

## Inbreeding and coancestry trends in Nordic Holstein

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### Abstract

Increased rates of inbreeding have been observed in several Holstein populations across the world since genomic selection (GS) was implemented into the breeding programs. The objective of this study was to test whether this is also the case in the Nordic Holstein population using pedigree data. Rates of inbreeding were estimated before, during and after the GS implementation. We could not detect any increase in inbreeding or coancestry rates in Nordic Holstein. Effective population size increased over the studied time periods from 68 to 104, despite fewer sires being used. This might be because more of sires of sons have been used to produce AI bulls compared to the time before implementation of GS.

### Introduction

Inbreeding rates have been higher in several Holstein populations around the world after genomic selection (GS) was implemented, compared to before GS (Doekes et al., 2018a; Doublet et al., 2019; Forutan et al., 2018). In theory, GS should decrease loss of genetic diversity (Meuwissen et al., 200; Meuwissen et al., 2016), but in practice the opposite has been observed in several breeds and populations. Loss of genetic diversity due to increasing rate of inbreeding in dairy cattle populations is concerning because it may lead to inbreeding depression, which affects many dairy cattle traits negatively e.g., milk yield, fertility, and udder health traits (Doekes et al., 2019; Makanjuola et al., 2020a), and loss of genetic variation. The Food and Agriculture Organization (FAO) recommends that the increase in inbreeding per generation should not exceed 1% to avoid negative effects of inbreeding depression (FAO, 2013).

Within the Nordic (Denmark, Finland and Sweden) Holstein population, inbreeding trends have not been investigated in recently. The analyses of Sørensen et al. (2005) were carried out prior to the introduction of GS in 2011. The Nordic countries have had a common Holstein breeding program since 2010 when the cooperative VikingGenetics (VG) was founded. For this reason, there is a demand for updated research on Nordic Holstein (NH), due to the changes in the breeding program after introduction of GS, to investigate how this has affected the population structure. Thus, the objective of this study is to analyse inbreeding and coancestry trends in the NH population based on pedigree data.

### Materials & Methods

Pedigree data was supplied by Nordic Cattle Genetic Evaluations. EVA software (Berg et al., 2006) was used to calculate inbreeding coefficient, expected inbreeding coefficient under random mating, alpha (deviation from random mating), coancestry (C), pedigree completeness index (PCI), average generation coefficient (Gencoef), and generation interval (L) (NordGen, 2022).

Nordic Holstein females expected to contribute to the next generation of the Holstein breeding population were selected as the base population. Selected females were candidates for VG' Holstein breeding program. They were from milk recording herds and born from January 2016 to November 2018. Only animals with a Nordic Total Merit value  $\geq 8$ , Holstein breed percentage  $\geq 97\%$  and PCI  $\geq 0.8$  were accepted into the base population for pedigree tracing. In total, pedigrees were traced for 372,955 females which reflect approximately 1/3 of the NH female population born in 2016-2018. Pedigrees of the selected base population animals were traced back to the known founders, on average 12.4 generations.

Rates of inbreeding were calculated from the regression of the natural logarithm  $\ln(1-F)$  on year of birth. Yearly rates of change in inbreeding ( $\Delta F$ ) and coancestry ( $\Delta C$ ) were calculated as  $\Delta F/\Delta C = 1 - e^{\beta_1}$  (Pérez-Enciso, 1995), where  $\beta_1$  is the regression slope. Effective population size,  $N_e$ , (Falconer & Mackay, 1996) was calculated from  $\Delta F$  as  $N_e = 1/2\Delta F \times L$ , where  $L$  is the generation interval. Expected future effective population size (Exp.  $N_e$ ) was calculated from  $\Delta C$  as  $N_e = 1/2\Delta C \times L$ . Animals were allocated to three different groups depending on birth year: before implementation of GS 2007-2010, during the implementation 2011-2014, and after implementation of GS 2015-2018. Calculations of effective population size were done separately for each group.

