Réseau laitier canadien
Canadian Dairy Network

# Haplotypes Impacting Fertility

The value and benefits of genotyping continues to grow. It almost seems endless! Although the original reason for DNA banking and genotyping was to improve the accuracy of genetic evaluations, other benefits have also become important very quickly. The most obvious of these has been parentage verification to ensure full accuracy for herdbook integrity and improved accuracy of genetic evaluation. In Canada, this benefit from genotyping has not been major since pedigree error rates have only been less than 4%. Beyond parentage verification, genotyping AI sires combined with whole herd genotyping of heifers and cows provides opportunities for discovering the parents of animals within the herd and/or population. This benefit can be very significant for herd owners that have traditionally not been recording the lineage of their animals in the breed association herdbook. In order to capitalize on this opportunity, Holstein Canada is planning to launch a new service in this area in the near future.

Correct parentage and lineage information also provides for more accurate measures and control of inbreeding. In addition to the traditional ways of estimating an animal's level of inbreeding based on pedigree analysis, genotyping data allows scientists to consider inbreeding from a whole new perspective. From an animal's genotype, inbreeding can also be quantified based on the proportion of its genes that are homozygous or "fixed". Such genes are automatically passed on to all progeny whereas progeny have a 50% chance of inheriting the best genes when the parent is in the heterozygous state.

**Newest By-Product of Genotyping**

Very recent research at the United States Department of Agriculture (USDA-AIPL), led by Dr. Paul VanRaden, has yielded another important value of genotyping within dairy cattle populations. Using the North American pool of 50K genotypes within the Holstein, Jersey and Brown Swiss breeds, the team of researchers started by locating regions of the genome that appear to be associated with infertility, embryonic death and/or stillbirth. Short sections of the genome that are transmitted as a block of DNA from parent to progeny are referred to as "haplotypes". Haplotypes may include genes associated with a specific trait expressed by the animal. An animal's genotype includes thousands of haplotypes on each chromosome, of which there are 30 pairs in the bovine genome. The specific approach of the USDA analysis was to identify any haplotypes that were never found in a homozygous state within the 50K genotypes for each breed, under the hypothesis that these would be associated with "lethal" genes. Lethal genes are so named because, when they are homozygous (i.e.: embryo has two copies, one from each parent), the resulting animal does not survive the embryonic stage or is born dead (stillbirth).

Following further analysis of identified haplotypes, a total of five were found to have an impact on reduced fertility including three in Holstein, one in Jersey and one in Brown Swiss. Table 1 provides details for each of these new haplotypes impacting fertility, which have been assigned a label representing the breed code (H, J or B), the letter "H" for haplotype, and a sequential numerical value (i.e.: HH1 for the first one found in Holstein, HH2 for the second one in Holstein and HH3 for the third one in Holstein). The estimated population frequency is 4 to 5% for the three Holstein haplotypes but those found in Jersey and Brown Swiss have higher frequencies at 23.4% and 14.0%, respectively. The frequency level in the population is a reflection of how easy or difficult it is to making matings that do not involve two carrier animals. As shown in Table 1, USDA scientists found that these haplotypes negatively impact fertility, as measured by conception rate and non-return rate. Also, when tracing back these haplotypes within the group of genotyped animals in each breed, they identified the earliest known ancestor(s).

**Table 1: Newly Identified Haplotypes Impacting Fertility in Holstein, Jersey and Brown Swiss Breeds**

| Breed | Label | Frequency | Impact on Conception Rate | Impact on Non-Return Rate | Earliest Known Ancestor(s) |
|---|---|---|---|---|---|
| Holstein | HH1 | 4.5% | -3.1% | -1.1% | Pawnee Farm Arlinda Chief |
| | HH2 | 4.6% | -3.0% | -1.7% | Willowholme Mark Anthony |
| | HH3 | 4.7% | -3.2% | -3.1% | Gray View Skyliner<br>Glendell Arlinda Chief |
| Jersey | JH1 | 23.4% | -3.7% | -3.7% | Observer Chocolate Soldier |
| Brown Swiss | BH1 | 14.0% | -3.4% | -2.5% | West Lawn Stretch Improver |

## Publication and Use of Haplotypes Impacting Fertility

The availability of the extensive database of 50K genotypes in North America has allowed for the discovery of these new haplotypes affecting fertility. These haplotypes do not, however, exist solely in genotyped animals but throughout the respective breed populations in North America and most likely globally. Simply because an animal is not genotyped does not mean it is not a carrier of any of these haplotypes. In the United States, the Holstein Association decided to publish the haplotype results for all animals genotyped with the 50K panel at the time of the August 2011 genetic evaluation release. Since the research results from the USDA-AIPL analysis are still quite recent, Canadian Dairy Network (CDN) and the respective breed associations are in the process of planning an appropriate publication policy and communication effort. It is expected that haplotype results will be made public in Canada effective the December 2011 genetic evaluation release to allow sufficient time for industry partners and producers to become familiar with this new by-product of genotyping and how to best use the resulting information within breed improvement programs.

## Summary

Five new haplotypes impacting fertility have been discovered by researchers at USDA-AIPL, including three in Holstein (HH1, HH2 and HH3), one in Jersey (JH1) and one in

Brown Swiss (BH1). The existence of thousands of genotypes within each of these breeds has now allowed for the identification of these negative haplotypes as an automatic by-product of DNA genotyping. This additional information can be used by industry organizations and dairy producers to help control the declining trend in fertility by minimizing the frequency of matings between animals that are both carriers of the same negative haplotype. While results have already been published in the United States, a publication policy and extension plan for Canada is expected by December 2011.

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