

## EVALUATION OF BOVINE HIGH DENSITY GENOTYPING IN KANKARAJ CATTLE POPULATION IN PAKISTAN

H. Mustafa<sup>1</sup>, H.J. Heather<sup>2</sup>, K. EuiSoo<sup>2</sup>, A. Ajmal<sup>1</sup> and T.S. Sonstegard<sup>2</sup>

*<sup>1</sup>Department of Livestock Production, University of Veterinary and Animal Sciences, Lahore-Pakistan; <sup>2</sup>Bovine Functional Genomics Laboratory (BFGL), U.S Department of Agriculture/Agricultural Research Services, Beltsville, MD, USA*

Corresponding author: hamidmustafa@uvas.edu.pk

The objective of this study was to evaluate the informativeness of Bovine high density single nucleotide polymorphism (HD SNPs) genotyping in Kankaraj cattle population. This is the first attempt to assess the Bovine HD SNP genotyping array in any Pakistani indigenous cattle population. To evaluate these SNPs on genome wide scale, we considered 777, 962 SNPs spanning the whole autosomal and X chromosomes in Kankaraj cattle population. Fifteen (15) non related gDNA samples were genotyped with the bovine HD infinium. Approximately 500,939 SNPs were found polymorphic (MAF > 0.05) in Kankaraj cattle population. The results of this study indicate potential application of Bovine High Density SNP genotyping in Kankaraj cattle population. The information generated from this array can be applied in genetic prediction, characterization and genome wide association studies of Kankaraj cattle population.

**Keywords:** Genotyping, Polymorphic SNPs, Sahiwal cattle