Genetic Potential of Icelandic Dairy Cattle

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ABSTRACT

The aim of the study was to measure the genetic progress in the Icelandic dairy cattle population since the current breeding program started in 1974. The goal was also to estimate the maximum genetic progress to be expected in the future. The data used were the results of the genetic evaluation from July 2010 which included 356,000 animals and all traits. The results showed that the annual genetic progress in dairy traits has been accelerating in recent decades and is now 10% of genetic SD (σ_G) per year for protein production. This is considerably less than the annual pro-gress of 16% of σ_G calculated from the component pathways showing what is theoretically possible with the current Artificial Insemination breeding scheme. The most likely explanations for less progress are extensive use of natural service bulls, that are clearly inferior to the AI stock, and the fact that the breeding goal today includes many traits besides milk production. Hence there is considerable genetic progress in all the traits involved.

Keywords: Generation interval, genetic evaluation, genetic progress, selection differential

YFIRLIT

Mögulegar erfðaframfarir hjá Íslenskum mjólkurkúm

Markmið rannsóknarinnar var að meta erfðaframfarir í íslenska kúastofninum síðustu áratugi eða frá þeim tíma er núverandi kynbótaskipulagi var komið á laggirnar árið 1974. Einnig að leggja mat á mögulegar hámarkserfðaframfarir í stofninum. Til grundvallar lágu niðurstöður útreikninga á kynbótamati allra gripa og eiginleika sumarið 2010, samtals 356 þúsund einstaklingar. Niðurstöður sýndu að hraði árlegra erfðaframfara í mjólkureiginleikum hefur farið vaxandi síðustu áratugi og er nú 10% af erfðafráviki (σ_G) á ári fyrir magn próteins. Þetta er nokkru minna en þær framfarir sem vænta mætti ef möguleikar núverandi kynbótaskipulags væru nýttir til hins ýtrasta en þá væru árlegar erfðaframfarir um 16% af σ_G. Líklegustu skýringarnar fyrir minni framförum eru tiltölulega mikil notkun á heimanautum sem greinilega eru af minni gæðum en sæð-inganautin og að nú er tekið tillit til margra annarra þátta en mjólkurframleiðslu í ræktunarstarfinu. Enda kemur í ljós að erfðaframfarir eru greinilegar í öllum eiginleikum.

INTRODUCTION

Nearly 50% of the gross income of Icelandic farmers comes from the cattle sector where milk production is of overwhelming import-ance. There are more than 26,000 dairy cows and over 600 farms producing milk. Both numbers have decreased sharply in recent years (Anonymous 2010).

The Icelandic cattle breed originates mostly from Norway and was brought by the original

settlers to the island in the ninth century (Adalsteinsson 1981). There are no signs of importation of other breeds since that time. The breed is in that sense genetically, historically and culturally unique (Kantanen et al. 2000).

Selection for breed characteristics like colors has apparently not been practiced and the breed shows more variation in that sense than most other breeds. In size the breed is rather small and the mature cow weighs 450-500 kg. The breed has solely been selected for milk production so that beef traits are rather variable.

The first step in organizing breeding work with cattle in Iceland was the starting of milk recording by the Farmers Association in 1903, taking the Danish recording system as a model. Use of Artificial Insemination (AI) started in 1946 when the first bull station was established. The application area of the bull station was however rather limited during the first years as only fresh semen was used (Torfason and Jonmundsson 2001).

The use of deep frozen semen started in 1970 and in 1974 the breeding plan for the population as one breeding unit was launched (Jonsson and Jonmundsson 1974). This plan was a small scale copy of the breeding plans already in use in the Scandinavian countries (Lindé 1968, Petersen et al. 1973, Skjervold and Langholz 1964). At the same time, calculation of selection indexes for bulls and cows started, based on contemporary comparison of yearly milk records corrected for effects of systematic environmental factors. Initially the selection was mainly on milk yield, but soon milking ease, udder and teat morphology as well as temperament were added. There were no definite weights for individual traits. The main attention was on yearly milk yield and other traits were seen as extra information to aid in selection between similar choices. Measurement of the protein content of the milk started in 1982, when the selection emphasis shifted from milk volume to protein yield.

