

Comparison of traditional and genomic breeding programs for organic and low input dairy cattle accounting for traits relevant in different macro-climatic zones.

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Introduction

In the past decade, successful selection on production traits for dairy cattle has greatly increased milk production. Recently, selection indices for female fertility were gradually and increasingly introduced into the overall breeding goals for dairy cattle (Miglior et al., 2005). As a by-product of fermentation in ruminants, enteric methane emissions (**ME**) should also be controlled and mitigated due to their contribution to global warming (Forster et al., 2007) and as a cause for inefficient use of dietary energy.

Moderate heritabilities ranging between 0.30 and 0.35 for predicted and real measurements of ME were reported for dairy cows and ewe lambs (de Haas et al., 2011; Pinares-Patiño et al., 2011), indicating that a heritable component for ME is available for implementing sustainable breeding strategies to reduce ME in dairy farms. In dairy cattle production systems, the traditional progeny testing substantially increases accuracy of selection especially for bulls. However, availability of high-density SNP arrays enable dairy cattle breeders to apply genomic selection in their breeding strategies. Consequently, the objective of this study was to compare selection response for a complex breeding goal comprising ME, milk yield (**MY**), days open (**DO**), clinical mastitis (**CM**), body condition score (**BCS**) and milking temperament (**MT**) and total discounted return for organic and low input dairy cattle (with organic Brown Swiss as an example) from progeny testing and genomic breeding program by applying ZPLAN+ (Täubert et al., 2010).

Materials and methods

Traditional progeny testing and genomic breeding programs (Table 1) were implemented separately in ZPLAN+. An organic population size of 25'000 was assumed for Brown Swiss in Switzerland. In the traditional breeding program, test bulls were selected based on phenotypes of their dams and paternal half sib sisters. For proven bulls and elite bulls their daughters' information were included in addition to relatives mentioned above. In genomic breeding programs, proven bulls were just selected based on own genomic information, while mothers', own genomic and paternal half sib sisters' information were available for elite bulls. Genetic and phenotypic correlations among the six traits ME, MY, DO, CM and BCS were calculated based on the data provided by Yin et al. (2014). The correlations between the five traits mentioned above and MT and phenotypic variances for MT were obtained from literature. The genetic and phenotypic correlations among the six traits are presented in Table 2. We assumed traits were not correlated with each other, if the correlations between the traits were not available from literature. Economic values of the traits were calculated based on the assumption that each trait constituted equal economic weight per genetic standard deviation within the overall breeding goal. In a separate run, economic weight was set five times higher

for MY than for the other traits to mimic a more conventional composite breeding goal allocating around half of the economic weight to production traits and half to functional traits, including ME. The assumed investment period for conventional and genomic breeding programs was 30 years. In the genomic breeding program, accuracy of genomic breeding values was varied from 0.2 to 0.8 with an increment of 0.2.

Table 1. Characteristics of traditional progeny testing and genomic breeding program for organic Brwon Swiss applied in ZPLAN+.

	Progeny testing	Genomic selection
Milking cow	25'000	25'000
Bull dam	250	250
Bull calves	125	125
Test bull	50	--
Proven bull	5	10
Elite bull	1	1
Bull sire	80% proven bull	97% proven bull
	20% elite bull	3% elite bull
Cow sire	40% test bull	--
	50% proven bull	67% proven bull
	10% elite bull	33% elite bull

Table 2. Estimated and assumed phenotypic standard deviation (SD), heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations between traits in the calculations. Economic values were calculated based on equal economic weight for the traits.

Trait	ME	MY	DO	CM	BCS	MT	Economic value
Methane emission (ME)	0.44	0.89	0.86	0.03	0.347	x	-6.84
Milk yield (MY)	0.92	0.34	0.93	0.04	-0.4	0 ¹	0.60 / 3.00
Days open (DO)	0.10	0.12	0.03	-0.18	-0.4	-0.028 ²	-0.10
Clinical mastitis (CM)	0.02	0.01	0.02	0.10	-0.26	0.19 ²	-1.66
Body condition score (BCS)	0.25	-0.01	-0.08	-0.01	0.15	x	6.11
Milking temperament (MT)	x	0 ¹	x	-0.67 ²	x	0.04 ³	8.01
Phenotypic SD	0.22	2.88	60.57	1.91	0.42	0.62	

x: not available from literature; ¹Orbán et al. (2011); ²Sewalem et al. (2011); ³Kramer et al. (2013).

