

Breed comparisons and genetic parameters regarding dairy cattle health and welfare in pasture based production systems

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1 Introduction

Breeding high-productive Holstein-Friesian cows has led to tall framed animals, mostly kept in indoor systems and demanding increasing amounts of energy rich concentrated feed (Burren *et al.*, 2010). As farmers have to rise to the challenging occasion of fluctuating milk and inclining fodder prices, in order to stay competitive, increasing interests in pasture-based systems have been observed (Macdonald *et al.*, 2008). Traditionally, Ireland and New Zealand strongly focus on grazing systems (Piccand *et al.*, 2011). In consequence, both countries sought on alternative breeding strategies, i.e. breeding rather small animals, emphasizing functional traits as a high fertility merit, longevity, robustness and efficient production of milk solids that are reflected in protein and fat yield per hectare grassland. Following the hypothesis that Holstein-Friesian (HF) genetics, selected in New Zealand are also superior in pasture based production systems in Germany compared to other Holstein-Friesian (HF) lines, the studies' objective was a comparison of different HF selection lines for novel functional traits reflecting health and welfare: body condition score (BCS), locomotion score (LS), hock lesion score (HLS) and total hygiene score (THS). Line comparisons also included traits from conventional performance tests: milk yield (M), fat-to-protein ratio (FPR), protein content (P%), somatic cell score (SCS), protein yield in kg (P) from test-days early in lactation and conception rate (CR). Genetic analyses further focused on the estimation of genetic (co)variance components for novel and conventional traits in pasture based production systems, and on the identification of potential genotype by environment interactions (GxE) via genetic correlations for same traits measured in different environments.

2 Material and Methods

In order to compare the effect of different sires on productivity and functional traits, twenty seven research farms with using intensive grazing systems were selected. Farms agreed to specific randomized mating plans and repeated novel trait recordings to generate a longitudinal data structure. The three HF selection lines resulted from mating using sires with different merits and from different countries: HF sires from Germany, mainly characterized by high EBV for milk volume (=HF_DEU), HF sires from Germany suited to grazing conditions, i.e. such sires reflecting superiority for estimated breeding values (EBV) with assumed relevance for

pasture based production systems (HF_DEU_P), and HF sires from New Zealand (=HF_NZL). Farm sizes varied from 20 to 200 milking cows per herd enabling in total 3682 observations. Novel functional traits included BCS (1=lean; 5=fat), (Edmonson *et al.*, 1989), LS (1=normal; 5=severely lame) (Berry, 2005), HLS (1=normal; 5= swelling/lesion) (Nocek, 2014); and THS consisting of the sum of single scores (0=clean; 5= dirty) for ventral side, udder, rear leg and back sight (Reneau *et al.*, 2005). Afterwards, the data for LS and HLS were transformed into binary traits where only scores of 0 and 1 were defined as healthy (2-5 defined as injured). The statistical model [1] defined for the analysis of the Gaussian traits (M, FPR, P%, P, SCS, BCS, THS) was:

$$Y_{ijklmno} = \mu + F_i + Lstage_j(YS_k) + G_l(Lact_m) + pe_n + e_{ijklmno} \quad [1]$$

where $Y_{ijklmno}$ = vector of observations, μ = overall mean of population, F_i = fixed effect of i^{th} farm, $Lstage_j$ = fixed effect of j^{th} lactation stage, YS_k = fixed effect of k^{th} season depicting data recordings (winter: Dec.-Feb.; spring: Mar.- May; summer: Jun.-Aug.; fall: Sep.-Nov.) within year (2013, 2014) of nearest test date to the farm visit or measurement date, G_l = fixed effect of l^{th} line (HF_NZL, HF_DEU_P, HF_DEU), $Lact_m$ = fixed effect of m^{th} lactation (parity 1, 2, >2), pe_n = random effect for permanent environment of n^{th} repeated measurement within same animal and $e_{ijklmno}$ = random residual effect. For the binary traits LS, HLS, and CR a generalized linear mixed model (GLMM) with a logit link function [2] was defined:

$$\text{logit}(\pi_{qrstuv}) = \log[\pi_{qrstuv}/(1-\pi_{qrstuv})] = \phi + F_q + Lstage_r(YS_s) + G_t(Lact_u) + pe_v \quad [2]$$

where π_{qrstuv} = probability of a cow for receiving the score 1 for LS, HLS, and CR, ϕ =overall mean effect and fixed effects as defined in model [1]. For genetic analyses, models [1] and [2] were used and extended by including the random additive-genetic effect via the additive-genetic relationship matrix. EBV for sires only based on daughters in pasture based production systems were correlated with their official breeding values from 08/2014 of the same trait. Correlations between EBV were transformed into genetic correlations applying the equation by Calo *et al.* (1973).

3 Results and Discussion

As expected, M and P were significantly higher ($P < 0.001$) for HF_DEU for all parities, but with antagonistic effects on P%. Especially HF_NZL were characterized by high values for P%, especially in the second parity (3.58%). Interestingly, HF_DEU were also superior over HF_NZL and HF_DEU_P with regard to SCS. Line effect was not significant on FPR (0.39). Least square means for CR were similar for HF_DEU_P (75%) and HF_NZL (77%) in first parity, whereas HF_DEU depicted a lower CR (66%). During first parity, HF_NZL recorded the highest body condition score (2.60), and the lowest locomotion- (0.09), hock lesion- (0.28)

and total hygiene score (3.62) which might be attributed to an enhanced robustness of the HF_NZL line (Fig.1).

