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Article · October 2016

DOI: 10.2527/jas2016-0632

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Published October 24, 2016

Genome scan for postmortem carcass traits in Nellore cattle[1]

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ABSTRACT: Carcass traits measured after slaughter are economically relevant traits in beef cattle. In general, the slaughter house payment system is based on HCW. Ribeye area (REA) is associated with the amount of the meat in the carcass, and a minimum of backfat thickness (BFT) is necessary to protect the carcass during cooling. The aim of this study was to identify potential genomic regions harboring candidate genes affecting those traits in Nellore cattle. The data set used in the present study consisted of 1,756 Nellore males with phenotype records. A subset of 1,604 animals had both genotypic and phenotypic information. Genotypes were generated based on a panel with 777,962 SNPs from the Illumina Bovine HD chip. The SNP effects were calculated based on the genomic breeding values obtained by using the single-step GBLUP approach and a genomic matrix re-weighting procedure. The proportion of the variance explained by moving windows of 100 consecutive SNPs was used to assess potential genomic regions harboring genes with major effects on each trait. The top 10 non-overlapping SNP-windows explained 8.72%, 11.38%, and 9.31% of the genetic variance for REA, BFT, and HCW, respectively. These windows are located on chromosomes 5, 7, 8, 10, 12, 20, and 29 for REA; chromosomes 6, 8, 10, 13, 16, 17, 18, and 24 for BFT; and chromosomes 4, 6, 7, 8, 14, 16, 17, and 21 for HCW. For REA, there were identified genes (*CDKN2A* and *CDKN2B*) involved in the cell cycle biological process which affects many aspects of animal growth and development. The *SLC38A1* and *SLC38A2* genes, both from *SLC38* AA transporter family, was also associated with REA. The AA transporters are essential for cell growth and proliferation, acting as carriers of tissue nutrient supplies. Various genes identified for BFT (*SORCS2*, *AQP3*, *AQP7*, *CDC42BPA*, *ASIP*, and *ACSS2*) have been associated with lipid metabolism in different mammal species. One of the most promising genes identified for HCW was the *PLAG1*. There is evidence, in the literature, that this gene is located in putative QTL affecting carcass weight in beef cattle. Our results showed several genomic regions containing plausible candidate genes that may be associated with carcass traits in Nellore cattle. Besides contributing to a better understanding of the genetic control of carcass traits, the identified genes can also be helpful for further functional genomic studies.

Key words: backfat thickness, beef cattle, carcass weight, genome-wide association study, ribeye area, single-step genomic BLUP approach

 J. Anim. Sci. 2016.94:4087–4095
doi:10.2527/jas2016-0632

[1]This work was supported by Sao Paulo Research Foundation (FAPESP grants #2009/16118–5 and #2015/06140–4), Brazil.

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Received May 13, 2016.
Accepted July 19, 2016.

INTRODUCTION

In beef cattle, carcass weight is the main measure used by the slaughter houses for payment. Ribeye area indicates the amount of meat in the carcass, and a minimum of backfat thickness is necessary to protect the carcass during cooling. Despite their importance, selection for these traits has been difficult since they are expressed late in life. In addition, the evaluation of bulls for postmortem carcass traits requires offspring information as the candidates to selection cannot be directly evaluated.

One approach that may contribute to the inclusion of carcass traits measured postmortem in the evaluation and selection of animals is the identification of genes and/or chromosome regions with major effects for these traits. In this context, genome-wide association studies (**GWAS**) have been an important tool for the detection of genetic variants associated with complex traits (Utsunomiya et al., 2013; Santana et al., 2014).

One of the methods used to implement GWAS is the single-step GWAS (Misztal et al., 2014). In this method, all available information (phenotypes, pedigree, and SNP) is used simultaneously in the analyses through a procedure that creates a combined pedigree-genomic relationship matrix, with subsequent prediction of genomic estimated breeding values (**GEBV**) of all animals. The SNP effects are then obtained from the GEBV of genotyped animals (Wang et al., 2012; Misztal et al., 2014).

