Réseau laitier canadien
Canadian Dairy Network

Genetic Diversity & Inbreeding: Before & After Genomics

Genomics has sped up genetic progress, but has it impacted inbreeding? Did genomics allow for a larger pool of bulls available for selection? We answer these questions in our current extension article.

The information presented in **Table 1** reveals bull numbers pre- and post-genomics on a global scale and in North America. In addition, it shows the number of bulls pre-screened with genotyping and the number of those that went on to enter A.I.

Table 1. Global and North American (NA) Bull Numbers, Before and After Genomics

		Pre-genomics	Post-genomics	
			Bulls entered AI	All genotyped bulls
Birth Years		2002-2008	2011	
No. of young bulls	Global	5,300	3,290	28,440
	NA	1,660	1,335	10,685
No. of sires of young bulls	Global	380	410	1,240
	NA	105	155	450
No. of most popular sires representing 50% of young bulls	Global	15	18	32
	NA	8	9	16
Average number of sons per sire	Global	14	8	23
	NA	15	9	24

- **Number of young bulls:** Before genomics, over 5,000 young bulls were sampled worldwide annually, of which over 1,600 were in North America. With genomics, well over 10,000 North American young bulls are being pre-screened with genotyping each year - a testament to the effort A.I. organizations are making to source new bloodlines. Of those pre-screened, approximately 1,300 will go on to enter A.I. annually**.**

- **Number of sires of young bulls:** Pre-genomics, sires of sons were predominately high-profile proven bulls. Post-genomics, the 1,300 bulls entering A.I. annually are the sons of 48% more sires (155 vs. 105) than the bulls entering A.I. before genomics. This is due to a shift towards young, unproven genomic bulls as sires of sons. In this regard, genomic technology is broadening the portfolio of bulls offered to farmers.

- **Number of most popular sires representing 50% of young bulls:** While the number of sires of sons has increased since genomics, the number of bulls siring 50% of the young bulls entering A.I. remains constant. This shows that while A.I. is trying to find new bloodlines, it's not translating into a greater number of bulls siring the majority of young bulls being offered. In 2011, 9 bulls sired 50% of the 1,300 young bulls that entered A.I. in North America and 18 bulls sired 50% of the 3,000 that entered A.I. globally. These bulls are listed in Table 2.

- **Average number of sons per sire:** Post-genomics, the average number of sons entering A.I. per sire has decreased significantly in North America from 15 to 9. With shorter generation intervals, the turnover of top bulls is faster than before meaning sires of sons aren't being used as long as they were previously.

Overall, genomics has allowed A.I. organizations to sample fewer bulls of greater genetic merit. The technology has diversified the portfolio of bulls available, yet the number of bulls siring 50% of sons remains largely unchanged.

Table 2. Most Popular sires representing 50% of young bulls born in 2011 that entered A.I. Globally versus North America

North America	
Sire	**No. Sons in A.I.**
Flevo Genetics Snowman	132
De-Su Observer-ET	98
Roylane Socra Robust-ET	86
Regancrest AltaIota-ET	85
Ladys-Manor PL Shamrock-ET	82
De-Su 521 Bookem-ET	81
Ronelee Toystory Domain-ET	54
Badger-Bluff Fanny Freddie	44
Co-op O-Style OMan Just-ET	35

