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Association of KiF12 Gene Related to Fatty Acid Composition in Javanese Fat Tailed Sheep

Kasita Listyarini[1], Mutasem Ali Abuzahra[1], Jakaria Jakaria[1], Cece Sumantri[1], Md. Jasim Uddin[2], Asep Gunawan[1]

[1] *Bogor Agricultural University, Animal Production and Technology, Indonesia*
[2] *Sylhet Agricultural University, Agricultural Economics, Bangladesh*

Abstract

Kinesin-like protein KIF12 gene are suggested as candidate gene involved in fatty acid metabolism. The aim of this study was to analyse the genotype polymorphism and to study association of KIF12 gene (g.9617965 C>T) related to fatty acid composition. Thirty five Javanese fat tailed sheep rams were used in this study. Identification of gene polymorphism and associations of KIF12 gene was performed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method and general linear model (GLM) analysis. The results of the identification of KIF12 gene polymorphism are polymorphic. The results showed that there were three genotypes (CC, CT, and TT) found in this study. Association analysis showed that KIF12 gene was significant ($p < 0.05$) associated with unsaturated fatty acids including Miristoleic acid (C14:1), Oleic acid (C18:1n9c) and saturated fatty acid including Lauric acid (C12), Myristic acid (C14), and Heptadecanoic acid (C17). The genotype CC exhibited greater the unsaturated fatty acid Miristoleic Acid (C14:1) and the saturated fatty acids Lauric acid (C12) and Myristic acid (C14) than the genotypes CT and TT ($p < 0.05$). The genotype CT exhibited greater the unsaturated fatty acid Oleic acid (C18:1n9c) and the saturated fatty acid Heptadecanoic acid (C17) than the genotypes CC and TT ($p < 0.05$). These results will improve the understanding of the functions of the KIF12 gene in fatty acid metabolism especially in terms of unsaturated fatty acid and will shed light on KIF12 as a candidate in the selection of sheep with high unsaturated fatty acids in Javanese fat tailed sheep.

Keywords: Association, fatty acid composition, Javanese fat tailed sheep, KIF12 gene

Contact Address: Kasita Listyarini, Bogor Agricultural University, Animal Production and Technology, Agatis Street, 16680 Bogor, Indonesia, e-mail: kasitalistyarini@gmail.com