Single-step GWAS permits us to estimate all effects (fixed and random) simultaneously and to include all animals (genotyped or not) in the analysis. Since one of the main limitations of GWAS has been the small number of data available for analysis (Dekkers, 2004), studies considering a model that uses all available information simultaneously could be important to obtain a more representative sample of the population. The aim of this study was to identify possible chromosome regions with greatest effect on carcass traits in Nellore cattle using the single-step GWAS method.

MATERIAL AND METHODS

Animal Care and Use Committee approval was not necessary for this study because the data were obtained from commercial herds.

Genotypes and Phenotypes

The data set used in the present study consisted of 1,756 Nellore males with phenotype records, for the following *postmortem* traits: Hot carcass weight (**HCW**), ribeye area (**REA**), and backfat thickness (**BFT**). The mean age at slaughter was 731.9 ± 83.0 d. The 1,756 males were the offspring of 294 sires and 1,546 dams, from 10 farms and 3 different breeding programs (DeltaGen, Paint, and Nelore Qualitas). Animals were distributed in contemporary groups (**CG**) defined by concatenating year and farm of birth, and management group at yearling. A subset of 1,604 animals had both genotypic and phenotypic information.

REA was determined using a grid of points, and BFT was measured with a caliper in millimeters. These 2 measurements were obtained over the *longissimus dorsi* muscle between the 12th and 13th rib of the left half-carcass according to United States Standards for Grades of Carcass Beef (USDA, 1997). For each trait, records outside the interval between 3.5 standard deviations above or below the average of the CG were excluded, and CG with less than 3 animals were removed.

Genotyping of the animals was performed using a panel of 777,962 SNP (Illumina Bovine HD). Only SNP located on autosomes with a GenCall score > 0.70 were included in the subsequent analyses. Fifty-four SNP pairs that had the same map locations were excluded from the data set. Quality control edits were applied including the removal of SNP with a MAF $\leq$ 0.02, HWE p-value $\leq 10^{-5}$, and call rate $\leq$ 0.98. Samples with call rate < 0.90 were also excluded.

After quality control of the phenotypic and genotypic data, there were 1,749 animals with records for REA, of which 1,569 animals had genotypic information of 462,518 SNP. For BFT, the data set contained 1,749 animals with phenotypic records, being 1,568 with genotypes for 462,688 SNP. There were 1,566 animals with phenotypes for HCW, being 1,409 with genotypes for 450,971 SNP. The descriptive statistics for each trait are summarized in Table 1.

It should be noted that 1 farm adopted castration of the animals, explaining the greater range in BFT values (Table 1). Additionally, there were differences in the feeding, environment, and management adopted, which are specific for each farm. As a consequence, the total range in BFT, REA, and HCW was large. Part of these differences was considered in the model by including the CG.

Before genome scanning, a principal component analysis based on the genomic relationship matrix was used to check for population stratification. Results (not

Table 1. Descriptive statistics of the phenotypic information for each trait[1]

Traits	N	Mean	SD	Minimum	Maximum
Ribeye area (cm^2)	1749	68.6	8.59	40.0	100.0
Backfat thickness (mm)	1749	4.84	2.59	1.0	23.0
Carcass weight (kg)	1566	277.9	23.4	206.7	370.6

[1]N = number of phenotyped animals; SD = standard deviation;

shown) did not indicate the existence of subgroups among the individuals from different breeding programs.

