Identification of SNPs located on BTA 6 and BTA 20 significantly associated with bovine respiratory disease in crossbred cattle

S.L. Miller[1], S. Mizell[1], R. Walker[2], T. Page[1] and M.D. Garcia[1,3]

[1]School of Animal Sciences, Louisiana State University/LSU Agricultural Center, Baton Rouge, LA, USA
[2]LSU Agricultural Center Hill farm Research Station, Homer, LA, USA
[3]Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, UT, USA

Corresponding author: M.D. Garcia
E-mail: Mgarcia768@aol.com / matthew.garcia@usu.edu

Genet. Mol. Res. 15 (4): gmr.15048861
Received June 7, 2016
Accepted July 29, 2016
Published October 6, 2016
DOI http://dx.doi.org/10.4238/gmr.15048861

ABSTRACT. The objective of the present study was to evaluate single nucleotide polymorphisms (SNPs) located in two quantitative trait locus (QTL) regions (BTA 6 and BTA 20) that are associated with bovine respiratory disease (BRD). A population of 323 crossbred steers sired by five purebred sire breeds during 2010-2013 (Angus, Braford, Braunvieh, Charolais, and Simmental) were evaluated for BRD susceptibility during the finishing process at a commercial feedlot. A total of 21 animals representing all sire breeds were affected with BRD at some time during the finishing process over the 4-year period. Although multiple sire breeds were evaluated in the present study, no sire breed effects were detected. A total of 82 SNPs were evaluated (58 on BTA 6 and 24 on BTA 20) in the present study for

potential associations with BRD incidence. When evaluating the previously described QTL regions on BTA 6, three SNPs (rs42968895, rs42823614, and rs43448463) were significantly ($P < 0.05$) associated with BRD incidence. Another three SNPs (rs42477340, rs42512588, and rs42524468) were identified as significantly associated with BRD on the previously described BTA 6 QTL region. For both of these regions, animals inheriting different genotypes differed in BRD incidence during the finishing period. Although multiple SNPs were identified as being significantly associated with BRD incidence in the present study, these SNP associations should be validated in larger and more diverse populations.

Key words: SNP; Bovine respiratory disease; Feedlot; Finishing

INTRODUCTION

Bovine respiratory disease (BRD) is the most common disease affecting feedlot cattle. It contributes to approximately 75% of morbidity and 50-75% of mortality in feedlots annually (Brooks et al., 2011). Economic losses incurred by animals contracting BRD, due to reduced feed efficiency, veterinary treatment, and death, are estimated to cost the U.S. beef industry 640 million dollars annually (Bowland and Shewen, 2000). Although cattle of all ages can be affected by BRD, most are susceptible during times of high stress as young calves (Schneider et al., 2010). Commonly referred to as shipping fever, BRD is most prevalent in calves being transported to feedlots after being weaned (Bowland and Shewen, 2000). The severity of bovine respiratory infection has been linked to a variety of factors, including environmental and nutritional changes, transportation, and weaning factors. Of these factors, transportation is the most accepted non-infectious risk factor for BRD (Bowland and Shewen, 2000). Fatal respiratory infections occur when a primary viral infection compromises host defenses and enhances the severity of a secondary bacterial infection (Hodgson et al., 2005).

Identifying animals with genetic predisposition to BRD susceptibility/resistance is vitally important, as BRD is a lowly heritable trait (Snowder et al., 2005). As such, identification of single nucleotide polymorphisms (SNPs) significantly associated with BRD resistance has become of great importance to the beef industry (Dekkers, 2004). Previous studies have reported quantitative trait locus (QTL) regions associated with BRD susceptibility located on BTA 6 and BTA 20 (Li et al., 2004; Casas et al., 2010). Moreover, the U.S. meat and animal research center reported 30 SNPs on 15 chromosomes that were associated with BRD, including the previously described regions located on BTA 6 and BTA 20 (Casas et al., 2010). Thus, the objective of the present study was to evaluate SNPs located in the previously described QTL regions BTA 6 and BTA 20 for potential associations with BRD incidence in a population of crossbred steers finished in a commercial feedlot.

