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Influence of temperament-related genes on live weight traits of Charolais cows

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ABSTRACT - We investigated whether a panel of molecular markers previously associated with temperament has an effect on live growth traits. Phenotypic data from 412 Charolais cows categorized according to their age in adult and young cows were used to determine Pearson's correlations between birth (BW), weaning (WW), and yearling live (YW) weight and temperament traits (measured as exit velocity [EV] and temperament score [TS]). For association analysis, selective genotyping of a group of 80 cows identified as the most docile and temperamental were genotyped with a 151-SNP (single-nucleotide polymorphisms) panel of molecular markers previously associated with temperament. Significant Pearson's correlations between birth weight and weaning weight and the two temperament measurements (EV and TS) were observed only in the young cow group. Significant effects of ten SNP on BW and WW were observed. Four markers located on candidate genes for temperament traits also had an effect on birth weight and weaning weight in Charolais cows, which indicates that both traits could be influenced by the same genes.

Keywords: beef cattle, behavior, body weight, candidate genes, SNP, temperament

Introduction

For beef cattle, birth weight is an important trait that represents the first phenotypic variable of a new individual in a population and is also considered an indicator of calving ease (Canellas et al., 2012). Furthermore, for beef cattle producers, calves with greater weights at weaning have the advantage of being more morphologically developed and better equipped to successfully cope with the environment (Jahuey-Martínez et al., 2016).

Databases with phenotypic records that describe growth usually include birth (BW), weaning (WW), and yearling (YW) weight (Jahuey-Martínez et al., 2016). The expression of growth traits is influenced by multiple environmental and genetic factors, and innumerable interactions of this trait with others, such as temperament, have been described. Temperament, defined as the response of an animal to handling by humans (Burrow and Dillon, 1997), has been studied in cattle using different testing approaches (Haskell et al., 2014; Friedrich et al., 2015). For example, flight speed is a measure of the time it takes for an animal to traverse a certain distance after being contained in a chute (Lindholm-Perry et al., 2015). Different studies have found that cattle with slower flight speeds gain weight more rapidly than those with faster flight speeds (Burrow and Dillon, 1997; Voisinet et al., 1997; Cafe et al., 2011) and that temperamental cattle have lower live weights than docile cattle (Fordyce et al., 1985).

Exit velocity (EV) is frequently used as a measure of cattle temperament. It is defined as the rate (m/s) at which an animal traverses a specific distance after exiting a squeeze chute (Curley et al., 2006). Petherick et al. (2002) found a negative correlation between flight speed and daily weight gain in 5/8 Brahman × 3/8 Shorthorn steers; they found that flight speed was a reliable predictor of the performance of the animals. Similarly, in a study with many animals, unfavorable genetic and phenotypic relationships were observed between average daily gain (ADG) estimated from weaning to yearling in *Bos indicus* (Nellore) cattle, demonstrating that animals with high flight speeds had lower body weights (Sant'Anna et al., 2012). Similarly, a study with *Bos taurus* cattle reported that animals exhibiting more excitable temperaments were phenotypically more likely to have a lower body weight at entry into the feedlot than more docile cattle (Reinhardt et al., 2009). Thus, investigators and producers have increasingly focused on the reaction of livestock during management using diverse methods to determine the temperament of the animals (Haskell et al., 2014). Such research is based on evidence from the literature, in which docility is correlated with not only the ease of managing cattle but also with economically relevant traits (Haskell et al., 2014; Friedrich et al., 2015).

Previous studies have identified growth-influencing genes in Mexican Charolais cattle (Jahuey-Martínez et al., 2016). Garza-Brenner et al. (2017) identified new genes and polymorphisms associated with bovine temperament as well as specific single-nucleotide polymorphisms (SNP) that showed effects on temperament-related traits such as EV and pen score (PS). Previous reports have not determined the effect of these genes on both characteristics (growth traits and temperament); however, these genes could have this potential due to their reported biological activities (e.g., the genes proopiomelanocortin [POMC], neuropeptide Y [NPY], and certain genes belonging to the solute carrier family [SLC18A2]).

