WHAT TO KNOW ABOUT INBREEDING AND PROFITABILITY

INTRODUCTION

The concept of inbreeding in dairy cattle has been widely debated for many years. Many producers still have many questions about the acceptable level of inbreeding on their farms to continue to make genetic progress, but not cause any harmful decrease in production, fertility, or health traits. Often, the increase of inbreeding is considered very negative and to be avoided. In a recent article in the Journal of Dairy Science, it was stated that "It is important to note that, in itself, inbreeding is neither good nor bad. In selecting for the improvement of a particular trait (in most cases, we are interested in increasing the yield of a particular production trait), the accumulation of homozygosity at favorable variants is the primary objective" (Maltecca et al. 2020). Inbreeding on its own is not a factor that should determine selection decisions. We need to understand how inbreeding affects profitability of an individual or a mating decision, so that our focus is on genetic progress and ultimately profitability.

> **"IT IS IMPORTANT TO NOTE THAT, IN ITSELF, INBREEDING IS NEITHER GOOD NOR BAD"**

WHAT IS **GENOMIC INBREEDING?**

Genomic inbreeding (gIB) can be identified for all genomically tested animals with a US evaluation **(Figure 1A)**. gIB is the relative percentage of homozygous alleles that an individual possesses in their DNA makeup. If the number is positive, this means that animal has a higher percentage of the same alleles at one location than the base population. Percentage of homozygosity means the proportion of the genome that has the same variant. If each location has two variants, B or b, a homozygous combination would be bb or BB. A heterozygous combination would be a Bb **(Figure 2)**. Genomic inbreeding is more accurate than pedigree inbreeding because with genomics we know exactly which alleles were transmitted from each parent and where the actual inbreeding (homozygosity) occurs.

551HO03713 NORTON

(https://www.stgen.com/sire-directory/dairy-bull-usa.aspx?code=551HO03713&language=english-cogentuk&title=mr-wings-norton-et)

Reg: HO840003132353282 **DOB:** 08/19/2017
RHA: 99% **DMS:** 234,345 aAa: 345 AA A2A2

Mr Wings Norton-ET TC **Wings x Nominee x Robust**

04/2020	**CDCB SUMMARY - GENOMIC**			**NM$ +754**
Milk	+1240	79%R	Fluid Merit $	+671
Fat	+73	+0.09%	Cheese Merit $	+793
Protein	+59	+0.07%	Grazing Merit $	+678
SCS	2.80	76%R	Gestation Len. +0	Fert. Index +1.0
PL	+5.9	75%R	Livability +2.2	Mastitis +1.5
DPR	+0.5	74%R	EFI 8.6% gEFI 10.9%	gIB 14.7%
HCR	+2.0%			
CCR	+1.8		0 Dtrs 0 Herds	100% US

Ⓐ **Norton's Genomic Inbreeding (gIB)**

Ⓑ **Norton's Genomic Expected Future Inbreeding (gEFI)**

Ⓒ **Norton's Expected Future Inbreeding (EFI)**

Figure 1 *shows Norton's bull page. Figure 1A shows Norton's* ***gIB*** *is 14.7%. Norton's* ***gEFI*** *is shown in Figure 1B as 10.9%. Figure 1C shows Norton's* ***EFI*** *is 8.6%.*

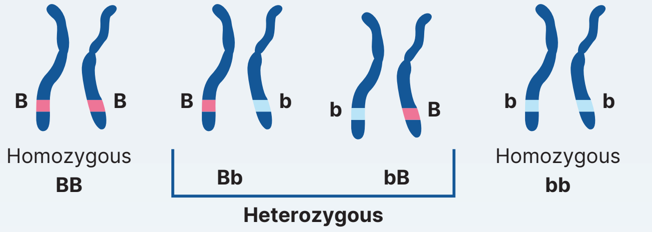
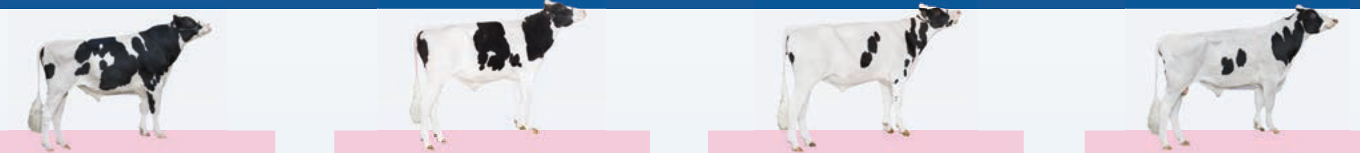