MATERIAL AND METHODS

All animals were treated and maintained in accordance with the principles and guidelines outlined in the Guide for the Care and Ethical Use of Agricultural Animals in Research and Teaching (Protocol #AE2009-21). The animals utilized in the present study were

comprised of 323 crossbred steers born at the Louisiana State University Agricultural Center Central Research Station in Baton Rouge, LA and the Agricultural Center Hill Farm Research Station in Homer, LA from 2010 to 2013. Calves were born during the spring calving season and were managed at these facilities until weaning, or until approximately six to seven months of age. Calves were sired by Charolais, Braunvieh, Simmental, Angus, or Braford bulls. The dam breeds at the Central Research Station utilized for this study have been previously described during the characterization of the Germplasm Evaluation VIII studies (Wheeler et al., 2010). The dams utilized by the Hill Farm Research Station in Homer, LA comprised various breed backgrounds. Steers were given a preconditioning ration at weaning and were fed 2.24 kg per head or 1.5% of the calves' body weight each morning for 45 days. Along with feed, calves had access to pasture grazing and bales of hay. At weaning, the calves were vaccinated with Bova Shield Gold FP5 and Clostra Shield 7. Calves were then boostered with Bova Shield Gold FP5 and Clostra Shield 7 approximately 30 days later. Steers that were deemed healthy enough for shipping were vaccinated and shipped to commercial feedlots in Texas and Oklahoma for the finishing process. During the finishing process, animals were recorded as 0 if it was never affected with BRD and 1 if it was affected by BRD at some point during the finishing process. In this study, a total of 302 animals over the four-year period were recorded as unaffected by BRD, whereas 21 animals were affected with BRD (Table 1).

Table 1. Total number of animals for each sire breed and total number affected by BRD for each sire breed.

Sire breed	Total No. of animals	Total No. affected by BRD
Angus	55	4
Braford	29	2
Braunvieh	46	0
Charolais	133	12
Simmental	60	3

Ear notches were collected from all calves at birth for future DNA extraction. Extraction of DNA was conducted using a saturated salt procedure previously described by Miller et al. (1988). DNA stock solutions were diluted to 25 ng/µL concentrations for future genotyping reactions. Fifty-eight SNPs were selected from a previously described QTL region associated with incidence of BRD, spanning between 40-80 Mbp on BTA 6 (Li et al., 2004). Another 24 SNPs were selected from a QTL region located on BTA 20 (0-30 Mbp) that has also been associated with BRD incidence (Casas et al., 2011). SNPs were selected using the QTL database (http://www.animalgenome.org/cgi-bin/QTLdb/index). SNPs, allele substitutions, and upstream and downstream genomic sequences are presented in Tables 2 and 3. SNP genotyping was performed by Neogen, Inc. (Lincoln, NE, USA) using the Sequenom platform.

The mixed model procedure of SAS (v. 9.4, SAS Institute, Cary, NC, USA) was utilized to evaluate potential associations of SNPs located on BTA 6 and BTA 20 with BRD incidence. Only SNPs with more than one genotype were included in the analysis. The LSMEANS function, along with a pre-planned pairwise comparisons procedure, was utilized to evaluate if significant differences existed between individuals inheriting different SNP genotypes identified as significant for BRD incidence. The dependent variable in the model was incidence of BRD. The independent variables included sire breed, SNP genotype, and birth year. Sire breed (year) was fit into the model as a random nested variable to account for confounding effects of sire breeds among the four years. Significance in the model was set at $P \leq 0.05$.

Table 2. Single nucleotide polymorphism ID, allele substitutions, and upstream and downstream genomic sequences utilized for amplification and visualization of genotypes for BTA 6.

