Swiss Brown Swiss in different environments: Does GxE play an important role?

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Abstract

Estimations of genotype by environment interactions have been carried out for Brown Swiss dairy cattle in Switzerland. Yield traits were considered as different traits in different environments. Genetic correlations were then estimated for the same trait in different environments.

First results from bivariate analyses showed that genotype by environment interactions might exist in the investigated population, especially for fat yield and protein yield. Further analyses are needed to prove genotype by environment interactions in Brown Swiss cattle in Switzerland.

Introduction

Brown Swiss is represented in various environments and production systems in Switzerland: From lowland to the mountain area with alpine summer pasture; from total mixed ration (TMR) to low input pasture based feeding systems and from conventional to organic production systems. Breeders often ask if breeding values for their specific production system are needed. If breeding values changed or bulls were re-ranked in different production systems, significant genotype by environment interaction (GxE) exists. This would imply that specific breeding programs should be designed for different regions or production systems. Therefore, the objective of this study was to investigate whether GxE interactions are relevant in Brown Swiss dairy cattle in Switzerland.

A simplified description of GxE interactions is the inclusion of an interaction term in the traditional quantitative genetic evaluation: P = G + E+ *GxE*, where P is the phenotypic value of an observed trait, G is the genotypic value of this trait, E is the influence of the environment and GxE is the interaction between the foregoing terms. In routine genetic evaluation for dairy cattle GxE interaction is usually not considered.

Materials and methods

Yield data (305-d lactation yields: milk kg (mkg), fat kg (fkg) and protein kg (ekg)) from 262,514 cows of 9,618 farms were used in the analysis. We applied a multiple trait animal model where the yield traits in different environments were treated as different traits. The extent of the genetic correlation (r_g) between the two traits indicates whether GxE interaction exists. For this purpose an animal model with repeated measurements was applied: $y_{iklmn} = \mu + h_i + ys_k + p_{lm} + la_n + a_m + e_{iklmn}$, where y_{iklmn} is the phenotypic observation for mkg, fkg, and ekg, μ is the overall mean, h_i is the random herd effect, ys_k is the fixed effect of year*season, p_{lm} is the random permanent environmental effect, la_n is the fixed effect of the lactation number, a_m is the random genetic effect and e_{iklmn} is the random residual effect. In each of three scenarios (i) milk yield level, ii) udder health, iii) farm altitude) two different environments were defined (Table 1). All scenarios included only farms with a minimum herd size of 10 cows. For scenario YL and UH only farms located in lowland areas (see also Table 1) were considered.

Table 1: Scenarios and definition of environments

Scenario	Environment 1	Environment 2	Comments
Yield level (YL)	Farms with annual average milk yield < 6,000kg	Farms with annual average milk yield > 8,200kg	Level of milk yield as an indicator for herd and feeding management
Udder health (UH)	Farms with annual average scc < 58	Farms with annual average scc > 170	Udder health as an indicator for herd management
Farm altitude (FA)	Level 1 (lowland)	Level 4 (highest mountain region)	Farms are grouped in 4 different levels according to altitude above sea level and their exposition following a governmental system. This may lead to different feeding strategies, climates and production systems.

scc= somatic cell count in 1000/ml milk

Results and Discussion

First results from bivariate analysis with different randomly drawn datasets are presented in Table 2. Genetic correlations for mkg in different environments were high (0.90 to 0.98) indicating almost no GxE. Genetic correlations for fkg and ekg were in the range of 0.66 to 0.86 indicating that slight GxE interactions exist in the defined environments.

Table 2: Genetic correlations (r_g) for mkg, fkg und ekg in different environments for scenarios YL, UH and FA

		Scenario	Environment 2		
			mkg	fkg	ekg
Environment 1	mkg	YL	0.97-0.98		
		UH	0.90-0.98		
		FA	0.96-0.97		
	fkg	YL		0.66-0.81	
		UH		0.73-0.80	
		FA		0.75-0.84	
	ekg	YL			0.71-0.86
		UH			0.71-0.78
		FA			0.75-0.79

These results are comparable to results found by Calus et al. (2002) who investigated GxE in Dutch Holstein for protein yield. Based on Robertson (1959) Yin et al. (2014) suggest a critical GxE threshold of $r_g \leq 0.80$ for which the inclusion of GxE interactions in genetic evaluations should be considered. Further investigations applying different methodology (modified models, multivariate analyses, reaction norm model), advanced environment definitions and including additional traits will be carried out to prove whether GxE interactions exist in Brown Swiss in Switzerland.

Acknowledgements

The author acknowledge the financial support for this project provided by transnational funding bodies, being partners of the FP7 ERA-net project, CORE Organic Plus, and the cofund from the European Commission.

We would like to acknowledge Braunvieh Schweiz for the permission to use data for this study.

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