

Common Misconceptions About Inbreeding

Do you really understand inbreeding? Do you know how it accumulates in a population and what determines the inbreeding level of a given animal? Of course, inbreeding must be considered when making mating decisions but are you doing this properly? In reality, the word "inbreeding" often arises in conversations about genetic improvement but there are many misconceptions that create confusion. Let's get all this straightened out into a clear understanding!

What is Inbreeding?

In cattle breeding, inbreeding refers to the mating of related animals. The closer the two animals are related to each other, the more the resulting progeny will be inbred. For example, mating a sire to its daughter or to its full-sister will both result in progeny with at least 25% inbreeding.

Is Inbreeding Good or Bad?

Usually, when we speak about inbreeding focus is given to its primary negative consequence, referred to as inbreeding depression. In cattle, high levels of inbreeding can be associated with decreased calf survival and fitness as well as poorer fertility. Over time, it can also reduce genetic variation in the breed and therefore in your herd. For this reason, it is important to manage the inbreeding level associated with each mating decision you make and to monitor the average level of inbreeding as it accumulates in your herd from year to year.

Notwithstanding the risk of inbreeding depression, there are some desirable outcomes associated with higher levels of inbreeding resulting from a mating that is specifically targeted. Mating two highly related animals together, increases the likelihood that the progeny would be "fixed" (i.e.: homozygous) for some of the positive genes contributing to successful performance and profitability. One might suggest that this was the case for popular Canadian-bred sires, Braedale Goldwyn, STBVQ Rubens and La Presentation Aerocerf, all of which were over 15% inbred and produced over 5,000 milk-recorded daughters. In fact, it can be argued that such planned "line breeding" should be part of a longer term strategy to manage inbreeding accumulation across generations.

Managing Inbreeding

Inbreeding gradually accumulates in a breed as elite animals, especially A.I. sires, get heavily used to produce the next generation of young bulls in A.I. as well as the next generation of replacement heifers in producer herds. Over time, it becomes increasingly difficult to find an interesting mating sire that is not at all related to the heifer or cow to be bred. Avoiding obviously close matings, such as a sire to its daughter, granddaughter or full-sister are easy enough by pedigree examination but that is not the key problem. For any animal born these days, a significant proportion of its inbreeding level will have accumulated due to multiple occurrences of several ancestors born decades ago on both sides of their pedigree. For this reason, inbreeding can only be accurately estimated when based on several generations of complete pedigree. The best source of such information is available by using the Inbreeding Calculator tool freely available on the Canadian Dairy Network (CDN) web site (www.cdn.ca).

Inbreeding and Sire Selection

One of the most common misconceptions associated with managing inbreeding is the belief that producers should avoid using sires with a high inbreeding level in their herd. This is not true at all! A highly inbred sire does not necessarily create inbred progeny. Inbreeding is not inherited

like genes and it is not calculated like a Parent Average (i.e.: [Sire + Dam]/2). To understand this better, let's take a look at a real comparison example based on two grandsons of Mountfield SSI DCY Mogul-ET with semen available as genomic young bulls in A.I. (Table 1). The selected bulls are Bandares with an inbreeding level of 8% and Sonic, who is 18% inbred since his dam is a granddaughter of Mogul and Snowman is the maternal grandsire of both his parents.

Using the CDN Inbreeding Calculator both bulls were mated to the group of Top 100 genomic heifers by Pro\$ to assess the inbreeding level that would result for each progeny. Table 1 shows that there was essentially no difference in the average inbreeding level of the resulting progeny from Sonic versus Bandares, with both groups slightly exceeding 14%. This example serves to demonstrate that a bull's own inbreeding level should not be considered when selecting bulls to include or exclude from your breeding program. What is important, however, is to look at the inbreeding that would result from each potential mating and then generally avoid all matings with a level of inbreeding that exceeds your threshold limit. Based on analysis at CDN of resulting inbreeding levels when active Holstein heifers and cows are mated to the Top 500 active genomic young bulls, 50% of all matings would yield an inbreeding of at least 10% so this level may be a useful guide when establishing your desired threshold limit.

Table 1: Analysis of Inbreeding Levels (%) Resulting from Matings Between Two Selected Active Genomic Young Bulls with Top 100 Pro\$ Holstein Heifers

| | Sonic (A) | Bandares (B) | Difference |
|---|-------------|--------------|------------|
| Bull's Own Inbreeding Level | 18% | 8% | 10% |
| Average Inbreeding Level (%) of Future Progeny | 14.3 | 14.7 | 0.4 |
| 5 Heifers with Largest Inbreeding Difference (A-B) | | | |
| PROGENESIS MODESTY PRAIRIE | 18.8 | 11.6 | 7.2 |
| PROGENESIS JEDI PRAXEUM | 19.1 | 11.8 | 7.4 |
| CLAYNOOK FIESTA MODESTY | 19.1 | 11.5 | 7.5 |
| STANTONS SILVER EMOTICON-ET | 23.1 | 12.2 | 10.8 |
| PROGENESIS SILVER PATTY | 23.1 | 11.9 | 11.2 |
| 5 Heifers with Largest Inbreeding Difference (B-A) | | | |
| LACTOMONT HATLEY BANDARES | 11.2 | 31.6 | 20.4 |
| BERNI BANDARES FELLY | 11.3 | 31.4 | 20.0 |
| CEDARWAL BANDARES CARAMILK | 12.1 | 31.6 | 19.6 |
| GLENHAVEN BANDARES CECILY | 13.5 | 33.0 | 19.5 |
| STE ODILE BANDARES EMPIRE | 12.5 | 31.7 | 19.3 |

Table 1 also provides the list of five heifers that have the largest difference in the level of inbreeding that would if they were mated to either Sonic or Bandares. As expected, the resulting inbreeding is highest when a sire is mated to a very close relative and Table 1 shows that levels exceeding 30% can result. In general, the results presented in Table 1 also indicate that it is very difficult to control inbreeding levels for matings among the highest genomic young bulls and the highest genomic heifers so producers should consider using outcross sires even if they are not at the top of the rankings for either LPI or Pro\$.

R-Value

For producers looking for outcross sires that would generally produce daughters with lower inbreeding levels, CDN also publishes the R-Value (i.e.: Relationship Value) for each animal. There are roughly 200 genomic young bulls with semen available in Canada that have an R-

Value of 14% or less, and 40 of these have a GLPI of at least 3000 or \$2200 Pro\$. On average, when used randomly to mate Canadian Holsteins, these sires will produce daughters with less than 7% inbreeding.

Summary

Inbreeding is more and more difficult to manage these days so CDN's Inbreeding Calculator is the best way to know the exact outcome of each mating. In sire selection, the inbreeding level of the bull itself is not relevant but their R-Value is available to identify outcross sires relative to the Holstein breed in Canada. Your Genetic Herd Inventory report available from CanWest DHI or Valacta provides an easy tool to monitor the average level of inbreeding in your herd.

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