Selection Of German Holstein Cows For Exceptional High Lifetime Performance And Long Productive Life

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Introduction

A serious decrease in longevity since more than 40 years is obvious in many dairy cattle breeds world-wide. Reduced longevity causes considerable costs to the dairy industry. Involuntary culling is mainly due to infertility, mastitis, feet and leg problems in dairy cows. With improved longevity, the age structure of the herd can be altered to more mature cows with higher milk yields and the rate of involuntary culling can be lowered. The possible benefits of increased longevity should outweigh the loss in revenue from shorter generation intervals in breeding cows and the salvage value of cull cows. Longevity is difficult to quantify because of the presence of incomplete records even if lifetime analysis models can handle censored data. A survey of milk recording data has shown that approximately 3-5% of the German Holstein dairy cows had a three-fold longer productive life than an average cow. The objective of our study is to collect detailed information on German Holstein (GH) cows with an exceptional long productive life at moderate to high lifetime performance and then to assess the predictive ability of single nucleotide polymorphisms (SNPs) genotyped on the Illumina bovine 50K Beadchip for longevity and lifetime performance.

Material and methods

Data sampling. Milk recording data were used to identify GH cows with more than eight lactations completed and not reported to have been culled. After confirmation via telephone calls that the cows were still alive the farms were visited to collect data and blood samples from these cows. The sampling strategy aimed at to collect cows with the highest lifetime performance in milk production and/or longest productive life. The cows with exceptional longevity and/or lifetime performance were not so closely related that half-sib groups could not be sampled. Therefore, we sampled two groups of GH cows with differing requirements for longevity and lifetime performance. The first group included 972 cows belonging to 26 paternal half-sib groups with a minimum of at least eight lactations completed and/or more than 90,000 kg milk produced (PH). The second group contained 497 cows with at least twelve lactations completed and/or more than 105,000 kg milk produced (EX). Data from 634 PH cows and 296 EX cows were collected using a questionnaire for farm management, cow management, fertility, disease and veterinary treatments of cows. Disease frequencies and veterinary treatments had to be evaluated by the farmer in comparison to the herd level

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(below, on average, above of all other herd mates). For genotyping, we selected EX cows with the most exceptional records for longevity and lifetime performance and per EX cow one herdmate with average milk production and having two or three lactations completed. In order to avoid stratification of the data by close ancestry, each cow chosen for genotyping had a different sire. Data and sample collection were performed in the years 2007 and 2008.

Genotyping. For genotyping, we employed the Illumina bovine 50K Beadchip. A total of 600 cows were genotyped for about 50,000 SNPs, whereof 50% of the cows belonged to the EX group (cases) and 50% to the herdmates (controls) matched by herd.

Statistical analyses. Genotyping data was analysed for minor allele frequencies (MAF), Hardy-Weinberg equilibrium, linkage disequilibrium, genetic distances within and between cases and controls. QQ-plots, multidimensional scaling and principal component analyses were performed for identification of stratification of data. Genome-wide association analyses were conducted using PLINK, version 1.07, and permutation procedures for all SNPs with a MAF greater than 0.05 to control multiple testing. Genomic breeding values were obtained in randomly selected subsamples and used as training samples to predict longevity and/or lifetime performance.

Results and discussion

The PH group had completed 8.75 lactations on average with a mean lifetime performance of 67,294 kg milk, 2,819 kg fat and 2,263 kg protein. The EX cows had completed 11.63 lactations on average and mean lifetime performances of 98,974 kg milk, 4,117 kg fat and 3,247 kg protein. The relative breeding values for the total merit and milk traits were below the average of the top 10 bulls from the same birth years (table 1). Particularly, relative breeding values for reproduction, functional longevity and somatic cell score were above the average, but did not exceed the relative breeding values of the top 10 bulls.

