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## Genetic analysis of superovulatory response of Holstein cows in Canada

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### ABSTRACT

Superovulation of dairy cattle is frequently used in Canada. The cost of this protocol is high, and so is the variability of the outcome. Knowing the superovulatory potential of a donor cow could influence the breeder's decision to superovulate it or not. The main objective of this study was to perform a genetic analysis for superovulatory response of Holstein cows in Canada using data recorded by Holstein Canada, and to investigate if these data could be used for genetic evaluation. Data contained the total number of embryos and the number of viable embryos from every successful flushing performed across Canada. After editing, 137,446 records of superovulation performed between 1992 and 2014 were analyzed. A univariate repeatability animal model analysis was performed for both total number of embryos and number of viable embryos. Because both data and residuals did not follow a normal distribution, records were subject to either logarithmic or Anscombe transformation. Using logarithmic transformation, heritability estimates (SE) of 0.15 (0.01) and 0.14 (0.01) were found for total number of embryos and number of viable embryos, respectively. Using Anscombe transformation, heritability estimates (SE) of 0.17 (0.01) and 0.14 (0.01) were found for total number of embryos and number of viable embryos, respectively. The genetic correlation between the 2 traits was estimated at 0.97 using logarithmic transformation and 0.95 using Anscombe transformation. Breeding values were estimated for 54,463 cows, and 3,513 sires. Only estimated breeding values of sires having a reliability higher than 40% were considered for estimated breeding values correlations with other routinely evaluated traits. The results showed that selection for a higher response to superovulation would lead to a slight decrease in milk production, but an improvement for functional

traits, including all reproduction traits. In all cases, the estimated correlations are either low or modest. We conclude that genetic selection for increased superovulatory response in donors is possible; daughters of sires with high estimated breeding values for superovulatory response will tend to yield more embryos, whereas the additive effect of service sire seems not to contribute to the variability of the 2 superovulation traits and was not significantly correlated with the additive effect of the donor.

**Key words:** superovulation, embryo production, Holstein, genetic parameter, breeding value

### INTRODUCTION

In the 1930s, AI (Hamilton and Symington, 1939) revolutionized the way breeding was done in the dairy industry. Genetically superior bulls were then able to have more offspring, therefore increasing the genetic gain more rapidly throughout the population. Similarly, superovulation and embryo transfer have increased the rate of genetic gain from genetically important cows. This technique has been commercially available since the 1970s as reported by several authors (Farin et al., 2007; Machaty et al., 2012; Hasler, 2014) and is commonly used by dairy producers worldwide. Globally, 700,000 bovine embryos were produced in vivo in 2012, and of that number 350,000 were produced by dairy donors. Also, 440,000 in vitro embryos were produced in the same year (International Embryo Transfer Society, 2012). Superovulation and embryo transfer is used frequently in the Canadian dairy population, with almost 10,000 donors flushed, and over 68,000 transferable embryos collected in 2013 (Canadian Embryo Transfer Association, 2013). In 2012, Canada produced more than 20% of the global in vivo production of dairy embryos (International Embryo Transfer Society, 2012).

The main disadvantages of superovulation/embryo transfer include cost and the high degree of variability in the number of embryos produced by individual cows (Hahn, 1992; Kanitz et al., 2002; Lonergan and

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**Table 1.** Summary statistics of the superovulatory data

Item	Total	Average <sup>1</sup>	SD <sup>1</sup>	Minimum <sup>1</sup>	Maximum <sup>1</sup>
No. of records (flush)	137,446	—	—	—	—
No. of cows	54,463	—	—	—	—
No. of sires	3,513	—	—	—	—
No. of service sires	2,250	—	—	—	—
No. of clinics	100	—	—	—	—
Total no. of embryos	1,265,333	9.21	7.24	1	87
No. of viable embryos	1,044,416	7.60	5.92	0	58

<sup>1</sup>On a per flush basis.

Boland, 2011). To date, no genetic analyses have been performed for superovulatory response of dairy cattle in Canada, and no breeding values are available for Canadian producers to select cows based on their superovulatory potential.

Therefore, the main objective of this study was to perform a genetic analysis for superovulatory response of Holstein cows in Canada using data recorded by Holstein Canada, and to investigate if these data could be used for genetic evaluation. The specific objectives were (1) to characterize the superovulatory response data set, (2) to estimate genetic parameters of superovulatory response traits, (3) to estimate breeding values (EBV) for superovulatory response traits and examine their relationship with other routinely evaluated traits in Canada, and (4) to assess the usefulness of having such EBV for the Canadian dairy industry.

## MATERIALS AND METHODS

### Data

**Database.** Superovulatory response data from April 1980 to March 2014 were obtained from Holstein Canada (Brantford, ON, Canada). Initially, the database consisted of 168,855 records, where one record corresponded to one flush. All records were from Holstein animals. The data set contained information about the donor (identification and birth date), service sire (identification and birth date), date of insemination of the donor, date of embryo recovery, service type, clinic, total number of embryos produced per flush, and number of viable embryos produced per flush. In Canada, all superovulatory protocols are prescribed by veterinarians and the embryos are recovered by the same practitioner. The procedure is usually performed in the barn of the donor's owner. Therefore, in this data set, the clinic corresponds to a veterinarian or group of veterinarians that were involved with the superovulation and embryo transfer of a particular donor.

**Data Editing.** It is worth noting that only successful flushes with at least one recovered embryo were

available, because unsuccessful flushes are not recorded in Canada. Considering the low number of flushes done between 1980 and 1991, only data with a recovery date between 1992 and 2014 were considered in the analysis. In addition, only animals also present in the Canadian Dairy Network database were included in the analysis. If the service sire, birth date, or clinic was missing for a record, it was excluded. Only 3 service types were considered: H, insemination done by a herd owner; I, in vitro; and T, service done by an AI technician. Therefore, any record having another code for service type was deleted. Records were included if the age of the female at recovery was at least 8 mo and no more than 180 mo (15 yr). Duplicate records with exactly the same recovery date, donor, and service sire were deleted. If for one flush, with a given recovery or service date, 2 records were present because 2 different service sires had been used, both records were deleted. Only clinics with 50 or more records were considered. Additionally, 4 clinics had recording problems between 1999 and 2001. Therefore, all the records from those clinics were deleted for those years, as well as records of January 2002 for one of those 4 clinics. Descriptive statistics of the edited data are presented in Table 1.

**Trait Definition.** The total number of embryos (**NE**) corresponds to all the embryos recovered from a flush, including degenerated or dead embryos. On the other hand, the number of viable embryos (**VE**) corresponds to the number of recovered embryos reported to Holstein Canada as transplanted or frozen by the practitioners.

**Data Transformation.** Test for normality was performed on the raw data and on the residuals of the model used in the analyses (described later) using SAS proc univariate (SAS Institute Inc., 2013). Because both data and residuals for total number of embryos and number of viable embryos did not follow a normal distribution, various transformations were tested to normalize the data. The ones that performed the best were the logarithmic (**log**) transformation and Anscombe (**ans**) transformation (Anscombe, 1948). Logarithmic transformation is used to normalize data

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