Statistical Analysis

The single-step GBLUP approach (Misztal et al., 2009) was used for the estimation of genomic breeding values (**GEBV**) for each trait. The general model was:

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}a + e$$

where **y** is the vector of observations for each trait; β is the vector of fixed effects; a is the vector of the additive effect of the animal, assuming $a \sim N(0, \mathbf{H}\sigma_a^2)$, where **H** is the matrix that combines the additive relationship matrix based on pedigree file and genomic relationship matrix and σ_a^2 is the additive genetic variance; e is the vector of residual effects, assuming $e \sim N(0, \mathbf{I}\sigma_e^2)$, where **I** is an identity matrix and σ_e^2 is the variance of residual effects; **X** and **Z** are incidence matrices that link each observation to their respective fixed and random effect. For all traits, fixed effects were: CG and animal slaughter age as covariable (linear effect). To correct for animal size, for REA, the linear effect of carcass weight, as the covariate, was added to the model. With the objective to correct for sequential selection effect, the genetic analysis for HCW trait was performed using a bivariate model, including weaning weight as anchor.

The inverse of **H** matrix was obtained according to Aguilar et al. (2010):

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

where $\mathbf{H}^{-1}$ is the inverse of the combined pedigree-genomic relationship matrix, $\mathbf{G}^{-1}$ is the inverse of the genomic relationship matrix, $\mathbf{A}_{22}^{-1}$ is the inverse of the pedigree-based relationship matrix for genotyped animals. The **G** matrix was computed based on VanRaden (2008), given by (Wang et al., 2014):

$$\mathbf{G} = \mathbf{ZDZ}'q$$

where **Z** is the matrix of genotypes adjusted for allele frequencies, **D** is a diagonal matrix containing weights for SNP effects (initially **D** = **I**), and q is a normalizing factor. Such a factor was derived by ensuring that the average diagonal in **G** is close to that of $\mathbf{A}_{22}$ (Vitezica et al., 2011).

The SNP effects were obtained based on the GEBV of the genotyped animals using an iterative procedure proposed by Wang et al. (2012). The equation used to compute the effect of SNP can be written as $\hat{u} = qDZ'G^{-1}\hat{a}_g$, where $\hat{u}$ is the vector of the effect of each SNP and $\hat{a}_g$ is the vector of GEBVs predicted for genotyped animals. The weight for each SNP effect was calculated as: $d_j = 2p_j(1-p_j)\hat{u}_j^2$, where p_j is the frequency of the second allele of the jth SNP and $\hat{u}_j^2$ is the square of the effect of the jth SNP (Zhang et al., 2010).

For this study, 2 iterations were considered. In the first round, D was an identity matrix, which means that both G matrix and SNP effects were obtained without any weighting. For the second round, D was a diagonal matrix containing the SNP weights computed in the first round, normalized to remain the total genetic variance constant (Wang et al., 2012). In this way, both GEBVs and SNP effects were refined using a weighted genomic relationship matrix (see "scenario S2" in Wang et al., 2012).

The percentage of genetic variance explained by 100-SNP windows was computed according to Wang et al. (2014):

$$\frac{Var(a_i)}{\sigma_a^2} \times 100\% = \frac{Var\left(\sum_{j=1}^{100} Z_j \hat{u}_j\right)}{\sigma_a^2} \times 100\%$$

where, a_i is the genetic value of the ith region consisting of 100 consecutive SNP, σ_a^2 is the total genetic variance, Z_j is the vector with genotype of the jth SNP for all individuals, and $\hat{u}_j$ is the effect of the jth SNP within the ith region.

Manhattan plots containing the variance explained by 100-SNP moving windows were used to identify chromosome regions with major effects on the traits. The average size ± standard deviations of the windows were 532,100 ± 210,390 bp, 532,100 ± 213,328 bp, and 546,200 ± 225,564 bp for REA, BFT, and HCW, respectively. The NCBI database (National Center for Biotechnology Information) was used to identify the candidate genes present in the top 10 SNP-windows considering the UMD3.1 bovine assembly. These genes were used in a gene-enrichment analysis with David software (Huang et al., 2009a; Huang et al., 2009b).

