Scholars Journal of Agriculture and Veterinary Sciences (SJAVS) **e-ISSN 2348–1854**
Abbreviated Key Title: Sch. J. Agric. Vet. Sci. **p-ISSN 2348–8883**
©Scholars Academic and Scientific Publishers (SAS Publishers)
A Unit of Scholars Academic and Scientific Society, India
www.saspublishers.com

Association of Several Genes and Genotype Combinations With Economic Traits in Beef Cattle

Hong Tian, Xiaojing Zhou*, Jinhua Ye, Yan Xu
Department of Information and Computing Science, Heilongjiang Bayi Agriculture University, Daqing, 163319, People's Republic of China

Review Article

***Corresponding author**
Xiaojing Zhou

Article History
Received: 02.04.2017
Accepted: 09.04.2018
Published: 30.04.2018

DOI:
10.36347/sjavs.2018.v05i04.006

Abstract: Beef quality is the most important index that consumers consider, which can be evaluated by detecting high-grade beef, marbling, eye muscle area, thickness of backfat and tenderness. The screening and identification of meat quality-related function gene have important significance for marker assisted selection. This paper explored the variation of 10 genes in 7 different populations of beef cattle. The association analysis of 10 genes and different genotype combinations with 14 carcass and growth traits of cattle was carried out by linear model using the SPSS software. PN3 gene had a significant effect on eight growth traits. Next, we studied association analysis between different genotype and growth traits, as well as the significance of different beef cattle breeds, different feed varieties and different months of age on important economic traits. Finally, the optimal prediction model of the trait LWBS with 13 traits was obtained by principal component regression. PN3 gene had a significant effect on the trait LWBS, among which individuals of BB genotype had significantly higher LWBS than those of AA and AB genotypes ($P<0.01$). The analysis results can provide scientific basis for improving the beef fat ratio and beef quality, and for the cultivation of new meat products.

Keywords: PN3; growth traits; genotype combination; association analysis; prediction.

INTRODUCTION

Carcass and meat quality traits of beef cattle are important economic traits and important indexes to measure breeding value and economic benefit. The quality of meat of cattle was evaluated by measuring the weight of high grade beef, marbling, eye muscle area, back fat thickness and tenderness of meat. Genetic marker information can improve meat quality and speed up the genetic process, and then select excellent individuals to obtain the desired genotype offspring. Detecting for relevant molecular markers can shorten the breeding period of growth traits.

Many studies have been carried out for exploring the association of traits of cattle and the genes [1-6]. The correlation analysis was carried out between each marker genotype and the economic traits of beef cattle by using the least square fitting linear model, and the main effect candidate genes of new beef cattle lines were found [7, 8]. Multiple comparisons showed that AA and AB were significantly higher than bb in 305 day corrected milk yield and milk fat percentage [9]. Through the correlation analysis of different genotypes and slaughter traits of cattle, the differences of individual genotypes were obtained [10, 11]. The correlation between AGP at 6 genes and fatty acid composition of Simmental in China was studied in order to provide experimental basis for molecular breeding and further improvement of meat performance of Simmental in China [12]. The effect of gene locus on growth traits of beef cattle was examined by association analysis method, and the candidate genes of beef were found [13-16]. The research progress of GWAS in complex economic traits of important livestock species was concluded, and the results obtained by GWAS in animal economic traits research in recent years were reviewed, and the research strategies and methods of GWAS were summarized [17]. The latest research achievements of molecular markers and molecular breeding related to beef cattle were overviewed, and the research progress of beef cattle growth and related production traits were mainly introduced [18].

In this paper, we first explored the variation of 10 genes in 7 different populations of beef cattle. The association analysis of 10 genes and different genotype combinations with 14 carcass and growth traits of cattle was carried out by linear model using the SPSS software. PN3 gene had a significant effect on eight growth traits. PI3_SSCP, PI6_TaqI and PE8 gene had a significant effect on five growth traits. Traits of CW, NMW, HGMW and BT were significantly affected by PN3, PI3_SSCP, PI6_TaqI. Next, we studied association analysis between different genotype and growth traits, as well as the significance of different beef cattle breeds, different feed varieties and different months of age on important economic traits. Finally, the prediction model of the trait LWBS with 13 traits was obtained by stepwise regression and principal component regression, and the prediction results of principal component regression were better than stepwise regression. The results showed that PN3 gene had a significant effect on trait LWBS, among which individuals of BB genotype had significantly higher trait LWBS than those of AA and AB genotypes ($P<0.01$). The analysis results can provide scientific basis for improving the beef fat ratio and beef quality, and for the cultivation of new meat products.

Analysis of important economic traits of beef cattle

Fat is not only the energy source of animals, but also affects the flavor quality and edible value of meat. One of the goals of beef cattle breeding is to increase the fat content in muscles to meet the needs of consumers for beef tenderness and flavor. Many internal factors related to the tissue structure and chemical composition of meat are related to meat quality, such as content and type of connective tissue, diameter, density, type of muscle fiber and sarcomere length, intramuscular fat (IMF) and so on. Tenderness is an important aspect of meat quality. The content of IMF has a great influence on the flavor of meat, and also has a certain influence on the tenderness of meat. Up to 10 % of intramuscular fat content can produce ideal marble pattern, thus forming high quality beef. Therefore, the IMF content can be genetically improved to improve the quality. The MyoD (MYOGenic determination gene, MyoD) family plays an important role in regulating myogenesis. The combination of muscle-specific genes and muscle-specific enhancers, which can activate the resting state, can promote transcription and promote the differentiation of some cells into skeletal muscle cells.

Marble pattern is the main factor affecting the tenderness of beef, the more the marble pattern, the better and the beef quality. The template can be referred to assess the level of marble pattern. The tenderness of meat is also affected by factors of pre-slaughter (month age, beef cattle variety and feed variety, and so on), post-slaughter and genetic factors. Huff-Lonergan thought that usually young animals have better tenderness than old animals. Studies have shown that heredity has a great influence on beef tenderness [20].

