Réseau laitier canadien
Canadian Dairy Network

Genetic Evaluations for Identical Genotypes

Prior to recent advances in genomic testing technology, it was very difficult to prove that animals were genetically identical. Natural occurrence of identical twins is relatively rare but amplified use of reproductive technologies such as multiple ovulation and embryo splitting for embryo transfer (ET), has increased their occurrence in dairy cattle populations. In today's pedigree-based genetic evaluation systems, identical animals are sub-optimally treated as full-sibs. This means it is assumed that only 50% of their genes are in common, when truly they have completely identical genotypes. Early in life, identical animals have equal Parent Averages (PA), as both the sire and dam would be the same. But as females start to produce milk and are classified, their own performance starts contributing to their evaluation. With limited ability to confirm if animals are in fact identical, the assumption that only 50% of their genes are in common can cause breeding values to vary significantly. Theoretically, evaluations of identical animals should be more similar than that of full-sibs because they actually have the same DNA and therefore transmit the exact same genetic potential. Wide-spread adoption of genomic testing has provided the missing piece of information required to precisely identify identical animals and methods have been developed to account for this additional information to improve genetic evaluations.

The Canadian Dairy Network (CDN) has implemented a process to easily locate and confirm identical genotypes via 3K or 50K SNP genomic testing. As a result, research has been conducted to modify existing evaluation methodologies for males to correctly account for identical animals having 100% of their genes in common. The CDN Board of Directors recently approved implementation of this new methodology and, effective April 2011, identical males born since April 1, 2006 will receive identical genetic and genomic evaluations in Canada.

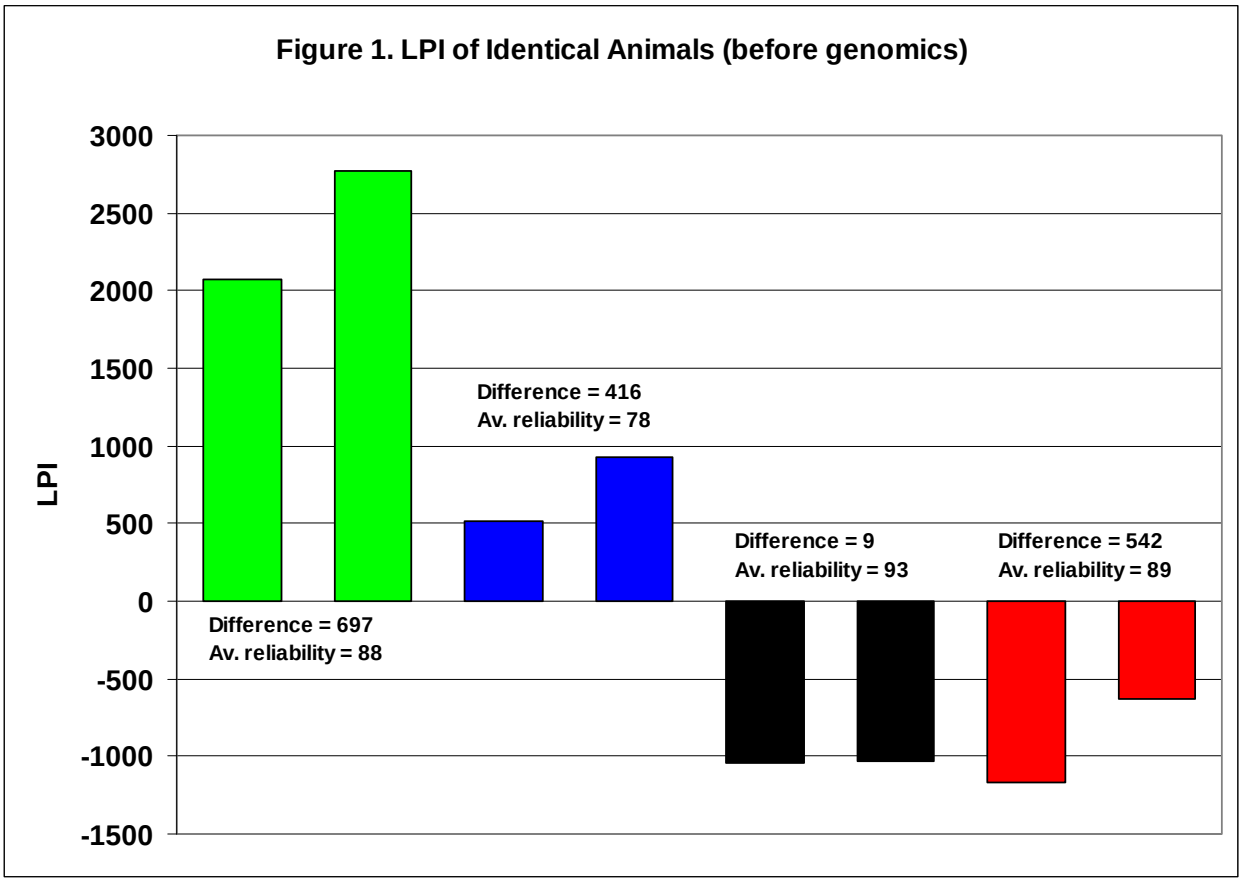
In February, more than 74,000 genotypes were scanned and 170 groups of identical animals were identified in the Holstein breed. A total of 343 animals were recognized as being identical, with 222 being female and 121 being male. A majority of these were young animals (PA) without progeny or performance data (Table 1). Under the current evaluation methods, these young genotyped animals would have identical GPA because they already have identical PA and, with the same DNA, would also have identical Direct Genomic Values (DGV). However, identical animals with an official LPI or MACE LPI will have identical genotypes but could have different EBV as a result of deviations in their own or progeny performances. Approximately 47% of the identical animals already genotyped were born and registered in Canada, 43% have a US registration number and the remaining 10% originate from other countries.

