APPENDIX 23

ALCASDE
Alternatives to Castration and Dehorning

Study on the improved methods for animal-friendly production, in particular on alternatives to the castration of pigs and on alternatives to the dehorning of cattle

D.2.2.2. Report on the assessment of breeding strategies in relation to the introduction of the polled gene

SP2: Alternatives to dehorning: To develop and promote alternatives to the dehorning of cattle.

WP2.2: Assessment of benefits and drawbacks of dehorning and alternatives to dehorning in dairy and beef cattle.

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Jack J. Windig. Wageningen UR, Animal Breeding and Genomics Centre, Lelystad The Netherlands.

André Eggen. INRA, UMR Genetique et Biologie Integr. Jouy en Josas, France.

Table of contens:

1.   Genetic background of horned and polled cattle

Since the rediscovery of Mendel's laws, inheritance of horns has been the subject of numerous studies, which have led to one model most commonly accepted and involving three loci *polled*, *scurs* and *African horn*, first proposed by White (1936) and revised by Long and Gregory (1978) and Brem *et al.* (1982). In this model:

1. The *polled* locus has two alleles: *P* (polled or absence of horns) dominant to *p* (horned) This was one of the first genes for which a Mendelian inheritance was reported (Bateson & Saunders 1902). The gene is known as the Polled-gene, and its alleles are designated as P for polled and p for horned. Polled is dominant over horned. Consequently animals carrying one or two P alleles are always polled while only animals homozygous for p are horned. Heterozygous (Pp) animals are thus always polled, and can be seen as carriers of hornedness. A cross of a heterozygous bull (Pp) with a homozygous horned (pp) cow will have a 50% chance of a polled calf (Pp) and a 50% chance of a horned calf (pp).

2. The *scurs* locus has two alleles: *Sc* coding for the development of scurs and *sc* for the absence of scurs. Scurs develop as small horn-like growths in the same area as horns but loosely attached to the skull. They can vary in size and shape to look like horns and in some animals, partial fusion to the skull has been observed with age. For the "scurs" phenotype to occur, the *polled* locus has to have at least one allele *P* (Table 1). Allele *Sc* is dominant to allele *sc* in *P/p Sc/sc* males but recessive in *P/p Sc/sc* females. The scurs phenotype has been observed in numerous breeds such as Angus, Hereford, Fleckvieh, Simmental, Pinzgauer, Limousin, Charolais and some other cattle breeds.

3. The *African horn* locus has two alleles: *Ha* (presence of African horns) and *ha* (absence) with allele *Ha* dominant to allele *ha* in *P/p Ha/ha* males and recessive in *P/p Ha/ha* females.

Thus, in contrast to the *polled* locus, expression of the *scurs* and *African horn* loci depend on the animal's sex. For breeding polled animals the polled gene is the most relevant since it is sex independent. Based on different studies it is shown that *scurs* and *African horn* loci are not alleles of the *polled* locus (e.g. Asai et al. 2004) and do not modify the horn shape on an otherwise horned animal (*p/p*).

The polled gene is located at one of the ends of the Bovine chromosome 1. This was first discovered at the university of Liege, where the proximity of two microsattelites (TGLA49 and AGLA17) to the polled gene was discovered (Georges et al. 1993). There is a recombination probability of 13% between these microsattelites and the polled gene, so that the accuracy of prediction of these microsattelites is limited. Since their discovery more molecular markers in proximity to the gene have been discovered (Schmutz et al., 1995; Brenneman et al., 1996; Harlizius et al. 1997; Drögemüller et al., 2005). Presently DNA-tests based on these markers are available commercially to distinguish between homozygous (PP) and heterozygous (Pp) polled cattle.

Genes lying in the region where the polled gene is located have been sequenced by a group based at Monsanto Company (Cargill et al. 2008). Thirteen SNPs were found with one of the alleles corresponding with polledness and the other with hornedness. These SNPs were not in the coding regions of the genes. One SNP was found in the 3'UTR (untranslated) region of the Synaptojanin gene, and it was shown that this SNP may disrupt a microRNA target site. Micro-RNAs regulate expression of genes generally on a tissue specific basis. Consequently, the most likely explanation for the mutation that leads to polledness is that it has not changed

any gene, but that the expression of a gene at the start of the pathway forming horns, in the tissue that is to form horns, is disrupted so that the development of horns does not take place.

