Identification of Markers Associated with Birth Weight in Boer Goat

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ABSTRACT

Genetic improvement of breeding depends on selective breeding of superior phenotypes. In order to increase accuracy of breeding and selection for efficient production systems, current trend is towards applying molecular markers. The purpose of the study was to identify markers associated with birth weight in Boer goats using 50k single nucleotide polymorphism (SNP) chip. A total of 657 Boer goats were selected based on the availability of birth weight data from a commercial farm. Individuals were genotyped using 50k SNP chip from Illumina using Illumina Genome Analyzer IIx. A genome wide association analysis using a mixed model was carried out and resulted in 32 detected markers for birth weight. In previous genotyping study done on the same population of goat using 20k custom-designed SNP chip resulted in 14 markers for birth weight. However, markers identified should be verified in an independent population before being applied in a Marker Assisted Selection (MAS) program. Further consideration should be on socio-economic factors as well as their sustainability in biodiverse environments.

Key Words: Molecular Markers, 50k SNP Chip, Boer Goat

INTRODUCTION

Genetic improvement of breeding depends on selective breeding of superior phenotypes. In order to increase accuracy of breeding and selection for efficient production systems, current trends is towards applying molecular markers. Molecular markers have been explored to evaluate the livestock performance for the purpose of genetic improvement (Montaldo & Meza-Herrera 1998; Dekkers 2004) as well for genetic diversity (Groeneveld 2010).

Currently, SNP panel are widely used to identify markers for various traits in livestock such as body weight (Esmailizadeh 2014; Jung et al. 2014; Somavilla 2014), reproductive (Tart et al. 2013; Sasaki et al. 2015; Farah et al. 2016; Ortega et al. 2016) and carcass traits (Onogi et al. 2015; Skok et al. 2016). SNP panel are also used in genetic diversity studies (Nicoloso et al. 2015; Manunza et al. 2016; Visser et al. 2016).

Based on these findings, there is potential of using markers in breeding and selection programmes. Birth weight is one of the traits of interest. Birth weight is an economically important trait and an important indicator of potential growth of livestock species. Birth weight has a direct effect on weights at subsequent ages, growth rate, rate of maturing and carcass characteristics (Greenwood et al. 1998). Low birth weight is normally associated with neonatal mortality (Morel et al. 2008). Weight is controlled by multigenes and environmental factors. Identification of markers associated with birth weight is important for genetic improvement program in a breeding population. The purpose of the study was to identify markers associated with birth weight in Boer goats using 50k single nucleotide polymorphism (SNP) chip.

MATERIAL AND METHODS

Biological samples and genotyping

A total of 657 Boer goats were selected based on the availability of birth weight data from a commercial farm at Negeri Sembilan, Malaysia. The parental stock of these Boer goats were imported from Australia.

DNA samples were extracted using a Promega Wizard Genomic DNA Purification System. Individuals were genotyped using the Goat SNP50 Beadchip (Illumina Inc., San Diego, CA) developed by the International Goat Genome Consortium (Tosser-Klopp et al. 2014). Genotyping was done at DNA Landmarks Inc. using Illumina Genome Analyzer IIx.

Whole genome association (WGA) and SNP Selection

To maximize the information from 50k genotyping, the samples with low call rate (<90%) and without phenotype data were excluded. Samples with the pedigree information were included in the 50k typing.

To select a panel of significant SNPs, those SNPs were selected based on their own *p*-value but also the P-value of the nearby SNPs. The regions that showed multiple SNPs with significant association were considered as promising regions.The most significant SNP was selected from such peaks. The minimum P-value is set as P<0.01 for SNP selection.

The statistical analysis was performed using ASREML by 2-step Mixed model (Aulchenko et al. 2007). The model for the body weight was: BW = Sex + Type of birth + Polygenic effect and SNP effect. In order to estimate polygenic effect, the relationship matrix was calculated using genotypes rather than pedigree due to some pedigree errors in the dataset. Sex and type of birth were estimated as fixed effects for birth weight. SNPs were selected based on the P-value of individuals SNPs as well as P-value of the nearby SNPs.

RESULTS AND DISCUSSION

Chromosomes and SNPs position from this study are shown on Manhattan plots in Figure 1. Different colors in the figures are used to separate different chromosome based on cattle genome. The position is also based on cattle chromosome. Each dot in the figure means a SNP. The SNP with high –log10 (P-value) indicate higher association with the trait. The –log10 (P-value) = 3 is equivalent to P= 0.001.
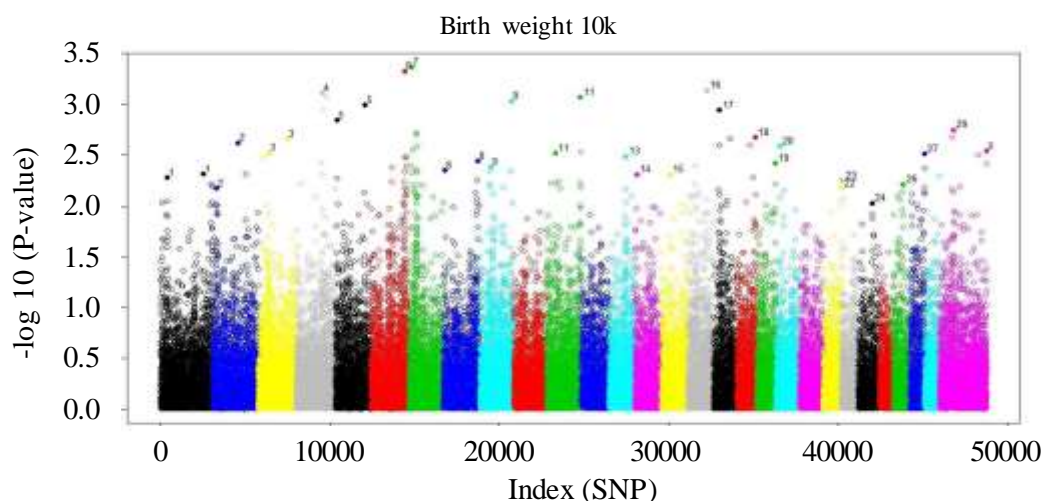