RESULTS AND DISCUSSION

Several genomic regions were identified that explained a moderate proportion of the genetic variance in each of the three traits (Fig. 1). The top 10 non-overlapping SNP-windows explained 8.72%, 11.38%, and 9.31% of the genetic variance for REA, BFT, and HCW, respectively. These windows were located on chromosomes 5, 7, 8, 10, 12, 20, and 29 for REA; chromosomes 6, 8, 10, 13, 16, 17, 18, and 24 for BFT, and chromosomes 4, 6, 7, 8, 14, 16, 17, and 21 for HCW. In total, 52, 76, and 59 annotated genes were identified for REA, BFT, and HCW, respectively (Tables 2, 3, and 4).

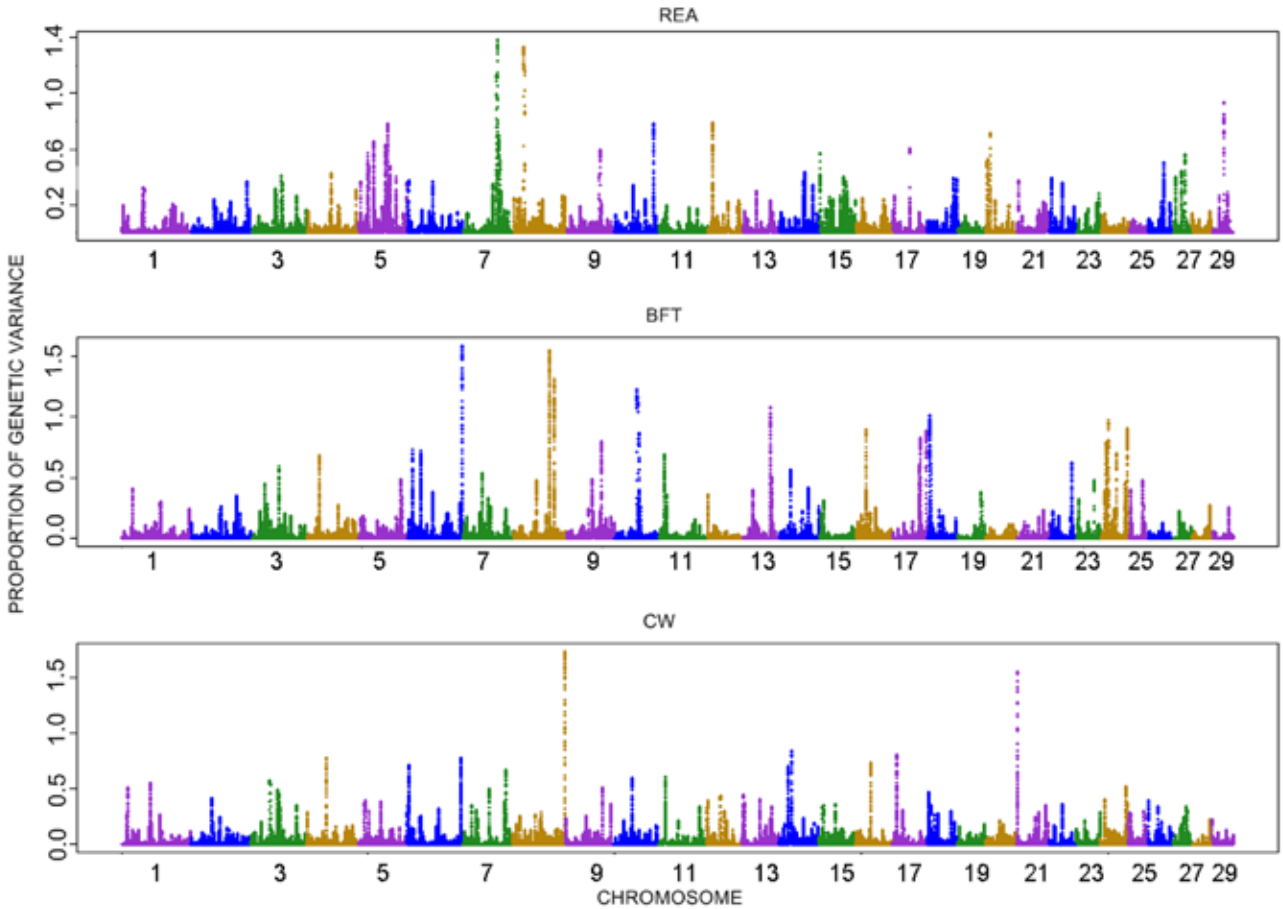

Figure 1. Manhattan plot of the variance explained by windows of 100 consecutive SNP for ribeye area (REA), backfat thickness (BFT), and carcass weight (CW).

