Kasetsart J. (Nat. Sci.) 47 : 228 - 237 (2013)

Genotype by Region Interaction on Milk Production Traits of Holstein Crossbred Dairy Cows in Thailand

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ABSTRACT

This study was designed to examine the existence of a genotype × region interaction on milk production traits in Holstein crossbred dairy cows in Thailand. The data set for this study was provided by Department of Livestock Development of Thailand. The data were divided into five regions (Central, East, North, Northeast and West). The factors having genotype × region interaction on milk production traits were region, year-season of calving, breed group and breed group × region interaction. The investigated traits were actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305), respectively. The breed group of cow had a significant ($P < 0.05$) effect on MY305 and a highly significant ($P < 0.01$) effect on ATMY and AJ305 while the effect of year-season of calving and region had very highly significant ($P < 0.001$) effects for all the studied traits. Breed group × region had a highly significant interaction ($P < 0.01$) for the milk production traits. The estimated heritability for the milk production traits ranged between 0.17 to 0.24 for the Central region and 0.29 to 0.57 for the Eastern region. It was suggested that the performance of breed group of cows from different regions should differ significantly or there was a genotype × region interaction in this particular study.

Keywords: genotype × region interaction, milk production traits, dairy cows, Thailand

INTRODUCTION

The genetic improvement of milk production traits in dairy cattle in Thailand is based on phenotypic selection. For more than 40 years, superior dairy sires and dam have been identified using quantitative genetic evaluations by the best linear unbiased prediction method (Tumwasorn *et al*., 2000). Selective use of these animals improved phenotypic measures for milk production and milk components in the Holstein dairy crossbred population in Thailand. However, there are some limitations on predicting the breeding values of an individual using quantitative analysis (Sanpote *et al.*, 2010). Once genotype has been fitted to the existing environment or region, then there would be less variation for more improvement through upgrading due to stress, high temperature and the humidity index level affecting the survival of a high-milk-producing cow while the marginal improvement from improving feeding and management tended to be greater than that of genetic improvement (Tumwasorn, 2012). There are major differences when considering the production system (that is, feed and feeding, and herd management) and the study of the magnitude

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Received date : 02/11/12 Accepted date : 21/01/13

of genotype × region or environment interaction on milk production traits in Holstein crossbred cows across regions of Thailand is of great importance. The interaction between an animal's genotype × region interaction can play a major role in the expression of the phenotype of productive traits and is very important when breeding value estimation is performed. Accordingly, the existence of a genotype × region interaction has not been reported before in Thailand. Thus, the aim of this study was to examine the existence of a genotype × region interaction on the milk production traits of Holstein crossbred cows in Thailand.

MATERIALS AND METHODS

Animals and data

The data comprised 1,561 first lactation records with 3,052 pedigree records from 1,561 Holstein crossbred cows that had calved at some time during 1993 to 2007. The data were collected by the Department of Livestock Development of Thailand from five regions (Central, East, North, Northeast and West). The average age at first calving of the cows was 32 mth and animals without records were excluded from the data set. All cows had their sires and dams identified for the analysis of genetic value and which indicated that the cows in the sample were the offspring of 12 sires and 1,561 dams. Moreover, all cows were assigned to one of five breed groups (genotypes), designated as BG1 to BG5, based on the Holstein fraction (H)—namely, BG1 ($H \leq 0.75$), BG2 ($0.75 < H < 0.875$), BG3 ($0.875 \leq H < 0.9375$) and BG4 ($0.9375 \leq H < 0.9687$) and BG5 ($H \geq 0.9687$). According to Koonawootrittriron *et al.* (2009), calving months were grouped into three seasons—winter (November to February), summer (March to June) and the rainy season (July to October). Animals were assumed to be grouped within year-season of calving contemporary group (a group of cows that calved in the same year and in the same season).The investigated traits were actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305), respectively.

