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Association of Several Genes and Genotype Combinations with Allometric Traits in Beef Cattle

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Abstract: Beef quality，except the milk production, is the most important index that both the consumers consider and the experts on genetic breeding care. The screening and identification of function gene meat quality-related and controlling the allometric traits have important significance for marker assisted selection. This paper explored variation of 10 genes in 7 different populations of beef cattle. The association analysis of 10 genes and different genotype combinations with totally 28 allometric traits was carried out by linear model using the SPSS software. Next, that we studied association analysis between different genotypes and the traits. PN3 gene had a significant effect on 12 important economic traits together with the LWBS. Finally, the optimal prediction model of the trait LWBS with 16 traits was obtained by principal component regression. 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; Allometric traits; Genotype combination; Association Analysis; Prediction.

INTRODUCTION

Allometry that describes the relationship in relative growth rate between biological traits or functions of organisms and body size is ubiquitously observed in nature. Allometry scaling, generally expressed as a power function, describes how morphological traits of organisms change with body size.

Since the introduction of allometry scaling equation by Huxley[1], a number of attempts have been made by biologists to justify the broad dependence of physiological, morphological, developmental, anatomic, life-historical, ecological as well as evolutional factors on body size[2-8]. Among diverse allometry scaling relationships, the most important and fundamental one is that metabolic rate scales to the three-quarters power of the mass of animals or plants, also known as Kleiber's law[2].

The quarter-power allometric scaling has been regarded as a universal phenomenon in biology, explained from fundamental principles of biology and biophysics. However, even with over a century of interest in the evolution of allometry, essentially nothing is known about the genetic and developmental mechanisms of differentiation in allometric scaling relationships, although developmental processes must have played a central role in maintaining the functional scaling relationships among traits as well as in their evolution.

The following three kinds of allometries are ordinarily used to describe scaling relationships between different organ parts, which are static allometry, ontogenetic allometry and evolutionary allometry[9-11]. The detail explanations for the three terms of allometries are displayed in the following. The relative growth between two different traits, or different organism or different functions can be described by static allometry, which also can describe relative growth between two different organs at a particular growth and developmental stage. The growth trajectory of one trait relative to the other trait in ontogeny can be expressed with ontogenetic allometry. By the stepwise regression analysis of the multiple regression analysis, relative growth of multiple partial body sizes to entire body size is measured by phenotypic joint allometry scaling model.

The genetic analysis of size change with increasing age, i.e., growth, has received considerable attention in quantitative developmental genetic studies, but the genetic architecture of ontogenetic changes in body shape and its associated allometry have been poorly understood partly due to the lack of analytical tools. The past three decades have witnessed a surge of interest in applying geometric morphometric approaches to understand how body shape changes and how such a change is associated with allometry during ontogeny[12-15].

Many studies have been carried out for exploring the association of traits of cattle and the genes[16-21]. 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[22, 23]. Multiple comparison showed that AA and AB were significantly higher than bb in 305 day corrected milk yield and milk fat percentage[24]. Through the correlation analysis of different genotypes and allometric traits of cattle, the differences of individual genotypes were obtained[25, 26]. The correlation between AGP at 6 gene 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[27]. 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[28-31]. The research progress of GWAS in complex economic traits of important livestock species was reviewed, 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[32]. The latest research achievements of molecular markers and molecular breeding related to beef cattle were summarized, and the research progress of beef cattle growth and related production traits were mainly introduced[33].

It is necessary to explore the internal mechanism and regularity of animal growth and developing, also it can help realize human intervention (including forecasting and control) and regulating the development of target traits.

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 28 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, HQW and BT were significantly affected by PN3, PI3_SSCP, and PI6_TaqI. Next, we studied association analysis between different genotype and growth 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 the pre-allometric weight, among which individuals of BB genotype had significantly higher pre-allometric weight 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.

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, Simmental). After weaning, the cows were transported to Beijing's JinWeifuRen dairy farm and fed under the same feeding and management system. Growth and development characteristics of all beef cattle were observed until allometric after 16 - 18 months.