Figure 1. Manhattan plots of SNP associated with birth weight using 50k SNP chip

The P-value for SNPs selected is shown in Table 1. The minimum P-value considered for SNPs selection in this study was P<0.01. The study identified 32 markers associated with birth weight from the Boer goat population (Table 1).

Table 1. Description of SNPs associated with birth weight in Boer goats

SNP name	Position	P-value	No. of animals
snp2671-scaffold1077-260243	19909684	0.005297	657
snp11813-scaffold1438-715481	129502496	0.004868	657
snp32307-scaffold367-263826	9767203	0.006697	657
snp50955-scaffold739-2803010	74046302	0.002391	657
snp37581-scaffold460-60946	33758693	0.002999	657
snp44026-scaffold595-5741464	93639804	0.002201	656
snp38964-scaffold494-3410708	80093565	0.000769	644
snp15225-scaffold1622-357391	5648416	0.001430	654
snp56986-scaffold903-353290	99263534	0.001016	657
snp25700-scaffold2643-789862	105389938	0.000470	657
snp22606-scaffold224-142058	8647570	0.000431	657
snp33318-scaffold391-2347591	4580242	0.004488	657
snp31895-scaffold356-4322178	106432736	0.003616	656
snp474-scaffold1011-1799744	33253406	0.004124	656
snp36799-scaffold447-297097	98382724	0.000933	657
snp9777-scaffold135-3200308	26279972	0.003015	657
snp17416-scaffold1803-76969	103665273	0.000856	655
snp13092-scaffold150-5061100	53167884	0.003260	657
snp21427-scaffold209-942795	7015359	0.004899	657
snp8602-scaffold131-1092240	61141555	0.000731	657
snp21169-scaffold207-2673559	18229249	0.001137	656
snp26870-scaffold283-439363	57378759	0.002129	657
snp41374-scaffold537-4310995	61758779	0.003800	657
snp14677-scaffold1591-1036604	11253247	0.002574	657
snp48747-scaffold692-580888	2654510	0.005606	657
snp22924-scaffold229-76929	44318631	0.003064	657
snp17566-scaffold182-238289	46847552	0.001783	657
snp54569-scaffold833-1768789	40801388	0.009374	657
snp31701-scaffold353-108154	30725050	0.006161	657
snp52571-scaffold783-10947	147516206	0.002885	657
snp4850-scaffold1162-146734	27736297	0.004901	657
snp56008-scaffold870-892566	60050800	0.006743	649

Discussion

A genome wide analysis using 50k SNP panel resulted in 32 detected markers. In previous genotyping study done on the same population of goat using 20k custom-

designed SNP chip resulted in 14 markers for birth weight (Saadiah et al. 2014). The chromosomal regions of SNPs selected from 20k do not completely overlapped with the ones selected from 50k. This indicate the challenges in identifying markers that control traits. Various factors have to be taken into consideration in order for the markers to be accurately utilised in breeding programme. In a study done by Brito et al. (2015) on characterization of linkage disequilibrium indicate that genome selection could be implemented within breed for a large training population but some breeds will require a denser panel. Multi-breed genomic evaluation require a denser panel as well (Brito et al. 2015).

Application of these markers in a biodiversed environment and geographical location requires further consideration as several studies indicate huge genetic diversity within different goat population and geography. Different pattern of diversity displayed in different goat population such as genetic drift in Spanish (Manunza et al. 2016) and Italian goats (Nicoloso et al. 2015); lack of gene flow (Nicoloso et al. 2015) and admixture with other goat breed (Manunza et al. 2016; Visser et al. 2016). Geographical locations cause genetic distiction between the population. Furthermore, for purebred population, inbreeding depression have impact on economic income of breeders (Leroy 2014). It is expected that the genetic background will affect different pattern of genome wide association of various traits.

CONCLUSION

The results give more insight into the trait of interest for breeding animals. More denser SNP panel such as 50k chip resulted to more markers generated as compared to less dense SNP panel. The study contribute to the understanding of genomic variability in relation to the birth weight in locally adapted Boer goat. However, markers identified should be verified in an independent population before application in a Marker Assisted Selection program (MAS) program. Further consideration should also be given to socio-economic factors as well as sustainability in a biodiverse environment.

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