It is worth mentioning that, even though some genomic regions with major effects were detected, the traits analyzed here are complex since there were many regions distributed across all autosomes contributing to genetic variation on each trait (Fig. 1).

The locations of the top 10 SNP-windows were different among REA, BFT, and HCW. The only exception was the window chr6:118.2–118.5 Mb that explained 1.59% of the genetic variance for BFT and 0.78% for HCW. This finding suggests that a possible pleiotropic effect may exist between BFT and HCW within this genomic region. This SNP-window harbors the *SORCS2* gene that is associated with the levels of *IGF1* and *IGFBP* (Kaplan et al., 2011). Circulating *IGF1* and *IGFBP* are involved in the regulation of carbohydrate homeostasis, can lead to the accumulation of energy in the form of fat, and were associated with height, weight, and body circumferences in humans (Kaplan et al., 2011).

In general, the chromosome regions identified for each trait corroborated the literature. For example, the SNP-window that harbors the *PLAG1* gene (chr14:24.7–25.4 Mb), which was associated with HCW in this study, has been previously associated with this trait in other studies (Nishimura et al., 2012; Saatchi et al., 2014). On the other hand, the results present here are different from those reported, for example, by Tizioto et al. (2013) in Nellore cattle. Tizioto et al. (2013) reported a different SNP-window with largest effect for REA (chr23:24.0–24.9 Mb) and for BFT (chr11:82.0–82.9 Mb), which explained 0.08% and 0.36% of the genetic variance, respectively.

The difference in GWAS results reported in the literature, considering the same breed and traits, might be explained by the fact that the influence of the genetic effect can be due to different genes and can manifest at different proportions in different environments. Furthermore, the use of different methods and differences in quality control may prevent a region that influences a certain trait in a population from being identified in another. Obviously, there are many other factors that could contribute to the different results found across studies, for example, the sample size used to estimate SNP effects, which influences the existence of false-positive or negative results (Dekkers, 2004).

In the present study, the gene *TSHR* on chromosome 10, which is involved with cell metabolism of the thyroid, was associated with REA. Thyroid hormones play a key role in differentiation, growth,

Table 2. Chromosome (Chr), position, candidate genes, and proportion of variance (Var) explained by the top windows of 100 consecutive SNP with higher effects for ribeye area[1]

Chr	Position (bp)	Genes	Var (%)
5	34041287–34787377	SLC38A2, SLC38A1, SCAF11, TRNAC-ACA, ARID2	0.66
5	68564812–68917492	CHST11, LOC101903254, SLC41A2, C5H12orf45, ALDH1L2	0.63
5	74084335–74493631	LOC101905402, LOC101905354, RASD2, MB, LOC616957, RBFOX2	0.79
7	77610842–78038681	TRNAE-UUC, LOC104968962	1.39
7	82358483–82707439	TENM2, MIR2462, WWC1	0.70
8	21487367–22408441	DMRTA1, LOC782525, LOC101907527, LOC101907577, LOC104969290, CDKN2B, CDKN2A, MTAP	1.33
10	93064242–93697011	LOC529746, LOC104973265, LOC510673, TSHR, GTF2A1, LOC101905498, STON2	0.78
12	11603434–11935366	RGCC, LOC104973536, LOC104973537, VWA8	0.79
20	9446860–10109158	LOC101905425, CARTPT, MCCC2, LOC101907652, LOC101902413, BDP1, SERF1A, LOC100847365, SMN1, NAIP	0.71
29	25401967–25724197	NAV2, LOC101905156	0.94

