Comparsion of Haplotype block stracture in Angus Bulls genotyped by 50k and 777k Bovine BeadChip

M. Nosrati*[a], M. vatandoost [b]
a, b Department of Agriculture, Payam Noor University, Tehran, PO BOX,19395-3697, Iran
*M_nosrati@pnu.ac.ir

Abstract: Haplotype blocks are defined as long stretches of SNPs on chromosome which have low recombination rates [3]. Understanding haplotype structure in genome can greatly facilitate linkage disequilibrium analysis [2]. Haplotype-based association analysis can offer a powerful approach for mapping functional genes [4]. Moreover, haplotye blocks analysis has important implications for genome wide association selection (GWAS) to identify the relevant variants and for genomice selection (GS) and to predict the genomic breeding values using reduced variable [1]. The aim of this study was calculated the haplotype block (HB) in genome in beef Angus Cattle. Blood samples were collected from 104 Angus bulls and Genomic DNA was extracted. The samples genotyped using Illumina’s bovine HD BeadChip (n=62) and Illumina’s bovine 50k BeadChip (n=42). Data were filtered by using PLINK v1.07 (Purcell et al. 2007). After filtering a total of 1280 loci for 50k and 14219 loci for Bovine HD with call rates <99% were pruned. After frequency and genotyping pruning, 535696 SNPs for Bovine HD and 38043 SNPs for Bovine 50k BeadChip were remaind. Only SNPs located on chromosome 1 was used to study HB stracture. For detecting HB, data anlysised by Haploview v3.1 in 100 kb distance. In total 3363 and 36 haplotype block were detected on Bovine HD and 50k Beadchip respectively. For Bovine HD 32% of HB had length less than 10 kb, more ever that was 1% for 50k Beadchip. It reveald denser chip not only detect most of HB, but also, it can detected small HB on genome which are not detectable by 50k chip. In contrast, the 55% of blocks on chromosome 1 which genotyped by 50k beadchip were between 60-100 kb lenght, and only 21% of animals genotyped by Bovine HD was in this distance. It seems 50k is powerfull for detecting long HB on genome and could not able to detect most of small block size. In coclusion previous studies reported the haplotype block properties in cattle could be influenced by many aspects, such as breed, marker types, marker density and chromosome region, which formed average haplotype block size.

Keywords: Genome; Angus cattle; BovinHD; 50k BeadChip; haplotype block

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