The objective of this study was to determine how a panel of molecular markers previously associated with temperament affect growth characteristics (BW, WW, and YW) in Charolais cows.

Material and Methods

The studied animal populations were included in the Animal Biotechnology Biobank and represented animals from four herds located in the northwest of México: herd 1 (n = 50), herd 2 (n = 77), herd 3 (n = 145), and herd 4 (n = 140). All cows in this study were born between 2004 and 2013, and similar management objectives in each herd are based on the sale of breeding stock and breeding purebred Charolais cattle. For correlation analysis of growth traits and temperament, data from selected animals (412 Charolais cows) were obtained from the Charolais Herd Book de México A.C.© (consulted July 2017) online database (http://www.ronbmexico.com/charolais/BusquedaAnimales.aspx), using the registration number of each cow. Data included the registered BW, WW, and YW. As the animal age is an important factor affecting temperament (Curley et al., 2006), cows were categorized into two groups according to age: mature cows ≥ four years old (n = 270) and young cows of 2-3 years old (n = 142).

Temperament was assessed using EV and PS. For EV, the velocity of a cow as it traversed a 1.83-m (6 ft) distance was recorded with a 2-infrared sensor (FarmTek Inc., North Wylie, TX, USA) following the stimulus of hair sampling before exiting a squeeze chute (Curley et al., 2006). The velocity was calculated as EV = distance (m)/time (s). Pen score was assessed by three evaluators using a five-point scale, with scores ranging from 1 (calm) to 5 (moving aggressively), as described by Hammond et al. (1996). Individual temperament score (TS) values were calculated by averaging the PS and EV [TS = (PS + EV)/2] (Garza-Brenner et al., 2017). Records of PS, EV, and TS were obtained for each animal from the available database of the Animal Biotechnology Laboratory; these data were recorded once at the time of hair sampling from each animal (Garza-Brenner et al., 2017).

Due to financial restrictions, we implemented a selective genotyping strategy for the association analysis. From the 412 analyzed cows, a group of 80 individuals identified as the most docile (n = 41) and temperamental (n = 39) were genotyped with a 151 SNP panel using the Sequenom MassARRAY® platform (GeneSeek, Inc., Lincoln, NE, USA). All SNP were selected from a previously reported SNV (single nucleotide variations) panel described by Garza-Brenner et al. (2017). The ID and gene location of each SNP are described in Table 1. The genotypic and allelic frequencies were estimated using Genepop® web version 4.0.10 software (Rousset et al., 2008). Before the association analysis, the quality of the genotypic data was verified. The SNP that were monomorphic (n = 14) or presented minor allele frequencies <0.01 (n = 19) (Table 1) were eliminated. The allelic frequencies of each tested SNP are shown in Table 1.

Pearson's correlation coefficients among traits evaluated were determined. A general linear model was fitted for BW, WW, and YW as follows:

$$Y_{ijk} = \mu + HD_i + GE_j + G_k + \varepsilon_{ijk},$$

in which Y_{ijk} = BW, WW, and YW, which represent the dependent traits of this study; μ = the overall mean value; HD_i = the *i*-th herd effect (herd 1, herd 2, ... herd 4); GE_j = the *j*-th age group effect (young and mature cows); G_k = the effect of the *k*-th genotype in each individual SNP; and ε_{ijk} = the random error. The genetic diversity information of those SNP that resulted with effect on live growth traits was calculated using the GenAlex Software (Peakall and Smouse, 2012).

The least squares mean of the genotypes was estimated for the SNP that demonstrated significant effects (P<0.05), and means were compared using the PDIFF statement. All statistical procedures were performed in SAS software (Statistical Analysis System, version 9.4).