Table 1. Weighting factors used for the official breeding goal ([a]TMI)

	1974	1993	1999	2003	2005
Protein Yield		65	60	55	44
Milking ease		10	10	9	8
Somatic cell count		5	10	8	8
Udder		4	8	8	8
Longevity		-	-	8	8
Fertility		4	4	4	8
Teats		4	4	4	8
Temperament		4	4	4	8
Quality rank		4	-	-	-
Yearly milk yield	100	-	-	-	-

[a]TMI = Total Merit Index

In 1993 the production trait definition was changed to a 305-day lactation yield with emphasis on protein production in the first three lactations. Because of the negative genetic correlation between protein yield and protein content (Sigurdsson 1993) both traits have been included with just enough weight on protein content to keep it stable (85:15). In later years the weight on production has been dropping and is currently only 44% as other traits have received more attention.

At the same time (1993) methodology for breeding value estimation was changed to the BLUP animal model and economic values were given to individual traits in the breeding goal in order to form a Total Merit Index (TMI). Table 1 shows how the weights in the breeding goal have changed since that time.

The main aim of this study was to investigate the genetic progress in milk production and functional traits in the Icelandic dairy cattle breed during the decades of systematic breeding. Secondly, the aim was to study the genetic potential of the breed and thus shed light on its future as a milk producing animal.

MATERIALS AND METHODS
Data used in this study were obtained from the main database of the cattle breeding industry

in Iceland (*www.huppa.is*). These data provided the information used for routine genetic evaluation of all traits and animals and consisted of all the data collected until July 2010 with pedigree information on approx. 356,000 animals. The main bulk of the data started with cows born after 1970, as the computerized national recording scheme did not begin until 1974. However, all known pedigree information was included in the database starting with the oldest animals born in 1910.

Production traits

Milk production records dating back to 1982 were used for genetic evaluations. Records from earlier years exist but can not be transformed to 305-day yields and were therefore not utilized. Information on 305-day milk, fat and protein yield, length of lactation, calving interval and cow survival is record-ed. Necessary information on calving dat-es and herd identifi-cation is also includ-ed. Information on the first three lactations is included. Records of second and third lactations are included if records on previous lactation exists in ord-er to account for selection. In the genetic ev-aluation procedure the records on production traits were corrected for herd-year-period (HYP), calving month (CM), age at calving in months (CA) and int-erval between calving (CI). The HYP was assigned in a flexible way, where the rule is to use months as the basic unit, but the period was lengthened until there were at least 2 cows per contemporary group.

Non-production traits

Breeding values are also routinely calculated for several traits other than milk production. These include somatic cell count, temperament, milking ease, feet and leg traits, udder- and teat traits, and several other conformation traits. The traits that were included in the routine genetic evaluations are listed in tables 2 and 3 together with specific information for each of them. For simplification only first lactation statistics and parameters are listed, but second and third lactation records were included in the evaluations.

The same environmental effects were defined for fertility as for the milk production traits. The only difference was that CI became the trait instead of being a fixed effect and CI for the first three lactations was considered. For somatic cell count (SCC) HYP, CM and CA were included as fixed effects. SCC was transformed to somatic cell scores (SCS) where $SCS = \log_2(SCC/100.000) + 3$. Individual SCC test-day records were corrected for days from calving and month of calving before they were included in the calculation of the geometric mean for each of the first three lactations (Sigurdsson 1997). For udder and teats, temperament and other conformation traits HYP, CA and number of lactation (first or second) were included as fixed effects. For milking ease only the mean was included as a fixed effect. Longevity is now part of the breeding goal (Benjaminsson 2002) but as this trait has only been included for a few years it was not included in this study.