Table 1: Comparison of animal model relative breeding values (RBV) among PH and EX cows as well as the top 10 bulls from the birth years 1983-1991 for the total merit RBV (RZG) and RBV for functional longevity (RZN) in German Holsteins

Breeding value	PH cows (n=26)	EX cows (n=236)	Top 10-RZG	Top 10-RZN
RZG	92	86	104	92
RZM	87	78	96	71
RZN	105	108	114	127
RZR	109	114	110	122
RZE	93	89	95	85
RZS	106	105	109	112

RZG: Relative breeding value for total merit; RZM: Relative breeding value for milk performance; RZN: Relative breeding value for functional longevity; RZR: Relative breeding value for reproduction; RZE: Relative breeding value for body traits; RZS: Relative breeding value for somatic cell score.

The analysis of the questionnaire clearly revealed that the EX cows had lower frequencies of claw, udder, fertility, metabolic and postpartal diseases than their herdmates. Only a very small proportion from the EX cows were scored as above the level of diseases of all other herd mates. In consequence, the EX cows also needed much less veterinary treatments.
Genotypes of 41,518 SNPs were available for 600 cows. The performance data of these cows by cases and controls is given in table 2. We could identify 22 QTL for lifetime performance and longevity reaching genome-wide significance levels below P<0.01 (table 3). QTL for milk, fat and protein yield in lifetime performance were consistently mapped on the same locations. However, for longevity further separate 6 QTL were found.

Table 2: Performance data of cases and controls genotyped on the bovine 50K Illumina Beadchip

Trait	Controls		Cases	
	Median	95% CI	Median	95% CI
No. of lactations	3	2-8	12	9-14
Lifetime performance				
-Milk yield	28,850	11,279-68,874	114,002	82,200-139,438
-Fat yield	1,207	451-2,909	4,609	3,401-5,919
-Protein yield	964	356-2,372	3,708	2,773-4,667

Training sets were generated by drawing random samples including 50 or 75 % from all 600 cows genotyped with each 50% cases and 50% controls. Using these training sets in more than 100 random replicates, genomic breeding values were developed employing a model with the quantitative additive effect of the animal and the allelic substitution effects for the SNPs weighted according to their variance for the respective phenotypic trait. An optimized SNP set was developed using those SNPs explaining the phenotypes best. So, we could develop a set of about 1500 SNPs that determined the exceptional phenotypes for lifetime performance and longevity with a reliability of more than 50%. In order to demonstrate the relationships between the genomic breeding values and the phenotypes, we plotted the probabilities for an extreme cow against the genomic breeding values in figure 1.

Conclusion

The approach to exploit extreme phenotypes for developing genomic breeding seems to be useful and an alternative to granddaughter designs. This approach should be also useful for disease traits and particularly for traits that can be measured only late in life or at very high costs. With the further development of high density beadchips, the genes and mutations underlying these QTL may be unraveled.

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Table 3: Distribution of genome-wide significant (P<0.01) quantitative trait loci (QTL) for lifetime performance and longevity in GermanHolstein cows

Bovine chromosome	Position of QTL in megabases	Number of genome-wide significant QTL for	
		Lifetime performance and longevity	Longevity
1	118, 126	2	
2	4, 82	2	
3	97	1	
5	114	1	
6	51, 76	1	1
7	85	1	
8	92	1	
9	77	1	1
14	7	1	
15	56		1
16	67		1
19	17	1	
22	58	1	
23	51	1	
25	11		1
X	12, 68	2	

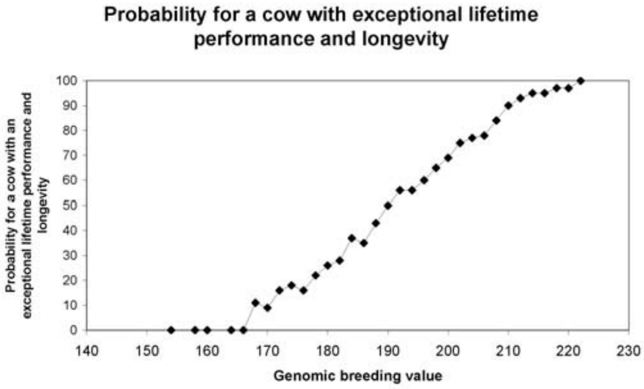

Figure 1: Estimated probability curve based on genomic breeding values for the likelihood of an extreme cow with exceptional longevity and lifetime milk performance (mean: 200, standard deviation 12)