Animal feeding and management practices

Dairy cattle in Thailand are usually raised in a small farm environment with varying feed and feeding methods. Farmers in the North feed their animals mainly with rice straw, waste from sweet corn factories and concentrates, whereas waste from tapioca flour and cassava byproduct are another source of fiber. In contrast, dairy farmers in the Central region feed their dairy cows with all available sources of fiber and this may vary from season to season. It is most common that farmers use fruit waste from factories as the main fiber source and also rice straw is an important fiber throughout the year. Fruit waste from pineapple factories and sweet corn factories is the main roughage feed covering up to 90% of daily feed especially in Prachuap Khiri Khan, Chiang Mai, and Kanchanaburi provinces (Endris *et al*., 2012). Farmers in the Northeast rely for their feed on rice straw and small cash crop residues on the farm. The feeding methods of dairy farmers also vary from region to region. In the South, where pineapple factories exist, farmers feed 30–40 kg of pineapple waste, 5–10 kg of concentrate and an additional 2–3 kg of rice straw per cow per day. In the Central and Northern parts, farmers feed their cows with 5–10 kg concentrate, 20–30 kg of silage from sweet corn and pineapple waste, 3–5 kg of rice straw and 2–3 kg of waste from ethanol factories. In the Northeast, farmers feed their cows with 5–10 kg concentrate, 20–30 kg of silage from sweet corn and pineapple waste, 4–6 kg of rice straw and 3–5 kg of waste from tapioca factories. Silage of mixed grass varieties from backyards is given in small amounts and is available only in the rainy season (Yeamkong *et al*., 2010)

Model description and statistical analysis

The data were subjected to analysis of variance to determine if there were any significant sources of variation affecting the traits. The fixed factors included in the model were year-season of calving, region, breed group (genotype), and breed group × region interaction. Ages at first calving and lactation length were included as covariate parameters in the model. Therefore, the general linear model analysis used the GLM procedure of the Statistical Analysis System software (SAS, 2002). It was assumed that with the varying feed and feeding methods given to dairy cattle in each region, the performance of each breed group of cows from different regions should differ significantly or there was a genotype × region interaction. The model was established according to Equation 1:

$$y_{ijkl} = \mu + YS_i + R_j + BG_k + (BG*R)_{jk} + b_1(L_{ijkl} - \bar{L}) + b_2(A_{ijkl} - \bar{A}) + e_{ijkl} \quad (1)$$

where, y_{ijkl} is the observation of the l^{th} animal, μ is the overall mean, YS_i is the fixed effect of the i^{th} year-season of calving, BG_j is the fixed effect of the j^{th} breed group (j = 1, 2, 3,…,5), R_k is the fixed effect of the k^{th} region (k = 1, 2, 3,…,5), $(BG*R)_{jk}$ is the fixed effect of the breed group × region interaction, b_1 is the coefficient of linear regression of ATMY on the lactation length, b_2 is the coefficient of linear regression of ATMY, MY305 and AJ305 on the age at first calving and e_{ijkl} is the residual error effect with $e_{ijkl} \sim N(0, \sigma_e^2)$.

Model for estimation of genetic parameters

The variance components and genetic parameter estimates for the investigated traits were compiled using the single trait animal model that had considered the general linear models indicated above. The direct additive genetic effect of animal was included as a random factor in the model. The variance components and genetic parameters were estimated with the restricted maximum likelihood method and by applying the average information algorithm program (AIREML; Gilmour *et al.*, 2000). The solutions for the fixed effects and simultaneously for the random effects were obtained by solving the mixed models equations. Heritability (h^2) was determined as the ratio of the additive genetic variance to the total phenotypic variance. The statistical model used was the same for all observations in the dataset and was expressed in matrix notation as shown in Equation 2:

$$y = X\beta + Za + e \quad (2)$$

where, y is the vector of observations, β is the vector of fixed effects including year-season of calving, region breed group of cow and covariates of the age at first calving and lactation length, a is the vector of random additive genetic effect of animal, e is the vector of random residual effect and X and Z are the incidence matrices relating fixed and random effect to the observation.

The assumptions about the variances of the random effects were var(a) = $A\sigma_a^2$ where A is the numerator relationship matrix and var(e) = $I\sigma_e^2$ where I is the identity matrix.