SNP ID	Allele substitution	Forward sequence	Reverse sequence
rs29025265	C/T	CAGTTAGAGTTCAAAGGGACTTTTG	GTCAAACTGAGTACAAAATCTTTTC
rs41626155	C/T	TCCTGCCCTGCCTTCTTTAACTTCT	TCCCCAATCTCTGGTTGCCATTCAT
rs41653357	A/C	TGGAGAATCCTTTAGACAATAGGAG	TTGGTGGGCTATAGTCCATGGGGTT
rs42402825	A/G	GAGAATCCAAAGACAATACCAAAAT	AAGTCTATTGAAAGCCCACTCCTTG
rs42403565	C/T	ATTTCTATTACCCTATGTGTCAGAT	TCTGATTCACTCTTCTGCCTCCTCT
rs42571566	A/G	GCCGTCTATGGGGTCGCACAGAGTC	GACACGACTGAAGCAACTTAGCAGC
rs42579150	C/T	ATATGCCAATGATCTTAAAATTACT	GGTAAATATTTGAACATTTTTCTGC
rs42579164	A/C	CTCTATTTTTACAACATGGATGGAC	TAGAGATGATTATACTAAGTGAAGA
rs42725112	C/T	TTCATTAAAACACAAAAATCACAAC	AACTGCTGAACAACCACCAGCAAAA
rs42823614	A/C	AGGCAAATTCTTCACCAGCTGAACC	CAGGGAAAGCCTAATTCCCACCTTC
rs42824344	C/T	GTAGCATCATTGCCCTTTAATTATC	AAACTAGAAGCAAACTGAATGTCCA
rs42880470	A/G	TCTGGAGTAGGTACTGTGGGAGCAA	CTCAATCAGAGTTGTGAATAGCCTC
rs42880522	A/G	CTGAGGCTGGCCCTGACCTGAGATA	CCACCCTTTCTTACTCTCTTTCTTC
rs42900120	G/T	GGGGAAGGGGAGGAAGGATAAATTG	GAGATTGGGACTGACATATACACAC
rs42900130	A/G	CACAGGAGATAATCCTCTGCCTCCA	TTATGGTCTTCTGTGAAAAGTACTG
rs42900481	A/G	ACTTTAGATTCAATTCTTCTTGGCT	GGGATGGAGAATCTTTGAATTTCTC
rs42961863	C/T	GGACCAGAAGTCCCTTTCCCTTGCT	ATGTGTATTTTTAATGGTGATGACA
rs42961866	G/T	TGTTGTTTCCAGCTCTCCAATCTAG	TATTGTCCATTACTATTAAACATTC
rs42961882	A/T	CTTCTTTTTTGGTATGATTTTGGTC	CTGTCTCCTATACACTATTACAGAT
rs42968197	C/T	TGACAAGTAGATGCTTTTTATTAAA	TCATTCTATGTAAGAGACAGCTGAG
rs42968891	A/G	TTCATACCTAGATAATTGCAATTTC	TACCTAGCCTTTCCAGTCCTTTGGA
rs42968895	C/T	TCATATTCAGAGGTGGGATGTCATT	TTAAGGCTTTCAAGGCACTAATCCT
rs43089863	C/G	CATCTCTCTGAGTTGTCCTCTATTG	AGTCAGGGAGCAGGGCCTTTTTACC
rs43138398	C/T	TTGCAAGATAATTACAGTCACTTCC	TTTTCATGATCATTGGCCTTGAGCT
rs43194943	A/G	ATATCTTCTTAATATCTTCTTTTTT	TTAGGTCTGCACCATTTCTGTCCTT
rs43446022	G/C	TATGTTCAGAGGAATTAAGTCTTGA	CTTGTCATAAATACAACAAAATGAG
rs43446601	G/T	GTTTCCTGGAATTTGGATGAAAATT	CCTTCAATGTTTATATCTGAATCTT
rs43446955	C/T	TGCTTGTTTATATCACTTTGATATA	ACTATATTAAATTATAATGCTCTTT
rs43447179	A/G	TTTCTTTTTTCCCACCAGGAAATAC	CATTTCCTGGCCTCATAAAGACCAT
