Inbreeding trends within the Holstein population worldwide

Gert Pedersen Aamand, Jukka Pösö, Ulrik Sander Nielsen, and Freddy Fikse

What is inbreeding?

Inbreeding is the mating of individuals that are related by ancestry and results in a reduction of heterozygosity and an increase in homozygosity. It can lead to a reduced biological fitness. The inbreeding coefficient (F) is the standard measurement of inbreeding. It can be defined as both:

- the probability that two alleles at any given locus are identical by descent
  and
- the probable proportion of an individual's loci containing alleles that are identical by descent.

It means the risk that an animal has got the same allele from its dam and sire originating from a common ancestor which occur in both the dam's and the sire's pedigree.

The reduction of biological fitness can manifest itself in two ways: genetic defects for monogenic traits and inbreeding depression for traits governed by many genes. For monogenic traits, allowing for matings with high inbreeding coefficients increases the chance that the offspring receives the unfavorable allele from both parents and suffers from the disorder or disease.

What is inbreeding depression?

Inbreeding depression is the effect of inbreeding measured as the reduction in mean phenotypic performance with increasing levels of inbreeding within a population e.g. reduced milk yield or fertility caused by inbreeding.

At farm level it is important to monitor inbreeding to avoid reduction of biological fitness due to monogenetic disorders/diseases and inbreeding depression. The inbreeding coefficient of planned matings can be used for this purpose. At population level, high inbreeding trends are related to loss of genetic diversity, which, among others, influences the prospect of achieving genetic gain in on a longer perspective. Here, the rate of inbreeding (average level of inbreeding in one time period compared to another time period) is more important to monitor than the inbreeding level itself.

How does inbreeding develop in the era of genomic selection?

The World Holstein Frisian Federation (WHFF) has in 2020 collected information about the development in inbreeding coefficients for cows and heifers from 26 countries worldwide including Denmark, Sweden and Finland. The information is collected in a presentation, which should had been given on the planned WHFF World congress in August 2020 but has been made available on the WHFF website instead. In table 1 the increase in inbreeding level (% units) per year are shown for different birth year periods of females for some of the largest Holstein populations in the world plus the three Nordic Holstein populations.

FAO recommends that increase in inbreeding level should be less than 1% units per generation, meaning that if the generation interval for dairy cattle today is 4 years then annual increase in inbreeding should be below 0.25% units per year to full fill that recommendation. In table 1 shows that some countries are close to or slightly above that threshold during the last 10 years.

Table 1 Average increase in inbreeding level (% units) per year and country in different time periods

Birth year of females	1990-2000	2000-2010	2010-2020
Italy	0.18	0.14	0.26
US	0.19	0.11	0.26
Canada	0.26	0.08	0.25
Finland	*0.09*	*0.19*	*0.20*
Netherlands	0.17	0.03	0.16
France	0.20	0.10	0.16
Germany	0.16	0.08	0.15
Sweden	*0.19*	*0.13*	*0.12*
Denmark	*0.18*	*0.12*	*0.10*

The results in Table 1 show large differences in increase in inbreeding coefficients during the last 10 years where genomic selection is the key tool for selecting breeding animals. Countries like Italy, US and Canada have an increase which is twice as high (0.25-0.26% units per year) as the one observed for Sweden and Denmark (0.10-0.12% units per year) in the same period. Finland deviates in magnitude from Sweden and Denmark, which is caused by the fact that introduction of the Holstein Frisian was much later in the Finnish population than in Sweden and Denmark. This led to a lower level of inbreeding in 1990-2000 and a higher in 2000-2020 in Finland than in Sweden and Denmark; even though the same pool of AI bulls has been used since VG was formed in 2008.

The results in table 1 show that inbreeding in the majority of cow populations has increased when genomic selection was introduced (2010-2020) compared to the situation when the traditional progeny test scheme was the key element in the breeding program (2000-2010). For the three Nordic countries the increase is kept at the same level in the period from 2000-2020.

Inbreeding can be controlled at:

- AI company level by considering future inbreeding when selecting young AI bulls
- farm level by using mating plans which consider inbreeding

Both elements are important to avoid inbreeding at population level in the short run, but in a longer perspective inbreeding needs primarily to be handled by the AI companies responsible for the breeding program.

Dealing with inbreeding in the genomic era

The results in table 1 indicate that AI companies in different countries deal differently with inbreeding in the breeding programs. Inbreeding has increased significantly after introduction of genomic selection in many of the countries, but the results from the Nordic countries prove that it by considering future inbreeding in the breeding program is possible to avoid an increased rate of inbreeding. Controlling of inbreeding in the breeding program requires that AI companies select more bull sires and make a tradeoff between the bull's genetic merit and his effect on future inbreeding.

Source World Inbreeding Trend in Holsteins - Presentation by Egbert Feddersen- view here http://www.whff.info/.