Figure 2 *shows a location on a chromosome with two different variants: B and b. A homozygous combination at this location would be BB or bb. A heterozygous combination would be Bb or bB*

Figure 3 shows the result of mating one cow with four full brothers: Delta, Denver, Drama, and Dion to demonstrate the difference in pedigree and genomic inbreeding. The pedigree inbreeding of the progeny created by mating the same cow to each of the four brothers is 11.5%. Progeny pedigree inbreeding is the same for the progeny of the four brothers because pedigree inbreeding calculates the pedigree relationship of the sire and dam based on common ancestry. Since each of these bulls has the same parentage information, they share the same pedigree relationship with the example female. The genomic inbreeding of the progeny from each of these sires is very different. Delta's progeny is expected to have 7% higher genomic inbreeding than Drama's progeny. Each sire in this example did not inherit the same genes from their parents, so each bull has a different genomic relationship with this female or genomic inbreeding of their expected progeny. The most accurate representation of inbreeding is genomic inbreeding because it utilizes SNP information to calculate the proportion of the genome that is homozygous.

SIRE: **Mogul**
DAM: **Miss Ocd Robst Delicious**
MGS: **Robust**
MGD: **OCD Planet Danica**
MGGS: **Planet**
MGGD: **Miss Elegant Delight**



Delta 523HO01468	**Denver 551HO00690**	**Drama 551HO00695**	**Dion 523HO01470**
909 NM$	**817** NM$	**804** NM$	**797** NM$
DELTA **Progeny Results:** Pedigree INB: **11.5%** Genomic INB: **21.5%**	DENVER **Progeny Results:** Pedigree INB: **11.5%** Genomic INB: **17.5%**	DRAMA **Progeny Results:** Pedigree INB: **11.5%** Genomic INB: **14.5%**	DION **Progeny Results:** Pedigree INB: **11.5%** Genomic INB: **17.0%**

***Figure 3** shows the progeny pedigree and genomic inbreeding results of mating one cow with four full brothers: Delta, Denver, Drama, and Dion. The pedigree inbreeding of the progeny created by mating the same cow to the four brothers is 11.5%. The genomic inbreeding of the progeny from each of these sires is very different. Delta's progeny is expected to have 7% higher genomic inbreeding than Drama's progeny.*

WHAT IS **EXPECTED FUTURE INBREEDING?**

Expected Future Inbreeding (EFI) is the estimated future inbreeding level of an animal's offspring if they were mated to the general population. The general population used by CDCB is females born in the last four years with pedigree information at CDCB. EFI is displayed on US proof information and is based on the average pedigree relationship of an individual to the base population **(Figure 1C).** gEFI can also be found on US proof information and is based on the relationship the individual shares with the genomically tested population average **(Figure 1B)**

WHAT MEASURE OF INBREEDING AFFECTS **GENETIC PREDICTIONS (PTA)?**

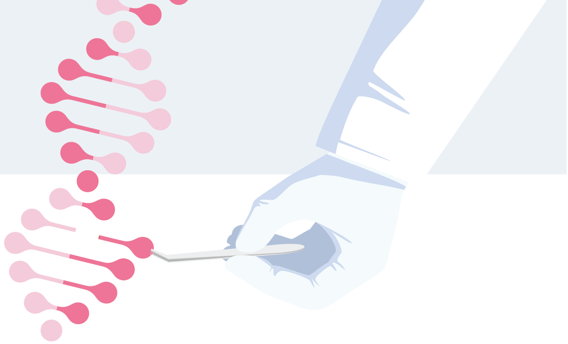
Since 2008, the US has adjusted evaluations for EFI. The May 2020 CDCB Connections by Duane Norman presented the current effects of an animal's expected future inbreeding (EFI) level. The USDA estimates the economic value of inbreeding depression associated with every 1% of inbreeding of an animal for each economic trait which is shown in **Figure 4**. For instance, for every 1% of inbreeding that an animal possesses, Net Merit (NM$) decreases by $25. Similarly, Milk decreases by 63.9 pounds for every 1% of inbreeding that an animal possesses. **Figure 5** shows an example of how inbreeding depression affects the NM$ evaluation of 4 bulls. Each of the 4 bulls have the same raw or unadjusted NM$ value of 1000 NM$. Each of these bulls' daughters perform identically; however, each bull has different EFI values from 7 to 10%. The last column shows the EFI adjusted and official NM$ which is published on the bull's proof. The difference between Bull 1's daughters and Bull 4's daughters' lifetime profitability is $75. The adjusted NM$ is determined by subtracting the EFI multiplied by $25 (inbreeding depression for every 1% of NM$) from the unadjusted NM$ value.