2 Data resources-population and phenotype of cattle

The total number of cattle is 189, which is from 7 breeds (Angus, Charolias, Jinnan, Limsion, Luxi, Qinchuan and Simmental). After weaning, the cows were transported to Beijing's jinweifu ren dairy farm and fed under the same feeding and management system. Growth and development characteristics of all beef cattle were observed until slaughter after 16 to 18 months. This study focused on phenotypic traits related to beef yield and meat quality traits. Meanwhile, measurements were made during slaughter in accordance with the standard meat procurement specification of the fresh beef guide. The live weight of beef cattle was measured 24 hours after fasting, and the area of the longest dorsalis muscle was measured 48 hours after slaughter, starting at the 12th and 13th rib joints, in square centimeters.

After collecting the original data, the fixed effect of phenotypic values was corrected, including slaughter year, feeding season, fattening days, weight when entering the farm and random effect.

The correction formula is given as follows：

$$y = \mu + Year_i + Season_j + Fattendays_k + Enterweight_m + e$$

Where y is the phynotype value, μ is the population value, $Year_i$ is the Slaughter year, $Season_j$为 breeding season (including three stage, December to April, May to August, September to November), $Fattendays_k$ is fattening days, $Enterweigt_m$ is weight when entering the farm, e is the random effect.

Association analysis between genes and important economic traits of beef cattle

There are 14 traits are analyzed, which are carcass weight, net meat weight, high-grade meat weight, marbling, intramuscular fat, eye muscle area, incarnadine, fat color , backfat thickness, average daily gain, muscle tenderness, acidity 1 and acidity 2 and live-weight before slaughtering, denoted by CW, NMW, HGMW, MB, IMF, EMA, IC, FC, BT, ADG , MT, A1, A 2 and LWBS respectively.

Significance analysis of each gene and important economic traits of beef cattle

By the significant tests of each gene and important economic traits of beef cattle (See Table 1), we can conclude that gene CAST had significant effect on trait BT only. PN3 gene had significant effects on traits CW, NMW, HGMW, MB, IMF, EMA, BT and ADG. PI6_TaqI gene had significant effects on traits CW, NMW, HGMW, BT and A2. PI3_SSCP gene had significant effects on traits CW, NMW, HGMW, IMF, EMA, BT and ADG. PE8 gene had significant effects on traits CW, NMW, HGMW and IMF. MyOD had significant effects on traits CW, NMW and HGMW. DGAT1 gene had significant effects on traits CW and BT.

Table-1: Significance test of each gene and some economic traits of beef cattle

Trait / Gene	Significance												
	CW	NMW	HGMW	MB	IMF	EMA	IC	BFS	BT	ADG	MT	A1	A2
CAST	0.810	0.947	0.956	0.870	0.724	0.847	0.675	0.869	0.041	0.987	0.356	0.958	0.970
Hfabp_2	0.430	0.514	0.580	1.000	0.821	0.787	0.674	0.868	0.839	0.082	0.993	0.872	0.320
PN3	0.034	0.000	0.001	0.000	0.016	0.021	0.316	0.300	0.002	0.001	0.274	0.928	0.641
PI6_TaqI	0.003	0.004	0.042	0.898	0.796	0.103	0.687	0.728	0.039	0.870	0.670	0.603	0.032
PI6_MspI	0.086	0.935	0.935	0.197	0.353	0.504	0.665	0.821	0.508	0.700	0.566	0.691	0.372
PI3_SSCP	0.001	0.003	0.003	0.851	0.019	0.006	0.808	0.924	0.009	0.020	0.907	1.000	0.456
PE8	0.043	0.045	0.045	0.858	0.017	0.912	0.484	0.687	0.660	0.983	0.421	0.585	0.978
MyOD	0.001	0.009	0.009	0.627	0.149	0.307	0.358	0.251	0.653	0.934	0.441	0.686	0.868
MYFi2	0.439	0.521	0.521	0.825	0.966	0.142	0.828	0.701	0.097	0.863	0.874	0.107	0.540
DGAT1	0.022	0.908	0.908	0.636	0.493	0.59	0.796	0.870	0.046	0.677	0.908	0.392	0.335

Table-2: Association of SNPs with growth traits

Gene	Genotype	MB	EMA	BT	ADG	MT
CAST	AA(n=43)	2.093(1.360)	76.233(15.104)	1.019(0.441)	0.535(0.217)	5.427(1.803)
	AB(n=50)	1.860(1.050)	74.840(13.886)	1.214(0.510)	0.508(0.220)	4.837(1.313)
PI6_TaqI	AA(n=164)	2.140(1.177)	77.317(14.102)	1.107(0.484)	0.580(0.305)	4.817(1.530)
	AB(n=13)	1.692(1.032)	76.615(16.756)	1.431(0.504)	0.367(0.213)	4.701(1.087)
MyOD	AA(n=144)	2.118(1.150)	77.910(14.136)	1.126(0.506)	0.570(0.321)	4.881(1.504)
	AB(n=17)	1.706(1.047)	67.941(10.256)	1.153(0.357)	0.452(0.190)	4.519(1.155)
PN3	AA(n=30)	1.333(0.661)	66.300(10.748)	1.283(0.477)	0.372(0.168)	4.421(1.155)
	AB(n=55)	2.218(1.272)	75.818(15.201)	1.258(0.551)	0.541(0.427)	4.806(1.384)
	BB(92)	2.261(1.157)	80.641(12.479)	1.013(0.427)	0.626(0.217)	5.050(1.671)
PI3_SSCP	AA(n=118)	2.229(1.187)	79.754(13.742)	1.071(0.489)	0.602(0.225)	4.950(1.635)
	AB(n=23)	1.826(1.072)	69.043(10.425)	1.352(0.527)	0.517(0.589)	4.613(1.344)
	AD(n=5)	1.600(0.894)	70.800(14.636)	1.120(0.427)	0.232(0.200)	4.252(1.398)
	CC(n=9)	1.667(1.414)	68.556(14.570)	1.244(0.464)	0.401(0.176)	4.311(1.013)
PE8	AA(n=137)	2.161(1.177)	78.307(14.524)	1.087(0.478)	0.579(0.236)	4.889(1.538)
	AE(n=14)	1.929(1.072)	74.071(11.228)	1.300(0.467)	0.595(0.759)	4.856(0.882)
	BB(n=14)	2.114(1.369)	76.786(15.353)	1.179(0.383)	0.507(0.236)	4.757(1.304)
	EE(n=7)	1.571(0.787)	71.714(6.576)	1.329(0.642)	0.364(0.209)	3.969(1.297)
dgat1	AA(n=6)	1.333(0.816)	68.333(12.111)	1.133(0.320)	0.239(0.210)	4.023(0.883)
	AB(n=111)	2.190(1.116)	78.500(13.890)	1.050(0.477)	0.591(0.350)	4.956(1.571)
	BB(n=29)	2.172(1.256)	77.310(12.584)	1.262(0.491)	0.587(0.233)	4.894(1.266)
	CD(n=18)	1.611(1.037)	71.444(12.268)	1.300(0.566)	0.500(0.178)	4.732(1.502)