Table 2. Statistics and genetic parameters for first lactation production traits included in the study

Trait	Mean[a]	SD	Min[b]	max	[c]ΔP^1	ΔP_2	ΔP_3	h^2	σ_G
Milk kg	4986	1413	802	15703	31	93	108	0.24	386
Fat kg	206	63	26	615	1.2	3.6	4.0	0.20	16
Protein kg	169	48	23	532	0.5	3.0	4.3	0.20	12
Fat %	4.13	0.42	1.88	7.37	-0.002	-0.003	-0.008	0.15	0.14
Protein %	3.38	0.16	2.52	5.71	-0.016	-0.002	0.014	0.32	0.09

[a] Mean and SD is given for all cows born in 2005

[b] Min and max are given for the whole data set of 115136 1st lactation records

[c] ΔP_{123}= Phenotypic change per year, birth year groups 1980-1989; 1990-1999; 2000-2007

Genetic parameters
Genetic parameters used for the routine genetic evaluation were in all cases estimated using REML methodology. Parameters for production traits were initially estimated in studies by Sigurdsson (1993). Genetic parameters for many conformation traits were investigated by

$$\Delta G = \frac{I_{SB} + I_{DB} + I_{SC} + I_{DC}}{L_{SB} + L_{DB} + L_{SC} + L_{DC}} \sigma_G$$

where I is the standardized selection differential and is the product of selection intensity (i) and accuracy (r_{TI}); L is the generation interval in years, i.e. the mean age of parents when the offspring is born; and σ_G is the genetic standard deviation for the trait being considered. The subscripts refer to the four pathways of selection: Artificial Insemination (AI) sires of AI bull (SB), dams of AI bulls (DB), AI sires of cows (SC), and dams of cows (DC).

For each selection path, realized selection differentials were

Table 3. Statistics, definitions and genetic parameters for functional traits included in the study

Trait	Records	Sub[a]	Description	h^2
Fertility	115136	3	Calving Interval (days)	0.04-0.06
Somatic cell count	64251	3	Somatic cell score[b]	0.09-0.14
Conformation	109547			
- Trunk		9	Linear scoring	0.10-0.28
- Legs		4	Linear scoring	0.14-0.29
- Udder		4	Linear scoring	0.12-0.20
- Teats		4	Linear scoring	0.10-0.18
Temperament	109547	2	Linear scoring	0.06
Milking ease	109547	3	Linear scoring, ranks	0.20-0.31

[a]Sub= Number of sub-traits evaluated within the category
[b]Somatic cell score (SCS)=$\log_2$(SCC/100000)+3

Sigurdsson (1995) and for somatic cell count by Sigurdsson (1997) but estimates for other traits have not been published officially before. Estimates for all traits together with some data statistics are listed in tables 2 and 3. These values represent the parameters that are being used in the routine evaluations.

Calculation procedures
The basic methodology used for the computations and solving of the mixed model equations is all well documented in Sigurdsson and Arnason (1995). A multitrait animal model with genetic groups for unknown parents was used throughout all genetic evaluations.

Realized genetic progress was studied by averaging the estimated breeding values (EBV) within year of birth and regressing these values on year of birth, giving the annual genetic change (ΔG). Genetic progress was studied in more detail by separating it into portions attributable to four pathways of selection as described by Rendel and Robertsson (1950):

estimated for each year birth group by the following method: Average EBV of the parents of each year of birth group of progeny minus the average EBV of all cows born one generation interval earlier. The contribution of Natural Service bulls (NS bulls) was calculated separately following the same method as described above for AI bulls. In addition, rate of inbreeding was assessed using procedures published in Sigurdsson and Jonmundsson (1995).

RESULTS AND DISCUSSION
Values for realized genetic change are listed for all traits included in the breeding goal in table 4. For the production traits the trend is reported in actual units, whereas for other traits the change is given in index units where 10 units equal the genetic standard deviation. The trend for all production traits followed the same pattern and the progress was found to have accelerated over the whole period, giving annual increases of 33, 1.4 and 1.2 kg of milk,

fat and protein respectively in the period after 2000. This is equal to 0.09 - 0.10 σ_G per year.

Kristofersson and Jonmundsson (2006) studied the economic return in milk production based on data from Icelandic farm accounts. They concluded that there is a clear effect of the genetic merit of the cows in the herd on economic return, and this effect is closely correlated to the production index.

