Comparision of ROH detection in Angus breed genotyped by 50k and 777k Bovine Beadchip

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Abstract: In Most of animal population rates of inbreeding have increased as intensive selection [2]. Increased levels of inbreeding result in increased probability that animals are homozygous for deleterious alleles and, decreasing fitness and lifspans [1]. Therefore, information on inbreeding is critical in the design of breeding program. For long time pedigree information has been used to calculate the estimated inbreeding [4]. However, incomplete pedigrees result in erroneous estimates and an underestimation of levels of inbreeding [1]. With the availability of SNP array genotyping technologies, long stretches of homozygous genotypes, known as runs of homozygosity (ROH) were be identified which it can reflect genomic regions which are IBD [2]. The inbreeding coefficient can be calculated as the proportion of genome covered by ROH and has been shown to be more informative than the inbreeding coefficient estimated from pedigree data [3]. The aim of this study was calculated of ROH in genome of Angus Cattle. Blood samples were collected from 104 Angus bulls and Genomic DNA was extracted from samples. These sample 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 Run of Hemozygosity. All 42 animals which genotyped with Bovine HD, displayed at least one ROH, moreover, only the 85% of animals which genotyped by Bovine 50k displayed a ROH. This revealed that marker density strongly affects ROH detection. Total length of ROH detected on samples genotyped by Bovine HD was 44.3 Mb which this was 3.3 on animals genotyped by 50k beadchip, and Differences among breeds existed in their frequency in different ROH length categories. The 96% of ROH detected by 777k were between 1-4Mb in length (1566 from 1625), moreover only 10% Of ROH detected by 50k were in this distance. It means genotypes denser than 50k detects accurately short ROH that are most likely identical by descent (IBD).

Keywords: Run of hemozygocity; Genome; Angus cattle; BovinHD; BeadChip

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