Interaction Effect of DGAT1 and Composite Genotype of Beta-Kappa Casein on Economic Milk Production Traits in Crossbred Holstein

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Abstract—The objective was to determine the single gene and interaction effect of composite genotype of beta-kappa casein and DGAT1 gene on milk yield (MY) and milk composition, content of milk fat (%FAT), milk protein (%PRO), solid not fat (%SNF), and total solid (%TS) in crossbred Holstein cows. Two hundred and thirty- one cows were genotyped with PCR-RFLP for DGAT1 and composite genotype data of beta-kappa casein from previous work were used. Two model, (1), and (2), was used to estimate single gene effect, and interaction effect on the traits, respectively. The significance of interaction effects on all traits were detected. Most traits have consistent pattern of significant when model (1), and (2) were compared, except the effect of composite genotype of beta-kappa casein on %FAT, and the effect of DGAT1 on MY, which the significant difference was detected in only model (1).The results suggested that when the optimum of all traits was necessary, interaction effect should be concerned.

Keywords—composite genotype of beta-kappa casein, DGAT1 gene, Milk composition, Milk yield

I. INTRODUCTION

MILK yield (MY), milk composition, FAT%, %PRO, %TS, and %SNF, are important for profitability of the dairy industry, particularly, in South East Asia. The farmers, however, have confronted with the low content of milk composition which is the main problem of dairy industry in this area. Genetic improvement is one in another ways to cope with this problem.It is undeniable that marker assisted selection has an important role in animal breeding to increase the accuracy and decrease the time of animal selection in this decade. From the mentioned problem, however, single gene marker may not enough to use in this purpose, since the traits are quantitative trait, which are controlled by polygene, it is possibility that interaction effect between genes on the traits may occur.

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Multi-loci marker may more suitable method than single marker to handle the problem.

The major composition of %TS and %SNF are milk protein. If the content of milk protein increases, the content of %TS and %SNF should be increased. Exceed than 80% of milk protein are casein protein [10]. Therefore, increasing casein protein, %SNF and %TS should be increased. Casein gene family which was composed with alphaS1, alphaS2, beta, kappa casein and locate on chromosome 6 are the group of gene which have the responsibility in casein synthesis process [8], [12]. Many previously studies [1], [3], [4], [5], and [7] found the significant association between the group of genes and milk production and milk composition. Therefore, it is possible to use the genes as gene marker in selection program.Additionally, from the study of [6], and [17], they found that Acyl-CoA:diacylglycerol acyl transferase 1 (DGAT1) enzyme which has a major role in the synthesis of triglyceride with the catalyzing of the reaction of diacylglycerol and fatty acid was encoded by DGAT1 gene. This gene is located on bovine chromosome 14. The study of them found that substitution of lysine with alanine (K232A) at the positions 10433 and 10434 in exon8 showed an association between milk production and composition traits. Moreover, many previous studies, [13], [15], and [16], those aimed to investigate this association and the significant association between the gene and the traits were detected. From these results, they are clear that DGAT1 gene has a strong association with milk production and milk composition.

However, as two previous paragraphs, there are questionable that which genes or how many genes will be used as gene marker to improve the milk production and milk composition. And interaction effect of the group of gene will affect on the trait, or not. Therefore, the objective of this study was to determine the single gene effect and interaction effect of composite genotype of beta-kappa casein and DGAT1 gene on MY, %FAT, %PRO, %TS and %SNF in crossbred Holstein.

II. MATERIALS AND METHODS

Data and Genotyping

Two hundred and thirty- one crossbred Holstein cows were genotyped and investigated the polymorphism of DGAT1 gene with the protocol which was reported by [11]. The

composite genotype data of beta-kappa casein gene from our previous work, "to be published" [1], were used in this study. The number of tested-day data about 2,500 record of milk yield, %FAT, %PRO, %TS and %SNF per cow per day were used in this study.

