Using Sexed Semen Has Limited Effect On Genetic Gain In A Dairy Cattle Breeding Scheme Using Genomic Selection

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Introduction

The use of female-sorted sexed semen in dairy cattle breeding has increased considerably during the last few years (Seidel Jr. (2009)). In spite of this fact, only a limited number of studies have addressed the question of what the long-term genetic consequence of this is.
The use of sexed semen in a dairy cattle breeding scheme can reduce the number of dams needed to maintain the population at a constant size. This in turn will increase the selection intensity on the dams and, as the annual genetic response in a population depends on the selection intensity in each individual selection path, it is expected that the genetic gain in the population will increase (Rendel and Robertson (1950)). This has not been demonstrated for a modern dairy cattle population using multiple ovulation and embryo transfer (MOET), and genomic selection (GS). However, we expect it to be the case.
The objective of this study was to test this expectation by simulating different strategies for use of sexed semen in combination with MOET in a breeding scheme where GS is applied. More specifically, it was examined how the concurrent use of these two reproductive technologies affects the rates of genetic gain and inbreeding.

Material and methods

Scenarios. We investigated the effect of varying both the use of sexed semen and the use of MOET. Two different levels of MOET were compared: No use of MOET versus all young bull (YB) candidates born from MOET. Within each of the two levels of MOET, three different levels of use of sexed semen were compared: 1) No use of sexed semen, 2) sexed semen used in the breeding nucleus, and 3) sexed semen used in both the breeding nucleus and the production population. In scenario 1) all inseminations were performed using conventional semen. In scenarios 2), two different strategies for using sexed semen were compared: x) X-sorted semen used for the 50% best bull dams (BD) and Y-sorted semen for the rest of the BD and y) Y-sorted semen used for 50% best BD and X-sorted semen for the rest of the BD. In scenario 3), the two scenarios (x and y) for use of sexed semen in the nucleus were combined with 100% use of X-sorted semen in the production population.

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We used the stochastic simulation program ADAM (Pedersen *et al*. (2009)) to simulate a population intended to resemble the breeding nucleus of a dairy cattle population. The level of genetic gain and inbreeding was monitored annually for 30 years. The simulations were replicated 100 times.

Population structure. The breeding nucleus consisted of 20,000 cows distributed equally among 200 herds. Each year, each nucleus cow produced one viable offspring with equal chance of it being a male or female, unless MOET or sexed semen was applied. As a result, approximately 10,000 female and 10,000 male offspring were produced every year.
When the offspring were one year old, the 2,000 best females and 2,000 best males were selected for genotyping based on their average parent genomically enhanced breeding value (GEBV). Also at the age of one year, the 200 best bulls were selected for progeny testing.
The 30 best sexually mature bulls were selected as active sires every year and randomly mated to the 20,000 selected dams producing 667 offspring each. When no reproduction technologies were applied, the number of BD was 4,000 and as a result approximately 2,000 bull candidates were born each year. All selected females were between one and five years old.
In the scenarios where reproduction technologies were applied, the following population parameters differed from that described above: When MOET was applied; five calves were born per BD. The number of BD was accordingly reduced from 4,000 to 800 to maintain the production of young bull candidates per year at approx. 2,000. When sexed semen was used, the probability of a female offspring was set to 90% (X-sorted) or 10% (Y-sorted) (Borchersen and Peacock (2009)).

Selection scheme. Two traits were included in the breeding goal: protein and mastitis resistance. The heritability of the traits was set to 0.30 and 0.04 with a genetic correlation of -0.30. The two traits were assumed to represent all milk production and functional traits, respectively, and the economic values were set to €83 and €82 per genetic standard deviation.
The traits were only realized in cows, and young bulls were progeny tested outside the breeding nucleus with 150 daughters per candidate for protein yield and 135 for mastitis.
In addition to the phenotypes, early predictors in the form of direct genomic values (DGV) were sampled for each of the two traits for genotyped animals. The DGV were sampled as individual traits, with a heritability corresponding to the heritability of the marker information, and a genetic correlation to the observed trait corresponding to the assumed accuracy of the DGV. The heritability of both DGV was set to 0.99 and the genetic correlation to the true breeding value of the realized trait was set to 0.71.
Selection was based on breeding values, estimated using a standard multivariate best linear unbiased prediction (BLUP) model based on phenotypic records and pedigree information. DGV were included in the model as information traits without any economic value and the breeding values thus resembled GEBV.

Results and discussion

Contrary to our expectations, the use of sexed semen only had a minor impact on the genetic gain (table 1). When MOET was not applied, the highest increase in total merit index was

6% which was observed for the scenario where X-sorted semen was used in both the nucleus and the production population. When MOET was applied, the effect of using sexed semen on the genetic gain was in most cases negative. The only scenario resulting in an increase in genetic gain was again X-sorted sexed semen used in both the nucleus and the production population. This corresponds with the fact that this scenario has the shortest generation interval both with and without the use of MOET. This shorter generation interval can be explained by the relatively larger competitiveness of one-year-old females, which will lead to a smaller proportion of older BD.

