

ESTIMATION OF DIRECT AND MATERNAL GENETIC EFFECTS FOR PRODUCTION TRAITS IN A CROSSBRED DAIRY HERD

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INTRODUCTION

Maternal effects can be defined the same as Phenotype = Genotype + Environment (Lynch and Walsh, 1998). By defining P as maternal effects, G is equal to maternal genetic effects (dam genotype) which can be separated into additive maternal genetic and cytoplasmic effects (Southwood *et al.*, 1989), and E is maternal environment or maternal ability such as intrauterine and postpartum nutrition provided by the dam, antibodies and pathogens transmitted from dam to her offspring, and maternal behavior (Albuquerque *et al.*, 1998). The genetic models can now be correctly partitioned into variations due to additive direct, additive maternal, cytoplasmic, and nonadditive effects. The objective was to quantify and compare the contribution of additive direct and maternal genetic effects to phenotypic variances of milk yield and milk composition in a crossbred dairy herd when the models were applied to field data.

MATERIAL AND METHOD

Data were the first lactation records of crossbred dairy cows from a commercial farm in Ratchaburi, Thailand which calved between 1986 and 2000. Crossbred cows comprised of 3 breeds, Holstein Friesian, Brown Swiss and Jersey, which could be separated into 6 breed groups in each breed. The traits used for analysis consisted of milk yield that were calculated by test interval method (TIM) (Everett and Carter, 1968), fat and protein percentage. Those cows with records from < 150 day in milk (DIM) were not included in the study. One hundred and thirty one cytoplasmic lineages were determined by tracing back to the founder females. The size of cytoplasmic lines ranged from 2 to 17 cows which mostly had 2 to 6 cows. There were 984 cows in pedigree file. The data were edited and analyzed using RENUMMAT and REMLF90, respectively. The algorithm was developed by Ignacy Misztal (Misztal, 2001). A complete animal model was fitted as:

$$Y_{ijklmn} = \mu + YS_i + BG_j + b_1(ACALV)_{ijklmn} + b_2(DIM)_{ijklmn} + A_k + M_l + C_m + e_{ijklmn},$$

where Y_{ijklmn} = milk, fat and protein percentage ; μ = overall means ; YS_i = fixed effect of year-season of calving which season was divided into three periods from March to May, June to October and November to February ; BG_j = breed groups which had 18 levels ; $b_1(ACALV)_{ijklmn}$ = linear regression of Y on age at first calving ; $b_2(DIM)_{ijklmn}$ = linear regression of Y on day in milk ; A_k = additive genetic effect of animal ; M_l = random effect of maternal genetic effect ; C_m = cytoplasmic lineage which was treated as fixed or random ; e_{ijklmn} = residual error. Four single-trait animal models were fitted : Model [1] was a general model excluding M_l and C_m , Model [2] excluding C_m was divided into 2 submodels with covariance between additive direct and maternal genetic effects (σ_{am}) as 0 (Model [20]) or 0.15 (Model[2]) (Southwood *et al.*,

1989), Model [3] excluding M_l was divided into 2 submodels which treated cytoplasmic lineage as fixed (Model [3F]) or random (Model [3R]), and Model [4] was a complete animal model and divided into 4 submodels (Model [4F], [4R], [40F] and [40R]) which were resulted from merging between model [2] and [3]. The additive direct, maternal genetic and cytoplasmic prior variance were 0.3 and 0.7 for the residual variance (Southwood *et al.*, 1989).

RESULTS AND DISCUSSION

Overall means and standard deviation (S.D.) were shown in table 1. The results of the analysis of three traits, milk yield, fat and protein percentage, were shown in tables 2, 3, and 4, respectively.