Table 1: Number of animals with identical genotypes by LPI type and country of registration (February 2011).

		Country of Registration		
Sex	Type of LPI	Canada	U.S.A.	Other
Male	PA	52	43	8
	OFFICIAL	11	-	-
	MACE	3	4	-
Female	PA	72	91	26
	OFFICIAL	23	-	-
	MACE	-	10	-

In order to comprehend the extent to which breeding values for identical sires can differ, traditional LPI for identical males that had an official proof in December 2010 were examined. Four identical male families are shown in Figure 1. Difference in LPI was as low as only 9 points but ranged up to nearly 700 points. In general, differences were higher for lower average LPI reliability. As daughter counts increase, it is expected that genetic evaluations for identical sires would become more and more similar. If GLPI values for identical twins are compared, differences would be smaller (almost halved). Having identical genotypes forces their DGVs to be very similar even with differences in data sampling due to different progeny groups. These four sire groups in particular will not be included in the methodology changes coming in April because they were already officially proven at the time of the December 2010 genetic evaluation release.

Figure 1. LPI of Identical Animals (before genomics)



The proposed methods suggest treating identical sires as one individual animal by pooling their daughter information and calculating one domestic genetic evaluation. For example, if one sire in the pair had 300 daughters and its identical partner had 200 daughters, both sires would receive a genetic evaluation based on the combined group of 500 daughters. Pooling daughter information will increase the reliability for both sires compared to treating them a full-sibs as in the past. Proof changes for identical sires will subsequently affect the official genetic evaluations of their progeny as well. The same EBV for identical sires will be sent to Interbull, however after conversion and contribution of foreign daughter information, their MACE LPI could be different on foreign scales.

Summary

In April 2011, any pair or group of sires identified as having identical DNA via genotyping will receive the same genetic and genomic evaluations as long as they were born after April 1, 2006. Identical sires already proven as of December 2010 (i.e., Gillette Jordan and Gillette Jerrick) will continue to be evaluated as if they were regular full-sibs. As reliability of their proof increases due to the accumulation of daughter information, their evaluations are expected to become more similar over time. Methods for handling evaluations of females with identical genotypes will continue to be developed at CDN for implementation in the future. Evaluation method for identical females are more complex given that each identical twin could have its own performance data, possibly in different herds and with different herd mate contemporaries.

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