Table 1 Horn and scurs inheritance models according to Long and Gregory, 1978 and Brem et al., 1982

	Sc/Sc	*Sc/sc*	*sc/sc*
P/P	S	Male NS or S Female NS	NS
P/p	S	Male S Female NS	NS
p/p	H	H	H

NS: non-scurred, S: scurred, H: horned.

2. General overview of presence in different breeds

The presence of polledness has been known for a long time in several breeds. A paper from 1887 describes extensively the occurrence of polledness in breeds across the world, known at that time (Auld 1887) and reports on Egyptian paintings and Greek and Roman coins with images of both polled and horned cattle in ancient times. From Scotland there are written accounts available that describe Galloway type of polled cattle at the end of the 18th century, while this type of cattle was already present in the Middle Ages, and possibly even in Roman times, although it is not clear whether or what percentage of these cattle was polled. However, the conclusion that polledness is not recent phenomenon is evident.

Completely polled breeds occur predominantly in Great Britain and Scandinavia (table 2). Polled Hereford has been used across the world for crossing to create new polled breeds. The Senepol on the Caribbean island St. Croix, for example, has been created by crossing N'Dama cattle from Senegal with polled Hereford. Similar breeds have been created in Brasil, USA and Australia. It is not always clear what the population size of these breeds is, and some are probably initiatives of local breeders which for marketing reasons created a separate name for their polled cattle.

Table 2 Presence of polledness in different breeds (not complete)

Category	Breed (Country of origin)
Completely polled	Aberdeen Angus (GB)
	Hereford Polled(GB)
	Belted Galloway (GB)
	British White (GB)
	Galloway (GB)
	Polled Red (GB)
	Swedish Red Polled (S)
	Old Norwegian Red Vestland (N)
	Old Norwegian Red Ostland (N)
	Estonian Red Polled (Est)
	Murray Grey (Aus)
	Senepol (St. Croix, Carib.) and other crosses
> 20% Polled animals	Norwegian Red (N)
	Welsh Black (GB)
	Sussex (GB)
	Several Beef Cattle (AUS)
< 5% Polled cattle	Holstein (USA/D/NL/F)
	Jersey (GB)
	Simmental (D/CH)
	Fleckvieh (D)
	Ayreshire (GB)
	Dexter (GB)
	Charolais (F)
	Limousin (F)
	Salers (F)
	Pie Rouge des Plaines (F)
	Parthenaise (F)
No polled cattle	Groningen White Headed (NL)
	Meuse Rhine IJssel (NL)
	Highland cattle (GB)
	…

In several breeds a substantial part of the animals is polled. An example is the Norwegian Red which originates partly from old Norwegian breeds that were polled. In Australian beef cattle polled animals are relatively frequent, probably originating from polled Hereford. In other breeds such as the Holstein-Friesian, Simmental and Jersey polledness is rare. A few polled bulls are available, but generally these are heterozygote and by far the largest part of the bulls is horned. In the Fleckvieh in Bavaria (Germany) a few polled bulls are available with high breeding values and are now used for most inseminations in that region.

Finally there are breeds in which polledness is completely absent, such as the dual purpose Meuse Rhine Ijssel in the Netherlands. The only option for breeding polledness in such a breed would be introgression. In, for example, the Scottish Highland cattle and the African Watutsi cattle horns mark the breed, and breeding polled cattle cannot be an issue.

3. Presence in the Holstein Friesian

3.1. History

The polled gene was probably more frequent in the 19th century in the Friesian Dutch cattle which is ancestral to the present Holstein Friesian breed. Göpel, a german breeder of polled cattle claims that around 1860 the dairy cattle in the North of Germany and the Netherlands was for a large part polled. When the pedigree of present day polled bulls is analysed, it seems likely that the present day polled bulls originate from Dutch cattle (Specht, 2008). Specht (2008) cites from a letter from 1914 from the Dutch secretary of the herd book who recounts polled cattle at an exhibition in 1886 in Amsterdam, and the use of a bull in 1884. Thus several polled cattle was around before 1900 in the Netherlands.

After 1900 polled cattle disappeared from the Netherlands. Probably selection for horned animals was intense, because in the then common tied stalls horned cattle was preferred. Horns prevented slipping of the chain over the Head. Moreover, horns were used to burn in ID numbers. In the USA a few breeders concentrated on breeding polled bulls (Specht 2008). The first bull available for AI was Burkett Falls ABC in the sixties of the previous century. All bulls nowadays available in the Holstein-Friesian are descendants of this bull.