From the analysis, it can be derived that, for CAST, PI6_TaqI, MyOD gene, the population mean value of individuals for backfat thickness (BT) trait with AA genotype was significantly lower than that with AB genotype, while for the other 4 traits, the population mean value for BT with AA genotype was significantly higher than that with AB genotype.

Table-3: Mean of each trait of different cattle breeds (standard deviation in brackets)

Trait	mean (standard deviation)	Angus	Charolias	Jinnan	Limsion	Luxi	Qinchuan	Simmental
CW	320.705 (3.894)	338.716 (10.135)	382.013 (10.382)	299.950 (6.744)	313.024 (5.595)	273.920 (4.890)	292.360 (7.965)	345.303 (7.384)
NMW	250.558 (2.902)	259.356 (7.421)	291.712 (6.872)	237.346 (5.869)	249.229 (4.806)	214.141 (4.049)	233.096 (7.103)	268.780 (5.917)
HGMW	31.386 (0.333)	31.415 (0.830)	36.088 (0.837)	30.208 (0.700)	32.474 (0.602)	27.486 (0.594)	28.924 (0.631)	33.007 (0.737)
MB	2.095 (0.086)	3.053 (0.259)	2.267 (0.219)	1.208 (0.134)	2.960 (0.220)	1.333 (0.146)	1.633 (0.182)	2.516 (0.160)
IMF	5.291 (0.242)	3.119 (0.291)	4.286 (0.369)	8.776 (0.916)	3.467 (0.340)	7.161 (0.767)	5.969 (0.467)	3.899 (0.182)
EMA	76.974 (1.046)	76.974 (1.046)	84.933 (2.492)	69.833 (2.345)	90.840 (2.580)	64.333 (1.641)	70.400 (1.993)	79.419 (2.263)
IC	4.476 (0.046)	4.476 (0.046)	4.737 (0.129)	4.375 (0.118)	4.320 (0.138)	4.400 (0.103)	4.250 (0.079)	4.742 (0.113)
BFS	1.283 (0.031)	1.342 (0.1150	1.267 (0.075)	1.250 (0.074)	1.200 (0.071)	1.350 (0.108)	1.300 (0.057)	1.274 (0.076)
BT	1.118 (0.035)	0.779 (0.076)	1.053 (0.060)	1.471 (0.131)	1.112 (0.115)	1.277 (0.025)	1.053 (0.060)	1.029 (0.086)
ADG	0.560 (0.022)	0.563 (0.065)	0.692 (0.038)	0.542 (0.118)	0.601 (0.028)	0.305 (0.025)	0.556 (0.043)	0.663 (0.030)
MT	0.11 (0.000)	5.396 (0.473)	4.838 (0.255)	4.332 (0.288)	5.359 (0.368)	4.751 (0.233)	4.365 (0.233)	4.958 (0.234)
A1	6.042 (0.015)	6.053 (0.053)	6.033 (0.033)	6.042 (0.042)	6.000 (0.000)	6.100 (0.056)	6.000 (0.000)	6.065 (0.045)
A2	5.751 (0.032)	5.684 (0.134)	5.767 (0.079)	5.625 (0.101)	5.680 (0.095)	5.933 (0.046)	5.667 (0.088)	5.839 (0.067)

For PN3 gene, the mean value of population for BT trait with BB genotype was significantly lower than that with AA and AB genotypes, while for the other 4 traits the population mean value for BT with AA genotype was significantly higher than that with AA and AB genotypes.

For PI3_SSCP gene, the population mean value of individuals for BT trait with AA genotype was significantly lower than that with AB, AD and CC genotypes, while for the other 4 traits the population means value for BT with AA genotype was significantly higher than that with AB, AD and CC genotypes.

For PE8 gene, the mean value of the population for BT trait with AA genotype was significantly lower than that with AE, BB and BE genotypes, while for the other 4 traits the population mean value for BT with AA genotype individuals was significantly higher than that with AE, BB and BE genotypes.

For dgat1 gene, the population mean value of individuals for BT trait with AB genotype was significantly lower than that with AA, BB and CD genotypes, while for the other 4 traits the population mean value for BT with AB genotype individuals was significantly higher than that with AA, BB and CD genotypes.

Association analysis of cattle breed and important economic traits

The results showed that different breeds had significant effects on the traits of CW, NMW, HGMW, MB, EMA and BT.