Table 1 - Allelic frequencies of tested SNP

GENE	SNP_ID	G	A	T	C	SNP_ID	G	A	T	C
DRD1	rs210683080	0.9889	0.0111			rs110957999	0.0116	0.9892		
DRD2	rs135155082	0.9101		0.0899		rs472600260	0.5		0.5	
	rs110214457	0.8833	0.1167			rs41749779		0.4828		0.5172
DRD3	rs109600560	0.267		0.733		rs208613784		0.1392	0.8608	
	rs109576799		0.6292		0.3708					
DRD5	rs385662606			0.0854	0.9146	rs382783250	0.8933		0.1067	
	rs42651237	0.6389	0.3611			rs42651238			0.15	0.85
	rs385679223	0.0824	0.9176			rs380555990	0.913	0.087		
HTT	rs384070463	0.9231	0.0769			rs110246370			0.7611	0.2389
	rs377978984			0.0761	0.9239	rs109786449			0.3895	0.6105
	rs42658479	0.5393	0.4607			rs110637774	0.7444	0.2556		
	rs211232205			0.2921	0.7079	rs210943488	0.2128	0.7872		
	rs208140118	0.7554	0.2446			rs109886127			0.7663	0.2337
	rs385032531			0.1044	0.8956	rs385973314	0.8391	0.1609		
	rs133165424	0.8571	0.1429			rs111003891	0.5899	0.4101		
	rs43703873			0.1099	0.8901	rs384532812			0.9261	0.0739
	rs110751698	0.7556	0.2444			rs137792823			0.4545	0.5455
	rs208081652			0.2889	0.7111	rs42659244	0.6724	0.3276		
HTR1A	rs525507540			0.0111	0.9889					
HTR1B	rs136136524	0.4			0.6	rs209984404		0.4185		0.5815
	rs722705037			0.0108	0.9892	rs133683693	0.3956	0.6044		
HTR2A	rs110801604			0.5543	0.4457	rs43696138			0.427	0.573
	rs43696137			0.1404	0.8596	rs43696136	0.7849	0.2151		
	rs382409204	0.9121	0.0879			rs208044329			0.011	0.989
	rs384853066	0.9125	0.0875			rs380120705			0.2079	0.7921
	rs209026145			0.7279	0.2721					
TDO2	rs523019968	0.9702	0.0298			rs518276997			0.0337	0.9663
	rs438426332	0.9894	0.0106			rs109119191			0.7989	0.2011
	rs211402172		0.0526		0.9474	rs385054562			0.7955	0.2045
TH	rs469153113	0.9889	0.0111			rs109268356			0.3222	0.6778
	rs108963205	0.9889	0.0111							

Continues...

Table 1 (Continued)

GENE	SNP_ID	G	A	T	C	SNP_ID	G	A	T	C
DBH	rs109353933	0.0111	0.9889							
ADRA2A	rs136394479	0.9695			0.0305					
ADRA2B	rs137223820	0.4663	0.5337			rs136350514	0.462	0.538		
	rs136116208	0.4615	0.5385			rs135185773			0.5247	0.4753
	rs134648419	0.6067	0.3933			rs133942464		0.4611	0.5389	
	rs133444985	0.4913	0.5389			rs133256867			0.5361	0.4639
	rs133007204			0.0759	0.9241	rs110927700	0.8	0.2		
	rs110649596			0.5337	0.4663	rs110575125	0.3889	0.6111		
	rs108982423	0.5444	0.4556			rs110898069	0.4663	0.5337		
	rs135723478			0.3889	0.6111					
PNMT	rs518562113			0.0112	0.9888	rs134932709			0.55	0.45
	rs133941642	0.5057	0.4943			rs133033392	0.456	0.544		
	rs109856434	0.5349	0.4651			rs384853211	0.467	0.533		
	rs137016655	0.0224	0.9776			rs136607942			0.5393	0.4607
MAOA	rs378587519			0.0178	0.9824	rs41626735			0.5165	0.4835
	rs41626734	0.4837	0.5163			rs134256715		0.8929		0.1071
	rs385873719	0.9889		0.0112						
MAOB	rs435106571	0.9402	0.0598							
TPH1	rs444271554		0.8807	0.1193		rs207553994			0.0122	0.9878
	rs207845864		0.0114		0.9886	rs134038223	0.8333	0.1667		
TPH2	rs208458809	0.1236	0.8764			rs209693095			0.1207	0.8793
	rs378572439	0.1429	0.8571			rs381772544			0.0272	0.9778
POMC	rs454703504		0.0106		0.9894	rs41257366	0.6	0.4		
	rs17871682			0.6833	0.3167	rs17871681			0.0489	0.9511
	rs17871680			0.2326	0.7674	rs136809285			0.4011	0.5989
	rs134604486			0.593	0.407					
	rs137756569	0.4	0.6							
NPY	rs110711537			0.9722	0.0278	rs385557691		0.9353		0.0647
SLC18AL	rs135217487			0.8763	0.1237	rs110011622	0.5769	0.4231		
	rs110365063	0.6534	0.3466			rs211305909			0.4239	0.5761
	rs211345511	0.9551		0.0449		rs207883889			0.0389	0.9611
FOSFBJ	rs385424680			0.011	0.989	rs43642463	0.9833			0.0167
DRD4	EF157845	0.4944		0.5056						