RESULTS AND DISCUSSION

Factors affecting milk production traits

To assess the effects of breed group (genotype), region and breed group × region interaction, a combined analysis of variance (ANOVA) was performed on ATMY, 305MY and AJ305 (Table 1). Accordingly, the breed group of cow showed a significant ($P < 0.05$) effect on MY305 and a highly significant effect ($P < 0.01$) on ATMY and AJ305. The results of these milk production traits across region showed very highly significant ($P < 0.001$) differences while the effect of year-season of calving had a very highly significant ($P < 0.001$) effect for all the studied traits. In addition, the results revealed that the linear regression on lactation length had a very highly significant ($P < 0.001$) effect on ATMY while age at first calving showed a highly significant ($P < 0.01$) effect on ATMY, MY305 and AJ305. The results of the combined ANOVA also showed highly significant ($P < 0.01$) breed group

Table 1 Analysis of variance for actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305) by the effect of breed group region, breed group × region interaction and year-season of calving.

Effect	Mean squares of traits				
	DF	ATMY (kg)	DF	MY305 (kg)	AJ305 (kg)
Breed group	4	2,216,109 **	4	2,086,377*	3,377,785**
Region	4	4,849,115***	4	5,534,540***	7,220,020***
Year-season of calving	37	1,801,769***	37	1,860,893***	2,071,751***
Breed group × region	16	1,721,317 **	16	1,887,740**	2,075,295**
Lactation length	1	485,510,804***		-	-
Age at first calving	1	5,545,359 **	1	8,880,559**	60,77,848**
Residual	1,497	640,724	1,498	837,901	791,665

***, ** and * indicate statistical significance at the 0.001, 0.01 and 0.05 probability levels, respectively, DF = Degrees of freedom = 1,497 for ATMY, DF = 1,498 for MY305 and AJ305.

× region interactions for all studied traits. Clearly, the presence of such sizeable G × E interactions will lead to changes in the ranking of genotypes; hence, certain genotypes exhibited their highest performance in selected regions while others showed their best performance in their respective favorite regions.

The genotype performances of ATMY, MY305 and AJ305 across regions are illustrated graphically in Figures 1, 2 and 3 and show a clearly observable oscillating performance of the genotypes in the different regions. However, there are changes in the magnitude of the difference among genotypes or changes in the relative ranking of the genotypes in different regions.

Overall, BG5 exhibited remarkably stable performance across all the regions considered in this particular study. BG4 followed BG5 with minimum oscillating trends (Figures 1, 2 and 3). Conversely, BG1 displayed the highest fluctuations in all milk yield traits, with the lowest of all of them being recorded in the Eastern region. BG1 showed its highest performance in the Northeastern region. Interestingly, all the remaining genotypes had relatively low values for ATMY, MY305 and AJ305 in the Central region (Figures 1, 2 and 3). Thus, BG2 seemed to be ideal for the Central and Western regions as it had a relatively better performance in the milk yield traits compared to the other genotypes. Contrarily, promotion of this genotype in the Eastern region does not reward livestock holders in this region as clearly noted from its poor performance. Such inconsistent performance of the genotypes in the milk yield traits across different regions has been reported by Parra-Bracamon *et al*. (2005) and Prempree *et al*. (2010).

Although several factors could be responsible for such performance oscillations, the contribution of feed and feeding management systems practiced in those regions is worth mention. In the current study, this factor showed a clear effect on all the breed groups. This was clearly manifested in the estimation of the genetic parameters of the milk production traits across regions. Clear estimates were obtained only for the Central and Eastern regions where the genotypes showed significant interactions (differences) unlike in the Northern, Northeastern and Western regions where all genotypes showed almost similar performance tendencies. Generally, the ATMY and AJ305 values of BG4 and BG5 did not show any cross-over interaction or qualitative interaction but did show a quantitative interaction or scaling effect which means there was no ranking shift among them (Figures 1, 2 and 3).

