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Identification of quantitative trait loci affecting economic traits based on divergently selected genomic regions between beef and dairy cattle

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ABSTRACT

In our previous study, we examined divergently selected regions between Japanese Black cattle and Holstein cattle based on a 50k single nucleotide polymorphism (SNP) panel and a Sliding Window Allele Difference method resulting in the identification of 11 genomic regions. The aim of the present study was to investigate the association between these genomic regions and economic traits, including seven carcass and five milk production traits. For this purpose, representative SNP markers were selected from the 11 genomic regions and used to estimate the effects on the traits in Japanese Black cattle ($N=488$) and Holstein cattle ($N=194$). Association analyses revealed that five SNPs showed a significant effect on the carcass traits in Japanese Black cattle and other five SNP showed a significant association with milk production traits in Holstein cattle ($P<0.05$). These results indicated that divergently selected regions identified using a Sliding Window Allele Difference method contain the quantitative trait loci (QTL) for economic traits. Furthermore, most of the QTL identified in this study were consistent with the previously reported QTL. Further investigations of these regions may lead to the identification of the genes and polymorphisms responsible for the economic traits.

1. Introduction

Domesticated cattle have been under strong artificial selection for various economic traits such as milk or beef production. Such selection increases the frequency of favorable alleles associated with production traits, and can lead to improved productivity in cattle populations. Therefore, the frequencies of favorable alleles are considered to be varied by breeds depending on the specific purposes and selection goals. For example, the allelic frequencies of a missense mutation in the diacylglycerol acyltransferase (DGAT1) gene, which has a major effect on milk yield and composition, vary between different cattle breeds (Grisart et al., 2002). This study suggested that allelic frequency differences could be one of the selection criteria.

The sliding window approach is a method which analyzes several consecutive single nucleotide polymorphisms (SNPs) simultaneously in order to identify genomic regions that have been differentially selected for production traits. Using this approach, Prasad et al. (2008) detected chromosomal regions that included some evidence of artificial selection for economically important traits in Angus and Holstein cattle. Additionally, Hayes et al. (2009) compared the allelic frequencies of approximately 10k SNP markers between dairy and beef cattle

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breeds to identify divergently selected genomic regions. They identified genomic regions which harbor some reported genes such as thyroglobulin (TG) on BTA6, DGAT1 on BTA14, and growth hormone receptor (GHR) on BTA20. Bovine TG gene mutations have significant effects on marbling in beef cattle (Barendse et al., 2004), and the GHR gene contains a mutation which markedly affects protein percentage in milk from dairy cattle (Blott et al., 2003). These results suggest that the sliding window approach has utility in identifying QTL for economic traits.

In our previous study, Hosokawa et al. (2012) identified the divergently selected regions between Japanese Black cattle and Japanese Holstein cattle based on genotypic information obtained using the BovineSNP50 Beadchip (Illumina Inc., San Diego, CA) and the Sliding Window Allele Difference method. We reported 11 genomic regions with large allele frequency differences between Japanese Black cattle and Japanese Holstein cattle. These identified regions were consistent with the previously reported QTL; therefore, they match the selection criteria and are good candidates for areas that harbor the causative gene mutations. The aim of this study was to investigate the association between these 11 genomic regions and the cattle production traits. For this purpose, we selected representative SNP markers from each of the 11 genomic regions and investigated associations between the SNP markers and economic traits.

Table 1
Eleven genomic regions with large differences in allele frequencies between JB and JH.

BTA	Chromosomal position[a]	Number of SNP[b]
2	71,717,547–72,527,749	10
3	57,315,260–58,584,905	11
4	78,918,962–80,063,330	15
5	43,372,802–44,075,126	16
5	120,674,019–121,384,505	13
12	52,526,705–52,919,033	10
13	46,222,327–46,536,277	10
13	58,861,890–59,278,090	10
21	14,946,223–15,643,297	13
21	49,338,616–49,993,221	11
26	21,814,970–23,604,860	28

[a] Chromosomal position was indicated as the map position from the most centromeric marker to the most distal one in each region based on bovine genome assembly (Btau 4.0).
[b] The number of SNP which were included Illumina BovineSNP50 BeadChip.

2. Materials and methods

2.1. Samples

Genomic DNA was extracted from the Musculus trapezius muscle of 488 Japanese Black cattle and 194 Holstein dams. The average age of the Japanese Black cattle at slaughter was 29.1 months. The intramuscular fat samples were collected from the diaphragm to analyze fatty acid composition in the meat of Japanese Black cattle. The average parity and days from parturition of Holstein cattle were 1.43 and 154, respectively. Equivalent quantities of milk samples were collected from each cow in the evening and the following morning (Matsumoto et al., 2012).

2.2. Economic traits

In Japanese Black cattle, carcass traits including dressed carcass weight (kg), rib-eye area (cm^2), rib thickness (cm), subcutaneous fat thickness (cm), yield estimate (%), and beef marbling score (BMS) were measured by official graders of Japan Meat Grading Association. The fatty acid profiles were measured according to a previous study (Taniguchi et al., 2004). The analyzed fatty acids were the following: C14:0, C14:1, C16:0, C16:1, C18:0, C18:1, and C18:2, monounsaturated fatty acid (MUFA) and saturated fatty acid (SFA). In Holstein cattle, the milk yield (kg), fat yield (kg), protein yield (kg), fat percentage (%) and protein percentage (%) were measured as milk production traits.

2.3. SNP selection and genotyping

In this study, we focused on 11 genomic regions which were previously identified by Hosokawa et al. (2012) (Table 1). Representative SNPs were selected from each of the 11 regions based on following criteria. (1) The difference of allele frequency between breeds was the largest in each region and (2) in view of statistical analysis,

Table 2
Detail of SWB markers.

Marker	Name	Chromosomal position[a]	JB MAF[b]	|JB-Holl[c]
SWB2-1	BTA-11592-rs29017351	BTA2: 72527749	0.16	0.77
SWB3-1	ARS-BFGL-NGS-12447	BTA3: 57339352	0.5	0.43
SWB4-1	ARS-BFGL-NGS-30005	BTA4: 79176999	0.22	0.5
SWB5-1	Hapmap52717-rs29026394	BTA5: 43372802	0.37	0.37
SWB5-2	Hapmap49920-BTA-23327	BTA5: 120980457	0.16	0.54
SWB12-1	BTA-23814-no-rs	BTA12: 52526705	0.18	0.65
SWB13-1	ARS-BFGL-NGS-63599	BTA13: 46505300	0.16	0.49
SWB13-2	BTB-00532606	BTA13: 58861890	0.23	0.68
SWB21-1	ARS-BFGL-NGS-112137	BTA21: 15362431	0.17	0.81
SWB21-2	Hapmap29405-BTA-159679	BTA21: 49338616	0.48	0.34
SWB26-1	BTB-00932483	BTA26: 23406738	0.18	0.76

[a] Chromosomal position was indicated based on bovine genome assembly (Btau 4.0).
[b] Minor allele frequency in Japanese Black cattle.
[c] Differences in allele frequencies between Japanese Black and Japanese Holstein.