3.2. Available Bulls

A number of bulls are available for AI. In april 2008, 39 polled bulls born after 1995 available for AI could be found on the internet. (e.g. https://www.cr-delta.nl/nl/index-producten.htm > stierzoeken) (table 3). There are several more bulls available for AI (e.g. Baldus David and Wietheges Dallas) but since they are still Young and do not have enough daughters yet that produce milk, no breeding values are available for these bulls. The young bull Baldus Davis is the only homozygous polled bull available for AI.

Table 3 Available bulls for AI with breeding values in april 2008 (source NRS Database)

Name		Polled Factor	Red factor	Father	Mothers father	NVI	Kg Milk	% fat	% protein	Longevity	SCS	Fertility	Conformation
T	Peter	P		Polled Plus	Celsius	114	118	0.04	0.05	398	103	102	105
Aggravation	Lawn Boy	P	Red	Bacculum	Manfred	85	1033	-0.54	-0.14	322	102	102	106
Hickorymea	Oswald	P	RF	Bosco	Bellwood	82	1423	-0.39	-0.33	375	105	101	103
Aggravation	Afterburn	P		BW Marshl	Manfred	97	1496	-0.37	-0.23	207	101	99	107
Burket-Falls	Polled Plus	P	RF	Aerostar	Fagin	57	-203	-0.07	-0.05	371	106	104	101
Burket-Falls	Perk	P	Red	Phideaux	Polled Plus	44	39	-0.21	0.12	46	96	99	101
Hickorymea	Tokyo	P	Red	Adam	Commotion	41	1000	-0.22	-0.06	112	99	103	
Hickorymea	Omar	P		Glenwood	Bellwood	31	792	-0.04	-0.12	110	105	97	99
Hickorymea	Ottawa	Pp	RF	Tripod	Bellwood	39	1247	-0.48	-0.3	150	108	102	98
Aggravation	Hardwood	P	Red	Redwood	Aerostar	36	-85	0.01	-0.06		104	107	96
Burket-Falls	Portrait	P		Taboo	Rudolph	35	275	-0.27	-0.09		102	103	
Hickorymea	Titus	P	Red	Colby Red	Cliffhanger	35	1192	-0.3	-0.21	47	101	98	104
Dansire	Pax	P	RF	Polled Plus	Lukas	27	587	-0.19	-0.27		101	104	100
Burket-Falls	Fortify	P	Red	Polled Plus	Blackstar	26	231	0.06	-0.16		103	101	98
Aggravation	Dieter	P	RF	Addison	Aerostar	21	1028	-0.55	-0.26		99	98	
Hickorymea	Ovation	P		Manfred	Bellwood	19	543	-0.46	-0.17	174		103	
Hickorymea	Omega	P		Inquirer	Bellwood	18	-6	-0.3	-0.05	191		99	
Weinberg	Lypoll	Pp	RF	Lyon	Cliffhanger	17	489	-0.22	-0.22	202	106	97	104
Burket-Falls	Preview	P		Marshall	Polled Plus	10	-12	-0.12	-0.16	157	105	102	
Burket-Falls	Clout	P		Polled Plus	Celsius	9	849	-0.61	-0.16	169	100	98	99
Hickorymea	Overtime	P		Forbidden	Bellwood	7	20	0.06	-0.09	174	106	102	104
Burket-Falls	Perfect	P		Polled Plus	Phideaux	5	-644	-0.12	-0.05	102	100	105	
Hickorymea	Tenor	P	RF	Manat	Commotion	6	1017	-0.3	-0.19	55	102	93	102
Dahlgaard	Var Hajo	P		Webster T	Funkis	-7	560	0.03	-0.08		96	95	100
Burket-Falls	Special	P	RF	Convincer	Polled Plus	-11	-310	0.2	0.1		95	97	100
Hickorymea	Turner	P		Bellwood	Commotion	-15	467	-0.04	-0.16	11	106	104	94
Wiethege	Dallas	P	Red	Darwin	Lateral	-18	-538	-0.13	-0.05		103	104	99
Ostretin	Gucker	P		Tucker	Zack	-18	314	-0.26	-0.17		101	102	100

