U.S. Genetic Trends, Production Numbers and Discussion on How Breed Associations May Need to Adapt

Robert Williams, Ph.D.
American-International Charolais Association
Director of Breed Improvement and Foreign Marketing

The importation of beef genetics, establishment of research, education and extension programs, the beef cattle performance revolution and in particular the Beef Improvement Federation, the printing of the first Sire Summaries have all had a profound impact on the U.S. beef population, increasing value and production.

Since the Spaniards first introduced cattle to the new world and through the great cattle drives of the late 1800s beef has become a major economic business in the U. S. As America became settled and our economy has grown, beef production and ranching has become a way of life.

The beef industry provides more than one million jobs in the U.S., creating a ripple effect in the economy. For every dollar of cattle sales, there is approximately five dollars in additional business activity generated. During the 1990s, U.S. Beef production generated more than $30 billion annually in direct economic output, plus about five times that amount per year in related economic output. (U.S. Environmental Protection Agency, 2009)

Regardless if genetics move from one breeder to another or across continents there is an anticipation of adding value, increasing output and/or creating efficiencies of the nations beef herd. This transfer of genetics wasn't only about serving domestic demand for beef but also enhancing our competitiveness in a global economy.

Given the U.N. has projected the world's population to reach 9 billion people by the year 2050 which has lead to the call for food production around the world to double by the year 2050 (Green) increasing production levels and efficiencies are a growing concern. Additionally, meat is demanding an increasing share of the global market as diets in developing countries are changing and as incomes rise (FAO). Opportunities exist for beef producers around the globe to capitalize.

Investments in public agricultural research have slowed since 1980 (Pardey) placing research stations and our land grant universities under growing budget constraints. During this same period of time the private sector has increased research and development significantly faster than the public sector (Huffman).

American beef producers historically have responded aggressively to an increasing demand for our product with increased production levels and improved efficiencies. While current beef cow inventories have returned to levels of the 1950s beef production has more than doubled (USDA) over the same period of time.

While much of the improvements in productivity can be traced to improvements in genetics, nutrition, management and improved health it has been the last 30-40 years that our increased focus on performance programs has been responsible for significant gains as well. Many of our successes can be traced to work done within the framework of the Beef Improvement Federation.

Genetic evaluations have played a significant role in the improvement of beef cattle in the United States for many characteristics with the first Sire Summary published by the American Simmental Association in 1971 and closely followed by every major beef breed in the U.S. Genetic trend tables, readily available on association websites, are a testament to our success domestically. Genetic trend tables published by the Meat Animal Research Center, Clay Center, Nebraska have shown as much as 60 pounds or more increase in the genetics for yearling weight alone since the early 1970s. Additionally, over this same period of time the combination of genetics, management, nutrition and health has seen average dressed carcass weights for steers increase by 150 pounds.

As the international community continues to develop stronger objective based performance and genetic improvement programs the intensity of identifying superior genetics continues to expand across borders for those breeds and breeders who can better characterize their populations for important traits. Joint international research projects which have shown when using current genetic evaluation methodology, sires ranked similarly across countries and within regions of the United States (de Mattos, Donoghue) which has lead to a greater interest for international evaluations.

The production of international genetic evaluations can provide improved marketing opportunities for genetics with increased accuracy, increase confidence of selection and accelerate genetic progress given the benefits of the larger pedigree and performance information that is made available. However, international evaluations are not without their problems given the timing of data collection, production sales and marketing competition.

Challenges faced by Beef Breed Associations

Both, the U.S. beef cow inventory and U.S. breed registries reached their peaks in the 1970s with breed associations recording record numbers of animals. However, a decline in the U.S. beef cow inventory (USDA) has created a shrinking demand for seedstock bulls since 1975. In fact the industry today needs approximately 400,000 fewer bulls than it did in 1974-75. The decreasing size of commercial beef cow numbers is the direct cause for a loss of approximately 430,000 registrations for U.S. beef breed associations over the same period of time (NPLC). This loss of registration numbers continues to strain association budgets for research and development as well as other services.

Beef breed associations have benefited greatly from the research and development from USDA ARS and land grant universities among others. However, development of new technology often takes a building-block approach where new discoveries are based on earlier discoveries and increased knowledge. We are a witness to this today as genomic enhanced selection continues to improve and the optimism that it will play a larger role in the genetic characterization of our

cattle. The question whether to use genomic information will be replaced by how to use it efficiently (Misztal).