Results

The least square mean values for live growth traits are described in Table 2.

In the young cow group, low and moderate but significant correlations with variables BW ($P<0.0001$) and WW ($P<0.03$) were found only for two temperament measurements (EV and TS). However, the variable YW was not correlated with any temperament measurements (PS, EV, and TS) (Table 3). In the mature cow group, no significant correlations were observed between temperament and weight traits (Table 3).

Ten SNP located on six genes (Table 4) resulted in an association with one or two of the growth measures (nine for BW and three for WW). No significant associations were found for YW. Genetic diversity parameters of the ten SNP are shown in Table 5, while in Table 6, the least square means of each growth trait are reported, also including the least square means data of temperament traits (Garza-Brenner et al., 2017). Seven markers (rs41749779 [DRD2]; rs134256715 [MAOA; monoamine oxidase A]; rs134604486, rs136809285, rs137756569, rs41257366 [POMC; proopiomelanocortin]; and rs43696138 [HTR2A; serotonin 5-hydroxytryptamine receptor 2A]) were associated with BW, in which the most significant associations were observed for markers rs41749779 and rs134256715 (P = 0.008 and P = 0.002, respectively). Marker rs17871681, located on the POMC gene, was significantly associated (P = 0.0085) with WW.

Table 2 - Least square mean values for weight variables ± standard error (SE)

Herd	Group[1]	BW±SE	WW±SE	YW±SE
1	Mature cows	34.80±0.95	202.84±6.72	-
	Young cows	36.25±0.99	210.50±7.19	331.50±29.9
2	Mature cows	40.52±0.75a	249.59±5.40	326.33±7.36
	Young cows	35.85±1.23b	244.70±5.93	338.15±9.16
3	Mature cows	33.88±0.49a	203.35±3.85	276.68±5.20
	Young cows	30.67±0.39b	201.89±4.71	285.96±6.91
4	Mature cows	41.03±0.77b	231.02±4.60b	336.47±5.80a
	Young cows	45.97±0.97a	248.85±4.24a	311.66±4.77b

BW - birth weight; WW - weaning weight; YW - yearly weight.
[1] Mature cows ≥ four years old; young cows = 2-3 years old.
a,b - Different letters indicate significant differences (P<0.05).

Table 3 - Pearson's correlation coefficients between temperament and growth

		PS	EV	TS
Mature cows	BW	0.055[1]	−0.008	0.033
		0.428[2]	0.901	0.635
	WW	0.031	−0.021	0.007
		0.652	0.760	0.920
	YW	0.021	−0.013	0.004
		0.796	0.867	0.953
Young cows	BW	0.146	0.514	0.521
		0.088	<0.0001	<0.0001
	WW	0.064	0.196	0.201
		0.455	0.021	0.018
	YW	−0.018	−0.143	−0.139
		0.842	0.118	0.127

BW - birth weight, WW - weaning weight, PS - pen score, EV - exit velocity, TS - temperament score.
[1] Pearson's correlation coefficient.
[2] Probability value.