Name		Polled Factor	Red factor	Father	Mothers father	NVI	Kg Milk	% fat	% protein	Long evity	SCS	Fertility	Confor mation
Carona	Enorm	P		Elevation	Polled Plus	-22	-99	-0.2	-0.15		101	104	98
Burket-Falls	Darwin	P	Red	Phideaux	Polled Plus	-25	-1301	0.22	0.08		101	105	101
Future	Genetic Perp	P	Red	Polled Plus	Deister	-26	-400	0.21	0.01		104	98	98
Hickorymea	Tripod	P	RF	Rudolph	Momentum	-26	460	-0.56	-0.35		105	103	102
Burket-Falls	Finishline	P	RF	Fred	Polled Plus	-27	-899	0.28	-0.04		107	107	97
Richter	Polar	P	Red	Polled Plus	Roels	-30	-624	-0.16	-0.06		107	107	101
Hickorymea	Overjoy	P	RF	Shandy	Bellwood	-31	635	-0.26	-0.21		101	100	
Dansire	Tucker	P		Tucker	Basar	-36	1075	-0.39	-0.24		102	97	
Weinberg	Pollent	Pp		Lentini	Polled Plus	-43	920	-0.69	-0.3	177	104	98	104
Hickorymea	Tucker	P	RF	Bellwood	Commotion	-46	1105	-0.63	-0.32		99	103	98
Hickorymea	Towaco	P	RF	Cliffhanger	Commotion	-56	110	0.06	-0.23		104	99	100

3.3. Breeding values

The breeding values for the Dutch-Flemish overall index (NVI) of 39 bulls available for AI in the Netherlands vary from -56 to +114. The NVI combines production traits with other traits such as fertility, survival and mastitis resistance. Compared with the top 100 of all bulls available the breeding values of polled bulls are clearly lower (table 4). The NVI of the top 100 varies from 161 to 309 and averages 185. Top 100 bulls rank also higher for milk, protein, fat and longevity, the difference is smaller for somatic cell count and leg conformation. Fertility is comparable for polled bulls and the top 100. In conclusion it is clear that polled cattle clearly lag behind in breeding values and breeding programs need to address this issue.

Table 4   Comparison of average breeding value for for Top-100 Holstein Friesian bulls and polled Holstein Friesian bulls (see table 3, april 2008)

	Top 100 horned bulls			Polled bulls		
	Average	min.	max.	average	min.	max.
NVI*	185	161	309	11	-56	114
Milk	880	560	2620	350	-1300	+1500
Fat (%)	-0.08	-0.59	0.86	-0.20	-0.69	0.28
Protein (%)	0.03	-0.25	0.31	-0.13	-0.35	0.12
Prod. Index	103	-38	201	-28	-114	57
Longevity	447	86	780	176	11	398
Cel count	103	90	112	102	95	108
Fertility	99	90	108	101	93	107
Leg conformation	106	97	112	100	94	103

*NVI = Dutch – Flemish overall index combining production, longevity, fertility, somatic cell count and conformation

4. Presence in the French Charolais

The value of Polled animals was recognized already in the 60's in the French Charolais breed and several breeders initiated some independent efforts in order to increase the frequency of Polled animals in their herd. One of them, Mr. Jumentier, succeed in having around 45-50 % of Polled animals in his herd at the end of the 80's. However, as the breeding strategy was not optimized, Polled animals were produced almost exclusively by inbreeding and the genetic value of the animals for future breeding programs was hopelessly low. Furthermore, the presence of scurs was compromising the production of true Polled cattle. A similar situation is also found in the Limousin breed.

At the beginning of the 90's, as the interest in Polled cattle was growing, a breeding organisation (France Charolais Optimal, today Genes Diffusion Optimal, www.genesdiffusion.com) initiated an introgression program based on 6 heifers from the above-cited herd (Mr Jumentier). For this purpose, sires of high genetic value were mated to Polled and Scurred Charolais cows in the first generation. In the next generation, heterozygote animals were crossbred to maximize the generation of Polled males that could tehn be progeny tested and become bulls of high genetic values (especially for carcass and maternal traits) for future artificial insemination. In order to maximize the success of the project, all the animals in the program are genotyped with genetic markers (microsatellites first and then SNP) to assist the selection of future animals and detect the presence of the Polled allele, leading to a rapid detection of potentially homozygous animals. However, according to recent observations (Capitan *et al.*, 2009), the frequency of the Scurs allele reaches 69.9% in the French Charolais.

Despite the high frequency of the Scurs allele that is negatively impacting the introgression program now running over 6 generations, several bulls of high genetic values are now commercialized (Table 1).