For fat and protein content the trend was negative in the period before 1990 but since then protein content has been increasing and can be considered to be stable now. Genetic changes in other traits were none or slightly negative in the period 1970-1990, whereas since then a significant positive trend can be confirmed. The genetic progress in udder and teats has been quite extensive and in SCS as well. A slight negative trend in fertility was revealed for the period 1990-1999 but it is much less than has been shown in many of the Holstein populations around the world (Van Raden 2006). This indicates that the relationship between production and fertility traits has not been as unfavourable in the Icelandic breed as in Holsteins. The weights on fertility and somatic cell score are thought to hinder a negative effect of selection for increased production because of the generally known unfavourable genetic correlation between the traits (Van Raden 2006, Boettcher et al. 1997). However, this has not yet been confirmed for the Icelandic cattle population and remains to be analysed, though assuming a similar pattern seems to give the expected response. The genetic trend in TMI is 0.7 units per year at present and can be compared to the 1.1 units per year for the protein production index. The genetic change for first lactation protein yield is

Table 4. Realized genetic progress per year

	Decade of birth			
	70-79	80-89	90-99	00-09
Production traits[a]				
-Milk yield kg	5	15	28	33
-Fat yield kg	0.1	0.5	1.1	1.4
-Protein yield kg	0.1	0.4	0.9	1.2
-Fat content	-0.002	-0.001	-0.004	0.003
-Protein content	-0.001	-0.002	0.001	0.003
Indices[b]				
-Fertility	0.0	0.0	-0.5	0.1
-Somatic cell score	0.1	0.0	0.1	0.5
-Trunk and legs	0.1	0.0	0.0	-0.1
-Udder	0.0	0.0	0.2	0.7
-Teats	0.1	0.0	0.1	0.8
-Temperament	-0.1	0.0	0.0	0.2
-Milking ease	0.0	0.0	0.1	0.4
-Protein production[c]	0.1	0.4	0.9	1.1
-TMI[d]	0.1	0.1	0.4	0.7

[a]Genetic progress for production traits is listed in actual units (kg or %) and only for first lactation; genetic progress very similar for second and third lactations.

[b]Genetic progress for indices is listed in standardized units where 100 is the average BV of cows born in 2000 and 10 points equal 1 genetic SD

[c]Production index = 0.85*(0,5*Pkg1+0.3*Pkg2+0.2*Pkg3) +0.15(0.5*P%1+0.3*P%2+0.2*P%3); where Pkg1 means first lactation protein yield in kg, Pkg2 means second lactation protein yield in kg, P%1 means protein percentage in first lactation, etc.

[d]TMI=Total Merit Index constructed according to the weighting factors listed in the last column of table 1
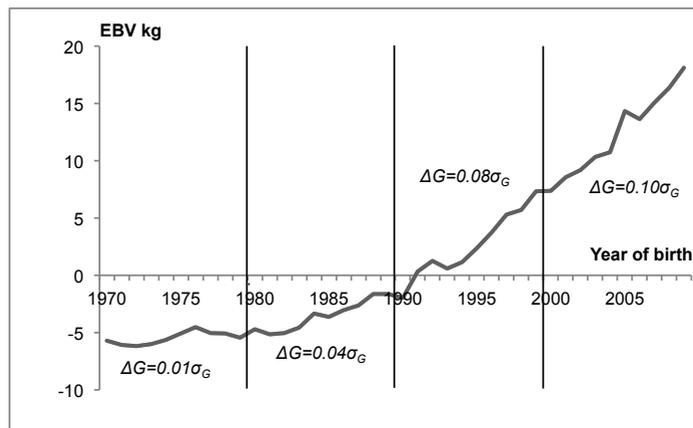
Figure 1. Genetic progress in first lactation protein yield.

plotted in figure 1. The change in protein production from 1970 to 2009 was approximately 24 kg of protein. The corresponding figures for fat and milk production were 28 kg and 727 kg respectively.

