Réseau laitier canadien
Canadian Dairy Network

Update on Proofs for Identical Twin Sires

Identical twins have identical genotypes. Pedigree-based genetic evaluation systems treat identical animals as full-sibs. This strategy was known to be suboptimal since it assumes that identical twins only have 50% of their genes in common, when in reality they have the exact same DNA and identical genotypes. For purposes of genetic evaluations, identical twins are expected to transmit the exact same genetic potential to their progeny. However, before genomics it was very difficult to prove that animals were genetically identical.

Since the identification of genetically identical animals was no longer an issue in the genomic era, Canadian Dairy Network (CDN) implemented an improved methodology in 2011 for handling proofs of identical males. As long as they were born after April 1, 2006, any pair of sires identified as having identical DNA via genotyping received the same genetic and genomic evaluations. Identical sires that were already progeny proven as of December 2010 continued to be evaluated as if they were regular full brothers.

Identical sires are treated as one individual animal by pooling their daughter information and calculating one domestic genetic evaluation. For example, if one sire in the pair has 300 daughters and its identical brother has 200 daughters, both sires receive the same genetic evaluation based on the combined group of 500 daughters. Pooling daughter information increases the reliability of their combined proof, compared to treating them as full-sibs in the past. The same proof for identical sires is sent to Interbull for the calculation of MACE evaluations on other country scales. Depending on how the other country, say United States for example, handles the MACE evaluation from Interbull in addition to any daughter data that either brother may have in that country, identical twins may receive differing official evaluations in other countries.

Case Study - Jordan and Jerrick

Identical twins Gillette Jordan and Gillette Jerrick were first progeny proven in August 2010 and ranked #1 and #7 LPI, respectively, including genomics. As a result, they were both returned to active service and widely used across the country, although Jordan was also previously used as a high-ranking genomic young bull. Since these bulls were born prior to April 1, 2006, their proofs remained separate. Now, both have thousands of daughters in lactation and type classified. Although over 80% of their daughter production data is still from first lactation, these bulls serve as an excellent example of how proofs of identical sires evolve over time (Figure 1).

When first proven in August 2010, the bulls had an LPI difference of 278 points based solely on their traditional proof without genomics. Over the following months and years, their traditional proofs fluctuated to some degree, both upwards and downwards, with the largest difference between them exceeding 400 LPI points. As of April 2013, the variation in the LPI scale was halved and the average LPI was increased by 1700 points so the differences between Jordan and Jerrick for LPI and its components were reduced as expected. Once both bulls reached over 1,700 production daughters in May 2014, their LPI difference before including genomics has consistently been less than 100 points.

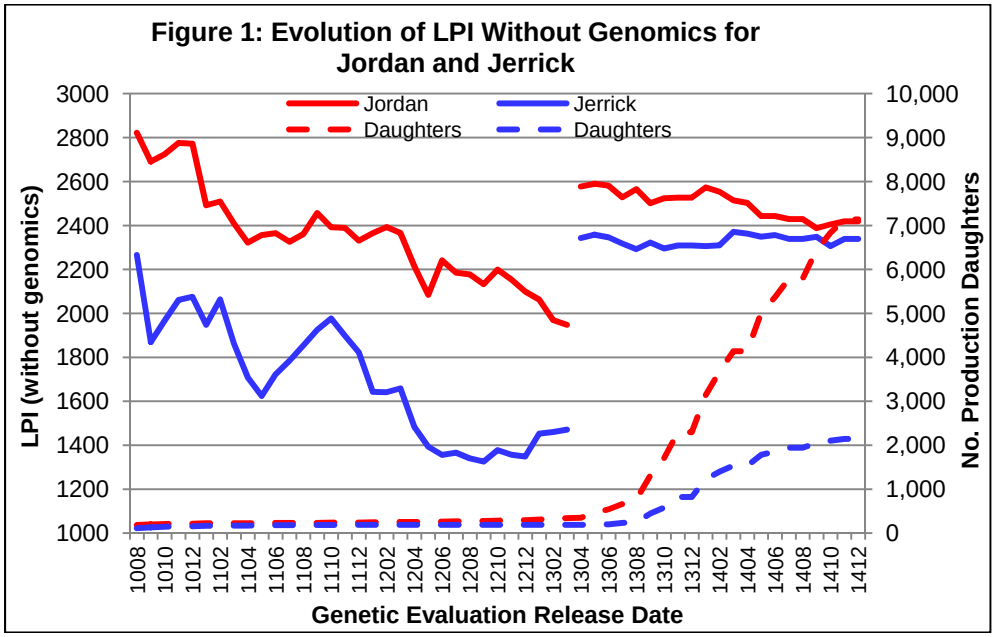

Table 1 shows the difference in traditional proofs without genomics between the identical brothers as of December 2014. Jordan is currently 80 LPI points higher than Jerrick, mainly because his production proof still exceeds that of Jerrick's, but by far less than it did during the first 6 months after these bulls were officially progeny proven. In terms of type traits, the brothers now only differ from each other by one point or less. Being that Health and Fertility traits are generally low heritability, more daughter data in first and subsequent lactations is required in order to reach high levels of reliability. For this reason, more difference between these bulls still exists for traits like Herd Life, Daughter Calving Ability, Temperament, Milking Speed and Mastitis Resistance. It is expected that as the reliability of their proofs for functional traits increases due to the accumulation of daughter information, their evaluations will continue to become more similar over time, as has been the case with Production and Conformation traits.

Table 1: Proof Differences as of December 2014: Jordan versus Jerrick

Trait	Difference during the first 6 months	Current Difference
LPI	341*	80
Production	334*	48
Milk	314 kg	43 kg
Fat	14 kg	5 kg
Protein	11 kg	3 kg
Fat Deviation	0.02%	0.04%
Protein Deviation	0.01%	0.0%
Durability	318*	10
Herd Life	1	-3
Conformation	5	1
Mammary System	3	1
Feet & Legs	6	1
Dairy Strength	1	1
Rump	5	0
Health & Fertility	30*	22
Somatic Cell Score	-0.05	-0.06
Mastitis Resistance	N/A	-2
Daughter Fertility	1	1
Milking Speed	4	2
Milking Temperament	-11	-4
Calving Ability	-1	-1
Daughter Calving Ability	1	-4

* Old LPI scale

Summary

The current CDN policy for calculating proofs for genetically identical brothers still raises some controversy and questions from breeders. Based on the observed evolution of traditional proofs for Jordan and Jerrick, excluding genomics, there is no indication that the policy should be altered. Since both bulls have the same genotype, the inclusion of genomic information for official proofs reduces the observed differences in published evaluations even further. Based on their semen usage in Canada, Gillette Stanleycup and Gillette Windhammer, and possibly Gillette Wildthing and Gillette Willrock, are two other pairs of identical brothers that may serve as case studies in the future but it will take a few more years before they have thousands of daughters with sufficient data for first and subsequent lactations.

Authors: Lynsay Beavers, Industry Liaison Coordinator, CDN
Brian Van Doormaal, General Manager, CDN

Date: December 2014