There are totally 25 allometric traits are analyzed. According to Institutional Meat Purchase Specifications (IMPS) for, Fresh Beef guidelines, the live weight (y) is measured before, allometric after fasting 24 h; Carcass weight (CCW) is done after allometric and bloodletting by eliminating the hide(HW), head, feet, tail, entrails and gut fill; Net meat weight of beef (NMW) is that of carcass after removing the bones, ligaments and breast; The high quality beef (HQW) includes tenderloin, striploin, ribeye and high rib. The intramuscular fat (IMF) is obtained from the sample of ribeye muscle.

The weight of bones (BW) is that of whole bones besides head (HW), tail (TW) and feet (FW). The red offal (ROW), pizzle (PW), oxtail (OW), white offal (WOW), mesentery and omentum (MOW), leaf fat (LF), kidney (KW) and diaphragm (DW) are collected by removing the surrounding fat and contents. The cowhide (CW) does not include the parts of head and tail. Among that, the red offal (ROW) includes heart, liver and lung; the white offal (WOW) consists of stomach and intestinal. Body length, bust circumference, abdominal circumference, carcass length, carcass chest depth, hind leg width, hind leg length, hind leg circumference, thigh thickness are denoted by BL, BC, AC, CL, CCD, HLW, HLL, HLC, TT, respectively.

After collecting the original data, the fixed effect of phenotypic values was corrected, including allometric year, feeding season, fattening days, admission weight and random effect.

The correction formula is 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 Allometric 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 enter the farm,e is the random effect.

Association analysis between genes and allometric traits of beef cattle.

Significance analysis of each gene and allometric 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 13 traits are significantly affected by the 10 genes. Gene CAST had significant effect on trait PW only. PN3 gene had significant effects on traits CCW, NMW, HQW, IMF, BW, HW, FW, OW, CW, MOW, LF and KW. PI6_TaqI gene had significant effects on traits CCW, NMW, HQW and LF. PI3_SSCP gene had significant effects on traits CCW, NMW, HQW and IMF. PE8 gene had significant effects on traits CCW, NMW, HQW, IMF and LF. MyOD had significant effects on traits CCW, NMW, HQW and LF. MYFi2 gene had significant effects on traits LF only and DGAT1 gene had significant effects on traits CCW only.

Table-1: Significance test of each gene with allometric traits (allometric traits) of beef cattle

Trait / Gene	Significance												
	CCW	NMW	HQW	IMF	BW	HW	FW	PW	OW	CW	MOW	LF	KW
CAST	0.810	0.947	0.956	0.724	0.121	0.282	0.236	0.043	0.545	0.748	0.691	0.501	0.330
Hfabp_2	0.430	0.514	0.580	0.821	0.403	0.378	0.320	0.572	0.121	0.405	0.762	0.366	0.474
PN3	0.034	0.000	0.001	0.016	0.001	0.000	0.000	0.315	0.002	0.001	0.018	0.000	0.025
PI6_TaqI	0.003	0.004	0.042	0.796	0.419	0.719	0.350	0.406	0.762	0.488	0.286	0.014	0.634
PI6_MspI	0.086	0.935	0.935	0.353	0.237	0.419	0.355	0.638	0.453	0.323	0.832	0.202	0.840
PI3_SSCP	0.001	0.003	0.003	0.019	0.900	0.930	0.813	0.845	0.797	0.927	0.492	0.677	0.329
PE8	0.043	0.045	0.045	0.017	0.943	0.964	0.900	0.961	0.993	0.972	0.775	0.000	0.408
MyOD	0.001	0.009	0.009	0.149	0.122	0.076	0.174	0.495	0.803	0.324	0.920	0.000	0.409
MYFi2	0.439	0.521	0.521	0.966	0.981	0.976	0.902	0.186	0.752	0.400	0.811	0.000	0.977
DGAT1	0.022	0.908	0.908	0.493	0.374	0.403	0.373	0.955	0.606	0.860	0.267	0.891	0.202

From Table2, we can see that MyOD, PN3, PI6_MspI and MYFi2 gene had a significant effect on 7 important allometric traits, among which individuals of AA genotype had significantly higher mean than those of BB and AB genotypes (P<0.01). MyOD, PI3_SSCP and MYFi2 gene had a significant effect on 7 important body measurements, also among which individuals of AB genotype had significantly higher mean than those of AA, BB, CD and EE genotypes (P<0.01).

