuracy values are not possible due to computing constraints; therefore, the accuracy values that are provided are approximations. The approximate accuracies used in previous years were generally higher than the actual accuracies, particularly for animals with low amounts of information. Because the procedures used to predict EPDs consider the actual amount of information as a part of the computations, EPDs for all animals can be directly compared even though there are differences in

accuracy. The accuracy is used to determine the extent of sire use in a program, with lower accuracy sires being used less because of higher risk of EPD change when new progeny are produced. Research has shown that equivalent or greater genetic progress per year can be made by using numerous low accuracy sires each year compared to using a few high accuracy sires. Therefore the inflated accuracy values that were used in previous years encouraged the use of young sires, which are genetically superior as a group compared to older, high accuracy sires. The new accuracy approximation that will be implemented will provide approximate accuracy values that are closer to the actual accuracies. The end result of implementing the improved accuracy computation procedure will be that computed accuracy values, especially for young animals, will generally be lower than in previous years, but they will be closer to the actual accuracies. This new change will help producers and breeders to more accurately assess their risk and make more informed selection and marketing decisions. It is important to understand that the EPDs produced using the new models will actually be more accurate than previous years; however, the approximate accuracy values will be less inflated than in previous years and closer to the actual values.

A last comment on the EPDs provided to AGA. In past years, the University of Georgia did not return EPDs for all animals that received an EPD in the evaluation. Genetic values on very low accuracy animals that did not have progeny or grandprogeny were not provided to AGA. We have decided to return all computed EPDs back to AGA, regardless of accuracy. Consequently, there are EPDs for some low accuracy animals that were not available before.

Even though there have been some improvements to the evaluation procedures to provide more useful and accurate genetic information to the breeders of Gelbvieh cattle, the basics of a sound genetic evaluation program have not changed. It is still very important that proper identification of contemporary groups be provided. The burden of proper contemporary group identification falls to the breeder, since the breeder is the only person who has the information on how animals were truly managed. The Gelbvieh Association provides codes and methods to assist breeders to identify contemporary groups. Most inaccuracies in National Cattle Evaluation programs trace back to improper identification of contemporary groups. Breeders must also do everything possible to provide correct weights and accurate animal identification and parentage. With the implementation of multi-breed evaluation, it is also now essential that breeders provide accurate breed designations on animal performance and pedigree information.

It is important to the cattle industry that Gelbvieh breeders continue a strong performance program. No genetic evaluation program or sire summary is possible unless Gelbvieh breeders and producers provide the necessary information to AGA. Participation in the performance and genetic evaluation program of AGA will help to ensure that the best Gelbvieh germ plasm is identified and available for use throughout the beef industry.