Table 1. Milk and milk compositions for the first lactation crossbred dairy cows

Traits	records	Means (S.D.)	Minimum	Maximum
Milk (kg)	596	3777.59 (1090.00)	1068.05	7018.90
Fat (%)	584	3.74 (0.58)	2.30	5.80
Protein (%)	587	3.30 (2.00)	2.00	5.50

Table 2. Heritability (S.E.) estimates for milk yield from specified models

Model	h_a^2 (S.E.)	h_m^2 (S.E.)	h_c^2 (S.E.)	-2logL
[1]	0.427 (0.017)			7643.964
[2]	0.431 (0.035)	0.109 (0.012)		7607.079
[20]	0.377 (0.021)	0.065 (0.005)		7607.535
[3F]	0.430 (0.034)			5924.280
[3R]	0.383 (0.029)		0.031 (0.012)	7643.600
[4F]	0.368 (0.043)	0.114 (0.033)		5888.679
[4R]	0.429 (0.059)	0.101 (0.065)	0.012 (0.002)	7607.055
[40F]	0.373 (0.021)	0.120 (0.024)		5888.690
[40R]	0.369 (0.021)	0.061 (0.003)	0.007 (0.002)	7607.556

Table 3. Heritability (S.E.) estimates for fat percentage from specified models

Model	h_a^2 (S.E.)	h_m^2 (S.E.)	h_c^2 (S.E.)	-2logL
[1]	0.315 (0.007)			-69.276
[2]	0.306 (0.057)	0.175 (0.013)		-60.776
[20]	0.232 (0.018)	0.116 (0.011)		-59.537
[3F]	0.241 (0.025)			89.821
[3R]	0.209 (0.028)		0.075 (0.020)	-71.805
[4F]	0.365 (0.076)	0.089 (0.025)		98.670
[4R]	0.296 (0.058)	0.119 (0.016)	0.061 (0.016)	-61.778
[40F]	0.240 (0.021)	0.030 (0.002)		100.591
[40R]	0.213 (0.030)	0.074 (0.003)	0.039 (0.021)	-59.897

Table 4. Heritability (S.E.) estimates for protein percentage from specified model

Model	h_a^2 (S.E.)	h_m^2 (S.E.)	h_c^2 (S.E.)	-2logL
[1]	0.265 (0.071)			-588.962
[2]	0.287 (0.050)	0.014 (0.009)		-574.997
[20]	0.263 (0.022)	0.014 (0.008)		-574.930
[3F]	0.290 (0.113)			-299.835
[3R]	0.203 (0.032)		0.048 (0.013)	-589.996
[4F]	0.357 (0.064)	0.031 (0.024)		-289.087
[4R]	0.268 (0.031)	0.023 (0.009)	0.061 (0.016)	-576.449
[40F]	0.290 (0.060)	0.014 (0.002)		-288.329
[40R]	0.215 (0.033)	0.010 (0.001)	0.043 (0.015)	-575.857

Comparisons within submodels under each model. Covariances between direct and maternal genetic effects did not differ from zero when declared the covariance were not equal to zero (Model [2]and[20] ; [4F]and[40F] ; [4R]and[40R]). These results are similar to those described by Albuquerque *et al.* (1998), Schutz *et al.*(1992),and Schnitzenlehner and Essl (1999). In this study, considering cytoplasmic effects as fixed effects may be more appropriate than random (Model [3F]and[3R] ; [4F]and[4R] ; [40F]and[40R]), which is in agreement with the finding results reported by Southwood *et al.* (1989), Faust *et al.* (1990), and Boettcher *et al.* (1996).

Comparisons between models. Most results indicated model [3F] and [40F] were fitted in this study by -2logL. The removal of maternal genetic effects (Model [1], [3F], and [3R]) increased estimates of variance components and heritabilities for milk yield as reported by Southwood *et al.* (1989) and Albuquerque *et al.* (1998), but not in fat (Southwood *et al.* 1989 ; Albuquerque *et al.* 1998) and protein percentage. Exclusion of cytoplasmic effects (Model [1], [2], and [20]) increased estimates of variance components and heritabilities for milk yield and fat percentage and there were greater than Albuquerque *et al.* (1998) when ignored both of those effects but there was no difference in protein percentage. The results suggested that maternal genetic effects were important and should be accounted for the phenotypic variance of milk yield while cytoplasmic effects should be accounted for milk yield and fat percentage.

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