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ADSA Multidisciplinary and International Leadership (MILK) Symposium: The Dairy Cow in 50 Years

272   The Dairy Cow in 50 Years: A symposium for all ADSA members and especially for graduate students in dairy production.   Michael VandeHaar*, *Michigan State University, East Lansing, MI.*

Dairy cattle have changed considerably in the past 100 years. They now are generally taller and thinner with larger udders that produce considerably more milk. Genomic selection and the ability to modify specific genes will enable us to make changes even faster in the future. The discipline of animal breeding is generally concerned with genetic change; however, all disciplines must adapt to the animals that are produced. Moreover, dairy cattle genetics are related across countries. Thus, it is imperative that we consider the future of the dairy cow from a multidisciplinary and international approach. Although the presentations in this symposium are led mostly by geneticists, this symposium is for all dairy scientists, especially for graduate students in the production division. You are the ones who will discover how to best feed and manage the cows of the future!

Key Words: genomics, selection, dairy production

273   A vision of the dairy farm and dairy cow in 50 years.   J. H. Britt*, *Jack H Britt Consulting, Etowah, NC.*

Dairy-based foods will increase in importance in human diets because of dairy's role in meeting protein needs sustainably. Dairy enterprises will relocate to regions that have adequate rainfall or water resources and suitable climates. Technologies that will be used have emerged conceptually at basic scientific levels. Dairy enterprises will use laterally-integrated systems comprising physically-separated facilities for pre-weaned heifers, replacement heifers, early dry cows, transition cows, milk cows and dairy beef. Each unit will be managed as if it were a superorganism. Scale of dairy enterprises will increase and manual labor will decrease through automation, robotics and sensors. Resources will be harvested from manure and reused. Perennial crops, including perennial maize and high-starch energy grasses, will replace annual maize as major feed sources. Dairy enterprises will be subjected to more regulations and will put greater emphasis on sustainable agro-ecological systems. Milk output will be contracted with processors and manufacturers, and milk will be separated automatically into pools at farms according to processing characteristics. Dairy cows worldwide will be gene-based rather than breed-based and will comprise genes that have been edited, synthesized or transferred. Cows will be smaller and healthier and selected for their environmental region. Milk yield will exceed 25,000 kg per cow per year in North America. Genetic introductions into herds will move from semen to embryos. Developmental programming and precision management will be used to regulate epigenetic and other gene-regulatory processes to control traits expressed in cattle weeks to years later. Microbiomes of cattle, crops and farmsteads will be manipulated strategically and a herd's genomic profiles will include genes of its cows and their microbiomes. Dairy beef with lower GHG footprints will grow in importance as proportion of dairy cows delivering male calves increases.

Key Words: future, dairy, cow

274   Possibilities in an age of genomics: The future of the breeding index.   J. B. Cole*, *Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD.*

Selective breeding has been practiced since domestication, but early breeders commonly selected on appearance (e.g., coat color) rather than quantitative phenotypes (e.g., milk yield). A breeding index converts information about several traits into 1 number used for selection and also to predict an animal's own performance. Calculation of selection indices is straightforward when phenotype and pedigree data are available. Prediction of economic values 3 to 10 years in the future, when the offspring of matings planned using the index will be lactating, is more challenging. The first USDA selection index included only milk and fat yield, while the latest version of the lifetime net merit (LNM) index includes 13 traits, with some traits actually composites of other traits. Selection indices are revised to reflect improved knowledge of biology, new sources of data, and changing economic conditions. Single-trait selection often suffers from antagonistic correlations with traits not in the selection objective. Multiple-trait selection avoids those problems at the cost of less-than-maximal progress for individual traits. How many and which traits to include is not simple to determine because traits are not independent. Many countries use indices that reflect the needs of different producers in different environments. While the emphasis placed on trait groups differs, most indices include yield, fertility, health, and type traits. Addition of milk composition, feed intake, and other traits is possible but are more costly to collect, and many are not yet directly rewarded in the marketplace, such as with incentives from milk processing plants. As the number of traits grows there is increasing interest in custom selection indices for closely matching genotypes to the environments in which they will perform. Traditional selection required recording lots of cows across many farms, but genomic selection favors collecting more detailed information from cooperating farms. A similar strategy may be useful in less developed countries. Recording important new traits on a small fraction of cows can quickly benefit the whole population through genomics. Gene editing may be used to increase the frequency of high-value Mendelian traits, such as polled.

Key Words: dairy cattle, genetic improvement, selection index

275   Building a better cow: The Australian experience and what's next.   J. E. Pryce*[1,2] and M. Shaffer[3], [1]*Agriculture Victoria, Bundoora, VIC, Australia,* [2]*La Trobe University, Bundoora, VIC, Australia,* [3]*DataGene, Bundoora,VIC, Australia.*

Genomic selection has opened up opportunities for developing new breeding values that rely on phenotypes that use dedicated reference populations of genotyped cows. There are also opportunities to advance phenotype collection through automation and identifying predictor traits that can be measured cost-effectively. One model is to identify the best phenotypes to measure in research herds and then increase observations (perhaps using predictors) in genotyped commercial herds. Further advances in the accuracy of genomic prediction can be gained from the use of sequence data, in addition to gene expression studies, which can lead to improved persistence of genomic breeding values across generations. In Australia integrating data collection with a research and implementation platform is the platform for delivering new methodologies and breeding values. For example, we have recently delivered the Feed Saved breeding values to industry and are soon to deliver genomic