

DAIRY PIPELINE

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Inbreeding in the Genomic Era

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“Genomics could help to reduce inbreeding using changes in genomic breeding programs, alternative measures of inbreeding, and selection against inbreeding depression.”

Selecting only the top percentage of animals in traits useful to humans has allowed dairy farmers to mold the dairy cow into the highly efficient, excellent producer that it is today. However, this intensity and speed of selection causes close genetic relatives to produce offspring, which is known as inbreeding. Inbreeding can lead to a reduced production, known as inbreeding depression. Dairy breeders have been combating inbreeding for decades, but it has continued to rise. Now, as genomic selection becomes more popular, it is important to consider the implications for inbreeding of this new component to dairy selection. Genomics could help to reduce inbreeding using changes in genomic breeding programs, alternative measures of inbreeding, and selection against inbreeding depression.

Since the first official genomic evaluation in 2009, genomic selection in the dairy industry has increased exponentially. The main advantage to this type of selection is that bull calves can be tested for their genetic merit before they even reach sexual maturity, which drastically decreases the generation interval as compared to traditional breeding programs. Although this has led to a much faster rate of genetic gain overall, shorter generation intervals has also meant a steep rise in inbreeding. However, Boichard et al. (2015) propose that a change in how genomics are currently being used inbreeding programs could start to reduce - and even reverse - this increase. Currently, genomic breeding systems are designed to be faster versions of traditional breeding programs, by testing a bull's DNA instead of his daughter's performance. There are two main areas where the researchers believe improvement can be made. First, testing more bull calves. Genotyping bulls is 5-10 times cheaper than progeny testing them, so increasing the genetic range of AI semen could be done without additional cost to suppliers. Second, reducing the number of offspring produced by each bull. Genotyping causes faster genetic gain, which should lead to newer bulls with

fresher genetics being chosen more rapidly anyway, so dairy breeds could easily promote this quicker bull turnover while still maintaining a profit. Overall, both changes would reduce the current increase in inbreeding that genomic selection is causing and would not be difficult or costly for dairy breeders to implement.

Traditional measures of inbreeding use pedigrees to calculate the probability of animals having the same alleles. Until recently, this estimation was the only way to consider how inbred offspring will be. However, Pryce et al. (2012) compared traditional measures of inbreeding to genomic inbreeding estimates from looking directly at animals' DNA. These researchers ran 50 simulations apiece for 3 measures of inbreeding: traditional, high-density genomic, and low-density genomic. The genomic measures compared the DNA of the animals themselves to determine the amount of inbreeding. Within these simulations, a selection of 2,117 bulls were “bred” using an equation that rewarded performance and penalized inbreeding. The simulated offspring were then compared to find which of the 3 methods allowed for the greatest reduction in inbreeding, without negatively impacting genetic gain. They concluded that both high- and low-density genomic selection were effective measures for reducing inbreeding with minimal effect on genetic gain.

There are two mechanisms by which inbreeding creates inbreeding depression, the recessive deleterious alleles and overdominance. Both of these stem from having a pair of identical alleles, otherwise known as homozygosity. But, homozygosity is not detrimental for every allele. In fact, most of a cow's DNA is made up of alleles in common with every other cow. To identify the specific genomic regions associated with inbreeding depression, Pryce et al. (2014) ran genome wide association studies to find specific genomic regions associated with inbreeding depression. Using this knowledge, inbreeding depression could be avoided by selecting against homozygosity in these specific regions. This would theoretically



Upcoming Events

See [VTDairy](#) for details.

April 1, 2017

VA Spring Holstein Show
Rockingham Co. Fairgrounds

April 25-26, 2017

Grazing School
McCormick Farm

May 13-14, 2017

[Show Like a Pro Workshop](#)
Frederick, MD

May 15, 2017

[Hokie Cow Classic](#)
Blacksburg Country Club

May 20, 2017

Dairy Judging Workout
New Market, VA

May 27, 2017

Breakfast on the Farm
Arbogast Farms

If you are a person with a disability and require any auxiliary aids, services or other accommodations for any Extension event, please discuss your accommodation needs with the Extension staff at your local Extension office at least 1 week prior to the event.