Table-4: Significant analysis on important economic traits of beef cattle between breeds

Trait	CW	NMW	HGMW	MB	IMF	EMA	IC	BFS	BT	ADG	MT	A1	A2
significance	0.000	0.000	0.001	0.040	0.185	0.015	0.781	0.424	0.000	0.476	0.586	0.915	0.698

Further, the analysis of the differences between the traits with significant effects was conducted as follows. (See Table 5)

For trait CW, there was significant difference between breed of Angus and Charolias, Limsion, Luxi, Qinchuan, Simmental. There was no significant difference among other varieties. For trait NMW, there was significant difference between breed of Charolias and Angus, Jinnan and Limsion and Simmental. There was significant difference between breed of Angus and Charolias, Limsion and Qinchuan. There was significant difference between breed of Jinnan and Simmental.

For trait HGMW, there was significant difference between breed of Angus and Charolias, Jinnan and Luxi and Simmental. There was significant difference between breed of Charolias and Angus, Jinnan and Qinchuan. There was significant difference between breed of Jinnan and Luxi, Luxi and Qinchuan, Qinchuan and Simmental.

For trait MB, there was significant difference between breed of Charolias and Qinchuan. There was significant difference between breed of Simmental and Jinnan, Luxi and Qinchuan.

For trait IMF, there was significant difference between breed of Charolias and Jinnan, Luxi and Qinchuan. For trait EMA, there was significant difference between breed of Angus and Charolias and Luxi. There was significant difference between breed of Limsion and Simmental.

For trait EMA, there was significant difference between breed of Angus and Charolias and Luxi. There was significant difference between breed of Charolias and Limsion, Limsion and Simmental.

For trait BT, there was significant difference between breed of Angus and Limsion. There was significant difference between breed of Charolias and Jinnan and Limsion, Jinnan and Limsion and Simmental. There was significant difference between breed of Limsion and Luxi, Simmental.

For trait LWBS, there was significant difference between breed of Angus and Charolias, Limsion, Luxi, Qinchuan and Simmental. There was significant difference between breed of Charolias and Angus, Jinnan, Qinchuan and Simmental. There was significant difference between breed of Jinnan and Limsion, Luxi, and Simmental.

There was no significant difference in trait of meat color, fat color character, daily gain, tenderness, acidity 1 and acidity 2 among different breeds.

Table-5: Significant difference of 8 traits between different breeds

Trait		Charolias	Jinnan	Limsion	Luxi	Qinchuan	Simmental
CW	Angus	0.000	0.100	0.001	0.000	0.045	0.000
	Charolias		0.001	0.154	0.121	0.001	0.121
NMW	Angus	0.000	0.222	0.004	0.003	0.107	0.001
	Charolias		0.001	0.147	0.131	0.002	0.212
	Jinnan			0.079	0.065	0.720	0.035
HGMW	Angus	0.000	0.226	0.041	0.001	0.215	0.002
	Charolias		0.011	0.099	0.789	0.006	0.486
	Jinnan			0.374	0.022	0.975	0.055
	Luxi					0.014	0.670
	Qinchuan						0.039
MB	Charolias		0.052	0.701	0.075	0.026	0.601
	Jinnan			0.134	0.792	0.874	0.015
	Luxi					0.655	0.021
	Qinchuan						0.006
IMF	Angus	0.301	0.414	0.808	0.424	0.405	0.518
	Charolias		0.044	0.397	0.038	0.035	0.654
EMA	Angus	0.007	0.204	0.416	0.009	0.266	0.004
	Charolias		0.139	0.044	0.919	0.069	0.821
	Limsion				0.054	0.771	0.025
BT	Angus	0.207	0.574	0.000	0.766	0.710	0.155
	Charolias		0.048	0.006	0.077	0.311	0.863
	Jinnan			0.000	0.755	0.304	0.032
	Limsion				0.000	0.000	0.009
LWBS	Angus	0.000	0.100	0.001	0.000	0.045	0.000
	Charolias		0.000	0.189	0.103	0.002	0.038
	Jinnan			0.010	0.014	0.316	0.037

Table-6: Further analysis on the significance of different breeds to each trait

CW	(12)0.004	(13)0.007	(16)0.022	HGMW	(12)0.0344	
NMW	(12)0.001	(23)0.022	(17).033	EMA	(34)0.008	(45)0.019

For trait CW, NMW, HGMW and EMA should strengthen the selection of Angus breed. The selection of variety 4 should be strengthened for the trait of EMA.

Association analysis of other factors and important economic traits

The results showed that feed varieties had effects on MB, IMF, EMA, BT, ADG, MT, A1 and LWBS.

Table-7: Mean of each trait of different feed varieties (standard deviation in brackets)

feed varieties / Trait	rbt	rby	zff
CW	352.993(7.464)	293.905(4.261)	315.707(6.002)
NMW	271.428(5.238)	232.220(3.640)	248.253(4.824)
HGMW	33.443(0.627)	30.058(0.502)	30.721(0.517)
MB	2.344(0.160)	1.934(0.158)	2.015(0.125)
IMF	4.741(0.400)	6.297(0.548)	4.875(0.265)
EMA	81.295(1.640)	75.410(2.186)	74.463(1.489)
IM	4.533(0.092)	4.426(0.079)	4.470(0.071)
BFS	1.287(0.057)	1.254(0.061)	1.306(0.044)
BT	1.067(0.064)	1.272(0.068)	1.024(0.049)
ADG	0.637(0.053)	0.460(0.025)	0.582(0.028)
MT	4.767(0.212)	5.071(0.205)	4.667(0.156)
A1	6.033(0.023)	6.066(0.032)	6.030(0.021)
A2	5.721(0.062)	5.754(0.056)	5.776(0.051)
LWBS	616.434(10.663)	511.115(6.183)	563.910(9.965)

Also, from the results of Table 8, it can be obtained that different months of age had effects on MB, IMF, EMA, BT, ADG, MT, A1 and LWBS.

