

DAIRY VETERINARY NEWSLETTER

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Holstein Inbreeding is Approaching a Level of Concern - but is There a Solution from the Past?

The first time I learned about AI breeding and influential bulls such as Round Oak Rag Apple Elevation, Pawnee Farm Arlinda Chief and Paclamar Astronaut was in a dairy genetics class over 40 years ago. Those bulls were all still alive and I saw Elevation on a dairy tour in 1976. A subject being broached at that time for all dairy breeds is now approaching a level of real concern even for what was once a comparatively outbred dairy breed - inbreeding in the Holstein breed.

A story by J. Dickrell in Dairy Herd Management October 24, 2019, states, “The current level of inbreeding in Holsteins calves born in 2019 is 8%, according to - - AgSource data. Eight percent is still considered to be a moderate level of inbreeding. ‘Inbreeding levels less than 3.15% is considered low while inbreeding levels over 12.5% are considered high,’ explains Nicole Nehls with AgSource.” However, Nehls adds: “The majority (76%) of Holstein cows born in 2011 fell in the low to moderate [inbreeding] category of 3.15 to 6.25% inbred. However, Holstein calves born in 2018 now fall in the moderate to high category (82%), which is 6.25 to 12.5%. Avoiding inbreeding will become harder as selection of top cows and bulls in the Holstein population are made.”

What is driving the inbreeding, and the faster increase in inbreeding of Holsteins?

Dickrell’s article summarizes: “The use of genomics is one reason inbreeding levels are increasing. The second reason is shorter generation intervals, say geneticists.” (More regarding this will follow later.)

Chad Dechow, Penn State University dairy geneticist, is quoted, “We refuse to use bulls that are not the best, and we’re having a tough time using a bull that is \$50 less on Net Merit but is still a good bull.”

The article has a good discussion of how not only breeding bulls selected as semen donors, but the mothers of the bulls are also coming from fewer cow families, thus “the genetic diversity that might be available from good (but less than elite) families will be lost. And that is happening quickly.”

Something I did not realize is pointed out; wildlife conservationists manage matings of wild species more effectively to reduce inbreeding, despite the logistic challenges, than we do in livestock genetics. This means that controversial species such as wolves have more management by humans of their inbreeding than we currently have in dairy cattle. The entire article is available at:

<https://www.dairyherd.com/article/holstein-inbreeding-reaching-moderate-high-levels>

Another article by D. Charles in Food For Thought October 17, 2019, is written primarily for the general public, but points out something interesting regarding Holstein inbreeding. Dechow is extensively quoted in this publication, basically an interview report, which can be read at:

<https://www.npr.org/sections/thesalt/2019/10/17/770696476/most-u-s-dairy-cows-are-descended-from-just-2-bulls-thats-not-good>

“A few years ago, Dechow and some of his colleagues at Penn State made a discovery that shocked a lot of people. All the Holstein bulls that farmers were using could trace their lineage back to one of just two male ancestors. ‘Everything goes back to two bulls born in the 1950s and 1960s,’ he says. ‘ - - Round Oak Rag Apple Elevation and Pawnee Farm Arlinda Chief.’”

Why is the inbreeding a concern?