The results from the study on the importance of different selection pathways are listed in table 5. The expected values according to the initial AI breeding scheme (Jonsson and Jonmundsson, 1974) are also given for comparison. The expected genetic gain in protein yield was 0.15 per year and the realized genetic gain in the first decade of the 21st century was close to that value or 0.16 σ_G. In the 1990s it was 0.05 σ_G and 0.13 σ_G in the period 1990-99. The most important path in terms of selection intensity is the SB pathway but if corresponding generation intervals are taken into account then it is presently the DB pathway.

The realized total selection intensity was very close to the expected value but the sum of the realized generation intervals was a little less than expected. It was mainly the generation intervals for cows that were shorter than expected and this has been happening gradually throughout the period investigated. The generation interval length in the DB path has dropped for two years during the period and the DC is now one year shorter than at the beginning of the period. The main reason for this shortening of generation length on the dam side can be traced to the early 1990s when the length of productive life of dairy cows dropped considerably due to the introduction of somatic cell count restrictions in payment for milk. The change in generation length in the DB pathway occurred mainly because of the current practice of selecting sons of top first calf heifers, something that was not done in earlier years. Selection intensity was very low in the pathway DC, meaning that more or less all cows were used to breed cows for replacements. This is especially clear for the most recent years as the population has been growing in numbers and demand for heifers has been high (Anonymous, 2010).

In small populations like the Icelandic one, the selection intensity will always be limited on the sire side. Selection intensity in the SB pathway is limited because of restrictions that have to be made to inbreeding accumulation and on the SC side the relatively high usage of young bulls for progeny testing will influence the selection possibility.

Comparing the realized values from the pathway study listed in table 5 to the genetic trend estimated by regressing average breeding values of each year birth group on year of birth plotted in figure 1 shows that the progress was in fact less than expected in the current AI scheme. There might be several reasons

Table 5. Expected and realized genetic progress based on current AI scheme

		SB	DB	SC	DC	Total	ΔG[d]
				Pathway[c]			
Expected[a]							
- proportion selected	%	10	4	30	80		
- selection intensity	i	1.76	2.15	1.14	0.35		
- accuracy	r_{TI}	0.90	0.50	0.88	0.40		
- selection differential	I	1.58	1.08	1.00	0.14	3.80	
- generation length	L	7.0	5.0	7.0	6.0	25.00	
							0.15
Realized[b]							
1980-1989	I	0.67	0.25	0.33	0.06	1.31	
	L	8.2	7.6	5.9	5.3	26.94	
							0.05
1990-1999	I	1.19	1.13	0.80	0.11	3.23	
	L	8.2	6.5	5.8	4.8	25.17	
							0.13
2000-2009	I	1.44	1.27	1.02	0.04	3.77	
	L	7.9	5.6	6.0	4.3	23.81	
							0.16

[a] According to breeding plan for the Icelandic dairy cattle
[b] Based on National Genetic Evaluation for first lactation protein yield in July 2010
[c] SB=Sire of bull; DB=Dam of bull; SC=Sire of cow; DC=Dam of cow
[d] ΔG = Genetic trend as proportion of genetic standard deviation

Table 6. Contribution of Natural service bulls to realized[a] genetic progress

| | | Pathway[b] | | | | | | | | [e]ΔG | |
| | | SB | | DB | | SC | | Total | | | |
		NS[c]	All[d]	NS	All	NS	All	NS	All	**NS**	**All**
1980-1989	I	0.43	0.51	0.18	0.19	0.05	0.31	0.71	1.06		
	L	6.9	7.4	6.1	6.6	2.6	5.8	20.93	25.05		
										0.03	**0.04**
1990-1999	I	0.81	0.88	0.30	0.43	0.24	0.75	1.46	2.17		
	L	6.5	6.8	5.6	5.7	3.1	5.5	19.88	22.77		
										0.07	**0.10**
2000-2009	I	1.12	1.18	0.28	0.38	0.19	0.81	1.62	2.41		
	L	6.6	6.7	5.2	5.3	2.6	5.3	18.76	21.65		
										0.09	**0.11**

[a]Based on National Genetic Evaluation for protein yield in July 2010
[b]SB=Sire of bull; DB=Dam of bull; SC=Sire of cow
[c]NS=Natural service bulls
[d]All bulls, i.e. AI and NS bulls
[e]ΔG = Genetic trend as proportion of genetic standard deviation

for this difference but the most likely ones are growing emphases on traits other than milk production, extensive use of inferior NS bulls, and accumulation of inbreeding. The first reason is clearly valid, as seen by looking at the changes in the weighting factors as shown in table 1. However, the main emphasis has for a long time been on dairy production traits and the effect of drop in weight from 65% down to 44% is yet to be seen in the years to come.