Months of age 20, 22, 23 and 25 had significantly affected trait of MB and EMA. Months of age 20, 22, 23, 25 and 42 had significantly affected trait of IMF and ADG. Months of age 20, 22, 23, 25, 30, 36 and 42 had significantly affected trait of BT. Months of age 36 had significantly affected trait of A1.

Table-8: Significant test of 8 traits of different month of age

significance	20	22	23	25	30	36	42	48
MB	0.000	0.008	0.043	0.007	0.441	0.343	0.187	0.833
IMF	0.001	0.001	0.017	0.003	0.102	0.112	0.036	0.323
EMA	0.002	0.004	0.054	0.034	0.386	0.307	0.660	0.734
BT	0.001	0.001	0.001	0.000	0.008	0.004	0.041	0.019
ADG	0.015	0.007	0.030	0.013	0.162	0.116	0.009	0.584
A1	1.000	0.306	0.663	0.800	1.000	0.025	0.158	1.000

Further analysis of the traits with significant impact was carried out.

For trait MB, there was significant difference between month of age 20 and 23, 25, 30, 36, 42 and 48. Also, month of age 22 and 30, 36 and 48, 23 and 30 and 48, 25 and 30, 36 and 48. While, there was no significant difference between other months of age.

Table-9: Significant difference of 5 traits between different months of age

Trait	significance	22	23	25	30	36	42	48
MB	20	0.448	0.003	0.027	0.000	0.000	0.026	0.000
	22		0.207	0.588	0.003	0.014	0.189	0.005
	23			0.248	0.022	0.096	0.661	0.032
	25				0.000	0.004	0.257	0.003
IMF	20	0.685	0.062	0.238	0.000	0.003	0.382	0.005
	22		0.113	0.275	0.008	0.015	0.317	0.011
	25				0.010	0.034	0.769	0.030
EMA	20	0.734	0.035	0.025	0.000	0.001	0.005	0.001
	22		0.092	0.101	0.002	0.008	0.011	0.004
	25				0.013	0.080	0.089	0.035
ADG	20	0.330	0.764	0.862	0.042	0.205	0.314	0.030
	22		0.270	0.384	0.029	0.083	0.877	0.015
	25				0.030	0.164	0.358	0.024
	30						0.041	0.361
	42							0.019
A1	36	0.076	0.000	0.000	0.008	0.081	0326	0.000

For trait IMF, there was significant difference between month of age 20 and 22 and 25, 30 and 36 and 48. Also, month of age 22 and 30, 36 and 48, 23 and 30 and 48, 25 and 30, 36 and 48. The growth and feeding of 30, 36 and 48 months old can be paid special attention to the choice of improving IMF. For trait EMA, there was significant difference between month of age 20 and 23, 25, 30, 36, 42 and 48, 22 and 30, 36, 42 and 48, 25 and 30 and 48. For trait ADG and A1, the results can also be observed from the table.

Association analysis between LWBS and important economic traits

Prediction of stepwise regression analysis

The stepwise regression analysis for LWBS with the important economic traits was carried out as listed in the following.

Table-10: Results of stepwise regression analysis for LWBS with other traits

	Constant	CW	NMW	ADG	MB	Constant	CW	NMW	ADG	MB
coefficient	71.836	0.782	0.95	22.475	-4.537	0	0.497	0.450	0.080	-0.063
Sig.	0	0	0	0.002	0.009	0	0	0	0.002	0.009
R square	0.904					0.904				
F value	433.293(p=0.00)					433.293(p=0.00)				

Note: Column 2 to 6 is the results of original data and column 7 to 11 is that of standardized data.

The prediction model with the original data was constructed in the following.

$$y=71.836+0.782x_1+0.950x_2+22.475x_3-4.537x_4$$

LWBS was significantly affected by NMW, CW, ADG and MB, and MB had a significant negative effect on LWBS.

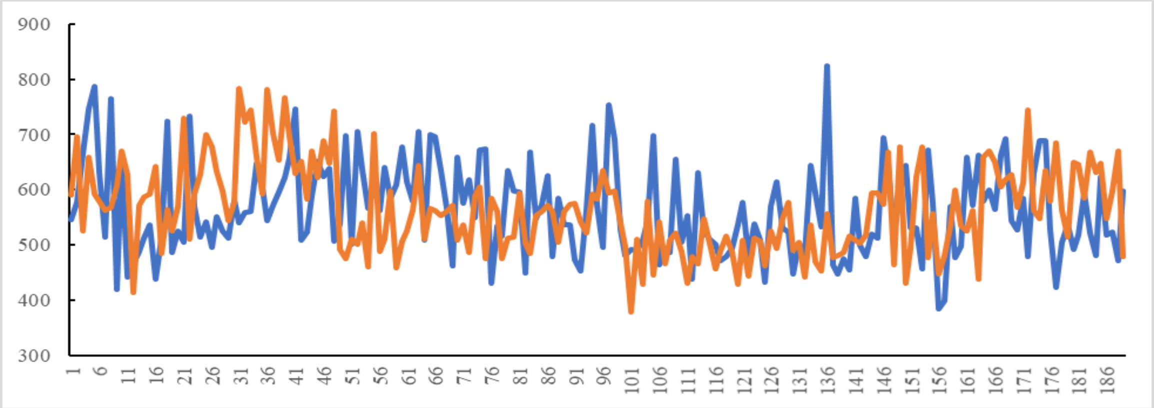

Fig-1: The prediction results of LWBS with 13 traits were described by stepwise regression analysis

Note：Blue line is the chart of LWBS trait and red one is the chart of stepwise regression prediction of LWBS trait.

Prediction of principal component analysis

Firstly, principal component analysis is carried out on each trait to obtain five principal components F1, F2, F3, F4 and F5, and then stepwise regression analysis is carried out by taking the LWBS as a dependent variable to obtain a regression equation.