Immunogenetics and lack of disease resistance is a major concern. As a breed or a species become more inbred, some of the immunogenetics are lost. We may be losing, for example, some haplotypes of the major histocompatibility complex (MHC) genes for cell surface proteins that recognize pathogens in the body among Holsteins and other breeds and species of farm animals. There is a vast number of different MHC genes and corresponding cell surface markers in all species and breeds. Heterozygosity in MHC is vital to a breed’s collective resistance to disease. A review paper by J. Bezdicsek et al. in Slovak J Anim Sci, Vol. 3, 2018 details the importance of MHC diversity in many wild and domestic species and breeds including Holsteins, and describes how many farm animal breeds are losing MHC genetic diversity. It also relates that isolated species such as cheetahs have lost MHC diversity and thus had reduced disease resistance. Closely related to this is an increase in recessive diseases. Holsteins are replacing indigenous breeds of cattle in many parts of the world besides North America and Europe. Trypanosomiasis, bovine leukocyte adhesion deficiency (BLAD), Brachyspina (causes spinal cord and leg deformities or internal organ defects), complex vertebral malformation (CVM), other genetic diseases, and intolerance of rising temperatures around the world are observed in Holsteins more than many indigenous species. A paper by Y. Zhang et al. in J Dairy Sci, January 2020, found that 26% of Chinese Holsteins tested carried recessive genes for at least 1 of 7 important diseases. While genomic testing can actually be used to reduce the prevalence of recessive carriers, many herds in Canada have 10% to 20% or more of their Holsteins carrying recessive genes for major diseases according to an April 2019 report by Van Doormall and Beavers for the Canadian Dairy Network. Selection for milk production and some type characteristics continues to be associated with inbreeding, including more concentration of recessive genes for disease because the latter are comparatively ignored in genomics based matings.

Does inbreeding increase infertility in Holsteins?

There is considerable speculation in dairy literature that infertility increases with inbreeding. There is evidence that in nature, many species seek mates with different MHC than their own (how they can detect this is unclear; opposites attract it seems, including in primates). The Bezdicsek review paper cites some evidence that embryonic mortality increases as MHC heterozygosity decreases in Holsteins. However, there are relatively few refereed papers from studies providing data regarding infertility related to Holstein inbreeding.

One such paper is by Pryce et al., Genetics Selection Evolution, November 2014. The authors used pedigrees and genotyping of 8853 Australian Holstein cows that also had complete genotypes for at least two generations on both parents and extensive production and reproductive records. An undisclosed proportion of cows they started with - in total they excluded 330,000 cows - were eliminated because genomics showed they could not possibly be daughters of their supposed parents. The authors looked for runs of homozygosity (ROH), proportion of all single nucleotide polymorphisms (SNP) that were homozygous, and the proportion of each cow’s genome that were ROH. All of these measures quantify how much cows’ genomes are alike in the genes from both parents for genes that are known to be potentially heterozygous.

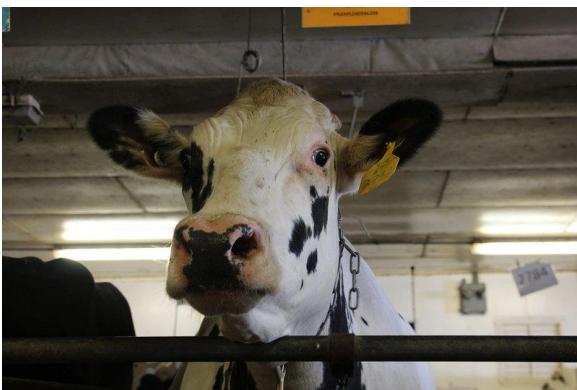
The average proportion of the Holstein genome that was homozygous was 0.66, and 5% of genomes had ROH of 50 SNP in a row, potentially heterozygous, that were homozygous. Calculations showed that a 10% increase in inbreeding was associated with a 1.8 day increase in calving interval, which does not sound like much. Unfortunately, like too much of the dairy industry still does, the authors only looked at days open and calving interval to measure fertility. The flaw in those measures is that cows must calve at least twice to be included at all. Cows not impregnated and then culled are never counted. A better measure of fertility is % of cows pregnant by 150 DIM, along with % pregnant by 200 DIM. Based on calving interval, the effect of inbreeding on infertility was apparently small. However, whether more cows simply never calved again was not detected. (Interestingly, the

paper found greater depression of milk and fat production associated with inbreeding than infertility effects. Despite genetic progress in milk production, some of the potential increased milk production is being lost by the resultant inbreeding.) The paper can be found at:

<https://gsejournal.biomedcentral.com/articles/10.1186/s12711-014-0071-7>

Will frozen semen from over 50 years ago be part of a solution?