[1]The UMD 3.1 bovine genome assembly was used for gene assignment

metabolism, and biological function in all tissues (Klimienė et al., 2008) and may therefore favor the deposition of muscle in the carcass. Two other genes, *CDKN2A* and *CDKN2B*, on chromosome 8, are associated with cell cycle regulation which affects many aspects of development. According to van den Heuvel (2005), cell cycle regulatory network might be associated with growth, differentiation, and tissue formation during development. It is worth mentioning that cell cycle regulation also involves genes of the *TGF-β* family. According to McPherron et al. (1997), the *TGF-β* family comprises a large group of growth and differentiation factors which are important for the regulation of embryo development and for the maintenance of tissue homeostasis in adult animals. Tizioto et al. (2013), highlighted that genes from *TGF-β* pathway are important regulators of muscle development.

Two other plausible candidate genes associated with REA are *SLC38A1* and *SLC38A2*, which are part of the *SLC38* family of AA transporters (Schiöth et al., 2013). Amino acids are the basic units of proteins and regulate metabolic pathways that are essential for the health, growth, and development of an organism (Wu, 2009). The supply of AA, which is directly related to the activity of their transporters, is a limiting factor for tissue protein synthesis during periods of rapid cell growth (Taylor, 2014) and is therefore important for muscle growth. Both *SLC38A1* and *SLC38A2* genes are located in the window chr5:34.04–34.79 Mb. Our results corroborate with Saatchi et al. (2014), who reported a QTL at 34 Mb on chromosome 5 affecting ribeye muscle area in Shorthorn cattle breed.

The chr7:82.35–82.71 Mb region, which explained 0.7% of the variance for REA, harbors the *TENM2*, *MIR2462*, and *WWC1* genes. The *WWC1* gene participates in cell proliferation and influences organ size in animals (Wennmann et a., 2014). This gene has been shown to play a fundamental role in the development of fibroblasts in mouse embryos (Martianov et al., 2014).

The windows with greatest effect identified for BFT also harbor genes with known function that could be associated with the expression of this trait. For example, the *SORCS2* gene that may be related to the expression of BFT, as discussed above. The *CDC42BPA* gene is a member of the *CDC42* gene family and this gene has been shown to be involved in the development of adipose tissue in humans (Shin et al., 2014). *ASIP* has been associated with obesity in mice (Bultman et al., 1991), regulates lipid metabolism in birds (Yabuuchi et al., 2010), and is present in bovine adipocytes (Albrecht et al., 2012). *ACSS2* provides acetate for lipid synthesis and is related to the production of fatty acids in milk of dairy cattle (Bouwman et al., 2011). The gene is also associated with other genes that stimulate the loss of lipids in mice (Garrido-Sánchez et al., 2012). The *AQP7* and *AQP3* genes facilitate the efflux of glycerol from adipocytes (Rodriguez, 2014) and are associated with obesity in humans (Miranda et al., 2010). Expression of the *AQP7* gene has been shown to be associated with intramuscular fat deposition in pigs (Puig-Oliveras et al., 2014). The metabolism of lipids is similar in mammalian species and the genes identified here by GWAS, which have been reported to be associated with similar traits in other species, are plausible candidate genes.

For HCW, there is strong evidence, in the literature, that the genomic region chr14:24.7–25.4 Mb, which contains the genes *LYN*, *RPS20*, *MOS*, *PLAG1*, *CHCHD7*, *SDR16C5*, *SDR16C6*, *PENK*, and *LOC101907667* are located in putative QTL affecting carcass weight in beef cattle (Nishimura et al., 2012; Utsunomiya et al., 2013; Saatchi et al., 2014). Among these genes, the *PLAG1* is the most reported in previ-

Table 3. Chromosome (Chr), position, candidate genes, and proportion of variance (Var) explained by the top windows of 100 consecutive SNP with higher effects for backfat thickness[1]

