



## Water buffalo genome characterization by the Illumina BovineHD BeadChip

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**ABSTRACT.** To define the best strategies for genomic association studies and genomic selection, it is necessary to determine the extent of linkage disequilibrium (LD) and the genetic structure of the study population. The current study evaluated the transference of genomic information contained in the Illumina BovineHD BeadChip from cattle to buffaloes, and assessed the extent of the LD in buffaloes. Of the 688,593 bovine single nucleotide polymorphism (SNP) that were successfully genotyped from the 384 buffalo samples, only 16,580 markers were polymorphic, and had minor allele frequencies greater than 0.05. A total of 16,580 polymorphic SNPs were identified, which were uniformly distributed throughout the autosomes, because the density and mean distance between markers were similar for all autosomes. The average minor allele frequency for the 16,580 SNPs was 0.23. The overall mean LD for pairs of adjacent markers was 0.29 and 0.71, when measured as for  $r^2$  and  $|D'|$ , respectively. The 16,580

polymorphic SNPs were matched to *Bos taurus* chromosome in the current bovine genome assembly (Btau 4.2), and could be utilized in association studies. In conclusion, the Illumina BovineHD BeadChip contains approximately 16,580 polymorphic markers for the water buffalo, which are broadly distributed across the genome. These data could be used in genomic association and genomic selection studies; however, it might be necessary to develop a panel with specific SNP markers for water buffaloes.

**Key words:** Buffalo; Genetic marker; Linkage disequilibrium; Illumina BovineHD BeadChip