

LACK OF EVIDENCE FOR CYTOPLASMIC INHERITANCE FOR MILK PRODUCTION TRAITS AT THE LANGHILL DAIRY HERD

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SUMMARY

Data on 717 first lactation cows at the Langhill Dairy Herd in Edinburgh, Scotland, were used to investigate the presence of a variance component attributable to cytoplasmic lineage. The cows, all Holstein Friesian, calved between 1979 and 1996 and were part of a long term selection experiment. Analysis was performed using an animal model and either fitting lineage, i.e. cow family, as a random variable or not including it. The analysis failed to provide any evidence of a significant variance component that could be attributed to cytoplasmic lineage, for milk, fat and protein yields, fat and protein percent or log transformations of the traits.

Keywords: cytoplasmic inheritance, milk yield, Holstein Friesian, dairy cattle, cow families

INTRODUCTION

Over recent years a great deal of interest has been expressed in the possible contribution of cytoplasmic inheritance to the inheritance of milk production traits in dairy cattle. The most likely cause of this relationship is the inheritance of mitochondrial DNA (mtDNA) which is additional to nuclear genetic inheritance (Gibson *et al.*, 1997). The reason for the interest in mtDNA is its exclusively maternal transmission in mammalian species (Hutchinson *et al.*, 1974). This might provide a possible explanation for the estimation of heritability being higher from daughter-dam regression than from paternal half sib correlations, (e.g. Seykora *et al.*, 1983).

Mitochondrial DNA only encodes about 0.05% of the total nuclear plus mitochondrial genes but the nature of the genes encoded make this a potentially important contribution. Mitochondria are responsible for a large part of the energy production of cells and as such it can be assumed that they will have a substantial effect on energetic processes such as the production of milk. The aim of this study was to investigate the presence of a cytoplasmic component of variance attributable to the cow families at the Langhill dairy herd for milk yield traits. The Langhill herd has been extensively recorded and a long term selection experiment has been in place there since the late seventies.

MATERIALS AND METHODS

Data description. Data were first lactation production records of 717 cows at the Langhill herd which calved between 1979 and 1996. The traits used for analysis were 305 day milk yield (MILK), fat yield (FAT), protein yield (PRT), fat% (FATP), protein% (PRTP), log milk yield (LMILK), log fat yield (LFAT) and log protein yield (LPRT). The reason for the inclusion of log transformations of the traits was intended to reduce the heterogeneous variance over time.

All cows were traced back to founder ancestors in the Langhill herd. These founder ancestors were then traced using the records of the Holstein Friesian Society to either the first point of registration of a founder female or to a cut off point of the year 1920, given no further convergence looked probable. The earliest cows traced were taken as being the points of cytoplasmic origin for the Langhill herd. This tracing resulted in the 717 first lactation cows being assigned to 78 cytoplasmic lineages (maternal lineages). The size of these groups ranged from the largest being 117 cows down to one.

Data analysis. Data were analysed with VCE (Groeneveld, 1996) using an animal model. Full and reduced models were fitted. The full model contained a cow lineage effect.

$$Y_{ijklm} = L_i + M_j + YS_k + b_1(\text{age}) + b_2(\text{age}^2) + a_i + f_m + e_{ijklm}$$

where Y_{ijklm} = MILK, FAT, PRT, FATP, PRTP, LMILK, LFAT, LPRT ; L_i = fixed effect of selection line, (i is selected or control line) ; M_j = fixed effect of month of calving, ($j=1,12$) ; YS_k = fixed effect of year-season of calving, (season was divided into three four month periods from Jan to April, May to Aug, Sept to Dec) ; age = age at calving; $b_1(\text{age})$ = linear regression of Y on age ; $b_2(\text{age}^2)$ = quadratic regression of Y on age ; a_i = additive genetic effect of animal ; f_m = random effect of maternal lineage ($m=1,78$) ; e_{ijklm} = residual error. In the reduced model the random effect of maternal lineage (f_m) was removed.

RESULTS AND DISCUSSION

Overall means and standard deviations for the traits analysed for the 717 cows are in Table 1.

The results of the analysis of traits of first lactation cows at Langhill (Table 2) failed to demonstrate any detectable component of variance attributable to cytoplasmic line based on standard errors (from VCE) or a log likelihood ratio test (under the null hypothesis of no variation due to maternal lineage, the asymptotic distribution of the log likelihood ratio test is $1/2\chi^2(0) + 1/2\chi^2(1)$, giving a 5% significance threshold of 2.7). It can however be seen that the standard errors associated with the components attributable to cytoplasmic lineage are equal

in magnitude to the components themselves and therefore we cannot rule out the presence of an effect.

The analysis corrected for the herd being composed of a selection and a control line by fitting the line as a fixed effect in the models. There was however the drawback, as with many experimental herds, of not being able to account for all the special management practices.

Table 1. Yield traits for 1st lactation records of 717 cows in 78 maternal lineages

Trait	Untransformed		Log Scale	
	Mean	SD	Mean	SD
Milk (kg)	6523	1255	8.76	0.19
Fat (kg)	274	52	5.59	0.19
Protein (kg)	213	39	5.34	0.19
Fat (%)	4.23	0.43		
Protein (%)	3.28	0.25		

Table 2. Heritability (\pm SE) estimates for the reduced model and the full (maternal lineage) model

Trait	REDUCED MODEL		FULL MODEL	
	h^2	h^2	f^2	LRT
MILK	0.32 (0.06)	0.28 (0.06)	0.03 (0.02)	1.62
FAT	0.37 (0.06)	0.35 (0.06)	0.01 (0.01)	0.54
PRT	0.25 (0.06)	0.23 (0.06)	0.01 (0.01)	0.44
FATP	0.64 (0.05)	0.60 (0.07)	0.02 (0.02)	0.48
PRTP	0.51 (0.06)	0.51 (0.06)	0.00 (0.00)	0.00
LMILK	0.31 (0.06)	0.27 (0.06)	0.03 (0.02)	1.52
LFAT	0.36 (0.06)	0.34 (0.06)	0.01 (0.01)	0.38
LPRT	0.23 (0.06)	0.21 (0.06)	0.01 (0.01)	0.48

f^2 is the proportion of phenotypic variance attributable to maternal lineage

LRT is twice the difference in log-likelihood between the full and reduced model

Mitochondrial inheritance would be expected to be responsible for a larger component of the traits highly dependent upon energetic processes. We would therefore expect traits such as fat yield or content to have a more significant variance component attributable to cytoplasmic lineage. The analysis did not provide significant evidence to support this theory. It was noticeable that protein% showed no variance component attributable to maternal lineage and fat% showed a larger maternal lineage component. If there was significant evidence for a maternal lineage component this is the trend we would expect.

The analysis was of data collected over seventeen years and there was a concern that the analysis would not be accounting for the change in variance over time within a selected herd. In order to correct in some way for this, log transformations of yield data were also analysed by the model. It was evident from the analysis that the transformed data provided the same results (Table 2) as the first analysis. Another concern was the effect of the use of selected bulls on the analysis. This selection effect is not properly taken into account, even when fitting an animal model, because selection took place in the national herd. We plan to investigate this either by fitting sire as a fixed effect, or regressing the data on the sire estimated breeding values.

The Langhill herd is extensively recorded for traits such as feed intake and the investigation will now move to look at traits such as production efficiency which are heavily energy dependent and therefore potentially dependent on mitochondria.

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