Chr	Position (bp)	Genes	Var (%)
6	118278729–118509372	TBC1D14, CCDC96, MIR2453, TADA2B, GRPEL1, LOC104968952, SORCS2	1.59
8	76184672–76810492	B4GALT1, SPINK4, BAG1, CHMP5, NFX1, AQP7, AQP3, NOL6, UBE2R2, UBAP2	1.55
8	86607283–87230586	LOC101907656, BARX1, PTPDC1, LOC104969435, LOC521737, MIRLET7A-1, MIRLET7F-1, MIRLET7D, ZNF169, LOC101908010, LOC101907893, LOC100141230, CDC42BPA, SPTLC1	1.31
10	54254562–54907844	LOC101906580, RFX7, TRNASTOP-UCA, LOC101908048, NEDD4, PRTG, LOC104973164, PYGO1, DYX1C1	1.23
13	63963608–65002717	RALY, EIF2S2, LOC104970069, ASIP, LOC104969994, AHCY, LOC101902488, TRNAG-CCC, LOC782136, ITCH, DYNLRB1, MAP1LC3A, PIGU, LOC786401, LOC100295994, TP53INP2, LOC101903101, NCOA6, GGT7, ACSS2, GSS, LOC104973865, MYH7B, MIR499, TRPC4AP, EDEM2	1.09
16	24682103–24999548	MARK1, C16H1of115, MARC2, MARC1	0.90
17	61166258–61527226	LOC104974661	0.82
18	5279153–5565447	WWOX	1.01
24	17017956–17509828	–	0.97
24	58401703–58708913	ZNF532, LOC510913, TRNAE-UUC, SEC11C	0.91

[1]The UMD 3.1 bovine genome assembly was used for gene assignment

ous studies as candidate not only to HCW but also to several other traits. This gene encodes a zinc finger protein that acts as a transcription factor for several genes, including *IGFII* which is related to the regulation of cell growth and differentiation. The *PLAG1* gene has been associated with carcass traits in Hanwoo cattle (Lee et al., 2013; Sharma et al., 2014), Japanese black cattle (Nishimura et al., 2012; Hoshiba et al., 2013), and Gelbvieh and Simmental cattle (Saatchi et al., 2014), as well as with growth traits, feed intake, and reproductive traits in different breeds (Littlejohn et al., 2011; Utsunomiya et al., 2013; Fortes et al., 2013; Saatchi et al., 2014; de Camargo et al., 2015). Fortes et al. (2013) observed a major pleiotropic effect of this gene, which has been correlated with several traits of commercial interest. According to these authors, this gene can be used in genetic evaluations.

Other genes identified for HCW are *ASTN2* (chr8:107.98– 108.27 Mb), *HAS2*, and *LOC100139328* (*OMA1*). The latter 2 genes are located on SNP window chr14:19.38–19.78 Mb. The *ASTN2* gene has been related to osteoarthritis in humans and apparently plays a role in bone development (arcOGEN Consortium et al., 2012). The *HAS2* gene was associated with birth weight in Colombian creole cattle (Martínez et al., 2014). The *LOC100139328* gene participates in mitochondrial activity and has been associated with an increase in body weight and adipose mass in mice (Quirós et al., 2012). Hence, these genes may influence carcass weight in cattle.

Enrichment analyses were done with the top 10 windows including all traits (HCW, REA, and BFT) using DAVID tools (Huang et al., 2009a; Huang et al., 2009b). Four over-represented gene ontology terms were identified (p-value < 0.01).

Two GO terms (GO:0044267~cellular protein metabolic process and GO:0019538~protein metabolic process) shared genes identified in genomic regions associated with REA (*LOC782525* and *CARTPT*), BFT (*GRPEL1, B4GALT1*, *SEC11C, PTPDC1, UBE2R2, MAP1LC3A, NEDD4, EIF2S2, ITCH, LOC782136*, and *NFX1*), and HCW (*GRPEL1, LYN, RIOK2*, and *MOS*). These 2 significant GO terms are related to protein turnover. There is a close relationship between protein turnover and animal growth and development (Buttery, 1981). Moreover, Gomes et al. (2013) have already reported that genes related to protein turnover were associated with growth and ultrasound carcass traits in Nellore cattle.

