



Breeding for polledness in Holstein cattle

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ABSTRACT

Currently almost all dairy cattle are dehorned as calf to avoid injuries later in life. A welfare friendly alternative to dehorning is to breed polled cattle. This paper explores the potential to breed for polledness in the Holstein breed, and investigates the genetic merit and relatedness of both polled and horned bulls. In 2009 there were 33 polled bulls available for artificial insemination (AI), two of them being homozygous for polledness. In 2014 more than 150 bulls were available, 31 of them being homozygous. Breeding values for the total merit index (NVI-Dutch Flemish Index) have increased considerably for polled bulls. In 2009 the difference in average Estimated Breeding Value (EBV) for NVI between polled bulls (available for AI) and the top 100 horned AI bulls was 180 points, equivalent to about 18 years of selection at that time. In 2014 the difference was reduced to 149 points, equivalent to about 5 years of (genomic) selection. Genomic selection has made an important contribution to this reduced difference between polled and horned bulls. Polled bulls in 2009 were more inbred ($F=0.045$) than horned bulls ($F=0.037$) but less related to cows born at Dutch farms in that year ($r=0.070$ vs. 0.089). Using optimal contributions and a combination of polled and horned bulls, a next generation of animals can be bred that combines a high genetic merit with a relatively low relatedness and higher frequency of polledness. However, homozygous polled bulls born in 2012–2014 had a relatively high average inbreeding level ($F=0.079$) and almost all originated from the same two polled founder bulls. This may form a potential risk for lethal alleles showing up with inbreeding. Overall, breeding high genetic merit polled Holstein cows has become a realistic perspective, but care must be taken to avoid high relatedness and inbreeding levels.

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1. Introduction

The Holstein Friesian is the largest dairy cattle breed in the world. Nearly all dairy cattle in NW Europe are dehorned, to avoid injuries among herd mates and increase safety for the farmer (Oliver, 2009; Cozzi et al., 2015). Dehorning is a painful process, although discomfort can be limited if correct procedures are followed and anesthesia is applied (American Veterinary Medical Association, 2007; Faulkner and Weary, 2000; Graf and Senn, 1999; Caray et al., 2015). Nevertheless, alternatives are sought to eliminate negative effects of dehorning on animal welfare altogether. One of the alternatives is to breed polled cattle that do not develop horns and consequently do not need to be dehorned (Prayaga, 2007; Götze et al., 2015).

Polledness is controlled by a major gene and is one of the earliest known examples of Mendelian inheritance in livestock (Bateson and Saunders, 1902; Schafberg and Swalve, 2015). Polledness (P) is dominant over horned (p). The gene is located at

the proximal end of Bovine chromosome 1 (Brenneman et al., 1996; Drogemuller et al., 2005; Georges et al., 1993; Harlizius et al., 1997; Schmutz et al., 1995). The exact molecular nature of the polled allele remained unknown for a long time, but was recently identified (Medugorac et al., 2012; Seichter et al., 2012) as two alleles: a 202 bp insertion–deletion in most breeds, and a 260 bp haplotype in Holstein cattle. The frequency of polledness varies over breeds, but is low in the Holstein breed. Consequently, farmers are faced with a limited choice of bulls that inherit polledness and a breeding program to increase the frequency of the polled allele is desirable. Such a breeding program carries the risk that, if low breeding values for other important traits are associated with the polled allele, the bulls will not be used for polled only. Moreover, if the polled locus is present in a small group of related bulls, such a breeding program can lead to substantial inbreeding with associated negative effects.

This paper describes genetic aspects relevant for a breeding program to increase polledness in the Dutch Holstein population. For this purpose, the history of polledness in Holstein is described, current breeding values for traits of polled bulls available for artificial insemination are compared to the breeding values for the

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current horned bulls, as well as their relatedness. The latter is important to estimate effects on inbreeding rates in a breeding program that intends to increase polledness.

2. Material and methods

2.1. Pedigree and breeding values of polled bulls

To determine the availability of polled animals in the Holstein Friesian breed, databases of the Dutch (CRV www.crv4all.nl) and Canadian (Canadian Dairy Network www.cdn.ca) breed associations were searched in April 2009 for polled bulls being available for AI. Since polledness at that time was not standardly registered by the herd books, initially polled animals were found by searching for names containing the word polled or the addition P. Polledness of animals found that way was confirmed as much as possible by other information (mainly advertisements on the web and in the press), where also some extra polled animals were identified. Parents and offspring of all polled animals were traced in the pedigree, and these were investigated for being polled as well, either by looking at the name or in the case of a parent by identifying the other parent as horned. The pedigree of all polled animals was traced back to at least 1960 to determine their polled ancestors.