Results and discussion

Response to selection and total discounted return for conventional and genomic breeding programs and two alternative relative economic weights for MY are depicted in Figure 1 and 2. Selection responses are reported in terms of genetic standard deviations instead of absolute values of selection responses to facilitate comparisons between scenarios. When equal economic weights for all traits were assumed, total discounted return was almost the same from conventional progeny testing and from the genomic breeding program with accuracy of GEBV of 0.2. Responses to selection in DO, CM, BCS and MT were smaller in the second scenario. A shorter generation interval can be one explanation for higher selection responses and dicounted returns in genomic breeding programs with lower accuracy. Average generation intervals in conventional and genomic breeding programs were 4.97 and 3.17, respectively.

Therefore, with an investment duration of 30 years, 6.04 and 9.46 generations were considered in the two programs respectively. With about 4 more generations for selection, higher gain can be expected in the genomic breeding programs. Total discounted return per animal increased from 4.62 to 7.97 gradually if the accuracy of GEBV increased from 0.2 to 0.8. The increase of accuracy in the genomic breeding program also improved the responses to selection for ME, DO, CM, BCS and MT. However, response to selection in MY was negative and continued to decrease with the increasing accuracy, which probably is due to the fact that ME and MY are highly positively correlated, but selection pressure acts in different directions (increase of MY and decrease of ME).