rs43448463	A/G	AGAATGCAAAGAGGAACTAAAGAGC	TCTTGATGAGGTTGAAGGAGAAGAA
rs43448512	A/C	AGATAAACTGAGACTTTCATGACGG	AGGCTCTTGAAGGAGAAGTTCTTTG
rs43449040	A/G	CACATTGATCGCTCTAATCTTAGAG	AAAAGTGCTTAAAAACTTAGACACT
rs43449194	C/T	TGAAAATGTTTCTTGCATTATTTTA	TATCAATTTCTTCATTTTGCTGTTA
rs43449209	A/G	AGTTGCTCAAGATCACACAGCATGT	TGCTGGAGCTAGGATTGAAAGCTCA
rs43449835	C/T	TAGTATCCTTTGCTAAATTTATCAT	AGTAGGTTAAAGAAGCCTTCAGGAT
rs43449896	A/C	TCCACTGGATGATCCACTGGATCAT	GAAAAAGCAAGAGAGTTCAAGAAAA
rs43451134	A/T	CATACTATATAGCACAGGAAACTAT	TTCAATATCCTGGGATAAATCATAA
rs42403543	C/T	AAGGAAATGCTTTCAATTTTTCACT	TTTATTATGATGCAAGCTGAAGGTT
rs42481129	A/G	TTCTCCCACACCACAGTTTAAAAGC	TCAATTCTTCGGCACTCTGCCTTCT
rs42579148	G/T	TATGACTTACCTACTGCTTTTCTTT	TATCTATGATGTCATAGAATGTAAG
rs42823610	C/T	GCCATCCAGCCATCTCATCCTCTGT	GTCCCCTTCTCCTCCTGCCCCCAAT
rs42824331	A/G	CATGGGGTCGCTGAGGGTCAGACAC	ACTGAGTGACTTCACTTTCACTTTT
rs42725042	G/T	AGGGGAGAAGGGGACGATAGAGGAT	AGATGGCTGGATGGCATCACTGACT
rs43080446	G/T	TTAAAGGAAAGATTACTTTATACAA	TATAAAGTATTGAAACAATAGTCTA
rs43185776	C/G	TCCTATGTCATCCCCTTCTCCTCCT	CCCTCAATCCCTCCCAGCATCAGAG
rs43178720	A/T	TGTATGTCTGTATGTACAGACATAC	GTGAAATATGTATATATGTACAGAC
rs43449906	G/T	TATATAAAATTGCATTTTAGAAAAC	TAAAGGTGATTAATGCTTTTTAATT
rs43449868	A/G	CCTAGAGCCAGACATCCTGGAATGC	AAGTCAAGTGGGCCTTAGGAAGCAT
rs43448433	A/G	ATTGAAGAATCTCTTTCTATATTCT	AATATTCTTAGTTTTCACATCCCCC
rs42940872	C/G	ATACAGCCAAAGGCTTTAGCAAAGT	ATGAAGCAGAAGTGTATGATTTTCT
rs43130086	A/G	AACTTAGGTGAGCTGAGGGGGCTGA	GGAAATCCACACAAGTCGCCCATGA
rs43444877	A/G	TCTGAAGAGTTCTTATCCCAAGAAA	AAAATTTTTTTTCTATTTCTTTAAT
rs43445941	G/T	AAACTCCAATACTTTGACCACCTGA	GCAAAGAACTGACTCATTAGAAAAA
rs43445971	A/G	TACATTTAGAACTGCTTACTTTCAT	TAAGTTCTTATGTAACACATAGATT
rs42900433	G/T	CTGACTCTTGGCGATCCCATGGACT	TAGCATACCAGGCTCCTCTGTCCAT
rs42961881	C/T	TGAATGCAACACTTTAACAGCATCA	CTTTAGTATTTGAAATAGCTCAGCT
rs42725037	A/G	ATATATGTTCCTTAAGAAACAAAAA	TAGACCTACCATATGTAATCTTGCA
rs43452444	C/T	AAGAAAAGGCAGTGTGCAAACAGGG	GTGAGCCACGTGAGAGAGAAGGTCG