The databases were searched again in December 2014. At this time the presence of the polledness gene in animals was registered, however for some older animals known to be polled the registration lacked. Another difference was that in 2009 the youngest bulls with estimated breeding values (EBV) were 5 years old, whereas in 2014 due to genomic selection EBVs were available for bulls of one year old as well. Bulls with only parental average as breeding value were not used in the evaluation, since the reliability was deemed to be too low.

2.2. Breeding polledness: farmers perspective

To determine the consequences of using polled bulls for farmers a cross section of all cows in the Netherlands in 2008 was used. From the central database in the Netherlands a random sample of 2000 farms with at least 60 cows was drawn. All the cows present in 2008 on these farms were analyzed. The total number of cows in this sample was 200 000. The pedigree of the cows was also available and was merged with the pedigree of the polled animals. The most popular 33 bulls, all horned, that sired 50% of the calves born on these farms in that and the preceding year were used as a representation of the horned bulls in the Holstein Friesian. Relatedness was compared with the polled AI bulls available at that time. Relatedness was determined within and between each of the three groups: polled bulls, horned bulls and the cross section of cows.

Genetic merit of the polled bulls born between 1985 and 2014 was compared with the average of all Holstein Friesian cows born in the Netherlands between 1985 and 2012 (CRV, 2014). Breeding values for the overall Dutch Flemish Index (NVI) which combines production, longevity, fertility, health and conformation traits were determined for all polled bulls born between 1985 and 2014. All breeding values were standardized to the same base.

2.3. Breeding polledness: Breeding companies perspective

To determine the consequences for a breeding program of bulls the breeding values of polled bulls available for AI were compared to those of the top 100 bulls in 2009 and 2014. Breeding values for production, longevity, fertility and udder health of bulls were retrieved from the Dutch database. Total genetic merit was evaluated

with the Dutch-Flemish Index (NVI).

In a breeding program both genetic merit and relatedness have to be taken into consideration. To maximise genetic diversity in future generations, the relatedness of the selected bulls should be minimised. Inbreeding rates in particular may increase to excessive levels when strong selection is performed by using a group of closely related animals as ancestors. Here we explore the possibility to maximize genetic merit while restricting relatedness of the bulls in a breeding program using the optimal contribution method (Meuwissen, 1997). The basic idea is that by using a combination of less related bulls and bulls with higher breeding values relatedness can be restricted.

With optimal contributions the average relatedness in the next generation is minimized or restricted by choosing the combination of parents according to their relatedness, and various other restrictions. The average relatedness in the next generation is given by:

$$r = c'Ac$$

where r is the average relatedness in the offspring, A is the numerator relatedness matrix of the current animals, and c is a vector with the contributions of the current animals to the next generation. The contribution vector sums to one, and by biological necessity the contribution of both females and males to 0.5. To find the contribution vector that minimizes the relatedness in the next generation the first derivative is determined of a function with the constraint that the contribution vector has to sum to one, that contributions of either sex sum to 0.5 and no negative contributions are possible. If the purpose at the same time is to increase the average breeding value in the next generation the average relatedness cannot be minimized anymore. Instead the average relatedness in the next generation is restricted to a predetermined value, and the breeding values maximized for that relatedness. This implies an extra constraint to the function determining the contributions to the next generation.

Optimal contributions can be applied to a single sex as well, and then the constraint for a total contribution of 0.5 for either sex is dropped. In that case the contribution of the members of the same sex is tailored in such a way that their relatedness is minimized or set to a predetermined value with their breeding values maximized.

Optimal contributions were calculated for three groups of bulls: the 38 polled bulls available for AI in 2009, the 33 bulls that sired 50% of the cows born in 2009 and 2008 and those two groups combined. First relatedness was minimized within each group. Then EBVs were maximized while restricting the relatedness to a value about 0.010 above the minimum (respectively 0.150 for polled bulls, 0.125 for horned bulls and 0.100 for the combination). Finally the EBV was maximized for the combined group while restricting the relatedness to the value of used for the horned bulls (0.125) to determine whether polled bulls may contribute to a higher EBV when restricting relatedness. In all cases the breeding values for NVI in the next generation was maximized.

3. Results

3.1. Pedigree and breeding values of polled bulls

All the polled Holstein Friesians bulls, originate from two polled ancestors born around 1960 (Fig. 1): the cow Princess Houwtje and her son Burket-Falls ABC. A limited number of bulls have Green Velvet Apollo L as another polled ancestor. The pedigree of both Princess Houwtje and Green Velvet Apollo L is incomplete and it is not clear whether they have a common polled ancestor,

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