From the analysis, it can be derived that, for PI3_SSCP, PI6_TaqI, dgat1 gene, the population mean value of individuals for intramuscular fat (IMF) trait with AB genotype was significantly lower than that with AA or BB or CD genotype, while for the other 6 traits, the population mean value with AB genotype was significantly higher than that with other genotypes.

For MyOD, PI6_MspI, MYFi2, PN3 gene, the mean value of population for intramuscular fat (IMF) trait with AA genotype was significantly lower than that with BB or AB genotype, while for the other 6 traits the population mean value with AA genotype was significantly higher than that with BB and AB genotype.

For PE8 gene, the mean value of population for IMF trait with BB genotype was significantly lower than that with EE genotype, while for the other 6 traits the mean value of the population with BB genotype individuals was significantly higher than that with EE genotype.

Table-2: Association of SNPs with allometric traits (7 important allometric traits)

Gene	Genotype	CCW	NW	HQW	IMF	ROW	HW	WOW
PI6_TaqI	AA(n=164)	305.738 (57.027)	238.613 (44.920)	29.593 (5.103)	6.906 (3.735)	12.988 (2.129)	39.846 (8.811)	16.755 (3.906)
	AB(n=13)	322.002 (54.201)	251.662 (40.462)	31.613 (4.550)	5.004 (3.254)	13.686 (2.304)	42.238 (8.859)	17.177 (3.025)
MyOD	AA(n=144)	321.847 (54.633)	250.897 (39.871)	31.527 (4.497)	5.029 (2.915)	13.666 (2.347)	42.076 (8.776)	17.114 (3.061)
	AB(n=17)	309.965 (55.064)	243.075 (43.907)	30.579 (5.180)	6.417 (3.559)	12.924 (1.913)	40.647 (8.902)	16.634 (3.542)
PN3	AA(n=30)	323.140 (55.319)	254.483 (46.695)	31.966 (5.089)	5.126 (2.398)	13.795 (2.193)	42.933 (9.584)	17.448 (2.944)
	AB(n=55)	316.815 (53.440)	249.208 (41.691)	31.370 (4.733)	5.593 (3.405)	13.744 (2.129)	41.400 (8.604)	17.269 (3.452)
	BB(92)	322.435 (55.154)	250.366 (38.583)	31.358 (4.405)	4.979 (2.830)	13.469 (2.427)	42.174 (8.824)	16.974 (2.919)
PI6_MspI	AA(23)	324.174 (67.644)	247.719 (35.223)	30.957 (4.138)	6.503 (3.343)	13.263 (1.714)	39.478 (8.107)	16.425 (2.417)
	AB(88)	321.477 (56.857)	251.410 (44.093)	31.484 (4.913)	5.260 (3.665)	13.755 (2.264)	42.761 (9.509)	17.264 (3.424)
	BB(58)	324.579 (48.130)	252.296 (40.294)	31.771 (4.681)	4.684 (2.445)	13.227 (2.579)	42.810 (8.317)	17.270 (2.690)
PI3_SSCP	AA(n=118)	304.835 (35.291)	239.121 (28.934)	30.814 (3.319)	5.098 (2.609)	13.091 (3.346)	37.348 (7.088)	16.446 (2.894)
	AB(n=23)	324.459 (55.978)	252.727 (40.051)	31.611 (4.593)	5.084 (2.973)	13.758 (2.089)	42.907 (8.759)	17.241 (3.086)
PE8	AA(n=137)	325.234 (56.621)	253.874 (41.976)	31.725 (4.764)	4.654 (1.552)	13.729 (2.093)	43.036 (8.879)	17.359 (3.035)
	AE(n=14)	300.357 (31.767)	234.796 (26.634)	30.185 (3.000)	5.045 (3.268)	13.607 (2.072)	37.714 (6.281)	15.932 (2.682)
	BB(n=14)	328.000 (56.368)	257.757 (44.968)	32.999 (4.508)	4.419 (2.235)	13.768 (4.155)	43.643 (11.119)	17.966 (3.791)
	EE(n=7)	283.857 (31.687)	223.544 (25.944)	28.290 (3.420)	7.707 (3.603)	11.800 (1.052)	36.000 (4.359)	15.020 (2.951)
MYFi2	AA(n=144)	321.096 (53.464)	250.445 (38.717)	31.497 (4.401)	5.086 (2.900)	13.611 (2.317)	41.986 (8.751)	17.134 (3.051)
	AB(17)	303.067 (58.707)	236.855 (46.448)	29.302 (5.216)	7.099 (3.833)	12.854 (2.166)	39.833 (9.203)	16.417 (3.875)
dgat1	AB(n=100)	328.560 (56.206)	256.116 (39.667)	32.018 (4.515)	4.886 (2.927)	13.809 (2.109)	43.640 (8.708)	17.362 (3.077)
	BB(n=29)	302.931 (42.270)	235.887 (32.795)	29.834 (3.796)	5.492 (3.072)	13.369 (1.846)	38.966 (7.562)	16.319 (2.753)
	CD(n=18)	314.122 (56.257)	246.464 (44.956)	30.989 (5.317)	6.360 (3.462)	13.086 (1.980)	40.500 (8.659)	16.682 (3.442)