Table 3. Single nucleotide polymorphisms ID, allele substitutions, and upstream and downstream genomic sequences utilized for amplification and visualization of genotypes for BTA 20.

SNP ID	Allele substitution	Forward sequence	Reverse sequence
rs41595713	C/T	TCTCGGTTCCTAACACAGCCAAGAC	GTTGTCCCGAACGGGTGAGGAATGG
rs41931108	C/G	TTGGTGTGCCAAGCACATCCCCAGC	GAGGAAGGCAGGTTGTGCCCATATT
rs42476237	C/T	CCTGGCCCACCCTTCCTTCCTTCCC	ATTTGTGGAGAAGCACGTGGGGAAC
rs42476290	A/G	CTGAGGCCAGAATTCTTGAAAGAAT	TGTTTGCATGGTGACAGCAAAGCAT
rs42477340	C/T	CTCCCGCCTCCTTCTCTGCTCCCTC	GGCTCCCTCTCTGCTCCCTCCGGCT
rs42480445	C/T	TGGCCCCAAATGCCAAAAGGTTATC	TCATTTTTTTCCAAGCAATCCCACC
rs42481107	A/G	AACAACACCTTCCACCGCCCCATCC	GGTCTCAGCCTAAGCATCAGCTCTT
rs42512588	C/T	GAATGGGGAGTGACTGCTTCCTAGG	CTGGGGTTTCTGTTGGGTTGATGCT
rs42520493	A/C	CATGCTGTATATCGGAGGGTCTAGG	CTGTTAAGCAGGAAATGAGAACTCC
rs42524445	C/T	GGTTCTTAAAAGTGAAATGATAATG	AGAAGAAATAGAGTGATGTGATGTG
rs42524450	C/T	TCCTTGGAAGTGGGGTTGCTCCTTC	GGCCGCCACCCCTGGCCTCAGGCGT
rs42524466	C/G	ATTTTATGTCGCAGTTTTCTCTCAC	AATCTAAGTTTAAATCTCTCAGAGG
rs42524468	A/T	AATAGACCCACAGACATAGAAAACA	ATGTATGGTTACCAAAGGGGAAAGG
rs42524472	A/T	AAAATAAATAGTAAATCACAAACAC	AATCACAGATAGGAAGAAAATGCAA
rs42524503	A/T	GTTGTATAGACAGATATCTGTCACT	ATTCTTTCCAAATGCTCTGACAGAT
rs43036576	A/G	TAATCATGAAGCCATCCTGTAGGGT	GAGCTAGGGTTTATAGCGGCTGTGA
rs42524459	C/T	ATCCACACAGTCAAAGCCTTTGGCA	AGTCAATAAAGCAGAAATAGATGTT
rs42481060	C/T	ACTGCCTCAGGCCTGGCACACAGCC	GAGAGGCCATGGGGCCCTGTGGAGC
rs41931083	C/T	GACTTCATTTCTCTCCGTGATAATC	TGCGGGGCAGGTCCCCAGGTCTGGA
rs42524449	A/G	TCTGCCCCTGCTGACCTTCAACGTG	AATAGCTCCTCTAGGACCTCCTGCG
rs42524457	G/T	GTTTATTGTGATCCACACAGTCAAA	CCTTTGGCACAGTCAATAAAGCAGA
rs42476309	C/T	GATGGTTTAGTCACTAAGTCATGTC	GACTCTTGAAACCCCATGGACTGTA
rs42236701	A/C/G	TCCACTTGATTTCACATTCCAGGAT	TCTGGCTCTAGGTGAGTGATCACAC
rs41931859	C/T	GAGGAGCCTGGGCTACAGTTCATGG	GTCACAGAGAGTCGGACACAACTGA

RESULTS

The analyses of BRD incidence revealed six significant individual SNPs. Three of the SNPs that were significant for BRD incidence were located on each of BTA 6 (rs42823614, rs42968895, and rs43448463) and BTA 20 (rs42477340, rs42512588, and rs42524468) (Table 4). Animals inheriting differing genotypes for each of the significantly identified SNP's had differing levels of BRD susceptibility or resistance (Table 5). Although multiple SNPs were described as significant sire breed was not identified as a significant source of variation, thus significance associations can be attributed to individual SNP and not sire breed.

Table 4. Level of significance and frequency of animals from each genotype associated with incidence of bovine respiratory disease.

BTA	SNP ID	Allele[1]	Minor genotype frequency	Heterozygous genotype frequency	Major genotype frequency	SNP P value	Sire breed P value
6	rs42823614	A/C	3	50	253	0.0396	0.9339
6	rs42968895	C/T	50	168	88	0.0234	0.9673
6	rs43448463	A/G	23	92	155	0.0334	0.9699
20	rs42477340	C/T	114	52	116	0.0192	0.9906
20	rs42512588	C/T	48	154	104	0.0167	0.9924
20	rs42524468	A/T	21	73	180	0.0324	0.6240

[1]The major allele is presented on the left.

Table 5. Single nucleotide polymorphisms associated with bovine respiratory disease and least square means estimate comparisons between reported genotypes for incidence of bovine respiratory disease.