The other 2 significant (p-value < 0.01) GO terms (GO:0016874~ligase activity and GO:0006518~peptide metabolic process) were enriched with genes identified in genomic regions associated with BFT, in which the genes *GSS*, *NEDD4*, *ITCH*, *ACSS2*, *NFX1*, and *UBE2R2* were related to GO:0016874, and *GSS*, *GGT7*, and *SEC11C* were related to GO:0006518. Although a direct association between these GO terms with BFT was not found, they are related to basic metabolism aspects that may influence many traits.

In general, the enrichment analyses complemented GWAS results and contributed to reveal the complexity of carcass traits. Different identified genes located in various genomic regions associated to carcass traits are part of the same biological processes influencing many traits simultaneously.

The present study indicated some genome regions that could be important to explain part of genetic variance for carcass traits in Nellore cattle. These regions harbor candidate genes that may be important for the understanding of genetic determinants that affect each

Table 4. Chromosome (Chr), position, candidate genes, and proportion of variance (Var) explained by the top 10 windows of 100 consecutive SNP with higher effects for carcass weight[1]

Chr	Position (bp)	Genes	Var (%)
4	49923242– 50539162	GPR141, NME8, SFRP4, LOC104972051, EPDR1, LOC101906678, STARD3NL, MIR2417, TRGC6, LOC781951	0.78
6	3506686– 3885921	ANXA5, LOC781203, LOC104972626	0.71
6	118199770– 118470818	TBC1D14, CCDC96, MIR2453, TADA2B, GRPEL1, LOC104968952, SORCS2	0.78
7	98827051– 99307994	LNPEP, LOC539264, LOC100296257, LIX1, LOC101902975, RIOK2, LOC104968996	0.67
8	107978188– 108270826	ASTN2, TRNAS-AGA	1.73
14	19379259– 19778580	LOC100139328, LOC522769, HAS2, LOC515601	0.70
14	24797724– 25354674	LYN, RPS20, MOS, PLAG1, CHCHD7, SDR16C5, SDR16C6, PENK, LOC101907667	0.84
16	37037143– 37377382	LOC104974416, LOC104974415, LOC104974414, DPT, LOC104974417, LOC104974418, TRNAC-ACA, LOC104974419, LOC104974420, TRNAC-GCA	0.73
17	10662312– 11068993	TMEM184C, LOC104974570, EDNRA	0.81
21	4684831– 5422909	LOC104975303, GABRG3, LOC783909, VIMP	1.56

[1]The UMD 3.1 bovine genome assembly was used for gene assignment.

of the traits studied. Further studies, such as fine mapping of these genes, are necessary to identify causal mutations that could be incorporated in customized chips. This information can be used in commercial genetic evaluations to increase the accuracy of carcass trait assessment. Furthermore, the association of this set of genes with the phenotypes described permits better interpretation of the biological role of these genes in cattle and closely related species, information that is generally scarce for this species. In addition, our candidate gene lists can be used as prior biological information in a further implementation of genomic selection for carcass traits in Nellore cattle. As stated by MacLeod et al. (2016), it is possible to increase the accuracy of genomic prediction by exploiting prior biological knowledge in the analysis of complex traits.

Conclusions

Association analysis indicated some chromosome regions with major effect harboring candidate genes with biological functions which could be directly or indirectly associated with the expression of carcass traits (REA, BFT, and HCW) in Nellore cattle. The candidate genes identified contribute to a better understanding of the genetic control of those traits in Nellore as well as can be helpful for further functional genomics studies. The results also showed that the genetic variance of each trait was distributed across the genome. Thus, despite potential genomic regions with major effects on carcass traits in Nellore were detected, these traits are primarily affected by many quantitative trait loci with small effects.

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