Statistical Analysis

Least square means from 2 different general linear model (GLM) which were shown below, (1) is the model was used to. estimate single gene effect of composite genotype of beta-kappa casein or DGAT1 gene on the traits, and (2) is the model was used to estimate single gene and interaction effect between composite genotype of beta-kappa casein and DGAT1 gene on the traits. Herd-year-season, day in milk, lactation, and the level of Holstein cattle were used as a fixed effect in the model. Relationship between genotype and the traits was considered significant when P < 0.05. Least significant different was used to compare the effect of each genotype. SPSS for windows (Release 10) (SPSS Inc., Chicago, IL) was used for statistical analysis.

$$y = X_1\beta_1 + X_2\beta_2 + \varepsilon \qquad (1)$$

When y, are the data of MY kg. per day per cow, %Fat, %PRO, %SNF, %TS while X_1, X_2 are incident matrix of fixed factor which include with Herd-year-season, day in milk, lactation, and the level of Holstein cattle, incident matrix composite genotype of beta-kappa casein or the DGAT1 genotypes, respectively, β_1, β_2 are the effect of fixed factor in X_1 and effect of composite genotypes beta-kappa casein or genotype of DGAT1, respectively. And ε is a random effect of residual.

$$y = X_1\beta_1 + X_2\beta_2 + \varepsilon \qquad (2)$$

When y, are the data of MY kg. per day per cow, %Fat, %PRO, %SNF, %TS while X_1, X_2 are incident matrix of fixed factor which include with Herd-year-season, day in milk, lactation, and the level of Holstein cattle, incident matrix of composite genotype of beta-kappa casein genotype, DGAT1 genotypes, and interaction between beta-kappa casein and DGAT1 genotype, respectively. β_1, β_2 are the effect of fixed factor in X_1 and effect of each genotypes and interaction effect, respectively. And ε is the random effect of residual.

III. RESULTS AND DISCUSSION

The significance of interaction effect on MY, %FAT, %PRO, %SNF, and %TS were detected at P-value < 0.0001, 0.01, <0.0001, <0.0001, and 0.036, respectively. The interaction effect which was detected in this study have

accorded with hypothesis and the previous studies, [2], [9], and [14], which studied the interaction effect of some gene on some economic traits in various dairy cattle population. Even the interaction effect was found, but if the effect do not affect on the pattern of significant, single gene marker should be more suitable used than multiple markers with the reason of simple and economical. As the mentioned, therefore, it is reasonable to compare the results from model (1), and (2).

Most traits have consistent pattern of significant effect when model (1), and (2) were compared, except the trait of %FAT in Table I which the significant difference was not detected in model (2), and the trait of MY in Table II which the significant difference was not detected in model (2). From the results, there are two points that need to discuss, consistent effect on %PRO, %SNF, and %TS from both model, and inconsistent effect on MY, and %FAT from both model. Firstly, the consistent pattern of significant difference least square means of %PRO, %SNF, and %TS, when model (1), and (2) were compared, the explanation of these situations are, beta-kappa casein gene have the main role in protein synthesis, [8], and [12] and showed the strongly effect on protein and some related traits, %SNF, %TS. Additionally, from previous research "to be published" [1], and [5] found that these loci also affect on milk production. Simultaneously, some previous studies, [13], [14], and [15], found that DGAT1 gene have also effect on milk protein. Therefore, there is possible that, beta-kappa casein and DGAT1 gene may have co-function in milk protein synthesis, and show the additive effect on the traits. Therefore, in some area where milk protein or related traits are the main problem, one of two groups of genes can use as gene marker for marker assisted selection. The second point, inconsistent effect on MY, and %FAT from both model were detected. The explanation of this point are, from some previous studies, [3], [4], and [7], event they found the composite genotype of beta-kappa casein has the significant effect on fat trait, however, should not stronger than DGAT1, since in model (1), when DGAT1 gene which affect on fat synthesis, [6], and [17], did not include in analysis, significant effect of beta-kappa casein on %FAT will be detected, but when DGAT1 gene was included in model (2) caused significant difference could not detect in composite genotype of beta-kappa casein. This is similar with the study of [14], which study the effect and interaction effect of DGAT1 and CSN1S1 gene, and the nonstrict additive effect was use to explain that result. The results could imply that DGAT1 gene may be more suitable than beta-kappa casein to be the gene marker for fat trait. In the case of MY, similar explanation with fat trait, that composite genotype of beta-kappa casein has the stronger effect on MY than DGAT1, since significant effect of DGAT1 on MY in model (2) which the effect of DGAT1 was separated by composite genotype of beta-kappa casein, and interaction effect, was not detected.