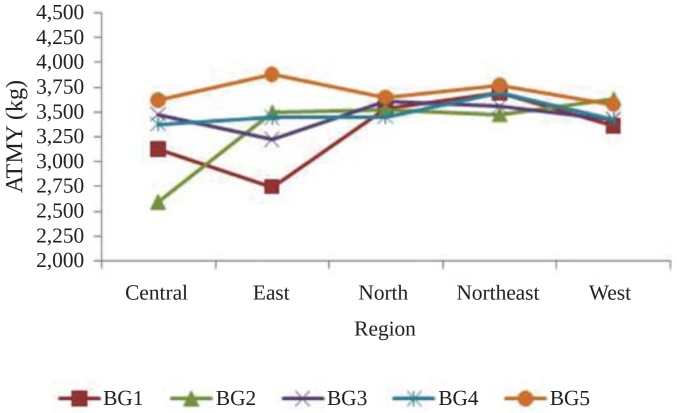

Figure 1 Least squares means of actual total milk yield (ATMY) for breed group (BG) by region interaction.

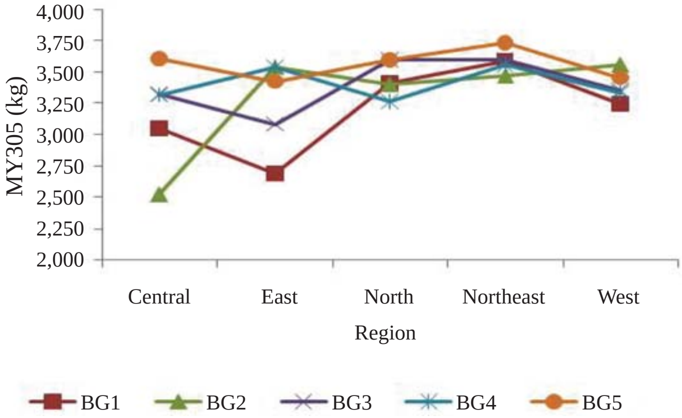

Figure 2 Least squares means of 305- day milk yield (MY305) for breed group (BG) by region interaction.

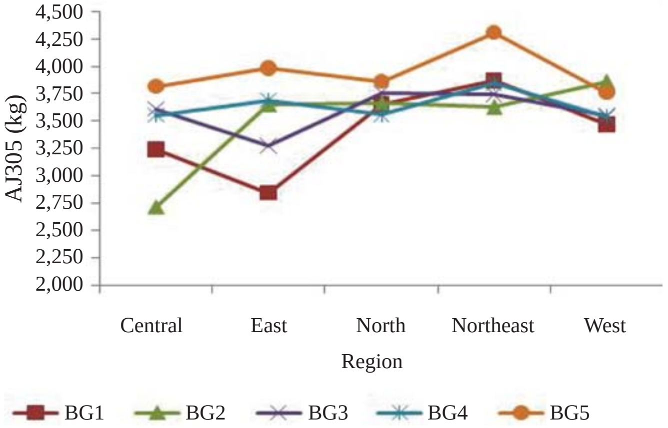

Figure 3 Least squares means of adjusted 305- day milk yield (AJ305) for breed group (BG) by region interaction.

The overall values for mean ± standard error for ATMY, MY305 and AJ305 were 3,590 ± 25.8 kg, 3,499 ± 24.1 kg and 3,767 ± 23.7 kg, respectively (Table 2). The highest values for MY305 of 3,526 ± 139 and AJ305 of 3,905 ± 135 were recorded from BG5 while the lowest values of all the above milk yield traits were recorded from BG1. Thus, this trend clearly revealed the strong and positive link between Holstein blood fraction and milk yield traits. The mean values for milk production traits per breed group of cow were within the range reported by other investigators in Thailand (Konig *et al*., 2005; Koonawootrittriron *et al*., 2009; Puangdee *et al*., 2012). The highest mean milk yield traits of ATMY (3,607 ± 73.8 kg), MY305 (3,557 ± 84.6 kg) and AJ305 (3,849 ± 82.1 kg) were obtained from cows raised in the Northeastern region. The lowest AJ305 and MY305 values were recorded from cows in the Eastern region. The lowest ATMY value of 3,238 ± 72.8 kg was obtained from the Central region.

The least squares means for milk yield traits estimated by region were in agreement with the findings of Parra-Bracamon *et al*. (2005) in Mexico and Prempree *et al*. (2010) in Thailand. In general, Vaccaro (1992) reported significant differences between localities in Venezuela for economically important traits in dairy herds. These reports associated these differences with management and the availability of feed and the feeding method. However, locality differences were also attributed to the breed group composition of the herds as well as differences in herd management. In the Northeastern region of Thailand, most herds had a high percentage of Holstein genetics and better management of the herd. In addition, the clear focus by farmers on milking cows in the Northeastern region resulted in the highest values for ATMY, MY305 and AJ305 of all regions.