Table 5. List of progeny tested Polled bulls in the French Charolais breed and their breeding values

Name	Sire	Mat.GF	Results at weaning on farm					Beef capacity on station				Beef capacity on farm		
			IFNAIS	CR	DM	DS	ISEVR	PCAR	CONF	RDT	IAB	ICRC	CONF	IAB
VIZIR SC	LE REBEL	HARNOIS	107	106	106	98	113	117	131	128	123	.	.	.
VIRGIL SC	LE REBEL	HELSINKI	110	104	111	99	115	106	118	122	111	.	.	.
UNO SC	SAKATA SC	TITAN	104	96	117	95	107	.	.	.	.	.	.	.
UNICO SC	ROOSVELT SC	HELSINKI	109	90	99	96	94	99	106	115	101	.	.	.
UFANO SC	ROOSVELT SC	HELSINKI	106	100	93	98	98	.	.	.	.	.	.	.
THUIR SC	PALADIN SC	MARTIEN SC	101	93	101	80	92	84	112	107	90	81	108	87
PALADIN SC	MARENGO sc	CAMUS	104	91	97	97	91	95	109	123	98	83	99	84

IFNAIS = calving ease, CR = Growth capacity, DM = muscle growth, ISERV = global weanibg, PCAR = carcass weight, CONF = carcass conformation, IAB = beef capacity

4.1. Other beef breeds in France

Since the late 90's, there is a growing interest in breeding Polled animals in French beef breeds, especially as it is also a very good argument for exporting animals. An introgression breeding programme has been initiated in the Limousin breed few years ago by importing semen from American Polled Limousin bulls and a study has been conducted in the Blonde d'Aquitaine. Unfortunately, no Polled animal has been identified in the Blonde d'Aquitaine and no progeny tested Polled bull is available for the French Limousin. One of the major drawbacks here is the very high frequency of the Scurred allele in the population (even higher than in the Charolais Breed).

5. Presence in Fleckvieh

In the German Fleckvieh breeding for polledness was initiated by the Bavarian Freestate (Landesanstalt für Tierzucht) in 1974 (Grupp 2009). The breeding started with the purchase of polled animals from farmers. Polled animals have been known in Bayern at least since the start of the 1900s. Initially breeding of the polled animals concentrated on suckler herds, at the start of the nineties beef lines and dairy lines were added. Initially breeding values for polled bulls were clearly lower than for horned bulls. After more than 30 years of breeding the gap in production is almost closed for dairy. In a test herd production was about the same for polled and horned animals (table 6).

Table 6 Average production in the Fleckvieh test herd LfL Grub for polled and horned animals in 2006-2008.

Genotype	Number	Milk (kg)	Fat (%)	Protein (%)
Polled (Pp)	48.3	7906	3.94	3.49
Horned (pp)	94.7	8122	3.96	3.19

Presently there are ample bulls available for AI in the Fleckvieh in Bavaria. For the suckler herds six homozygous bulls can be used, while for the dairy and beef herds six heterozygous bulls are available. In the suckler herds new born animals are almost all polled, while in dairy herds about 40% are polled.

Two traits are observed that occur frequently in polled bulls. One is that the eyelid is folded, giving the bulls a sleepy appearance the other is a prolaps of the preputium. Both traits may be caused by the use of a few ancestors (i.e. genetic drift or inbreeding effects)

6. Opportunities for breeding programs

The availability of bulls with the polled gene opens up the possibility for breeding programs. The first thing that needs to be answered is whether breeding has the potential to produce enough polled animals of sufficient quality to offer an alternative for the current horned animals. Two aspects are important: 1) can the current gap in breeding values between polled and horned animals be closed and 2) how long does this take? Traditionally an introgression program is used to introduce a required gene in a (sub)population without the gene. Modern molecular techniques may help in this process. At the same time breeding value estimation can be used to introgress and select for higher genetic merit at the same time. Genomic selection is the latest development where dense marker maps are used to estimate breeding values early in life. Here we investigate with model calculations and computer simulations the potential of breeding programs for polled cattle.

6.1. Classic introgression program

With an introgression program a specific allele of a population (= donor population) id introduces into another population where the allele is absent. This is done in such a way that introduction of large amounts of other genetic material coding for other traits is not introduced into the receiving population as well. Generally the donor population is a low production merit breed with one interesting gene for a high production breed. The situation in regard to the polled gene is similar. In this case the bulls with the polled gene form the donor population.

