

Genotype by Housing Interaction in Danish Holsteins

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Introduction

Genotype by environment interaction manifests itself in many situations and levels. In this study, the environment in question is the housing system which is defined as either confinement or loose housing. In Denmark, many new free stall barns have replaced tie stall barns during the last couple of decades and this development is expected to continue. Therefore, the breeding goal should be performance in free stalls. If substantial genotype by housing interaction exists then the breeding program and genetic evaluation should account for this. That is, performance in tie stalls should receive relatively less emphasis than today. The aim of this study was to quantify the degree of genotype by housing

interaction for production, health and fertility traits in Danish Holsteins.

Material

Housing system information for Danish dairy cattle herds from 1997 to 2002 were merged with 1st parity Danish Holstein data used in the joint Nordic routine genetic evaluations and conformation data used in Lassen and Mark (2007). The proportion of cows in free stall barns increased from 48% in 1997 to 75% in 2002 (Fig. 1). Data used in the analyses are summarised in Table 1 for all the traits considered in this study.

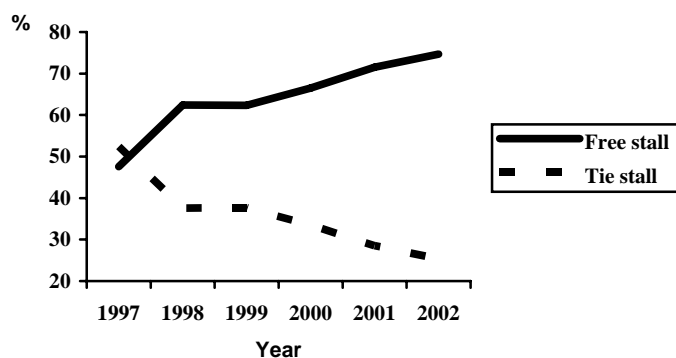


Figure 1. Trend in percentage of tie and free stalls in Denmark during 1997 to 2002.

Table 1. No. records for tie- and free stalls used to estimate genetic parameters

Trait-group	Total	Tie stall	Free stall
Production	29,863	10,723	19,140
Somatic cell count	29,626	10,662	18,964
Health ¹	24,840	8,880	15,960
Fertility	25,292	9,203	16,089

1) Health traits other than somatic cell count.

Methods

Genetic parameters were estimated using AI-REML (Jensen *et al.*, 1997; Madsen and Jensen, 2004) and a bivariate model which assumed performance in each housing system to be a different trait. The model included a fixed herd effect (529 herds), a fixed year-season of calving effect (four seasons per year), a fixed regression of days in milk, a fixed regression of age of the cow at calving as well as random additive genetic and residual effects.

Results and Discussion

The genetic correlation between performance in tie and free stall was near unity ($r_g = 0.95$ to 0.99) for all traits (Table 2), except for non-return rate ($r_g = 0.63$), non-udder diseases ($r_g = 0.87$) and days from calving to first insemination ($r_g = 0.89$). However, standard errors of the latter three estimated correlations were all high (se = 0.09 to 0.42). Thus, there seemed to be little or no genotype by housing interaction for individual traits.

Table 2. Ratio between average¹ performance in free and tie stalls, ratio between additive genetic variance in free and tie stalls, ratio between residual variance in free and tie stalls, heritabilities, additive genetic correlation (r_g) between performance in free and tie stalls; standard errors (se) are to the right of their associated parameters.

Trait	$\frac{\mu_{\text{free}}}{\mu_{\text{tie}}}$	$\frac{\sigma_{a,\text{free}}^2}{\sigma_{a,\text{tie}}^2}$	$\frac{\sigma_{e,\text{free}}^2}{\sigma_{e,\text{tie}}^2}$	h^2_{free}	se	h^2_{tie}	se	r_g	se
Production:									
Milk yield	1.01	1.07	1.30	.38	.02	.40	.03	.99	.02
Protein yield	1.01	1.00	1.36	.31	.02	.37	.03	.97	.02
Fat yield	1.01	0.90	1.40	.31	.02	.42	.03	.96	.03
Health:									
Mastitis occurrence	1.00	0.62	1.12	.04	.01	.09	.02	.97	.11
Non-udder diseases	1.08	1.00	0.99	.04	.02	.04	.02	.87	.19
Somatic cell count	0.98	0.95	1.01	.20	.02	.21	.02	.98	.03
Female fertility:									
Non-return rate 56d	1.06	0.60	1.00	.012	.007	.022	.014	.63	.42
No. inseminations	0.91	0.67	1.03	.027	.011	.058	.020	.96	.18
Days 1 st to last AI	0.89	0.55	0.99	.022	.010	.062	.021	.95	.21
Days calving to 1 st AI	0.92	0.89	0.98	.096	.016	.097	.021	.89	.09
Calving interval	0.97	0.85	1.07	.081	.016	.107	.023	.96	.07
Days open	0.91	0.82	1.08	.075	.015	.108	.023	.96	.08

1) Based on raw averages

Heritabilities were lower for free stalls than tie stalls for most traits (Table 2). For production, health and fertility traits, respectively, the heritability in tie stalls compared with free stalls was 20, 43 and 76 percent higher on average. There seemed to be different reasons for this difference in heritability for each group of traits. For production traits, it was mainly explained by a higher residual variance in free stalls than tie stalls, whereas for fertility there was a lower genetic variance in free stalls than tie stalls. For mastitis occurrence there was both higher residual variance and a lower genetic variance in free stalls compared with tie stalls.

Reasons for higher estimated residual variances and lower estimated genetic variances in free stalls compared to tie stalls may be that there are more identification errors in free stalls. This could for instance happen if several cows calve at the same time in the same calving pen. Identification errors should affect all traits, but its effect may be counterbalanced by other factors for some traits. Disease traits are recorded by veterinarians and the farmers themselves and there may be differences in recording and management between free and tie stalls that affect the estimated parameters. Likewise with fertility traits, which are highly influenced by

management. There seems to be a better fertility in free stalls than tie stalls (Table 2). This may be because it is easier to observe heat and because more exercise leads to better fertility in free stalls compared with tie stalls. Another explanation could be if farmers with free stall barns are less patient with cows having poor fertility. Then cows with poor fertility in free stalls would get fewer opportunities to get pregnant and to show true genetic fertility. The average performance for production and health was quite similar in free and tie stalls.

In a similar study of genotype by housing interaction for conformation and workability traits in Danish Holstein (Lassen and Mark, 2007) similar results were found. Unity or near unity genetic correlations were found between conformation measured in tie and free stalls. However, heritabilities were higher for tie than free stalls for most traits. That is, 17 % and 20 % higher on average for 16 and 2 conformation and workability traits, respectively. The reason for this could be that classification is often more difficult in free stalls.

Although no genotype by housing interaction is evident for individual traits, there may well be significant genotype by housing interaction for the total merit index. This is because the relative weights of the index change as heritabilities change.

Conclusion

The genetic correlation between performance in tie and free stalls was near unity for most of the investigated production, health and fertility traits. Heritabilities were, however, higher in tie compared with free stalls. Therefore, genotype by housing interaction could exist for total genetic merit in Danish Holsteins.

Implications

It does not seem necessary to treat traits measured in free and tie stalls as separate traits in genetic evaluations, but it seems important to account for heterogeneous variances, also for functional traits. Genetic parameters for free stalls should be used to calculate relative weights in the Danish total merit index.

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