Genomic selection strategies to optimize the use of multiple ovulation and embryo transfer schemes in dairy cattle breeding programs

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ABSTRACT

The aim of this study was to assess the impact of varying features of an open multiple ovulation and embryo transfer (MOET) nucleus used in a genomic dairy cattle breeding scheme on both genetic gain and inbreeding rates. The Viking Red breeding scheme served as a case study to design scenarios that were stochastically simulated. We analyzed the number of AI sires used in the breeding population, the number of flushed heifers, the number of flushings per heifer and the genotyping capacity allocated to young females. The results supported that setting up a MOET program in a genomic dairy cattle scheme increases genetic gain without increasing inbreeding rates when the MOET nucleus size and the number of AI sires in service are large enough. Secondly, it was shown that increasing the number of genotyped heifers could not compensate the loss in genetic gain caused by closing the MOET nucleus. On the contrary, when extending the flushing capacity of the MOET program, increasing the number of flushings per heifer had a greater impact on genetic gain, but also on inbreeding rates, than increasing the number of flushed females. So, when a constraint applies on the flushing capacity in an open MOET scheme and the achieved inbreeding rate permits it, it seems more relevant to increase the number of flushings per heifer than the number of flushed heifers. Results also indicated that the number of genotypings allocated to females had to be sufficient to get maximal returns from the MOET scheme. In this case study, little extra genetic gain could be obtained by extending the MOET scheme size with the initial genotyping strategy (800 genotyped females). Indeed, the genotyping capacity should permit to genotype all heifers produced in the MOET scheme to discriminate the best heifers within families, and should be also sufficient to identify the best heifers outside the MOET nucleus.

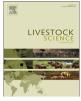© 2015 Elsevier B.V. All rights reserved.

1. Introduction

Multiple ovulation and embryo transfer (MOET) has been common practice in dairy cattle breeding schemes for the

last 30 years. For instance, a MOET program has been running in the Finnish Ayrshire (FAY) breeding scheme since the early 1990s, (Mäntysaari et al., 1996). This program, called ASMO, was structured as an open MOET nucleus and aimed at providing the progeny-testing scheme with bull calves from the best breeding heifers. The use of MOET on young heifers was expected to speed up genetic gain by increasing selection intensity and reducing the generation interval in the bull dam selection path (Nicholas and Smith,

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1983). However, with conventional selection methods, the use of MOET had to be carefully optimized to achieve genetic gain at reasonable levels of risk, i.e. at reasonable inbreeding rates. Actually, the selection of heifers for flushing and of calves born from flushings was undertaken with limited accuracy and giving a large weight to parental information. Hence, the progeny testing of young bulls was still critical to select both within and between families the best sires for artificial insemination (AI) (Strandén et al., 2001).

The development of genomic selection (GS) opened new opportunities to alleviate some of these limitations (Pryce and Daetwyler, 2011). By integrating dense SNP information in statistical models used for genetic evaluation, GS assists the early selection of breeding individuals from both sexes with reasonable accuracy (Meuwissen et al., 2001). Furthermore, the use of genomic breeding values (GEBV) allows discriminating prospective calves within sib families because it capitalizes on individual genomic information to estimate the Mendelian deviation of breeding values. As a result, larger rates of genetic gain are expected from using MOET in genomic schemes (Pedersen et al., 2012; Pryce et al., 2010; Sørensen and Sørensen, 2009). However, even though the number of calves produced by elite bull dams is enlarged, the resulting increase in selection intensity is expected to only have a small impact on genetic diversity when the number of selected candidates is maintained (Daetwyler et al., 2007).

The first GEBV were officially released in 2011 in the Viking Red (VR) breeding scheme which resulted from the association of the breeding programs of the FAY, the Danish Red (DR) and the Swedish Red (SR) breeds. Selection accuracy was increased for young male and female candidates compared with conventional selection methods (Su et al., 2012). In this new context, questions about the optimality of the ASMO program were raised by the industry with respect to its size and structure.

Increasing the number of flushings on the very best females should give more superior offspring for selection in the next generation. So, at a given flushing capacity, we could hypothesize that breeding fewer heifers with more flushings give more genetic gain than breeding more heifers with fewer flushings, but also more inbreeding. In GS schemes of dairy cattle, enlarging the number of AI sires used in the population is a strategy to curb inbreeding rates without markedly reducing genetic gain (Lillehammer et al., 2011). Hence, it was tested if using more intensively MOET on females together with a larger panel of genomic bulls could generate more genetic gain and lower inbreeding. Finally, in a breeding scheme integrating MOET, achieved genetic gain critically depends on the relative proportions of genotypings allocated to males and females (Sørensen and Sørensen, 2009). Indeed, a sufficient number of genotypings must be allocated to males and females to ensure detecting the best breeding individuals within each sex. When the number of genotypings allocated to females is too limited, little genetic gain is expected of increasing the MOET scheme size. Therefore, we suppose that the genotyping capacity spent on females should be carefully defined in order to get maximal genetic gain from the MOET scheme. Based on the VR case study, strategies to optimally combine genomic selection and MOET in an open nucleus were investigated.

2. Material and methods

To test hypotheses, different scenarios mimicking the size and structure of the VR breeding population were stochastically simulated. The optimality of the MOET nucleus was investigated focusing on 4 parameters, namely the number of AI sires used in the breeding population, the number of heifers recruited for the MOET nucleus, the number of flushings carried out per heifer in the MOET herd and the genotyping capacity spent on females. The interaction between parameters was studied by simulating scenarios with all possible combinations of parameters.

2.1. Description of the genomic VR breeding scheme

The simulated population was made up of three different entities mimicking the DR, FAY and SR sub-populations with 7000, 9000 and 9000 females, respectively, i.e. 25,000 females in total. Breeding cows were selected within country among 1- to 5-year-old females. All cows were inseminated with conventional semen and produced one calf per year. The first calving occurred at two years of age and all cows older than six years were systematically culled. Each year, 15% of all females were culled at random.

In the basic scenario, 1800 male and 800 female calves were annually genotyped at birth, which corresponded to the situation in 2010. Calves from both sexes could be genotyped and were chosen based on mid-parental EBVs. Genomic EBVs were used to directly select AI sires with GEBVs among genotyped young bulls aged from 1 to 4 years, i.e. no progeny testing was undertaken before selection. GEBVs were available at one year of age when selecting males for AI and females for the ASMO program. At five years of age, all AI bulls were culled for age reasons. Involuntary culling concerned 15% of males in each age class.

The management of genetic resources was achieved by constraining the use of bull sires. No more than four (and six) active bulls descending from the same sire could be used every year (and in total).

2.2. Use of MOET in the VR population

The ASMO program has been running as an open juvenile MOET nucleus since the early 2000s (Korpiaho et al., 2003; Strandén et al., 2001). In this scheme, the best 75 1-year-old heifers were annually recruited in the Finnish population based on GEBV. All selected heifers were gathered in a central station and were flushed twice at one year of age to produce four offspring per flushing. Hence, each 2-year old donor produced eight viable offspring from two different matings. All produced embryos were implanted in recipient cows that were not considered for breeding.

To mimic real practices, a few flushings were also carried out on breeders' own initiative, i.e. outside the ASMO program. This concerned the best 10 DR, 20 SR and 100 FAY females on GEBV across age groups. These heifers were flushed once and produced four calves per donor with equal probability of having males and females. In the FAY population, priority was given to ASMO for the selection of heifers, i.e. 1-year old heifers were not considered for an extra