The classical introgression program can bes een in the figure. It start with crossing animals from the low genetic merit population with the high genetic merit population. Assuming that the low genetic population is homozygote for the required allele and the high genetic merit population is homozygote for the not wanted allele all offspring will be heterozygote. The other genetic material is also for 50% of high genetic origin and for 50% of low genetic origin. By crossing this offspring again with the high genetic merit population and selecting offspring with the required gene, the proportion of DNA originating from the low genetic population will be reduced to 25%. In subsequent generations the proportion will be halved each time, until the reduction is deemed sufficient. Then heterozygous animals have to be crossed to produce homozygous animals for the required gene.
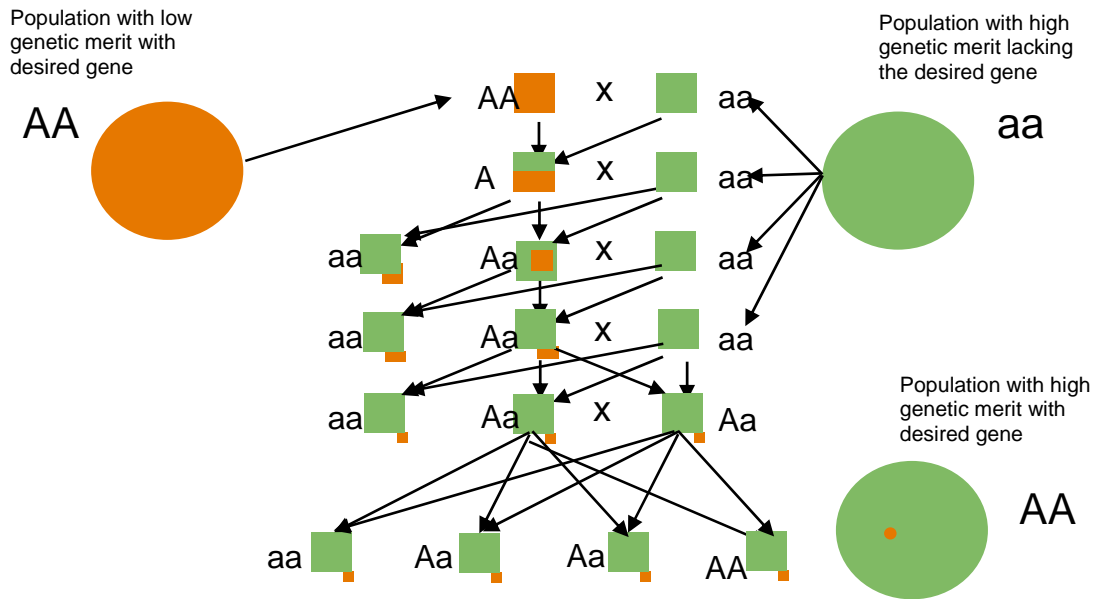
Figure 1. Schematic overview of a classical introgression breeding program

In the Holstein Friesian the first phase of crossing polled bulls with high genetic animals has in fact already been carried out, resulting in the currently available heterozygote polled bulls. We have used model calculations to estimate how many generations of introgression will be needed, and what the loss in genetic merit will be compared to the currently available top bulls.

6.2. Loss of genetic merit in introgression program

The receiving population will lose genetic merit when crossed with animals of the low genetic merit donor population. This is because DNA from the low genetic merit population implies a lower genetic value, but also during the introgression program the increase in genetic merit is largely halted. We used the formulas developed by Wall et al. (2005) to estimate the loss in genetic merit. In these calculations the assumption is that the proportion of DNA from the donor population is linearly related to the difference between the two populations in genetic merit. We used data from table 4 to estimate the total loss. In table 7 the parameters used in the calculation are summed up.

Table 7 Parameters used for the calculation for the expected difference in genetic merit (NVI) after introgression of the polled gene into the top breeding bulls of the Holstein Friesian in the Netherlands.

Parameter	Value	Source
Difference in genetic merit	185 vs. 11	Table 4
Genetic gain per generation	14 = 8%	NRS
# generations	4	
Generation interval	4	
Length total genome	35	
Length carrier chromosome	1.54	
Position on chromosome	0.1	Brenneman et al. 1996

After for generations of backcrossing and one generation of crossing for obtaining homozygote bulls (5x4 = 20 years) the estimated proportion of donor DNA is 6.8%, Taking the genetic gain in the regular population into consideration this would result in a genetic merit (NVI) of 662 points in 20 years without introgression. This would be reduced to 458 points with introgression, the difference being roughly equal to 10 years of selection. Althogh this calculation is quite rough it is safely to conclude that a classical introgression program is long, and will not clese the gap between polled and horned bulls in genetic merit.