Table 6 shows clearly that the rather heavy use of NS bulls was probably the main reason that realized genetic progress was lower than could be expected. Figures are given for the pathways SB, SC and DB based firstly on NS bulls only and secondly on all bulls, both AI and NS. The selection differential was lower in all cases compared to the AI bulls in table 5. The generation intervals, on the other hand, were shorter, especially for the paths SC and SB, as there were no proven bulls involved given that the NS bulls were mainly young bulls that had been used for only a few years. The main difference was clearly in the path DB where the selection differential dropped considerably. In the period after the year 2000

the DB selection differential for NS bulls was 0.28 compared to 1.27 when looking at AI bulls only. The same trend can be seen regarding ΔG in tables 5 and 6 where genetic progress is shown to have been accelerating every decade. The genetic trend based on all bulls is estimated to be $0.11\sigma_G$ per year. As expected, this result is very close to the genetic progress estimated by regressing average breeding values within each birth year group on year of birth plotted in figure 1. It should be pointed out that NS bulls were inconsistently recorded in the earlier years but more reliably later on and, according to the pedigree files, around 25% of the replacement heifers are sired by NS bulls at present.

Kristofersson and Jonmundsson (2006) found a clear negative effect of the use of NS bulls on the economic return from milk production in Iceland.

A third reason for less progress than expected might be increased inbreeding. The development in inbreeding is shown on figure 2. Three lines are plotted, the lowest one showing mean inbreeding within year of birth group based on all animals; the middle line only
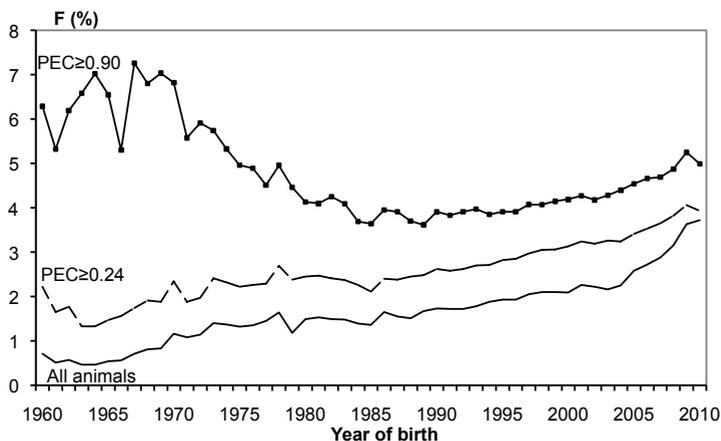
Figure 2. Average inbreeding within year of birth and different levels of pedigree completeness (PEC).

includes animals with at least both parents and one additional ancestor recorded; and the top line gives results based on animals with very dense pedigrees, i.e. at least 5 generations known. To draw conclusions about the level of inbreeding one should use the results based on the most dense pedigree tables, showing that average inbreeding is presently around 5%. The fluctuations in the early years were because of general lack of pedigree information resulting in the large effect on the mean of involving only a few animals. The trend is similar for all the lines showing that inbreeding has been accumulating at a pace of about 0.07 % per year for the last two decades. This means that it will take roughly 15 years to raise the inbreeding level by 1%. In a study by Sigurdsson and Jonmundsson (1995) inbreeding depression in Icelandic dairy cattle was estimated to be in the range of 11-18 kg of milk or 0.3-0.5 kg of protein per 1% increase in inbreeding in the first three lactations. According to these findings inbreeding depression will slow down genetic progress by 0.03-0.04 σ_G per 15 years, which is much less than the effect of extensive use of inferior NS bulls. The increase in inbreeding does not seem to be alarming compared to the results shown by Philipson et al. (2009) for many of the largest dairy cattle populations in the world and despite the fact that outcrossing bet-

ween populations in different countries is a common practice.

