# The functions and mechanisms of sequence differences of DGAT1 gene on milk fat in between dairy cow and buffalo

Dinesh Bhattarai[a], Tesfay Worku[a], Sutong Xu[a], Zia ur Rehman[a], Xing Chen[a], Farman Ullah[a], Min Zhang[a], Xianwei Liang[b], Tingxian Den[b], Mingxia Fan[c], Shujun Zhang[a]*

[a]Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Education Ministry of China, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan 430070, People's Republic of China b

[b]Key Laboratory of Buffalo Genetics, Breeding and Reproduction technology, Ministry of Agriculture, Buffalo Research Institute, Chinese Academy of Agricultural Sciences, Nanning, 530001China

[c]Renmin Hospital of Wuhan University. Wuhan. 430060. People's Republic of China

Short Title**:** DGAT1 **gene for milk fat in dairy cow and buffalo**

***Correspondence**

Shujun Zhang

Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction,

College of Animal Science and Technology, Huazhong Agricultural University

Wuhan 430070, People's Republic of China,

Email id: sjxiaozhang@mail.hzau.edu.cn

**Summary**

The experiments reported in this research communication is aimed to describe DGAT1 sequence and promoter region in dairy cows and buffalo and compared the activity between the two species to know the cause for milk fat variation. pGL-3 basic vectors were used to construct the reporter gene. Based on the predicted promoter region, 4 truncated plasmid vectors were constructed in cow-DGAT1 and 3 plasmid vectors in buffalo-DGAT1. Each reporter plasmid was transfected into the Bovine mammary epithelial cell (BMEC), 293T cell, and CHO cells to analyze the activity using Dual-Luciferase Reporter Assay System. The results show that the region between -93 to -556bp was essential for cow promoter activity while -84 to -590bp was essential for buffalo promoter activity revealing these regions contain core promoter. The buffalo has higher promoter activity than cow yet it was not statistically significant. Comparison of candidate mutation K232A between cow and buffalo population revealed the presence of both the allelic population in dairy cows (lysine and alanine) however, only K (lysine) allelic amino acid was found in buffalo population. The absence of the alanine allelic population from buffalo explains the higher fat content of buffalo milk.