Trait	BTA	SNP ID	Allele[2]	Major genotype mean	Heterozygous genotype mean	Minor genotype mean
BRD[1]	6	rs42823614	A/C	0.071 ± 0.059^{a}	0.179 ± 0.071^{b}	0.033 ± 0.157^{ab}
BRD	6	rs42968895	C/T	0.028 ± 0.061^{a}	0.121 ± 0.058^{bc}	$0.057 \pm 0.065a^{ac}$
BRD	6	rs43448463	A/G	0.061 ± 0.050^{a}	0.090 ± 0.053^{a}	0.232 ± 0.074^{b}
BRD	20	rs42477340	C/T	0.093 ± 0.062^{ab}	0.162 ± 0.068^{a}	0.030 ± 0.063^{b}
BRD	20	rs42512588	C/T	0.047 ± 0.058^{a}	0.072 ± 0.055^{a}	0.184 ± 0.064^{b}
BRD	20	rs42524468	A/T	0.119 ± 0.037^{a}	0.017 ± 0.046^{b}	0.025 ± 0.074^{b}

Different superscripted letters indicate significant differences of means at $P \leq 0.05$ within rows. [1]BRD = Bovine respiratory disease. [2]The major allele is presented on the left.

DISCUSSION

Three of the SNPs identified in the present study that were located on BTA 6 were significantly associated with BRD incidence. These results are in agreement with previous research that identified a significant QTL region along with significant SNPs associated with BRD incidence located on BTA 6 (Li et al., 2004). However, BRD was not the only economically important trait to be significantly associated with this region on BTA 6. Growth traits such as birth weight, weaning weight (Lu et al., 2013a), hip height (Bolormaa et al., 2014), and carcass traits, such as carcass weight (Lu et al., 2013b), rib eye area (Casas et al., 2000), marbling (Lee et al., 2012), and back fat thickness (Li et al., 2004), have also been found to be significantly associated with this region.

Furthermore, three identified SNPs located on BTA 20 were also associated with BRD incidence. These results are in agreement with a previous study that identified SNPs significantly associated with incidence of BRD on BTA 20 (Casas et al., 2010). Like the BTA 6 region, BTA 20 has also been associated with other economically important traits such as the growth traits birth weight, weaning weight (Saatchi et al., 2014), and hip height (Bolormaa et al., 2014), and carcass traits such as carcass weight (McClure et al., 2010), yield grade, marbling (Saatchi et al., 2014), rib eye area (Garcia et al., 2010), and back fat thickness (Garrett et al., 2008).

These results indicate that BRD susceptibility may have a strong genetic component in conjunction with an environmental influence. To validate the results of the present study, a larger, more diverse population of animals should be utilized. Additional SNPs located on BTA 6 and BTA 20, as well as evaluation of SNPs in other regions of the bovine genome, should be evaluated. This will ensure that SNPs accounting for the most variation in BRD susceptibility are identified, which will lead to improved accuracy for identifying genetic predisposition to BRD. Furthermore, the identified SNPs in these regions should be evaluated for multiple traits so that selection for specific SNPs associated with BRD does not result in detrimental selection of other economically important traits.

Conflicts of interest

The authors declare no conflict of interest.

ACKNOWLEDGMENTS

Research supported by the Louisiana Agricultural Experiment Station through the use of State and Federal Hatch funds.

REFERENCES

Bolormaa S, Pryce JE, Reverter A, Zhang Y, et al. (2014). A multi-trait, meta-analysis for detecting pleiotropic polymorphisms for stature, fatness and reproduction in beef cattle. *PLoS Genet.* 10: e1004198. http://dx.doi.org/10.1371/journal.pgen.1004198

Bowland SL and Shewen PE (2000). Bovine respiratory disease: commercial vaccines currently available in Canada. *Can. Vet. J.* 41: 33-48.

Brooks KR, Raper KC, Ward CE, Holland BP, et al. (2011). Economic effects of bovine respiratory disease on feedlot cattle during backgrounding and finishing phases. *Prof. Anim. Sci.* 27: 195-203. http://dx.doi.org/10.15232/S1080-7446(15)30474-5

Casas E, Shackelford SD, Keele JW, Stone RT, et al. (2000). Quantitative trait loci affecting growth and carcass composition of cattle segregating alternate forms of myostatin. *J. Anim. Sci.* 78: 560-569. http://dx.doi.org/10.2527/2000.783560x

Casas E, Kuehn L, Snelling W and Wells J (2010). Genomics of disease in beef cattle. Proceedings of the 9th World Congress on Genetics Applied to Livestock Production, Leipzig, Germany. August 1-6, 2010. CD-ROM Communication No. 0125.

