Keeping the "Genetic Doors" Open between Canada and the U.S.

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The first question to ask is how did we have open "genetic doors" between Canada and the U.S. in the past? We can then address why we need to keep those doors open into the future. An obvious answer to the above question is that our two beef cattle industries have historically been tied through the exchange of germplasm, particularly through use of common AI sires. That has been the foundation of the open doors and has bound the two industries together in a real and measurable fashion. These genetic ties have influenced interactions among the respective breed associations in the two countries relative to sharing databases for genetic evaluation. Prior to merging databases, some associations (e.g., American and Canadian Simmental Associations) had separate genetic evaluations, which lead to confusion, especially when bulls did not rank the same. In addition, the existence of these genetic ties also obligates those of us who support these industries with services, education and research to a commitment of collaboration. We owe it to the success of these industries to ensure that we provide educational materials and research findings in a timely and organized fashion. In an era of dwindling resources, we need to avoid excess duplication of effort and resource expenditures as might occur if we did not keep the genetic doors open.

The beef industry (and all of animal agriculture for that matter) is in the midst of a transition motivated by new technology that is moving us from sole use of performance and pedigree records for genetic assessment (used for the computations of expected progeny differences, EPDs) of animals to DNA inferences of genetic merit. One could argue that as important as it was to interact on developing and implementing genetic tools such as EPDs in concert, it will be even more important to interact into the future as we navigate our way through this transition. How long the process will take is not the issue; the issue is how to evolve our national and international strategies for genetic programs and collaborations to accommodate this transition.

Transitions in beef genetic programs are not new. Many historical transitions are documented in the proceedings of the Beef Improvement Federation (BIF). BIF was founded, in fact, to address one of the most significant transitions in the beef industry, that being the movement towards performance-based selection. BIF was also central to the development and delivery of EPDs, providing the forum for discussion and education and in the development of universally accepted guidelines. So, for the last 40 years, BIF has been THE meeting at which U.S. and Canadian producers, support industry representatives, and scientists have met to address current issues and envision the future. As we look to future opportunities for collaboration between the U.S. and Canada and synergism between our industries, it seems fitting that BIF continues to be the forum in which we discuss and delineate strategies to move through this next transition period.

Why is the transition to DNA-based marker selection inevitable? To me it a simple function of the investment that has and continues to be made in DNA technology and the increasing technical know-how in using that technology that exists in young scientists from both countries. Perhaps the most aggressively funded program in science in

the last decade or two has been the sequencing of genomes. Starting with the human genome sequencing project and cascading through other relevant species (including bovine), the concept of sequencing the genome has stood out as the most important effort in genetics, maybe in all of biological science. Genome sequences provide a foundation for developing tools of unprecedented power, but knowing the sequences themselves does not harness that power. From the information generated through numerous investments by both government, industry, and the scientific community, high-density single nucleotide polymorphism (SNP) assays are now available to the research community. As an example of international collaboration between the U.S. and Canada, one of those assays, the Illumina BovineSNP50, was developed by the iBMAC (Illumina, Beltsville, Missouri, Alberta, and Clay Center) consortium. Large SNP panels are now being run against numerous population resources. The associations among the SNPs on these assays and phenotypes for many traits will be forthcoming as these projects mature.

Scientists in disciplines other than genetics have the technical know-how to build their research programs around the use of molecular tools. Animal breeders are quite happy with markers that are in linkage disequilibrium with causal mutations somewhere in their near vicinity for the purpose of selection. They do not need to know in which genes those mutations reside to implement successful selection strategies. However, it would seem that to achieve an understanding of the genetic control of biological pathways supporting traits like muscle development, fat deposition, reproduction, and lactation requires knowledge of the genes and the mutations within them. Hence, as we use the large SNP arrays to identify DNA segments that become interesting targets for selection, we are also identifying, for other scientists, fertile regions of the genome for in-depth exploration of casual mutations. The discovery of casual mutations will then find their way back to genetic programs for use in selection if we develop strategies for connecting the discipline-based scientists to our data resources.

So, why does the impending success of DNA marker-based selection increase the need to collaborate and keep the genetic doors open? First, results of associations will be useful, at least within-breed, across both industries. If we proceed in concert then both industries would be testing for the same polymorphisms in markers (mutations). Commercial DNA companies will provide the connection between our industries as AI companies have and will continue to do. Second, the obstacles to the successful transition to DNA marker-based assessment are plentiful and will require significant investment of time, energy and resources to circumvent. For example, as marker information initially will likely explain only a portion of total genetic variation for a trait, first efforts should be to combine that information with EPDs, a very logical convergence of technologies. However, an obstacle to this effort is our inability to capture the DNA test information being generated. This is true in both countries, and until this constraint is removed, effective merger of the breed databases and the DNA information will be impossible. Building the appropriate infrastructure to capture and store DNA information should not be duplicated. In fact, we should be considering a universal database of DNA information so that the infrastructure does not have to be duplicated even across breed associations.

A second obstacle to the merger of these two technologies is the need to develop genetic evaluation systems that actually accomplish the task. Building duplicate systems is a waste of resources, and hence, capitalizing on the historical collaboration on joint EPDs between countries and breeds seems intuitively appealing.

A third obstacle relates to having DNA-based predictions of genetic merit for traits for which there are no EPDs available or prior to them being merged with EPDs for traits where they do exist. Standardized methods for this prediction need to be developed and implemented so that there is a consistent interpretation of resulting genetic assessments across different panels being offered by genetic service providers. This interpretation of DNA-based predictions should be consistent with that of EPDs to capitalize on decades we invested in the education on using those values. Appropriate methods for obtaining accuracies for these predictions also need to be developed.

An additional challenge we face is that with DNA technology, we will be increasing the number of traits in the selection portfolio to include tenderness of meat products, efficiency of feed conversion, health, and healthfulness of beef products. We need to develop decision-support programs to help producers use these economically relevant traits (ERTs).

The current thrust in the application of DNA technology to selection is the concept of "whole genome enabled animal selection". As the high-density SNP panels are run against larger and larger data sets, more of the genetic variation for ERTs will be explained by the panels. At some point, we will need to reflect on whether routine data collection is necessary. It may be that the industries instead move resources into developing targeted data collection, identifying large populations of animals that are well characterized and then measured for many traits. Although this is not in the immediate future, it makes imminent good sense that planning for collaborative efforts in developing and sharing these datasets be undertaken. A recent meeting between the Australian Beef CRC management team, the US MARC research group, and Canadian and New Zealand researchers was held in January, 2008 at the Plant and Animal Genomics meeting to discuss just such strategies of collaboration.

There will be numerous presentations at this BIF meeting regarding topics I discussed. I encourage us to think creatively about this transition period. The genetic doors between our breeding populations will stay open at the producer level. The populations are tied together now and will stay tied into the future. Both industries will face the same issues as we transition to DNA marker-assisted selection and marker-assisted EPDs. The infrastructure needed to accommodate this will be the same for both countries. The extension materials needed to educate producers on how to adopt the new technology and research into how best to use it will be the same. It seems that there is only one mistake we can make going forward and that would be closing the genetic doors between our two counties.