Table 4 - Probability values of associations with single nucleotide polymorphisms (SNP) affecting growth

Gene	Chromosome	Genome position	SNP ID	P-value	
				BW	WW
DRD2	chr15	24309558	rs41749779	0.008	
DRD3	chr1	59343756	rs109576799[1]	0.015	0.025
MAOA	chrX	105395894	rs134256715	0.002	
POMC	chr11	74116762	rs134604486[1]	0.030	
		74116738	rs136809285	0.026	
		74116786	rs137756569[1]	0.027	
		74116629	rs41257366	0.021	
		74116182	rs17871681		0.0085
TDO2	chr17	44388366	rs385054562	0.042	0.043
HTR2A	chr12	44388366	rs43696138[1]	0.027	

BW - birth weight, WW - weaning weight; PS - pen score, EV - exit velocity, TS - temperament score.
[1] Previously associated with temperament traits (PS, EV, TS).

Table 5 - Genetic diversity parameters of temperament-related genes with effect on live growth traits of Charolais cattle

Gene	SNP	Freq. genotype (N)			Freq. allele		Ho	He	Ne	PIC	χ2
		AA	AB	BB	A	B					
DRD2	rs41749779	23	38	25	0.488	0.512	0.437	0.502	1.999	0.375	1.153
DRD3	rs109576799	38	38	14	0.625	0.375	0.427	0.469	1.882	0.358	0.546
MAOA	rs134256715	74	2	8	0.893	0.107	0.024	0.192	1.237	0.173	64.96
	rs134604486	9	50	26	0.400	0.600	0.581	0.486	1.923	0.366	31.92
	rs136809285	27	52	9	0.602	0.398	0.582	0.483	1.920	0.365	4.79
POMC	rs137756569	26	52	9	0.598	0.402	0.578	0.483	1.926	0.365	5.131
	rs41257366	9	51	27	0.397	0.603	0.578	0.483	1.918	0.365	4.398
	rs17871681	80	8	0	0.955	0.045	0.500	0.435	1.095	0.339	0.200
TDO2	rs385054562	4	28	56	0.205	0.795	0.318	0.327	1.482	0.272	0.043
HTR2A	rs43696138	15	7	63	0.218	0.782	0.472	0.492	1.516	0.370	48.86

SNP - single nucleotide polymorphism; N - number of observations; Ho - observed heterozygosity; He - expected heterozygosity; Ne - number of effective alleles; PIC - polymorphism informative content; χ2 - chi-square value.

Table 6 - Least square means for live weight and temperament traits of several SNP located at temperament related genes in Charolais cows

Gene	SNP	Genotype	Growth trait (kg)			Temperamental trait		
			BW	WW	YW	PS	EV	TS
DRD2	rs41749779	AA	40.6a	231.7a	315.8a	1.88a	1.94a	1.91a
		CC	37.6b	235.6a	314.5a	1.98a	1.27a	1.63a
		CA	35.9b	225.5a	316.8a	1.94a	1.46a	1.70a
DRD3	rs109576799	AA	36.3a	231.0a	322.4a	1.96a	1.28a	1.57a
		CC	41.6b	246.6a	316.7a	1.89a	2.34b	2.17b
		CA	37.0a	221.0b	308.2a	1.94a	1.31a	1.58a
MAOA	rs134256715	AA	38.2a	232.5a	317.4a	1.96a	1.64a	1.80a
		CC	31.9b	209.7a	308.7a	1.76a	0.96a	1.36a
		AC	-	-	-	-	-	-
	rs134604486	CC	41.7a	233.2a	295.5a	2.19a	1.74a	1.99a
		CT	36.7b	225.5a	312.4a	1.91a	1.34a	1.59a
		TT	36.6b	234.6a	322.8a	1.66b	1.84a	1.93a
	rs136809285	CC	36.7a	234.2a	309.7a	2.02a	1.85a	1.93a
		TT	41.9b	233.2a	284.9a	2.26a	1.77a	2.01a
		TC	36.7a	224.1a	302.0a	1.84a	1.34a	1.60a
POMC	rs137756569	AA	36.8a	234.7a	322.8a	1.58a	1.94a	1.99a
		AG	36.5a	225.6a	312.5a	1.76b	1.36a	1.60a
		GG	41.8b	233.1a	295.4a	1.99b	1.77a	1.99a
	rs41257366	A	42.0a	233.3a	285.0a	2.26a	1.77a	2.01a
		AG	36.6b	224.0a	301.9a	1.85a	1.34a	1.59a
		GG	36.8b	234.2a	309.7a	2.02a	1.84a	1.93a
	rs17871681	CC	38.0a	232.8a	314.8a	1.95a	1.51a	1.73a
		CT	35.0a	202.5b	276.8a	2.03a	1.95a	1.99a
		TT	-	-	-	-	-	-
TDO2	rs385054562	CC	39.3a	240.2a	322.1a	1.93a	0.72a	1.32a
		TT	36.7b	224.4b	310.1a	1.96a	1.71a	1.84a
		CT	-	-	-	1.90a	1.49a	1.69a
HTR2A	rs43696138	AA	38.2a	250.1a	331.7a	1.98a	1.69a	1.68a
		GG	37.7b	228.0a	311.8a	2.02a	1.38b	1.64a
		AG	-	-	-	1.65a	2.59c	2.30b