A genetic change of 20% of σ_G per year, for dairy production traits, is generally accepted as the optimum for a wellexecuted selection program in a large dairy cattle population (e.g. Schaeffer 2006). In small populations this optimum can hardly be reached for reasons that include fast inbreeding accumulation and less accurately estimated breeding values. More rapid genetic change in classical AI schemes is attributed to extensive international selection of genetic material like the genetic lift that was experienced in the Italic population of Holstein Friesian dairy cattle (Burnside et al. 1992).

FUTURE OUTLOOK
One of the burning questions in Icelandic dairy cattle breeding is whether we should continue to breed this closed population or start importing foreign breeding material. There is no clear comparison of the Icelandic cattle with other dairy breeds. Only one direct comparison has been made. It was in the Faroe Islands where the Icelandic cow was compared to Norwegian red cattle (NRF). The NRF breed showed superiority for most of the traits studied (Rikhardsson & Jonmundsson 1996). Kristofersson et al. (2007), using model calculations, found that by using other breeds (NRF, Swedish red and white, Swedish black and white, New Zeeland Friesian) to produce milk in Iceland, a considerable gain in net economic return could be expected. Even though there are limited comparisons there is hardly any doubt that more progress can be made in milk producing traits by simply moving towards internationalization of Icelandic dairy cattle breeding. That would of course mean drastic changes for the future of the native breed and pose some

serious questions about conservation of genetic resources and genetic diversity. However, the competitiveness of the breed might depend on other factors and an interesting question that remains to be answered is whether there is a real marketing value in producing dairy products with such a historic and culturally unique cattle breed. This paper does not answer these questions; it only shows what can be done with the closed population as such.

In the past, selection for economically important traits in animal breeding has been solely based on statistical processing of phenotypic measures of related individuals assuming the infinitesimal model. These methods have proven to give remarkable results with regard to genetic progress. For many years we have been waiting for the availability of data and expansion of knowledge so as to utilize effectively genomic information directly for selection and genetic improvement. Selection based on known individual genes and specific clearly active parts of the genome (QTLs) has been practiced and has given additional progress to traditional methods. Knowledge in genetics is steadily growing and in recent years we have had great progress in technology to scanning the whole genome directly with the help of SNP chips. This is becoming cheaper and faster every year. Recent simulation studies have shown that it is possible to use single nucleotide polymorphisms (SNPs) as a base for genetic evaluation (Meuwissen et al. 2001, Schaeffer L.R. 2006). If this turns out to be the fact we can talk of a revolution of similar magnitude as when AI was first introduced in the 1940s. This is happening very fast and most of the greatest milk producing countries of the world are now changing their plans to rely on "Genome-wide selection" in their breeding programs. All scientific research indicates that this will be the case, resulting in doubling genetic progress, according to Schaeffer (2006).

This view may be a little optimistic and in practice the progress may be a little slower as there seem to be some unsolved problems before this method can be used in small populations like the Icelandic dairy cattle population (Hayes et al. 2009, Goddard et al. 2010). It is, however, most likely that these methods will in due time be applicable for any population of livestock. Although the focus has mainly been on larger populations Schaeffer (2006) has clearly pointed out that these methods can be applicable to populations like the Icelandic dairy cattle by simply moving to routine genotyping of all individuals. Whether this is possible in terms of cost remains to be answered but in the meantime genetic progress in Icelandic dairy cattle will continue at the maximum rate of approximately 16% of genetic standard deviation per year.

CONCLUSIONS

There have been improvements in the Icelandic dairy cattle population. Calculations based on component pathways show that genetic progress has been accelerating and is now equal to the expected maximum of the AI based breeding program in place since 1974. The overall genetic progress in production traits is however less than maximum and extensive use of natural service bulls and increased emphases on non-dairy traits seem to be the main reasons. Genetic progress is confirmed in all traits investigated and inbreeding accumulation does not seem to be alarming.

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