6.3. Genomic selection breeding program

To reduce the loss in genetic gain during an introgression program selection on genetic merit can be applied simultaneously. This requires a breeding program of some substance since breeding values need to be estimated. Traditionally breeding value estimation combines the phenotype of relatives into one prediction for the breeding value of an individual (= BLUP-estimation). Generally, a bull needs a number of milk producing bulls before a breeding value can be estimated. With genomic selection breeding values are estimated based on markers. First some generations are needed to estimate the contribution of marker alleles to the genetic value of an individual. In subsequent generation the breeding value can be estimated directly at birth using markers. The biggest advantage is that the long time before breeding values can be estimated with BLUP selection (4-6 years minimum) is not needed anymore.

To explore the potential advantage of genomic selection computer simulations were run. A population was generated with 11,000 markers and 1000 loci coding for a phenotype (following Calus et al. 2007). The heritability of the trait was set to 25%, similar to heritabilities of genetic merit indexes used in cattle breeding. The population was split into two subpopulation. No selection was carried out on population 1, in population 2 BLUP selection was carried out. At this stage the population size was 50 male and 50 female animals. After 10 generations of selection the difference in phenoytype was 150 points on average, roughly equal to the difference between polled and horned bulls in the Dutch genetic merit index (NVI).

In the second stage the population size was 100 males and 900 females. No overlapping generations were simulated. In this stage either BLUP selection or genomic selection was performed. For genomic selection marker effects were estimated once at the start of the second stage, and used in subsequent generations. Each generation 10 bulls were selected as father. The bulls with the highest breeding value were selected in three ways 1) The top 10 bulls based on breeding values without taking the polled gene into account. 2) The one polled bull with the highest breeding value and the other 9 bulls as in 1 3) as 2, but not 1 polled but at

least 5 polled bulls. For BLUP selection 10 replicates were run for genomic selection only 1 replicate due to time constraints.

Results

Within analysed cases breeding values for polled and horned animals converged after 4 generations of selection. The breeding programs with selection for polled animals lagged 10-20% behind the breeding program without selection for polled animals (table 8). Using more polled bulls also resulted in somewhat lower breeding values but the number of polled animals increased more quickly.

Table 8 Breeding value after 4 rounds of selection in non-overlapping generations and number of polled cows in breeding program (out of 500) . BLUP 0 no selection on polled animals, BLUP 1 and GS 1: at least 1 of the 10 selected sires was polled, BLUP 5 and GS 5: at least 5 of the 10 selected sires was polled. BLUP = BLUP selection based on 10 offspring, GS ins genomic selection based on dense marker map. Pp heterozygote polled, PP homozygote polled animals.

	BLUP 0		BLUP 1		BLUP 5		GS 1		GS 5	
Average True breeding value in Generation 4	212		196		172		178		162	
# of polled animals in Generation	Pp	PP	Pp	PP	Pp	PP	Pp	PP	Pp	PP
1	0	0	74	2	283	37	72	0	329	29
2	0	0	78	6	344	37	83	0	329	41
3	0	0	91	3	314	54	98	1	351	58
4	0	0	81	2	371	53	111	2	393	79

