



## Interest and limits of a bovine MD chip to study *Bos taurus* x *Bos indicus* crossbred animals in India

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### **Interest and limits of a bovine MD chip to study *Bos taurus* × *Bos indicus* crossbred animals in India**

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BAIF is an Indian NGO serving 4 million poor rural families in 16 states. Besides improvement of indigenous breeds, BAIF promotes the use of Holstein/Jersey purebred and crossbred bulls to improve *Bos indicus* non-descript cows with limited production. BAIF runs a big bull stud producing 8 million semen doses a year. A total of 288 animals from BAIF stud and nucleus farm were genotyped with the Illumina Bovine SNP50 Beadchip<sup>®</sup> (MD chip). These included Holstein (59 males (M), 23 females (F)) Jersey (39M), Holstein-Bos indicus crossbreds (78M, 7F), Jersey-Bos indicus crossbreds (28M) and Bos indicus animals (54M) mainly of Gir and Sahiwal breeds. After quality control, 43,167 SNP were kept but 18,191 of these were monomorphic in Gir and Sahiwal. These genotypes were analyzed using Principal Component Analysis (PCA) which clearly separated Holstein, Jersey and Bos indicus breeds with their crosses in intermediate positions. PCA revealed a large heterogeneity among Holstein animals, due to varied procurement sources over time. However, SNP information appeared limited to distinguish between indigenous breeds. Breed composition was studied using the Admixture software. It showed good agreement with known pedigree for Jersey crossbreds but the proportion of Holstein genes among Holstein crossbreds was frequently overestimated and Bos indicus breed composition was often incorrect. The results illustrated the necessity to genotype a larger number of local Bos indicus animals. More importantly, there is a need for the development of a more adequate MD chip with more polymorphic SNP. Being more cost efficient than the current bovine HD chip, such a MD chip could be used for determination of breed composition of crossbreds and Bos indicus animals, for genetic diversity studies but also for genomic selection of animals adapted to the local environment.