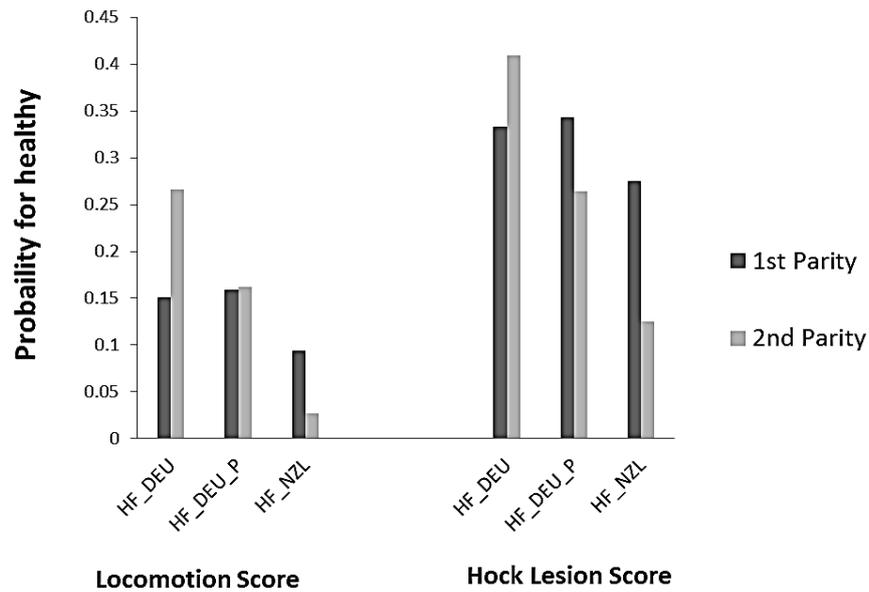


Figure 1: Least square means for locomotion score (LS) and hock lesion score (HLS) of HF lines and parities one and two.

In support of previous studies, Sogstad *et al.* (2007) associated higher milk yields with a higher risk for hock lesions, resulting from larger body sizes in high-yielding animals, and explaining higher HLS for HF_DEU. THS increased in the second lactation for HF_NZL (4.38), like the scores of HF_DEU (4.69). However, the scores of HF_DEU_P (4.24) slightly decreased, indicating changes of lying and feeding behavior between animals and lactation periods. HF_DEU recorded a steady BCS of 2.37-2.39 across lactations, while BCS of HF_DEU_P (1st parity=2.44, 2nd parity=2.49) slightly increased over parities. Higher metabolic stress due to increased milk yield within the first parity is the major explanation for a lower BCS of HF_DEU when comparing to the two other lines. Genetic parameters for conventional traits, based on data from pasture system, reflect the parameter range for same traits in indoor systems (Table 1). A moderate heritability of FPR (0.18) indicates suitability for genetic selection. Importance of FPR for the explanation of cow disposals early in lactation based on energy deficiencies was carried out in previous studies (Bergk and Swalve, 2011). Novel traits based on own recording schemes (BCS, HLS, LS, THS) revealed moderate heritabilities justifying their inclusion in overall breeding goals. THS might be a future interesting trait regarding the analysis of genetic components of dairy cow behavior (Andreasen and Forkman, 2012). Correlations for same traits between the two sets of EBV were: M (0.40), P (0.44), SCS (0.35), CR (-0.10), BCS (0.34) and LS (-0.27). Genetic correlations between same traits, i.e. accounting for reliabilities of EBV, indicated GxE for all traits when using the threshold of $r_g < 0.80$ as indicated by Robertson (1959): M (0.60), P (0.70), SCS (0.62), CR (-0.20), BCS (0.46) and LS (-0.47).

Table 1: Additive genetic (σ_a^2), permanent environmental (σ_{pe}^2) and residual variances (σ_e^2) and heritabilities (h^2) with standard errors (SE) for conventional and novel traits recorded in grassland systems.

Trait	σ_a^2	σ_{pe}^2	σ_e^2	h^2	SE
M	4.223	2.029	17.658	0.177	0.052
FPR	0.005	0.003	0.020	0.179	0.059
P%	0.021	0.015	0.045	0.259	0.065
P	0.003	0.002	0.018	0.135	0.050
SCS	0.190	0.482	1.329	0.095	0.050
CR	0.379	2.043	1.000	0.066	0.057
BCS	0.036	0.025	0.087	0.242	0.048
THS	0.951	0.000	5.864	0.140	0.041
LS	0.378	0.000	1.000	0.103	0.044
HLS	0.125	0.000	1.000	0.037	0.041

The negative genetic correlation for LS suggests a re-rankings of sires in pasture based production systems. However, the pronounced negative correlation might be also due to differences in the LS trait definition along with the scoring system. Nevertheless, GxE were more obvious for functional traits compared to higher heritability production traits.

In conclusion, results from the present study do not justify general utilization of HF sires from NZL to improve productivity and functional traits in grassland systems in Germany. Heterogeneous results were found with e.g. advantages for NZL_HF regarding health composites of feet and legs, but in contrast impaired udder health. The broad pool of German Holstein sires should be used to select specific sires for distinct environments and breeding goals, e.g. HF_DEU_P for grassland systems. Furthermore, the present study revealed genetic background for traits that are generally related to cattle husbandry and farm management, e.g. the welfare indicator THS.

4 References

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Acknowledgements

We thank the Federal Ministry for Food and Agriculture for providing the Grant (no. 12NA035) supporting the research project ‘economic evaluation of breeding strategies in pasture-based production systems to improve animal health and animal welfare’.