Trait	Inbreeding depression / 1%
Milk	-63.90
Fat	-2.37
Protein	-1.89
Productive Life	-0.26
Somatic cell score	0.004
Daughter pregnancy rate	-0.13
Cow conception rate	-0.16
Heifer conception rate	-0.08
Cow livability	-0.08
Net merit $	-25.00

***Figure 4** displays the inbreeding depression associated with each economic trait for every 1% of inbreeding that an animal possesses according to the USDA.*

Sire	Unadjusted NM$	Percentage EFI	Adjusted NM$
Bull 1	1000 NM$	7%	825 NM$
Bull 2	1000 NM$	8%	800 NM$
Bull 3	1000 NM$	9%	775 NM$
Bull 4	1000 NM$	10%	750 NM$

***Figure 5** shows an example of how inbreeding depression affects the NM$ evaluation of 4 bulls. Each of the 4 bulls have the same raw or unadjusted NM$ value of 1000 NM$. Each of these bulls' daughters perform identically; however, each bull has different EFI values from 7 to 10%. The last column shows that the EFI adjusted and official NM$ which is published on the bull's proof. The difference between Bull 1's daughters and Bull 4's daughters' lifetime profitability is $75. The adjusted NM$ is determined by subtracting the EFI multiplied by $25 (inbreeding depression for every 1% of NM$) from the unadjusted NM$ value.*



WHAT MEASURE OF INBREEDING AFFECTS **PERFORMANCE OR PROFITABILITY?**

Genomic inbreeding (gIB) affects performance or profitability. EFI estimates what the inbreeding level of the offspring of an individual would be if they were mated to the general population. gIB indicates the actual inbreeding of an individual from genes contributed by their sire and dam.

HAS INBREEDING INCREASED DUE TO **GENOMIC TESTING?**

Initially, genomic testing gave the dairy industry the ability to evaluate the genetic potential of a larger group of animals with high accuracy than previously available through parent averages. This possibility could have led to more variety of animals used to make the next generation of parents; however, producers are also likely to utilize the highly accurate genomic PTAs from genomic evaluations to choose the highest genetic value sire or dam to make replacement females. This narrows the genetic pool to a few select individuals. Also, genomic testing has decreased the timeframe needed to determine the value of an animal. This means that a young animal can be evaluated to have a high genetic value prior to breeding age and be utilized as a parent for the next generation. This decreases the generation interval or the average age of an animal when its replacement is born. The CDCB reports that since the introduction of genomic testing, generation interval of the sires of bulls has decreased from 7 to 2.5 years and for the dams of bulls from 4 to 2.5 years. During this same time period, inbreeding in Holstein cows has increased from 5.66% in 2010 to 8.49% in 2020 and 6.84% in 2010 to 8.74% in 2020 in Jersey cows (https://queries.uscdcb.com/eval/summary/inbrd.cfm) **(Figure 6 and 7)**. It is important to note that genomic testing did not increase the amount of inbreeding in our dairy cattle population, but rather inbreeding increased because of the strategies that are used to make sire and dam selections based on genomic information (Norman 2020). Inbreeding occurs in each generation, and decreased generation interval as well as an increase in selection intensity speeds up the increase of inbreeding.