Casas E, Garcia MD, Wells JE and Smith TP (2011). Association of single nucleotide polymorphisms in the ANKRA2 and CD180 genes with bovine respiratory disease and presence of Mycobacterium avium subsp. paratuberculosis(1). *Anim. Genet.* 42: 571-577. http://dx.doi.org/10.1111/j.1365-2052.2011.02189.x

Dekkers JC (2004). Commercial application of marker- and gene-assisted selection in livestock: strategies and lessons. *J. Anim. Sci.* 82 (E-Suppl): E313-E328.

Garcia MD, Thallman RM, Wheeler TL, Shackelford SD, et al. (2010). Effect of bovine respiratory disease and overall pathogenic disease incidence on carcass traits. *J. Anim. Sci.* 88: 491-496. http://dx.doi.org/10.2527/jas.2009-1874

Garrett AJ, Rincon G, Medrano JF, Elzo MA, et al. (2008). Promoter region of the bovine growth hormone receptor gene: single nucleotide polymorphism discovery in cattle and association with performance in Brangus bulls. *J. Anim. Sci.* 86: 3315-3323. http://dx.doi.org/10.2527/jas.2008-0990

Hodgson PD, Aich P, Manuja A, Hokamp K, et al. (2005). Effect of stress on viral-bacterial synergy in bovine respiratory disease: novel mechanisms to regulate inflammation. *Comp. Funct. Genomics* 6: 244-250. http://dx.doi.org/10.1002/cfg.474

Lee JH, Li Y and Kim JJ (2012). Detection of QTL for carcass quality on chromosome 6 by exploiting linkage and linkage disequilibrium in Hanwoo. *Asian-australas. J. Anim. Sci.* 25: 17-21. http://dx.doi.org/10.5713/ajas.2011.11337

Li C, Basarab J, Snelling WM, Benkel B, et al. (2004). Identification and fine mapping of quantitative trait loci for backfat on bovine chromosomes 2, 5, 6, 19, 21, and 23 in a commercial line of *Bos taurus*. *J. Anim. Sci.* 82: 967-972. http://dx.doi.org/10.2527/2004.824967x

Lu D, Sargolzaei M, Kelly M, Vander Voort G, et al. (2013a). Genome-wide association analyses for carcass quality in crossbred beef cattle. *BMC Genet.* 14: 80. http://dx.doi.org/10.1186/1471-2156-14-80

Lu D, Miller S, Sargolzaei M, Kelly M, et al. (2013b). Genome-wide association analyses for growth and feed efficiency traits in beef cattle. *J. Anim. Sci.* 91: 3612-3633. http://dx.doi.org/10.2527/jas.2012-5716

McClure MC, Morsci NS, Schnabel RD, Kim JW, et al. (2010). A genome scan for quantitative trait loci influencing carcass, post-natal growth and reproductive traits in commercial Angus cattle. *Anim. Genet.* 41: 597-607. http://dx.doi.org/10.1111/j.1365-2052.2010.02063.x

Miller SA, Dykes DD and Polesky HF (1988). A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res.* 16: 1215. http://dx.doi.org/10.1093/nar/16.3.1215

Saatchi M, Schnabel RD, Taylor JF and Garrick DJ (2014). Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. *BMC Genomics* 15: 442. http://dx.doi.org/10.1186/1471-2164-15-442

Schneider MJ, Tait RG, Jr., Ruble MV, Busby WD, et al. (2010). Evaluation of fixed sources of variation and estimation of genetic parameters for incidence of bovine respiratory disease in preweaned calves and feedlot cattle. *J. Anim. Sci.* 88: 1220-1228. http://dx.doi.org/10.2527/jas.2008-1755

Snowder GD, Van Vleck LD, Cundiff LV and Bennett GL (2005). Influence of breed, heterozygosity, and disease incidence on estimates of variance components of respiratory disease in preweaned beef calves. *J. Anim. Sci.* 83: 1247-1261. http://dx.doi.org/10.2527/2005.8361247x

Wheeler TL, Cundiff LV, Shackelford SD and Koohmaraie M (2010). Characterization of biological types of cattle (Cycle VIII): carcass, yield, and longissimus palatability traits. *J. Anim. Sci.* 88: 3070-3083. http://dx.doi.org/10.2527/jas.2009-2497