



## Estimation of effective population size ( $N_e$ ) in Angus breed by 777K Bovine BeadChip

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**Abstract:** Effective population size ( $N_e$ ) is an important population parameter that helps to explain how the populations evolved and expanded, and to improve the understanding and modeling of the genetic architecture underlying complex traits [2]. Traditionally,  $N_e$  has been estimated by comparing DNA sequences. However,  $N_e$  is unlikely to have been constant during the evolution of humans, and so DNA sequence heterozygosity estimates some average  $N_e$  over a long period of time.  $N_e$  can also be estimated from linkage disequilibrium (LD) data [4]. This approach will estimate  $N_e$  over more recent history than DNA sequence heterozygosity [1] and can therefore complement evolutionary studies of human populations. Until recently it has not been possible to estimate  $N_e$  from LD due to the large number of closely linked markers required to do so. The aim of this study was calculated  $N_e$  in genome of Angus Cattle. Blood samples were collected from 42 Angus bulls and Genomic DNA was extracted from samples. The samples were genotyped by using Illumina's bovine HD BeadChip. Data were filtered by using PLINK v1.07. After filtering a total of 14219 loci with call rates <99% were pruned. After frequency and genotyping pruning, 535696 SNPs were remained. Only SNPs located on chromosome 1 was used to calculate  $r^2$  and  $N_e$ . the ped and map file were analyzed by Haploview v3.1. In this study, the formulation  $N_e = \left(\frac{1}{4c}\right) \left(\frac{1}{E(r^2)} - 1\right)$  was used to estimate  $N_e$ , where  $c$  is the marker distance in Morgan on autosomes assuming 100 Mb per Morgan [3]. And the age of  $N_e$  for any distance is calculated by  $1/2c$ . We inferred  $N_e$  on autosomes at distance bins of 0.001>, 0.001-0.002, 0.002-0.003, 0.003-0.004, 0.004-0.005, 0.005-0.006, 0.006-0.007, 0.007-0.008, 0.008-0.009, 0.009-0.01 cM. In this study, that the average  $r^2$  decreased with the increasing distance of SNP pairs. Specifically, the average  $r^2$  was equal to 0.6 when the SNP pair distances were less than 10 kb. With the SNP pairs increase to 100 kb, the average  $r^2$  was only 0.02. This Result showed the estimated  $N_e$  decreased through time and  $N_e$  for Angus from 1666 at 5000 generation ago were decreased to 1065 animals in the last generation (500 generations ago).

**Keywords:** effective population size; Genome; Angus cattle; BovinHD;  $r^2$

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