Chad Dechow, again quoted in the Food For Thought article, says, “We've lost genetic variation. Now, some of that variation was garbage that we didn't want - - but some of it was valuable.” Dechow obtained semen from bulls that were alive decades ago, including University of Minnesota Cuthbert and Zimmerman All-Star Pilot. The USDA keeps some of their semen deep-frozen in Fort Collins, Colo. Following AI, some calves were born from sires that have been dead for half a century, and “now it's possible to see some lost pieces of the Holstein family tree come to life in a barn at Penn State - in the form of three cows.” [Dechow describes one] - - “If you notice, if you look over her back - see how that cow to her left is a little more bony? [The cow from past genetics] definitely carries more body condition. She's a little bit fatter.” Dechow suggests a number of advantages from a reinfusion of some genes that have been lost into Holsteins, but he acknowledges that milk production has to be high enough for producers to use semen from bulls from the past, and eventually their offspring carrying more of the nearly lost genetic variation. “So Dechow is carefully monitoring his experimental cows. So far, he says, it's going pretty well. Two of the three cows are producing at least as much milk as the industry average.”



Cow at Penn State University whose sire lived a half century ago, from Charles et al., Food For Thought

These concerns about lack of genomic diversity and worldwide extinction of nearly 100 livestock breeds since 2010 are not limited to what is cited here. Many experts in both the developed and developing world are equally concerned, and where it is available, beginning use frozen semen from generations long past to inseminate Holsteins on a small experimental basis.

I asked our clinical and reproductive veterinarian, Dr. Rusty Stott about this, and he said I could share these observations, which we both recognize as experience-based “Cowboy Science”. However, that is useful:

- Some heifers with high production genomics are now used to harvest oocytes using ovum pick-up (OPU) well before puberty; oocytes have been harvested from calves as young as 2 months old resulting in daughters with a markedly shorter generation time. Inbreeding is accelerated by this practice.
- Genomics proponents state (correctly) that Holstein herds neither routinely using genomics nor producing bulls for bull studs could be genomically tested. We would likely find some great genetics in cow families more outbred to expand the gene pool. However, such herds rarely if ever are genomically tested now.
- Fortunately, there is some genetic diversity maintained in the Holstein breed. Purebred show breeding herds using their own bulls and cows, producers who primarily select AI sires mainly on low semen price, and producers using outcrossing such as with Jersey, Swedish Red, Danish Red, Viking Red (a “crossbred breed” itself), or Montbeliarde are contributing to genetic diversity.

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- According to a University of Minnesota study reported in extension press in 2018, the main advantages with many dairy crossbreds were increased conception, decreased stillbirth, more value of baby bull calves, and reduced mastitis. However, they had lower milk production than purebred Holsteins.

Considering what might be lost in the next great bovine disease epidemic and/or with continuing climate change, steps to re-diversify the Holstein gene pool may be paramount, something we cannot afford to ignore. How future generations survive may depend on it.

What does this mean for veterinarians, including dairy veterinarians?

My perception is that dairy veterinarians have less input into mating decisions and choice of AI bulls than they once did, but I hope I'm wrong. It cannot be good to have such a loss of genetic diversity in Holsteins if for no other reason than immunogenetics and possible susceptibility to a great "cow plague" of disease someday, whether within a few years or 100 years. Veterinarians should advocate to all of their bovine clients using AI breeding to consider the use of more outbred sires, consider crossbreeding, and pay at least some attention to the available information regarding important recessive genes in semen donor selection. We should be advocates for more outbred genetics; all dairy producers and other livestock owners need to be receptive to reintroducing some of the genetic diversity of the past while not sacrificing the ability to profitably feed the world in the future.

Please let us know your comments and suggestions for future topics. I can be reached at (435) 760-3731 (Cell), or David.Wilson@usu.edu.



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