SNP - single nucleotide polymorphism; BW - birth weight; WW - weaning weight; YW - yearling weight; PS - pen score; EV - exit velocity; TS - temperament score.
a,b,c - Different letters in the same column differ significantly (P<0.05).

Markers rs109576799 and rs385054562, located on the dopamine D3 receptor (DRD3) and tryptophan 2,3-dioxygenase (TDO2) genes, respectively, were significantly associated (P = 0.05) with BW and WW. Cows with genotype CC of marker rs385054562 had a higher BW than cows with the TT genotype (39.36 vs 36.74 kg; P = 0.042); similarly, for WW, cows with CC genotype had higher WW than cows with the TT genotype (240.19 vs 224.49 kg; P = 0.043). Cows with the CC genotype of marker rs109576799, located on the DRD3 gene, had higher BW and were 5.32 kg (P = 0.004) and 4.59 kg (P = 0.014) heavier than cows with the AA and CA genotypes, respectively.

Discussion

From a molecular perspective, the use of candidate genes that affect economically important traits has been shown to be a direct method of understanding biological functions that focuses on the trait of interest. This approach consists of exploring genes that are implicated in known biological pathways and define whether the genetic variation present in populations is associated with phenotypic differences (Mormède et al., 2005). By using this approach, investigations have been performed to elucidate the molecular basis of bovine temperament (Glenske et al., 2011; Lühken et al., 2010). Recently, Garza-Brenner et al. (2017) conducted a study of genes and markers associated with bovine temperament in Mexican Charolais cows. The selected markers were located on genes of the dopamine and serotonergic pathways as well as five protein-protein interacting genes. Among complex and productive traits of interest, growth has been extensively studied, and its genetic architecture is currently under investigation (Lühken et al., 2010). Because cattle temperament affects other important traits such as cattle weight, we analyzed whether SNP known to be associated with temperament traits are also associated with live weight traits.

Results of Pearson's correlation coefficient in this study were inconsistent with those described in other studies focused on correlating temperament with growth, because all the correlations found here were positive. This finding could be related to the time at which temperament was recorded (Curley et al., 2006; Schmidt et al., 2014). Temperament of animals is usually recorded around weaning time, either pre- or post-weaning. The mature cows likely did not show a correlation with the temperament traits because of their age; therefore, age could have had an influence, because older cows are acclimated to the location and environment where they have lived for years (Curley et al., 2006; Schmidt et al., 2014).

Using the 151 SNP panel previously reported by Garza-Brenner et al. (2017), we identified associations of ten SNP located on six genes with two of the three recorded growth measures (BW and WW). Interestingly, four of the SNP associated in this study have been previously described as having associations for temperament traits (Table 4) (Garza-Brenner et al., 2017).