Breeding values were lower for genomic selection than for BLUP selection. This was largely due to a single replicate effect. The average breeding value in generation 0 was relatively low for the horned animals in the single genomic selection replicate, 7 out of 10 replicates in BLUP selection were higher. When compared to the lower replicates of BLUP selection GS legged only a few points behind after 4 generations of selection
This will have been mainly due to not reestimating the marker effects every generation. Overall the conclusion has to be that GS gives results similar to BLUP estimation with 10 daughters or slightly lower. The real gain is in the generation interval. Here no overlapping generations were simulated and BLUP values were assumed known at the time of birth. In reality these will take 4-6 years to be realized. GS thus seems a promising method to use for breeding polled cattle.
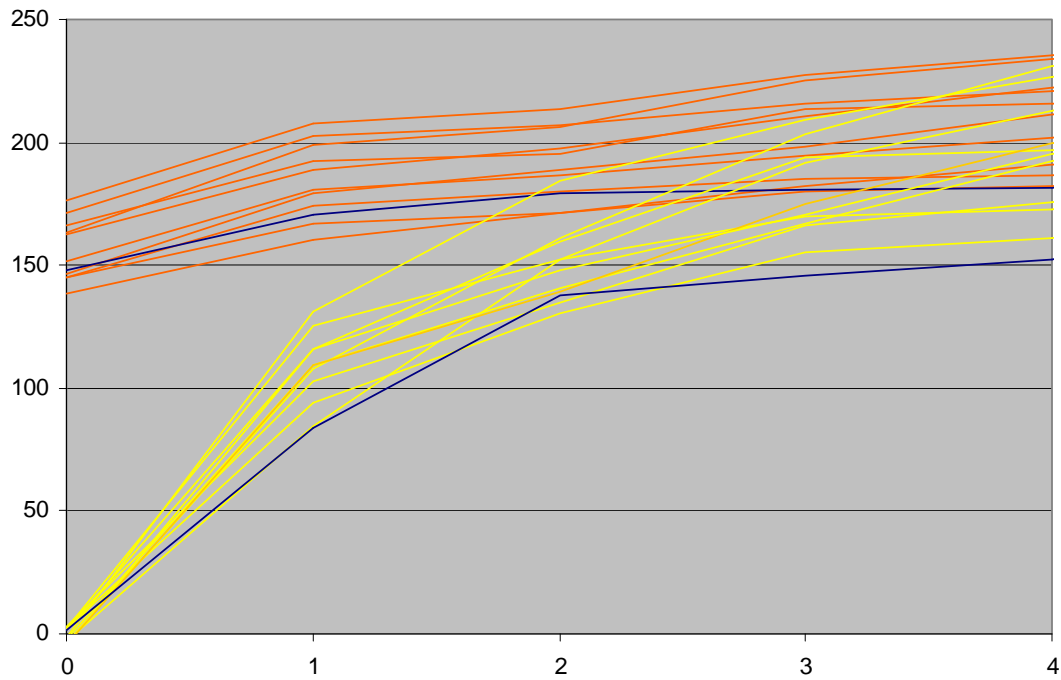
Figure 2   Breeding value for BLUP selection base don 10 daughters or on Genomic Selection (dark blue lines). Orange: horned bulls, yellow: heterozygote polled bulls. For BLUP 10 replicates were run, for GS only 1.

7. Attitude of farmers and breeding companies

7.1. Farmers

The attitude of farmers to breeding polled cattle is generally neutral to positive. Only some farmers in organic farming (bio-dynamic section) do not accept polled animals as an alternative. In a survey with Dutch farmers on priorities for breeding polledness was not highly ranked as a trait to breed for. Since dehorning was commonly accepted, the need to breed polled animals was not widely felt. Since presently polled bulls have low breeding values and choice between polled bulls is limited most farmers are not interested in polled bulls. However, if a wide variety of polled bulls of high genetic merit would be available farmers would prefer these bulls. Concequently whether farmers will start using polled animals depends on whether the breeding companies succeed in producing high genetic merit polled bulls,. The example of the Fleckvieh in Bavaria shows that if this is the case the switch to polled animals may take place quickly.

7.2. Breeding companies

Currently there are a few small breeding companies that specialize in polled cattle. In the Holstein breed present day polled bulls originate from the Hickorymea breeding company in the USA or descend from bulls of this company. In Europe the Göpel breeding company specializes in polled bulls. For Fleckvieh the Grub company together with the Institut fur Tierzucht of Bayern have a breeding program for polled bulls that started in 1974. In France efforts are undertaken in the Charolais and Limousin breed, while some polled animals are present and used for breeding in the Holstein and the "Rouge des Plaines" breeds. The large breeding companies such as CRV (The Netherlands) and Alta (Canada) are now considering to start a breeding program for polled bulls. Monsanto sequenced the polled region and filed a patent for the discovered SNPs, but what their further plans are is not known.

7.3. Future of polled cattle

How the use and breeding of polled cattle will develop is hard to predict. The policy in several countries is directed at limiting dehorning. Using polled cattle may be an interesting option. In the Netherlands research on the acceptability of breeding polled cattle (Windig et al. 2008) showed that this may be an acceptable alternative if polled cattle is seen as a natural phenomenon and if the distinction between classical breeding and genetic modification is clear. One can expect that if the large breeding companies invest and put a substantial effort in breeding programs for polled cattle that in about 10 years time sufficient polled bulls with high genetic merit may be available. In that case the cattle population may change quickly to more than 90% polled animals. The plans of Monsanto are not known, but this company has produced numerous varieties of plants with genetic modification. Production of high production polled bulls with genetic modification is for the Dutch general public (and probably in more European countries) not acceptable, but in America the situation may be different.

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