Variances and heritabilities within region analyses

The variance components and heritability were estimated after the non-genetic factors affecting the traits were identified and accounted

Table 2 Least squares means (± SE) for actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305) of Holstein crossbred cows by percentage of Holstein fraction (H) by region and cow breed group (BG1–BG5).

Factor	Number	Trait		
		ATMY(kg)	MY305(kg)	AJ305 (kg)
Overall mean		3,590 ± 25.8	3,499 ± 24.1	3,767 ± 23.7
Region				
Central	335	3,238 ± 72.8^{c}	3,174 ± 83.5^{c}	3,391 ± 81.1^{c}
East	202	3,242 ± 121^{bc}	3,132 ± 138^{c}	3,369 ± 134^{c}
North	277	3,496 ± 96.8^{ab}	3,406 ± 111^{ab}	3,636 ± 107^{ab}
Northeast	314	3,607 ± 73.8^{a}	3,557 ± 84.6^{a}	3,849 ± 82.1^{a}
West	433	3,392 ± 83.4^{bc}	3,318 ± 95.7^{bc}	3,543 ± 92.8^{bc}
Breed group of cow				
BG1 ($H \leq 0.75$)	278	3,170 ± 94.6^{c}	3,095 ± 108^{b}	3,276 ± 105^{c}
BG2 ($0.75 < H < 0.875$)	107	3,315 ± 86.1^{bc}	3,252 ± 98.8^{a}	3,470 ± 95.8^{bc}
BG3 ($0.875 \leq H < 0.9375$)	546	3,408 ± 63.8^{b}	3352 ± 73.1^{a}	3,542 ± 70.9^{b}
BG4 ($0.9375 \leq H < 0.9687$)	463	3,429 ± 75.4^{ab}	3,363 ± 86.4^{a}	3,595 ± 83.8^{b}
BG5 ($H \geq 0.9687$)	167	3,653 ± 121^{a}	3,526 ± 139^{a}	3,905 ± 135^{a}

^{a,b,c} = Least squares means in a column with different lowercase superscript letters within factors and traits are significantly different ($P < 0.05$).

for in the mixed model equations (MME). Tables 3 and 4 present the results of single trait analysis with respect to additive genetic, residual, phenotypic variance and heritability using a univaraite animal model. The overall heritability estimates (± SE) of ATMY, MY305 and AJ305 were 0.20 ± 0.13, 0.24 ± 0.12 and 0.37 ± 0.11, respectively (Table 3). The heritability estimates found in this study for milk yield traits were lower than those reported by other authors in Thailand (Tumwasorn *et al*., 2000; Topanurak *et al*., 2001; Koonawootrittriron *et al*., 2003, 2009; Seangjun *et al*., 2009; Sarakul *et al*., 2011). However, the low estimates were in close agreement with the findings of Asaad *et al*. (2011). The heritability estimates of the present study differed from other investigations due to the fluctuations in feed availability and environmental factors.

The phenotypic variances of the milk yield traits obtained (Table 3) were larger than those reported by Sanpote and Buaban (2003) of 553,060 kg^2 and Koonawootrittriron *et al*. (2009) of 663,652.0 kg^2 in Thailand but the estimates of phenotypic variance were in close agreement with the findings of other countries—Morocco, 846,641.5 kg^2 (Boujenane, 2002), Kenya, 658,516 kg^2 (Amimo *et al.*, 2007) and Iran, 799,598.5 kg^2 (Hashemi *et al*., 2009).

Table 3 Estimates of variance components and heritability for actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305) of Holstein crossbred cows.

Trait	Variance component (kg^2)			Heritability
	σ_a^2	σ_ε^2	σ_p^2	
ATMY	195,657	786,802	982,459	0.20 ± 0.13
MY305	207,135	648,213	855,348	0.24 ± 0.12
AJ305	301,373	507,652	809,025	0.37 ± 0.11

σ_a^2 = Additive genetic variance, σ_ε^2 = Residual variance, σ_p^2 = Phenotypic variance.