“The compulsory compliance of Dutch dairy farmers to the ANCA model provides an important lesson to American agriculture.”

For more information on Dairy Extension or to learn about current programs, visit us at VT Dairy—Home of the Dairy Extension Program on the web at: www.vtdairy.dasc.vt.edu.



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allow for dairy breeders to benefit from inbreeding without the detrimental effects of inbreeding depression.

In conclusion, genomics is a growing area of dairy breeding. Currently, the sharp reduction it produces in generation interval has led to an

REFERENCES:

- Boichard, D., et al (2015). “Sustainable dairy cattle selection in the genomic era.” *Journal of Animal Breeding and Genetics* **132** (2): 135-143.
- Pryce, J.E., et al. (2012). “Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information.” *Journal of Dairy Science* **95**(4): 377-388.
- Pryce, J.E., et al. (2014). “Identification of genomic regions associated with inbreeding depression in Holstein and Jersey dairy cattle.” *Genetics Selection Evolution* **46**(1): 71-71.

Reflections on International Dairy Federation World Summit

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In October 2016, I attended the International Dairy Federation World Dairy Summit held in Rotterdam, Netherlands. Over 1,200 participants from every continent attended including many heads of government agencies, research institutes and national dairy organizations... seven percent were dairy farmers...few were American. Presentations addressed a wide range of topics important to the dairy industry ranging from animal well welfare, food safety, economics, nutrition, marketing, environmental challenges and sustainability. Not surprisingly, the issue of environmental quality was a “hot” topic of great interest.

Environmental regulations focusing on greenhouse gas emissions are significantly impacting financial and production decisions implemented on Dutch dairy farms. For example, in the Netherlands all manure lagoons are required to be covered to limit greenhouse gas emissions. In 2016, the Annual Nutrient Cycling Assessment (ANCA) model was implemented in the Dutch dairy sector. The goal of the ANCA model is to produce more milk and pollute less. The inputs for the ANCA model are milk produced per cow, manure, animals and land. A national database is used to aggregate inputs and outputs for each farm per year. Follow-up includes the potential for motivational calls.

The leaders of milk producers organizations, the farmers’ union, feed suppliers and farm accountants signed on to the ANCA model, making it mandatory for all Dutch farms. Beginning in January 2017, the penalty for non-compliance on a particular farm means milk cooperatives will not buy that farm’s milk.

What Implications Might This Have For American Dairy Farmers? The compulsory compliance of Dutch dairy farmers to the ANCA

increase in inbreeding. However, through increased bull testing, decreased offspring per bull, genomic measures of inbreeding, and selection against inbreeding depression, genomics has the potential to combat inbreeding’s detrimental effects.

model provides an important lesson to American agriculture. As succeeding generations have become more removed from the experience of their farming ancestors, a large disconnect has emerged between the nostalgic vision of the Old MacDonald family farm and realities of large, technology-driven, commercial farms. Similar to European animal rights and environmental groups, their American counterparts tend to portray the large farms as “industrialized” agriculture, both harmful to animals and the environment. An immediate and proactive response by America’s agricultural community would provide an opportunity to shape future legislation and cultural beliefs.

The American agricultural community **must immediately** consider undertaking a social media campaign and public education programs detailing the story of production agriculture in America through time...the good, the bad, and the ugly, as well as the resultant improvements and future directions. Since large commercial farms engaged in dairy, beef, crop and poultry are the most visible for critiquing, they have the most to gain from starting Facebook pages and/or blogs for their farms, providing regular updates about day to day activities. This type of campaign would illustrate how farmers utilize latest agricultural technology to improve the environment and quality of life/care to animals on their farms, while producing a safe, abundant food supply. Extension specialists at Virginia Tech are willing to collaborate with farmers to develop effective communication strategies with the urban consumers.

The agricultural community needs to define itself proactively in a positive, plausible light. Otherwise, animal rights and environmental groups will promote and encourage the public to approve the passage of legislation that will

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