Table-11: Variance explained by the principal component analysis

	Original eigenvalue			load sum of squares Extracted		
component	Total	contribution rate	Cumulative contribution rate	Total	contribution rate	Cumulative contribution rate
1	3.797	42.192	42.192	3.797	42.192	42.192
2	1.665	18.500	60.692	1.665	18.500	60.692
3	0.892	9.913	70.605	0.892	9.913	70.605
4	0.824	9.158	79.762	0.824	9.158	79.762
5	0.650	7.219	86.981	0.65	7.219	86.981
6	0.541	6.011	92.992			
7	0.425	4.724	97.715			
6	0.541	6.011	92.992			
8	0.144	1.606	99.321			
9	0.061	.679	100.000			

Table-12: coefficient derived by the principal component analysis

component	1	2	3	4	5	component	1	2	3	4	5
CW	0.45	0.22	0.13	-0.05	-0.13	EMA	0.38	-0.12	-0.04	-0.17	-0.03
NWBS	0.46	0.23	0.13	-0.04	-0.14	BT	-0.09	0.46	0.13	0.83	0.09
HGMW	0.45	0.25	0.2	-0.01	-0.12	ADG	0.29	0.14	-0.52	-0.01	0.78
MB	0.27	-0.45	-0.18	0.32	-0.26	MT	0.11	-0.42	0.73	0.08	0.51
IMF	-0.23	0.46	0.27	-0.42	0.09						

Table-13: Prediction of LWBS trait by principal component analysis

	constant	F1	F2	F3	F4
coefficient	-2.019E-15	0.442	0.246	0.082	-0.078
Sig.	0	0	0	0.009	0.016
R square	0.842				
F value	0.000				

$$y=0.442*F1+0.246*F2+0.082*F3-0.078*F4$$

Note: F1, F2, F3 and F4 were the four principal components that affect the LWBS trait significantly. The prediction model with the standardized data was constructed in the following:

Comparison between stepwise regression analysis and principal component analysis

In order to compare the advantages and disadvantages of stepwise regression and principal component regression, we draw the normal p-p graph and histogram of regression residuals under the two models.

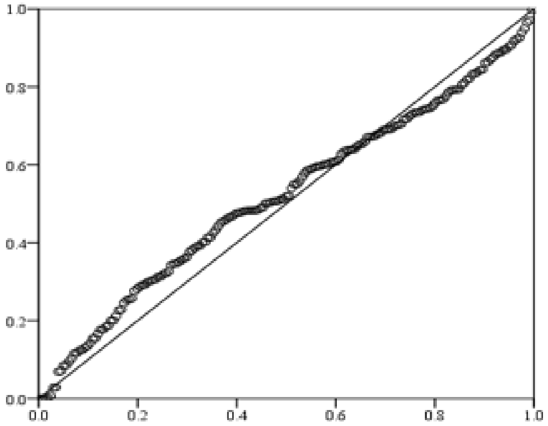

Fig-2: Histogram of regression residuals

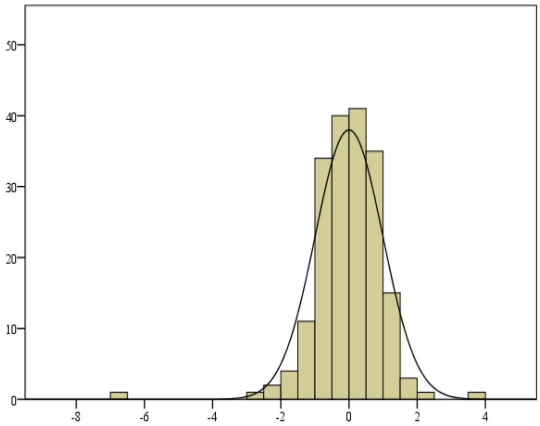

Fig-3: Residual normal graph of regression

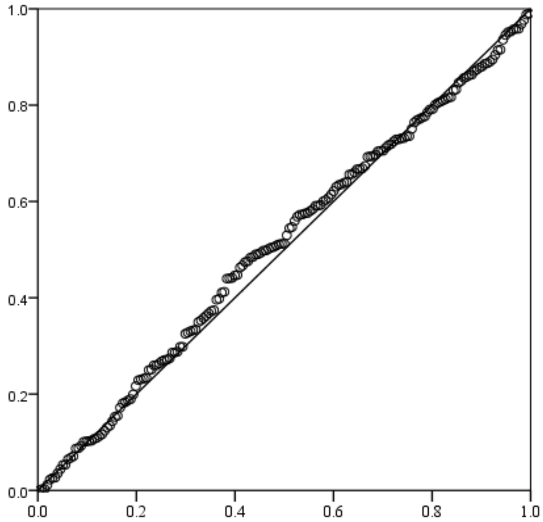

Fig-4: Histogram of PCA residuals

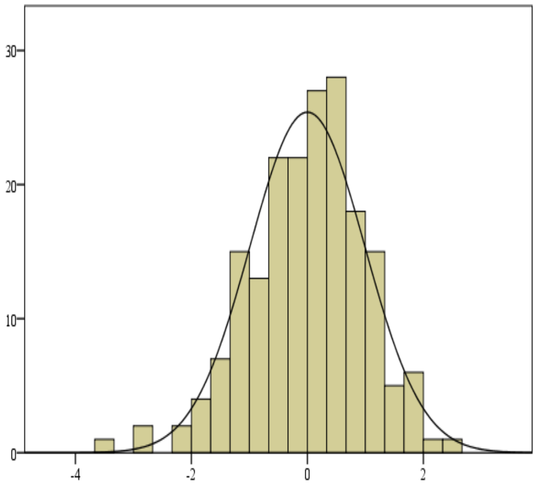

Fig-5: Residual normal graph of PCA

Note: For the left figure, the horizontal axis denoted the normalized residual and the vertical axis denoted the frequency. For the right figure, the horizontal axis denoted the measured cumulative probability, and the vertical axis denoted the expected cumulative probability.

The durbin-Watson statistic of stepwise regression was 1.929 and that of the principal component regression was 1.941.