Historically in the United States genetic evaluation services have been provided by a few land grant universities. However over the course of the last several years genetic evaluations have moved in house for some breeds (Angus and Simmental) while others have contracted with service providers other than the traditional land grant universities. This change was necessitated as budgets became strained or the retirement of faculty, which have not been replaced, and an increasing need and desire to focus more efforts on improving genetic evaluation models.

Our transition is far from complete, however. Today we spend more time trying to access, prepare and manipulate data sources and less time modeling data and applying expertise to improve and expand evaluations. The challenge is compounded further as the amount of data and complexity of problems increase. Additionally, new technology will offer more computing options and new genetic tools. DNA technology has rapidly decreased in costs allowing for research to move forward at a faster pace to incorporate genomics into existing genetic evaluations. For example, the cost for DNA sequencing has decreased per genome from $100 million dollars in 2001 to under $10,000 in 2011 (NHGRI). This technology will further assist associations to offer genetic selection tools for additional traits which have historically been more difficult to characterize for our evaluations.

The current system of “islands of data” is inefficient and inhibits active associations from moving forward in an efficient way. We need to begin capturing data more efficiently which can benefit the building of resource populations for research and development of genomic tools. The current situation is that we have multiple and disparate sets of data that are intended to represent the same or similar concepts.

The cornerstone for our success the last 30-40 years has been the collection of quality phenotypic data which has allowed our producers to capitalize on research/technology transfer programs for genetic improvement. This will continue to be important or research into genomic markers may have little if any impact. The old adage “genetic evaluations are only as good as our data” will continue to be true and will be important information as the expansion of genomic data will require large volumes of phenotypic data and will be required to update existing marker effects (Funk).

We must identify synergies and further evaluate the sharing of resources between associations and internationally. I believe synergies exist that will make each of us stronger and ready to address the challenges. We must concentrate our efforts to build a more efficient information infrastructure which supports the formation of research and technology development and partnerships. This will help provide a quality genetic evaluation service which incorporates the best technology to provide superior responses to the needs of our producers.

Literature Cited

de Mattos, D. J. (2000). Investigation of genotype x environment interactions for weaning weight for Herefords in three countries. *Jounal of Animal Science* , 78: 2121:2126.

Donoghue, K. A. (2004). Investigation of genotype by country interactions for growth traits for Charolais populations in Australia, Canada, New Zealand and U.S.A. *Livestock Production Science* , 85:129-137.

FAO. (2002). *World Agriculture: toward 2015/2030.* Retrieved April 25, 2011, from Food and Agriculture Organization of the United Nations: ftp://ftp.fao.org/docrep/fao/004/y3557e/y3557e.pdf

Funk, D. (2009). *DNA Markers: Revolution of Evolution.* Retrieved 2011, from ABS Global, Inc.: http://www.absglobal.com/media/files/feature-articles/DNA_Markers.pdf
Gawande, A. (2009). Testing, Testing. *The New Yorker* , 34.

Green, R. e. (2009 307.5709). Farming and the Fate of Wild Nature. *Science* , 550-555.

Huffman, W. G. (2011). *Investing in a Better Future through Public Agricultural Research.* Retrieved from Council for Agricultural Science and Technology: http://www.cast-science.org/websiteUploads/publicationPDFs/Ag%20Research%20final%20QTA2011-1171.pdf

McDonald, A. (2007). *International Benchmarking of Genetic Trends of the Australian Beef Cattle Seedstock Industry.* Meat and Livestock Australia.

Misztal I., I. A. (2010). A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation. *Proceedings of the 59th Annual National Breeders Roundtable,* (pp. 79-89). St. Louis, MO.

NHGRI. (2012). DNA Sequencing Costs. National Human Genome Research National Institute. Bethesda, MD.

NPLC. (2009-2010). *Annual Report, Directory & Career Opportunities.* The Villages, FL: National Pedigree Livestock Council.

Pardey, P. B. (2006). *Agriculture Research: A Global Divide?* Washington, D.C.: International Food Policy Research Institute.

U.S. Environmental Protection Agency. (2009). *Ag 101: Beef Production.* Retrieved 2011, from U.S. Environmental Protection Agency: http://www.epa.gov/agriculture/ag101/printbeef.html

U.S.D.A. (2011). *National Agriculture Statistics Service, Data and Statistics*. Retrieved from http://www.nass.usda.gov/Data_and_Statistics/Quick_Stats_1.0/index.asp