Research focusing on determining pleiotropic interactions has recently increased because of the availability of dense SNP arrays and the development of statistical methodologies capable of probing multitrait-marker interactions (Gianola et al., 2015). In cattle, for instance, Lindholm-Perry et al. (2015) analyzed the role of SNP located on BTA6 previously associated with phenotypic and efficiency traits, including frame size, average daily gain, and average daily feed intake. The authors found that they were also associated with flight speed. The markers identified are located within a coding region of non-SMC condensin I complex subunit G (NCAPG) and in the 30-UTR of the ligand-dependent nuclear receptor corepressor-like (LCORL) gene.

The present study revealed that the markers rs109576799 (DRD3), rs134604468, rs137756569 (POMC), and rs43696138 (HTR2A), previously associated with bovine temperament traits (Garza-Brenner et al., 2017), were also associated with live weight traits (BW and WW). Further studies analyzing our results could determine whether the four markers had a pleiotropic effect on temperament and live weight traits. The results of these studies require the conformation and analysis of a larger cattle population to confirm the effect of the identified markers on the traits of interest.

Except for the POMC gene, there are no previous reports describing any associations between the genes found in the present study and body weight. For the POMC gene, an association was reported between polymorphisms located at the 3' flanking region with body weight and weight gain of Nanyang cattle (Zhang et al., 2009).

The specific association of marker rs134256715, which is located on the MAOA gene, with BW found in our study is important because it is a non-synonymous SNP (Cys/Trp) and, therefore, has the potential to modify the protein structure. The MAOA gene has been termed as "warrior gene" because of its association with the response to aggression in several behavioral studies, mainly in humans (Kim-Cohen et al., 2006; McDermott et al., 2009). The MAOA gene plays an important role in inter-individual variability in aggressiveness, impulsive response, and serotoninergic response capacity of the central nervous system (CNS) as well as in complex behavior regulation. Lühken et al. (2010) studied the genetic variation of the gene in two cattle breeds (Angus and German Simmental), which are known to differ in their behavior during handling (German Simmental was reported as more difficult to handle than Angus). The authors evaluated five SNP different from those included in our study and did not observe a significant association between the polymorphism and the recorded behavioral scores.

An interesting result of our study was the novel associations found for two body weight traits (BW and WW) and marker rs385054562 located on TDO2 and marker rs109576799 located on DRD3. The TDO2 gene does not have any reported associations in cattle. In studies conducted with humans and mice, TDO2 has been identified as a potential candidate gene for autism and as a modulator of behavioral diseases associated with inflammatory states, psychiatric disorders, behavioral modulation, and cognitive function (Nabi et al., 2004; Too et al., 2016). Marker rs109576799 is located in an intron of the DRD3 gene and has been associated with EV and TS (Garza-Brenner et al., 2017). It is important to determine the role of this marker in gene function, because variations in non-coding regions may be involved in splicing (and alternative splicing) and in splicing efficiency, thus affecting gene expression and regulation (Ramírez-Bello and Jiménez-Morales, 2017).

Further attention should be given to polymorphisms and genes that have shown important associations with the studied traits to validate their effects on other cattle populations, especially because four of the same markers previously associated with temperament have also been associated with growth traits.

Conclusions

This report presents the first findings in which single-nucleotide polymorphisms located on candidate genes for temperament traits also had an effect on birth weight and weaning weight in Charolais cows, which indicates that both traits could be influenced by the same genes. Once validated, this information would assist in the selection of appropriate genotypes for the economically relevant traits temperament and live weight.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Formal analysis: E. Garza-Brenner, A.M. Sifuentes-Rincón and F.A. Rodríguez-Almeida. Investigation: E. Garza-Brenner, A.M. Sifuentes-Rincón, F.A. Rodríguez-Almeida and W. Arellano-Vera. Methodology: A.M. Sifuentes-Rincón, F.A. Rodríguez-Almeida, R.D. Randel and G.M. Parra-Bracamonte. Project administration: A.M. Sifuentes-Rincón. Writing-review & editing: E. Garza-Brenner and A.M. Sifuentes-Rincón.

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