J. Dairy Sci. 100:1–8
https://doi.org/10.3168/jds.2016-12075

Estimating variance components and breeding values for number of oocytes and number of embryos in dairy cattle using a single-step genomic evaluation

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ABSTRACT

Reproductive technologies such as multiple ovulation and embryo transfer (MOET) and ovum pick-up (OPU) accelerate genetic improvement in dairy breeding schemes. To enhance the efficiency of embryo production, breeding values for traits such as number of oocytes (NoO) and number of MOET embryos (NoM) can help in selection of donors with high MOET or OPU efficiency. The aim of this study was therefore to estimate variance components and (genomic) breeding values for NoO and NoM based on Dutch Holstein data. Furthermore, a 10-fold cross-validation was carried out to assess the accuracy of pedigree and genomic breeding values for NoO and NoM. For NoO, 40,734 OPU sessions between 1993 and 2015 were analyzed. These OPU sessions originated from 2,543 donors, from which 1,144 were genotyped. For NoM, 35,695 sessions between 1994 and 2015 were analyzed. These MOET sessions originated from 13,868 donors, from which 3,716 were genotyped. Analyses were done using only pedigree information and using a single-step genomic BLUP (ssGBLUP) approach combining genomic information and pedigree information. Heritabilities were very similar based on pedigree information or based on ssGBLUP [i.e., 0.32 (standard error = 0.03) for NoO and 0.21 (standard error = 0.01) for NoM with pedigree, 0.31 (standard error = 0.03) for NoO, and 0.22 (standard error = 0.01) for NoM with ssGBLUP]. For animals without their own information as mimicked in the cross-validation, the accuracy of pedigree-based breeding values was 0.46 for NoO and NoM. The accuracies of genomic breeding values from ssGBLUP were 0.54 for NoO and 0.52 for NoM. These results show that including genomic information increases the accuracies. These moderate accuracies in combination with a large genetic variance show good opportunities for selection of potential bull dams.
Key words: ovum pick-up, multiple ovulation and embryo transfer, accuracy, genomic breeding value

INTRODUCTION

Nowadays, reproductive technologies such as ovum pick-up (**OPU**) and multiple ovulation and embryo transfer (**MOET**) are broadly used in cattle breeding (Betteridge, 2003). Although both technologies are used to produce embryos, the major difference between them is the place of maturation and fertilization of the oocytes. With MOET, the maturation and fertilization of the oocytes and the embryo growth until d 7 is in vivo, but with OPU, it is in vitro (Pieterse et al., 1988; Merton et al., 2003).

Worldwide, 1,531,609 oocytes were collected using OPU and 339,969 embryos were transferred in dairy cattle in 2013 (IETS, 2014). The quantity of embryos collected after MOET or oocytes collected by OPU in one session depends on several factors. Nongenetic factors such as hormone-related factors, technician, age of the animal, and interval between sessions influence the quantity of embryos and oocytes collected with MOET or OPU (Merton et al., 2003).

Although the main focus in most studies was on nongenetic factors, some research has also been done on genetic factors. For number of oocytes (**NoO**) collected with OPU, a heritability of 0.25 was reported (Merton et al., 2009). For number of MOET (**NoM**) embryos, a heritability of 0.17 was reported (Jaton et al., 2016). The MOET and OPU can accelerate genetic improvement due to higher selection intensity when selecting bull dams, because more offspring per bull dam can be produced and therefore fewer dams can be selected compared with classical breeding (Hanenberg and van Wagtendonk-de Leeuw, 1997; Merton et al., 2003). With the introduction of genomic selection in dairy cattle, MOET and OPU can further accelerate genetic improvement, because with genomic selection

Received September 30, 2016.
Accepted February 6, 2017.
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relatively accurate breeding values can be estimated for animals at a relatively young age, even at birth or at embryo level (Schaeffer, 2006).