Table 4 Estimates of additive genetic variances (σ_a^2), residual variance (σ_e^2), phenotypic variance (σ_p^2) and heritabilities (h^2 ± SE) of actual total milk yield (ATMY), 305 d milk yield (MY305) and adjusted 305 d milk yield (AJ305) within regions.

Trait	Parameter	Environment	
		Central (Region 1)	Eastern (Region 2)
ATMY	σ_a^2	160,940	263,458
	σ_e^2	706,446	639,092
	σ_p^2	867,338	902,550
	h^2	0.19 ± 0.19	0.29 ± 0.25
MY305	σ_a^2	176,056	293,778
	σ_e^2	830,009	502,239
	σ_p^2	1006,065	796,017
	h^2	0.17 ± 0.18	0.37 ± 0.27
AJ305	σ_a^2	235,180	395,395
	σ_e^2	736,001	303,765
	σ_p^2	971,181	699,160
	h^2	0.24 ± 0.27	0.57 ± 0.34

Variances are all measured in kg^2.

The result revealed that the estimated phenotypic variance (σ_p^2) for milk production traits within region analysis ranged from 699,160 to 1,006,065 kg^2 (Table 4). The findings for this phenotypic variance for the milk production traits were within the range reported by Nauta *et al*. (2006) and Sofla *et al*. (2011) in the Netherlands and Iran, respectively. In addition, the results revealed that the estimated heritability for milk production traits ranged between 0.17 to 0.24 for the Central region and 0.29 to 0.57 for the Eastern region (Table 4). These results were similar to the findings of Prempree *et al*. (2010), who estimated the heritability for milk production traits in different regions of Thailand, with the heritability estimate of ATMY being 0.19 for the Central and 0.29 for the Eastern regions. In the present study, the heritability of MY305 was 0.17 for the Central and 0.37 for the Eastern regions. Similarly, the estimated heritability of AJ305 was 0.24 for the Central and 0.57 for the Eastern regions. The higher standard error of heritability estimates for all the traits under study indicated that these traits were highly influenced by environmental factors and management of the herd such as feed and feeding, and health care could also contribute to the variation. A high standard error of the heritability estimates for milk yield was reported by Usman *et al.* (2012) in Holstein Friesian cattle in China, with the corresponding value being 0.26 ± 0.33.

The estimated heritabilities of the milk yield traits under the Eastern region conditions were higher than in the Central region. The main reason for this was that the residual variance (σ_e^2) of the milk yield traits was lower for the Central region. In addition, the estimate for the additive genetic variance (σ_a^2) of the yield traits was higher in the Eastern region than for the Central region (Table 4). Fikse *et al*. (2003) evaluated the records for first lactation in dairy cows in four countries (Australia, Canada, the USA and South Africa) to determine the genotype × environment interaction for milk production, using different statistical models. The estimated heritability for the milk yield traits in the present investigation was within the range of Sofla *et al*. (2011), who estimated heritability values of 0.48, 0.39, 0.59 and 0.70 for milk yield in conventional, pre-organic, converting-organic and organic production environments, respectively.

CONCLUSION

The ANOVA results showed a significant genotype × region interaction. This interaction resulted in inconsistent performance and a ranking shift of genotypes across regions. BG5 exhibited remarkably stable performance across all the regions considered in this study. In addition, BG4, like BG5, had minimum oscillating trends. Hence, these two breed fractions are recommended for further promotion. For the estimation of genetic parameters, clear estimates were obtained only for the Central and Eastern regions where genotypes showed significant interactions (differences) unlike for the Northern, Northeastern and Western regions where all genotypes showed almost similar tendencies in performance. The estimated heritabilities of milk yield traits in the Eastern region were higher than in the Central region.

ACKNOWLEDGEMENTS

The authors wish to acknowledge the Department of Livestock Development of Thailand for making their field data set available for this study. The authors are grateful for the financial support from the Rural Capacity Building Project under the Ministry of Agriculture of Ethiopia. For additional support, the authors thank the Integrative Research Center for Animal Science, Aquaculture and Animal Health (ASA-AH) of Kasetsart University under the National Research University Project of Thailand.

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