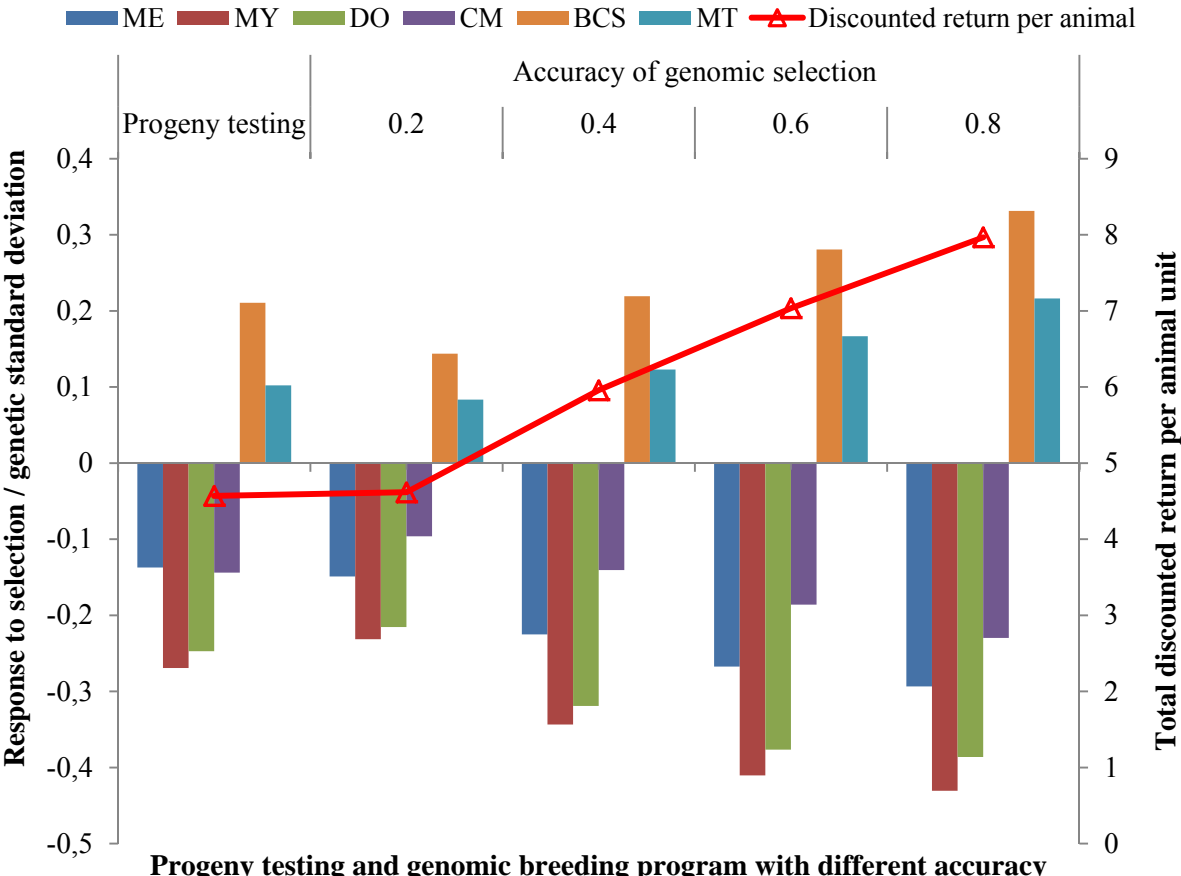
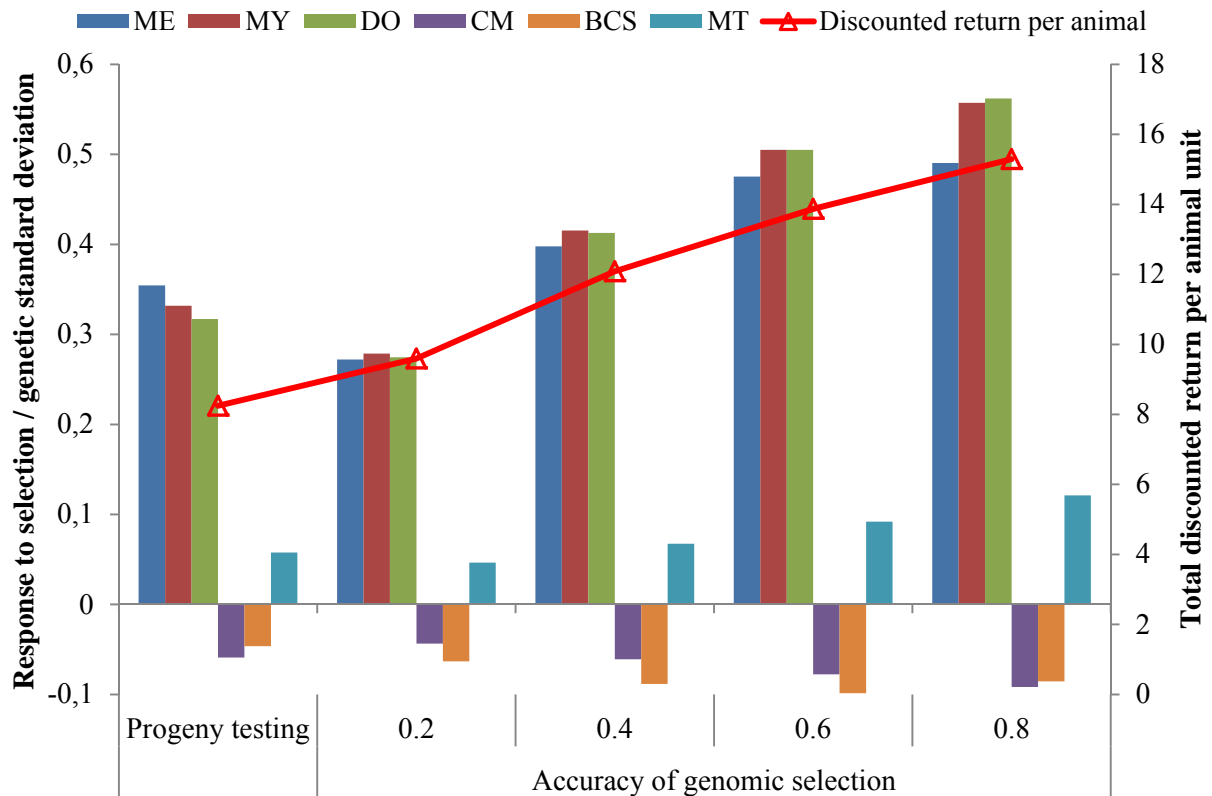


Figure 1. Responses to selection in terms of genetic standard deviations and total discounted return per animal when equal economic weight was assumed for the six traits.

When relative economic weight for MY was 5 times higher than for the other traits, total discounted returns doubled compared to scenarios with equal economic weight. Even with an accuracy of 0.2 for the 6 traits, genomic breeding program achieved higher response to selection (9.60) than conventional progeny testing (8.25). Within the genomic breeding programs, total discounted return increased dramatically from 9.60 to 15.29 when accuracy of GEBV increased from 0.2 to 0.8. Therefore, compared to the conventional breeding program, total discounted return from genomic breeding program increased 68.18%, even when only a moderate to high accuracy (0.6) was applied for all traits. However, responses to selection in ME, DO and BCS ran in the opposite of the desired direction and those responses became worse when the accuracy of GEBV increased. This probably resulted from the antagonistic

genetic correlations of 0.89, 0.93 and -0.4 between MY with ME, DO and BCS.



Progeny testing and genomic breeding program with different accuracy

Figure 2. Responses to selection in terms of genetic standard deviations and total discounted return per animal when economic weight for milk yield was five times higher than for other traits.

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