## Results and discussion

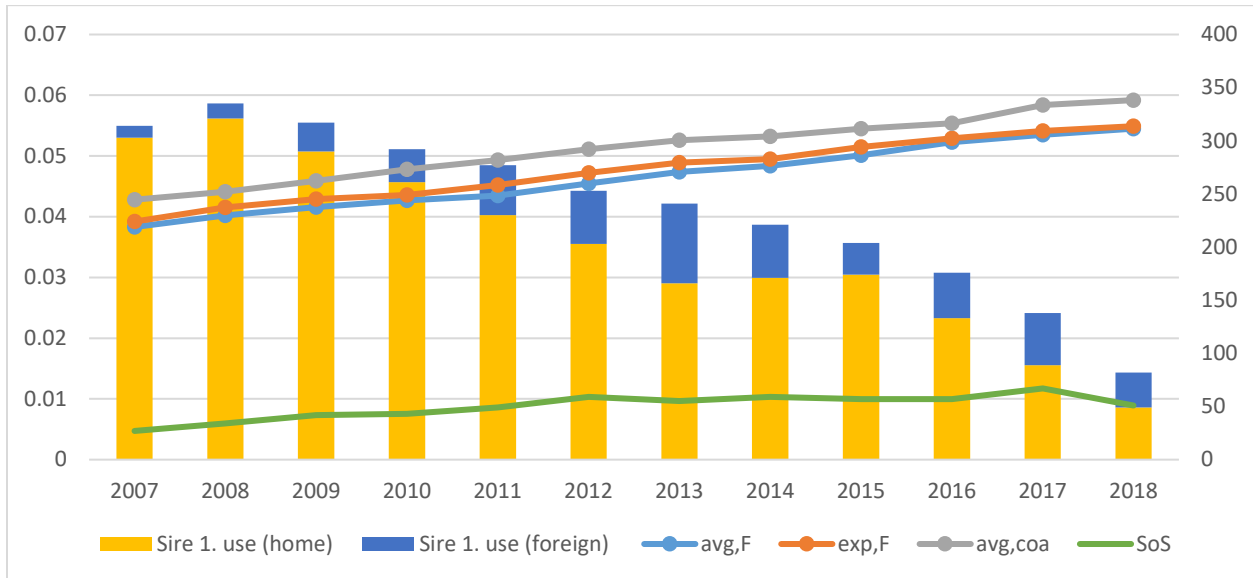
The generation interval has decreased in NH after implementation of GS. Before GS, the generation interval was on average 4.9 years, and it has decreased to 3.2 years on average after the implementation (Table 1). Inbreeding and coancestry trends (Figure 1) have been stable in NH across time periods, and we were not able to detect any increase in inbreeding in contrast to what has been seen in some other Holstein populations (Doekes et al., 2018b; Forutan et al., 2018; Makanjuola et al., 2020b). On the contrary,  $\Delta F$  in NH has remained unchanged (0.0016) from before to after implementation of GS. This was also seen for the  $\Delta C$  (0.0018). Over the time periods number of starting AI sires has decreased, but in the last time period a wider range of sires of sons has been used compared to earlier periods (Figure 1). These observations agree with the theory of decreasing loss of genetic diversity with genomic selection. Similar results for Nordic animals were seen in the inbreeding survey by World Holstein Friesian Federation (Feddersen, 2020).

**Table 1.** Yearly rates of change of inbreeding ( $\Delta F$ ) and coancestry ( $\Delta C$ ), generation interval ( $L$ ), effective population size ( $N_e$ ) and expected future effective population size (Exp.  $N_e$ ) in each group of animals before, during and after genomic selection was implemented in NH.

	$\Delta F$	$\Delta C$	$L$	$N_e$	Exp. $N_e$
2007-2010	0.0016	0.0018	4.86	68	59
2011-2014	0.0017	0.0014	4.08	71	88
2015-2018	0.0016	0.0018	3.17	104	87

The increase in effective population size ( $N_e$ ) from 68 to 104 across the time periods supports the theory, because even though rates of changes have been the same over the time periods, generation interval has decreased which leads to larger  $N_e$ . Expected future effective population size similarly increased over the time periods, but is smaller than the  $N_e$ , which might indicate that even though animals are less inbred, they are still related to each other. This might be caused by more intense use of related bulls from same imported sires. This will cause a decrease in inbreeding, but

coancestry will increase or remain at the same level. After implementation of GS, sires have been used more equally meaning that all bulls will have offspring in the breeding population even though they might not be used as much in the Holstein production population. GS has made selection of AI sires more reliable, and daughter proven sires has become less competitive; therefore, bulls can be circulated faster in the breeding program. In this study focus was more on the inbreeding trend behind NH females. Studying inbreeding trends behind Nordic AI sires will be beneficial because other studies show that increase in inbreeding is higher for the bulls (Doekes et al., 2018a; Doublet et al., 2019).



**Figure 1.** Number of starting Nordic and foreign AI bulls, average inbreeding, expected inbreeding, average coancestry and number of sires of sons (SoS) between years 2007-2018 in NH population.

Considering the effective population size, there has been improvement since the last study on NH from 2005 (Sørensen et al., 2005), where the historical  $N_e$  was 49-69 and expected future effective population size was 43-51 across the time periods. Even though  $N_e$  for NH has increased, there is reason to monitor the development and improve the breeding scheme to gain higher  $N_e$ . Populations with  $N_e$  between 50-100 are facing risk of inbreeding depression, and even higher  $N_e$  might be needed for long-term (FAO, 2013; Frankham et al., 2014). After the implementation of GS, NH is above the short-term threshold but in the long-term the breed might be in danger of facing issues related to inbreeding depression, when the expected future effective population size is on the threshold for short-term survivability. Therefore, methods for controlling future increase in inbreeding more efficiently need to be developed.

Breeding programs today are based on genomic selection and there has been recommendations that methods to control inbreeding should then be based on genomic information (Sonesson et al., 2012). There has been debate about the best way to manage inbreeding in livestock populations (Meuwissen et al., 2020; Henryon et al., 2019a; Henryon et al., 2019b) and more research on the topic is required. In the future research, inbreeding and coancestry trends should be based on genomic information to investigate whether similar results are seen when studying only genomic tested animals in the breeding population for NH.

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