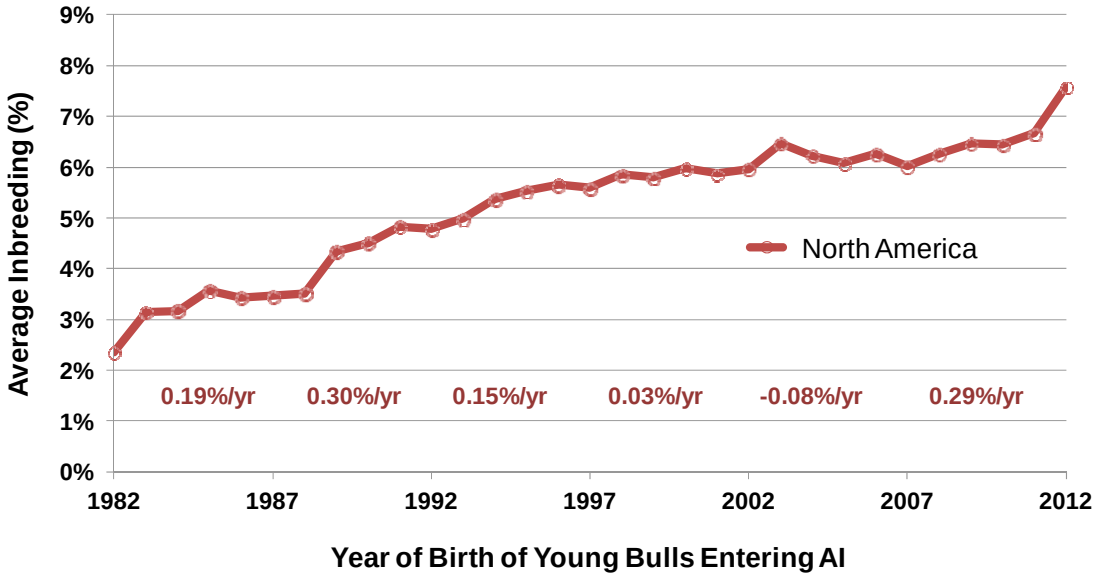
Globally	
Sire	**No. Sons in A.I.**
Flevo Genetics Snowman	243
Regancrest AltaIota-ET	178
End-Road Beacon-ET	121
De-Su Observer-ET	116
Schillview OMan Gerard-ET	112
Charlesdale Superstition-ET	104
Ladys-Manor PL Shamrock-ET	101
Roylane Socra Robust-ET	97
De-Su 521 Bookem-ET	93
Badger-Bluff Fanny Freddie	80
Long-Langs OMan OMan-ET	79
Ronelee Toystory Domain-ET	62
Ri-Val-Re 2338 Niagra-ET	54
Gillette Windbrook	51
Laeschway Jet Bowser-ET	51
Gillette Jordan	47
Bosside AltaRoss-ET	43
Co-op O-Style OMan Just-ET	41

Inbreeding after Genomics

Despite the fact that genomics has diversified bulls available, the arrival of the technology coincides with the highest average inbreeding levels among young bulls entering A.I. seen in the past 15 years (Figure 1). Most noteworthy is the rate experienced from 2011 to 2012, which hovers at 1% increase that year alone. Depending on how these young bulls are used in the breed, this increasing trend may also translate to average increases in the heifer population going forward.

On one hand inbreeding is associated with an increased frequency of desirable genes in a population as a result of selection. On the other, it is related with lower than expected performance, especially for economically important traits. At what extent does inbreeding hurt more than help the breed? This question still warrants more research. Of particular concern is the fact that with genomics a shorter generation interval may not allow enough time for natural selection to counter balance the negative effects of inbreeding.

Figure 1: Average inbreeding of bulls entering A.I. in North America over time



Controlling Inbreeding

On a breed level, CDN is exploring crediting outcross genomic young bulls in the LPI formula to promote the exposure and usage of bulls with superior genetics that are less related to the population. While geneticists study ways to control inbreeding on a breed basis, producers should focus on controlling inbreeding in their own herds. For individual matings, CDN's Inbreeding Calculator (http://www.cdn.ca/inbreeding/selectlist.php) can be used to confirm inbreeding and genetic potential of possible mates. In addition, A.I. mating programs can also be useful tools to monitor and maintain inbreeding at a level the producer has decided is acceptable to them.

While genomics provides an array of benefits, one of the technology's current drawbacks is increased average level of inbreeding. Nevertheless, we wouldn't trade today's more productive and more inbred cow with her less productive and less inbred ancestors. Maximizing genetic gain while controlling inbreeding levels will remain a high priority goal of the dairy cattle breeding industry.

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Date: September 2014