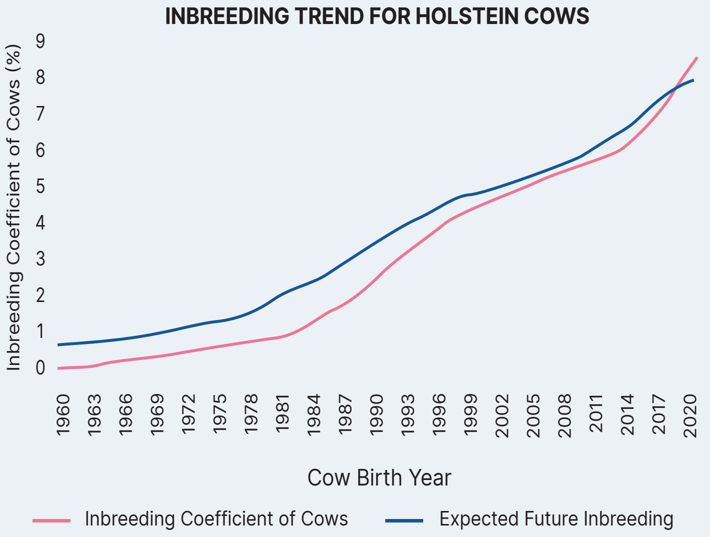


Figure 6 *shows the inbreeding (IB) and Expected Future Inbreeding (EFI) trends for Holstein cows since 1960.*

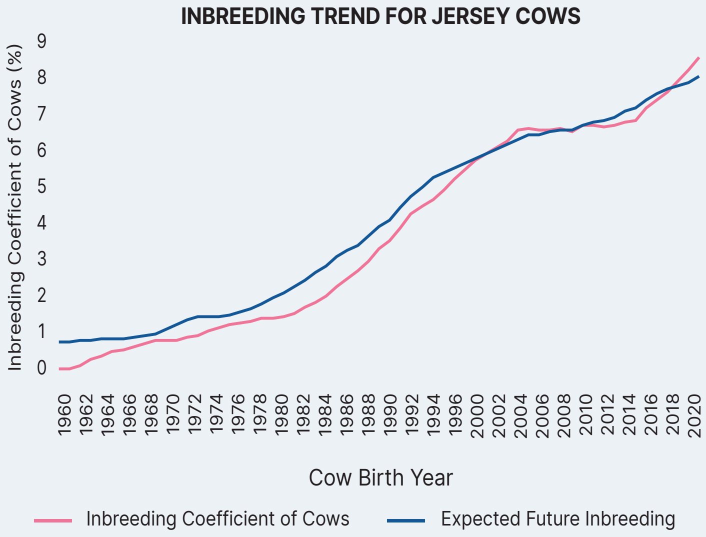


Figure 7 *shows the inbreeding (IB) and Expected Future Inbreeding (EFI) trends for Jersey cows since 1960.*

WHAT IS CURRENTLY BEING RESEARCHED **ABOUT INBREEDING IN DAIRY COWS?**

Currently, researchers are working to identify lethal or negative recessives. We are currently able to identify 16 of these negative recessives when animals receive a genomic evaluation (Cole et. al, 2018). We need to continue to identify areas of the genome that are impacted negatively by increased homozygosity of inbreeding as well as areas that are impacted positively by increased inbreeding.

HOW IS **INBREEDING ACCOUNTED** FOR IN CHROMOSOMAL® MATING

The goal of Chromosomal Mating® is not to reduce inbreeding. Chromosomal Mating® selects the best mating pairs to drive profitability which takes into account the inbreeding depression caused by the inbreeding (IB or gIB) of the proposed progeny. A formula to determine economic value of the progeny of a mating scenario is genetic gain minus inbreeding depression. The equation that STgenetics® uses in the Chromosomal Mating® program calculates the Predicted Producing Value (PPV) which forecasts how the animal will perform in the herd (Sun et. al, 2013). The first step of the formula removes the EFI penalty from the sire and dam PTA values. The second step determines the actual relationship of each mating pair as calculated by CDCB. This relationship can be used to predict the progeny's inbreeding level. In the third step, the formula penalizes the inbreeding of the proposed progeny by multiplying the inbreeding depression of the selected trait for optimization by the progeny's inbreeding. While maximizing PPV in Chromosomal Mating® does not limit inbreeding, optimizing for PPV creates lower inbreeding in the progeny of the matings compared to just optimizing for PTAs in a mating program. For more information about PPV, please see the article Predicted Producing Value (PPV) What Is It and Why Is It Important?