Including NoO and NoM in selection decisions can improve the efficiency of embryo production programs by selecting donors with a high MOET or OPU efficiency (Merton et al., 2009). The aim of this study was therefore to estimate variance components and (genomic) EBV for NoO and NoM based on Dutch Holsteins. The second aim was to assess the accuracy of pedigree and genomic breeding values for NoO and NoM using cross-validation.

MATERIALS AND METHODS

Data

In this study, NoO and NoM were the 2 traits analyzed, and for each trait a different data set was used (data provided by CRV, Arnhem, the Netherlands). For OPU, immature oocytes were collected once or twice per week at 5 nucleus herds in the Netherlands. The OPU sessions were performed in teams of 2 persons: the technician, responsible for the manipulation of the ultrasound probe and the ovary, and the assistant, responsible for the punctures of the follicles (Merton et al., 2009). The information collected from the OPU sessions were NoO collected per OPU session, the quality of the oocytes, OPU technicians, location of OPU, date of OPU, frequency of OPU, parity, and lactation stage of the cow. This data file contained information from OPU sessions from January 1993 to April 2015. Data were collected for 56,058 OPU sessions from 4,273 animals. Data were excluded if OPU sessions were not at nucleus farms (too few observations per location), if OPU technicians had less than 10 observations, and if OPU intervals were of 1, 2, 6, or 8 d, because usual intervals were of 3, 4, or 7 d. After data editing, the data file contained 40,734 OPU sessions and 2,543 animals with an average of 17.8 sessions/donor. The pedigree of the 2,543 animals with OPU data contained 11,807 animals and 27 generations in total. From the 2,543 animals with OPU data, 2,049 animals did not have progeny with OPU observations. Dams had between 1 and 49 offspring with OPU observations and sires had between 1 and 59 offspring with OPU observations.

For MOET, multiple oocytes were recruited for ovulation after hormone stimulation (superovulation). The ovulated ova were fertilized by AI and the fertilized ova developed into embryos. The ova migrated from the oviducts into the uterus. Approximately 7 d after insemination, the uterus was flushed (Merton et al., 2003; van Wagtendonk-de Leeuw, 2006). The information from the MOET sessions included in the data file were NoM, MOET technician, location, protocol, and date of session. This data file contained information from MOET sessions from June 1989 to August 2015. Data were collected for 43,810 MOET sessions from 18,822 animals. In the data editing, records were excluded when locations or technicians had less than 10 sessions, when sessions were performed before 1994 or without superovulation and when non-Holstein Friesian animals were used. After data editing, the data file contained 35,695 MOET sessions and 13,868 animals with an average of 3.0 sessions/animal. The pedigree of the 13,868 animals with MOET data contained 41,231 animals and 27 generations in total. From these 13,868 animals, 10,383 animals did not have progeny with MOET observations. Dams had between 1 and 57 offspring with MOET observations and sires had between 1 and 370 offspring with MOET observations. Summary statistics are shown in Table 1.

Genomic Data

Part of the animals with OPU or MOET data were genotyped using the Illumina 10 or 50K SNP chip. The animals genotyped with a 10K SNP chip were imputed to 50K SNP. For imputation, a combination of Phasebook software (Druet and Georges, 2010) and Beagle (Browning and Browning, 2007) was used (Mulder et al., 2012). For OPU, 1,144 animals of the 2,543 animals with observations were genotyped. From these 1,144 animals, 890 animals did not have progeny with OPU observations. For MOET, 3,716 of the 13,868 animals with observations were genotyped. From these 3,716 animals, 2,729 animals did not have progeny with MOET observations. Both for OPU and MOET, geno-

Table 1. Summary statistics of number of oocytes with and without log-transformation (NoO and NoO_{log}) and number of multiple ovulation and embryo transfer embryos with and without Anscombe transformation (NoM and NoM_{Ans}) after data editing

Trait	No. of records	Mean	SD	Minimum–maximum
NoO	40,734	7.716	5.283	0–81
NoO_{log}	40,734	0.867	0.260	0–1.914
NoM	35,695	9.273	7.260	0–97
NoM_{Ans}	35,695	2.872	1.184	0.612–9.868