By the residual normal graph and durbin-Watson statistic of the two models, it can be concluded that the result of principal component regression residual test is better than that of stepwise regression residual test。

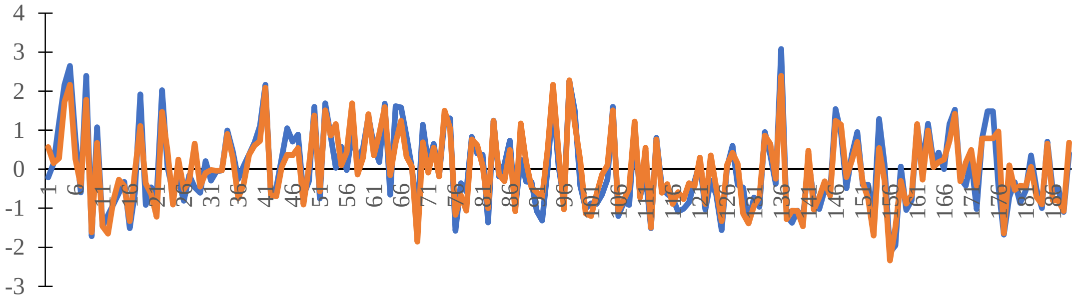

Fig-6: The prediction results of LWBS with 13 traits were described by PCA (standardized data)

Note：Blue line is the chart of LWBS trait and red one is the chart of PCA of LWBS trait.

Significance analysis of each gene on LWBS trait

Table-14: Significance test of each gene on LWBS trait

Trait	CAST	Hfabp_2	PN3	PI6_TaqI	PI6_MspI	PI3_SSCP	PE8	MYOD	MYFi2	dgat1
Significance	0.645	0.183	0.005	0.454	0.285	0.42	0.877	0.187	0.532	0.846

Further, the analysis of the impact of PN3 on trait LWBS, Levin test results showed that variances of different gene types of LWBS were different, from the robustness test results of PN3 gene, three types of genotypes (AA, AB and BB) on the impact of LWBS were significantly different, which can be seen in the following table and figures.

Table-15: Effect of PN3 gene on trait LWBS

		Statistic	df1	df2	Significance
homogeneity of variance test	Levene	6.263	2	174	0.002
robustness test of mean equality	Brown-Forsythe	21.235	2	150.391	0.000

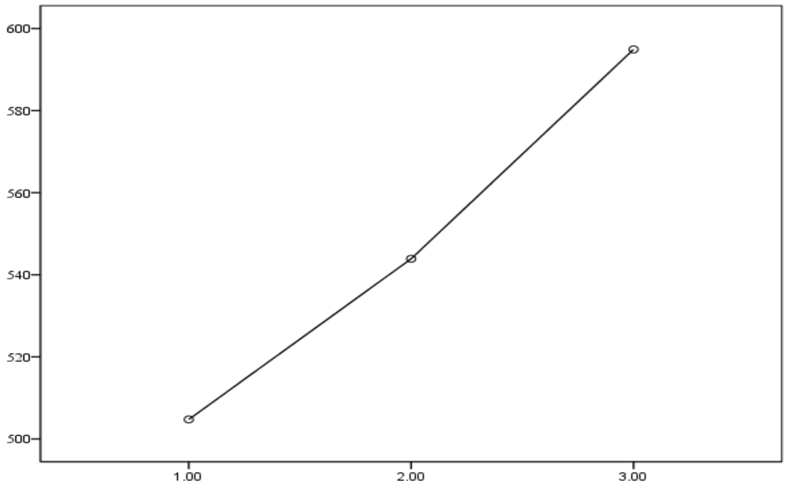

Fig-7: Mean values of three PN3 genotypes with LWBS under single-factor variance analysis

Note：1.00, 2.00 and 3.00 denoted AA, AB and BB genotypes. It can be seen that BB genotype had significantly higher LWBS than those of AA and AB genotypes (P<0.01).

CONCLUSIONS

The improvement of beef meat quality is always an important topic in beef breeding. It is an important way to solve the related problems and speed up the progress of beef breeding to find the relevant candidate genes and carry out marker-assisted selection.

In this paper, the single-factor variance analysis and LM model were used to study the association between target traits and genes. The significant test results of 10 genes and important economic traits of beef cattle showed that CW was affected significantly by 7 genes, and NMW HGMW was affected significantly by 5 genes. Trait MB was significantly by PN3 gene and IMF by 3 genes, EMA and ADG by 2 genes, BT by 5 genes, A2 by only 1 gene. The association analysis between different genotype combinations and growth traits was further discussed, and it was concluded that AA genotype could be used as marker genotype for that selection of CAST, PI6_TaqI, MyOD, and PI3_SSCP and dgat1 gene. For PN3 gene, BB genotype can be selected as marker genotype. For dgat1 gene, AB genotype can be selected as marker genotype.

Meanwhile, we tried to analyze the relationship between the important economic traits of different beef cattle breeds, different feed breeds and different months of age. Finally, we carried out the correlation analysis of important economic traits of LWBS, and obtained the results with biological significance. These important functional genes can provide important reference materials for the production of high-grade beef in the future. However, due to the high slaughter cost of cattle, the data and meat quality traits analyzed in this study are relatively small, and other meat quality traits need to be analyzed in more varieties and larger populations, and more gene functions and related regulatory mechanisms need be studied in a deeper level at the cellular level.

ACKNOWLEDGEMENT

The preparation of this manuscript is supported by the instructive program of science and technology plan from Daqing City: Bayesian mapping method for detecting QTL controlling dynamic traits and a real dataset analysis(No. zd-2016-089), University training project: Hierarchy strategy of animal genome-wide association study- based on stochastic regression model (XZR2017-13).