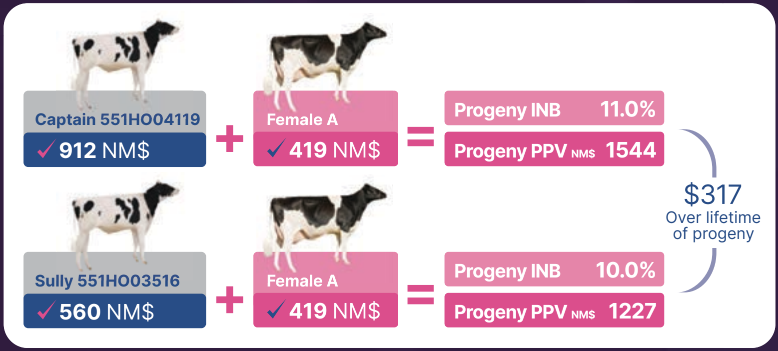


Figure 8 *shows the difference in the Predicted Producing Value (PPV) of progeny created from mating Female A to Captain and Sully. Captain's progeny had 1% higher inbreeding than Sully's progeny, but Captain's progeny is expected to produce $317 more in her lifetime than Sully's progeny.*

DOES **HIGH GIB** INDICATE A LOW PERFORMING OR LESS PROFITABLE ANIMAL?

No, remember gIB is a percentage of homozygous alleles that an individual possesses in their DNA makeup. More homozygosity means less diversity in the genetic makeup, but it does not necessarily mean less genetic value. As stated in the introduction, a recent article in the Journal of Dairy Science affirmed, "It is important to note that, in itself, inbreeding is neither good nor bad. In selecting for the improvement of a particular trait (in most cases, we are interested in increasing the yield of a particular production trait), the accumulation of homozygosity at favorable variants is the primary objective" (Maltecca et al. 2020). Genomic inbreeding (gIB) is not enough to determine the production value of an animal. We also have to look at the genetic value of an animal first, and then adjust for the inbreeding depression. Duane Norman also wrote in the May 2020 CDCB Connection, **"Inbreeding does negatively impact most individual performance traits. Nevertheless, genetic gains resulting from intense selection can outpace whatever losses are inflicted from inbreeding depression. Figure 8** shows an example of using Chromosomal Mating® to mate one female to two different bulls, Captain and Sully. Captain's progeny is expected to have a higher inbreeding value by 1% but is also predicted to produce $317 more in her lifetime than Sully's progeny. This reinforces that **additive genetics and inbreeding depression must be considered when determining genetic value, and there can be an opportunity cost to lowering inbreeding instead of increasing genetic gain.**

May 2020 CDCB Connection
(https://www.uscdcb.com/wp-content/uploads/2020/05/Microsoft-Word-CDCB-Norman-Inbreeding-05_2020-CDCB-Norman-Inbreeding-05_2020.pdf)

IS THERE A CERTAIN **INBREEDING COEFFICIENT** THAT I SHOULD NOT EXCEED IN MY HERD?

Historically, dairymen were encouraged to minimize the increase of inbreeding in their herd or simply not exceed an arbitrary average level of inbreeding. Prior to genomic testing, increasing homozygosity in an individual or increasing inbreeding could have resulted in the expression of negative haplotypes. For example, before we discovered the Holstein Cholesterol Deficiency (HCD) haplotype, there was an increased risk of mating related animals together that both carried the HCD haplotype resulting in a calf with the lethal cholesterol deficiency. Genomic testing has allowed us to identify individuals with negative haplotypes and now dairymen can avoid mating carriers with Chromosomal Mating®. At this time, there is no known threshold for inbreeding that results in catastrophic loss; therefore, the best strategy for managing inbreeding is to avoid matings of two carrier parents for the same negative haplotype and using actual inbreeding to maximize herd performance in the Chromosomal Mating® program.

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Maltecca, C., Tiezzi, F., Cole, J.B., and Baes, C. 202. Exploiting homozygosity in the era of genomics- selection, inbreeding, and mating programs.
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