Table 1: Average annual rate of change in total merit index in € (ΔTMI), protein in genetic standard deviations (ΔPRO), mastitis resistance in genetic standard deviations (ΔMAST), generation interval in years (L), and average rate of inbreeding per generation in percent (ΔF).

	Strategy		ΔTMI[1]	ΔPRO[2]	ΔMAST[3]	L[4]	ΔF[5]
MOET	Sexed semen	Semen type					
No	No	Conventional	37.56	0.24	0.21	2.52	0.73
	Nucleus	X to top 50%	38.12	0.25	0.21	2.50	0.74
		Y to top 50%	36.28	0.24	0.23	2.55	0.74
	Nucl. & prod.	X to top 50%	40.00	0.26	0.21	2.30	0.76
		Y to top 50%	38.10	0.25	0.22	2.35	0.80
Yes	No	Conventional	46.33	0.30	0.27	2.35	0.82
	Nucleus	X to top 50%	45.88	0.30	0.26	2.34	0.79
		Y to top 50%	44.85	0.29	0.25	2.36	0.73
	Nucl. & prod.	X to top 50%	46.88	0.31	0.27	2.19	0.87
		Y to top 50%	45.59	0.29	0.26	2.22	0.79

[1]Standard errors in the range: 0.11 to 0.14, [2]0.001 to 0.002, [3]0.001 to 0.002, [4]0.0013 to 0.0021, [5]0.017 to 0.029.

As expected, when conventional semen was used, MOET significantly increased the rate of genetic gain and inbreeding by 23 and 13%, respectively. When sexed semen was used, MOET still increased genetic gain substantially (17-24% increase in TMI). However, inbreeding was not increased when the best half of the BD was inseminated with Y-sorted semen. The reason for this is probably that when Y-sorted semen is used, the full-sib bull calf families born by top BD are on average larger compared to when conventional semen is used. This allows GS to increase within-family selection thus causing less full-sib sires to be selected. When conventional semen is used, the full-sib bull calf families born by top BD are on average too small for GS to counteract the increase in inbreeding caused by MOET. When X-sorted semen is used to the best BD, within-family selection have little importance, as the superior bull calves have almost no brothers, and the large full-sib bull calf families have a lower genetic merit on average.

The use of sexed semen also only had a minor effect on the rate of inbreeding compared to MOET. Although an increase of 2 to 10% was observed when MOET was not applied; this was only significant when the use of Y-sorted sexed semen to the breeding nucleus was combined with X-sorted semen to the production population. When MOET was applied, the

only significant effect was observed in the scenario where Y-sorted sexed semen was used to the breeding nucleus. In this case, the rate of inbreeding was lowered by 11%.
When using sexed semen, combining use in the breeding nucleus with use in the production population always increases genetic gain and rate of inbreeding significantly compared to using it exclusively in the breeding nucleus.

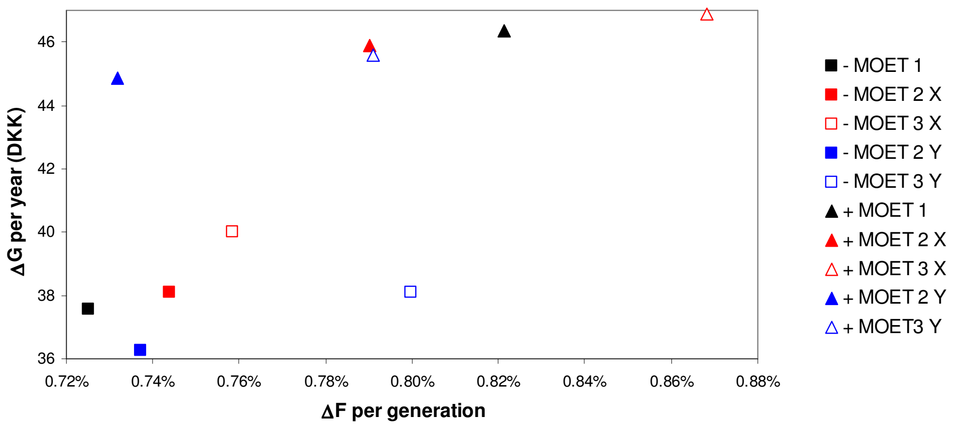

Figure 1: Rate of total genetic gain per year in DKK as a function of rate of inbreeding per generation for each of the ten scenarios.

Finally, when comparing the ten scenarios as illustrated in figure 1, where the rate of genetic gain is depicted as a function of the rate of inbreeding, it is clear that the increase in genetic gain that can be achieved when using MOET is not necessarily accompanied by an increase in the rate of inbreeding. This indicates, that a dairy cattle breeding scheme using GS can benefit from the use of MOET at a relative low cost in inbreeding due to increased within-family selection among dams.

Conclusion

The results show that in a dairy cattle breeding scheme applying GS, the use of sexed semen can increase the rate of genetic gain. This effect is, however, somewhat counteracted when MOET is applied, where only the use of X-sorted semen in both the breeding nucleus and the production population will result in an increase in genetic gain. However, the increased rate of inbreeding that is observed when MOET is applied can be offset by the use of Y-sorted sexed semen in the breeding nucleus as this enables GS to increase within-family selection.

References

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