TABLE I

LEAST SQUARE MEAN AND STANDARD ERROR (SE) OF COMPOSITE GENOTYPE

OF $\beta, \kappa - casein$ WHEN WAS ANALYZED IN MODEL (1), AND (2)

Trait		A1A2 AA	A1A2 AB	A1A2 AE	A2A2 AA	A2A2 AB	A2B AB
MY	(1)	10.59[a]	9.95[b]	10.18[ab]	10.37[ab]	9.13[c]	10.38[ab]
		(0.23)	(0.27)	(0.37)	(0.25)	(0.30)	(0.32)
	(2)	10.50[a]	10.37[a]	10.24[ab]	10.66[a]	9.59[b]	10.79[a]
		(0.25)	(0.32)	(0.57)	(0.33)	(0.36)	(0.35)
%FAT	(1)	3.87[a]	3.89[a]	3.76[a]	3.86[a]	3.40[b]	3.90[a]
		(0.05)	(0.06)	(0.08)	(0.05)	(0.07)	(0.07)
	(2)	3.88	3.87	3.72	3.86	3.92	3.93
		(0.05)	(0.07)	(0.12)	(0.06)	(0.08)	(0.07)
%PRO	(1)	2.94[bc]	2.94[bc]	2.89[c]	2.97[b]	3.03[a]	3.01[a]
		(0.02)	(0.03)	(0.04)	(0.02)	(0.03)	(0.03)
	(2)	2.90[b]	2.88[b]	2.89[b]	3.02[ab]	3.07[a]	2.95[b]
		(0.02)	(0.03)	(0.05)	(0.03)	(0.03)	(0.03)
%SNF	(1)	8.29[b]	8.26[b]	8.25[b]	8.31[b]	8.45[a]	8.34[a]
		(0.03)	(0.04)	(0.06)	(0.04)	(0.05)	(0.05)
	(2)	8.25[c]	8.23[c]	8.18[c]	8.38[b]	8.52[a]	8.30[b]
		(0.04)	(0.05)	(0.09)	(0.05)	(0.05)	(0.05)
%TS	(1)	12.23[bc]	12.22[bc]	12.09[c]	12.25[b]	12.53[a]	12.40[ab]
		(0.07)	(0.09)	(0.12)	(0.08)	(0.10)	(0.10)
	(2)	12.17[b]	12.16[b]	11.96[b]	12.32[ab]	12.51[a]	12.29[ab]
		(0.08)	(0.10)	(0.18)	(0.09)	(0.11)	(0.11)

(1) model: single gene of $\beta, \kappa - casein$ composite genotype was analyzed, (2) model: multiple gene, $\beta, \kappa - casein$ and DGAT1 gene were analyzed.

MY, %FAT, %PRO, %SNF, TS are milk yield,kg./cow/day, percentage of fat , percentage of protein, percentage of Solid not fat, and percentage of total solid, respectively.

Where [a,b,c] in each row means significant difference at p<0.05.

IV. CONCLUSION

The results suggested that event the significant of interaction effect were detected but did not change the pattern of significant in the %PRO, %SNF, and %TS. We can use single gene, either composite genotype of beta-kappa casein, or DGAT1 gene as gene marker for improve the traits. However, if the breeding goal is trying to improve and optimize the trait of milk yield and milk composition, %FAT, %PRO, %SNF, and %TS, animal breeder need to concern the interaction between gene. Which combination of these group is the most suitable, should be the further studied.

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