REFERENCES

1. Chunping Zhao, Linsen Zan, Yan Wang, M. Scott Updike, George Liu, Brian J. Bequette, Ransom L. Baldwin VI, Jiuzhou Song. Functional proteomic and interactive analysis of proteins associated with beef tenderness in Angus cattle [J]. Livestock Science. 2013.
2. Wang LJ, Liu XL, Wang HL, He H, Li ZX, Chen L. Expression analysis, single nucleotide polymorphisms and combined genotypes in candidate genes and their associations with growth and carcass traits in Qinchuan cattle. Molecular biology reports. 2013 Mar 1;40(3):2335-46.
3. Venhoranta H, Bauersachs S, Taponen J, Lohi H, Taira T, Andersson M, Kind A, Schnieke A, Flisikowski K. Fetal growth restriction caused by MIMT1 deletion alters brain transcriptome in cattle. International Journal of Developmental Neuroscience. 2013 Nov 1;31(7):463-7.
4. Cao XK, Zhan ZY, Huang YZ, Lan XY, Lei CZ, Qi XL, Chen H. Variants and haplotypes within MEF2C gene influence stature of chinese native cattle including body dimensions and weight. Livestock Science. 2016 Mar 1;185:106-9.
5. Huang YZ, Jing YJ, Sun YJ, Lan XY, Zhang CL, Song EL, Chen H. Exploring genotype–phenotype relationships of the LHX3 gene on growth traits in beef cattle. Gene. 2015 May 1;561(2):219-24.
6. Gandolfi G, Pomponio L, Ertbjerg P, Karlsson AH, Costa LN, Lametsch R, Russo V, Davoli R. Investigation on CAST, CAPN1 and CAPN3 porcine gene polymorphisms and expression in relation to post-mortem calpain activity in muscle and meat quality. Meat Science. 2011 Aug 1;88(4):694-700.
7. Zhao Jx, Chen Xj, Gao X, Xu Sz, Li Jy, Gao Hj, Zhang Lp. Genetic Polymorphisms of the GH, CAPN1 and CASTGenes and their Association with Economic Traits in Snow Dragon Black Cattle. China Animal Husbandry & Veterinary Medicine. 2014;12:045.
8. Gao JB, Zan LS, Yang N, Li YK, Huangfu YF, Hao RJ, Ma XH, Fu CZ, Jiang BJ, Cheng G. Polymorphismsof DKK1 gene and its association with body measure-ment and meat quality traits in Qinchuan cattle. Acta Veterinaria et Zootechnica Sinica. 2013;44(3):376-86.
9. Yuwei Zhan, Zhidong Tan, Shengxian Fu, Linglong Zhao, Haibing Yang, Shenglin Yang. Analisis of the Polymorphisms of DGAT1 Gene and its Association with Molk ProductionTraits in Guizhou Holstin Cows[J]. China Animal Husbandry & Veterinary Medicine. 2013,40(12):56-61.
10. Zhong-cheng YA, Yu GO, Yong-qiang YA, Ruo-yu LI. Correlation analysis of SOCS4 gene polymorphism with growth traits in Weining cattle. Journal of Southern Agriculture. 2015 Apr 1;46(4).
11. Yuni1 Yao, Enliang Song, Guifen Liu, Haijian Cheng, Wei You, Xiaomu Liu. Correlation between Polymorphisms of SIRT1 Gene and Carcass Traits in Beef Cattle[J]. ChineseJournal of Animal Science. 2015, 51(1):15-19.
12. Yu H, Zhao Z, Yu X, Li J, Lu C, Yang R. Bovine lipid metabolism related gene GPAM: Molecular characterization, function identification, and association analysis with fat deposition traits. Gene. 2017 Apr 20;609:9-18.
13. Xiuxiang Wu, Zhangping Yang, Yongjiang Mao, Xiukui Shi, Bizhi Huang. Genetic distribution of GHR gene and its association with carcass traits in Chiness Simmental cattle[J]. Journal of Yangzhou Universiy (Agricultural and Life Scinece Edition). 2015, 36(4): 31-34.
14. Haibin YU, Hang Xiao, Tian Wei, Yaolu Zhao, Xianzhong Yu, Lupei Zhang, Zhihui ZZhao.

Polymorphisms of GPAM gene oxonand their assocoation with economical traits and fatty acid composition in cattle [J].Chin J Vet Sci. 2015, 35(4): 649-654.

15. Wangqiang Tian, Chugang Mei, Changzhen Fu, Yaping Xin, Song Zhang, Guoqiang Wang,Linsen Zan.SNPs of bovine PRKAA2 gene and its association with growth and meat quality traits[J]. Joutnal of Northwest A&F University (Nat.Sci.Ed.). 2016, 44(7): 1-15.
16. Linsheng Gui, Linsen Zan, Hongbao Wang, Hongcheng Wang. Effects of Single and Combined Genotypes of SIRT1 and SIRT2 Genes on Meat Quality Traits in Qinchuan Cattle [J]. Acta Veterinaria et Zootechnica Sinica. 2015, 46(10):1741-1749.
17. Xian Qiao, Lei Zhang, Xiaokai Li, Yixing Fan, Yuhao Ma. Progress of Genome-wide Association Analysis on Impoetant Economic Traits of Livestock and Poultry [J]. Acta Ecologiae Animalis Domstici Oct. 2017, 38(10):1-9.
18. Hong Guo, Yang Lv, Jian-xing Chen，Guangpeng Li. Ｒeceat Progress and Trend of Molecular Breeding in Beef Cattle[J]. Journal of Agricultural Science and Technology. 2014, 16(1):24-31.
19. Huff-Lonergan E, Mitsuhashi T, Beekman DD. Proteolsis of specific muscle structureproteins by mu-calpain at low PH and temoerature is similar to degradation in postmortem bovine muscle [J]. J Anim Sci .1996 May, 74(5):993-1008.
20. Morgan JB, Miller RK, Mendez FM, Hale DS, Savell JW. Using calcium chloride injection to improve tenderness of beef from mature cows. Journal of animal science. 1991 Nov 1;69(11):4469-76.