Significance analysis of each gene and body measurements traits of beef cattle

Table 3 shows the significant tests of each gene and body measurements of allometric traits of beef cattle, it can be concluded that 10 traits are significantly affect by the 8 genes. PN3 gene had significant effects on traits AC, TC, CL, HLC and HLW. PI6_TaqI, PI6_SSCP, PE8, MYFi2 and DGAT1 only affect one trait, which are CD, CC, HLL, HLW and CC, respectively. MyOD had significant effects on traits HLW and TMT.

Table-3: Significance test of each gene with allometric traits (body measurements) of beef cattle

Trait / Gene	Significance									
	C	C	C	L	CD	D	LC	LW	LL	T
PN3	.572	.021	.028	.034	.363	.649	.007	.000	.068	.172
PI6_TaqI	.258	.412	.146	.345	.211	.031	.702	.359	.201	.720
PI6_MspI	.260	.513	.093	.637	.014	.066	.483	.180	.685	.887
PI3_SSCP	.037	.257	.176	.569	.407	.246	.272	.107	.723	.919
PE8	.954	.881	.920	.763	.582	.388	.719	.630	.015	.916
MyOD	.784	.462	.796	.416	.886	.160	.250	.042	.212	.004
MYFi2	.936	.907	.831	.619	.586	.832	.865	.040	.638	.739
DGAT1	.021	.365	.379	.699	.398	.218	.359	.675	.051	.619

Table-4: Association of SNPs with allometric traits (8 important body measurements)

Gene	Genotype	BL	BC	AC	CL	CCD	HLW	HLL	TT
PI6_TaqI	AA(n=164)	147.583 (5.125)	197.417 (8.163)	216.000 (7.699)	131.385 (4.501)	73.231 (2.587)	42.000 (7.649)	78.769 (2.555)	14.308 (1.548)
	AB(n=13)	155.435 (7.822)	206.400 (10.340)	228.832 (18.116)	138.640 (6.389)	75.098 (3.311)	43.104 (4.096)	80.354 (3.457)	14.159 (1.701)
MyOD	AA(n=144)	155.606 (7.905)	206.303 (10.381)	229.718 (16.879)	138.549 (6.574)	75.014 (3.337)	43.417 (4.424)	80.458 (3.284)	14.340 (1.673)
	AB(n=17)	151.353 (6.717)	200.938 (10.181)	220.176 (11.137)	134.941 (4.930)	74.941 (3.307)	40.235 (3.649)	78.412 (4.388)	12.647 (1.057)
PN3	AA(n=30)	150.556 (7.062)	201.593 (9.569)	216.481 (26.180)	133.867 (5.387)	74.967 (3.557)	40.567 (3.739)	78.467 (3.137)	13.667 (1.768)
	AB(n=55)	153.855 (7.768)	203.296 (10.477)	224.382 (14.534)	137.182 (6.736)	74.509 (3.447)	42.291 (4.630)	79.855 (3.285)	14.200 (1.715)
	BB(92)	157.033 (7.676)	208.418 (10.047)	233.791 (14.466)	140.109 (5.966)	75.315 (3.169)	44.043 (4.049)	81.043 (3.406)	14.283 (1.633)
PI3_SSCP	AA(n=118)	155.547 (8.318)	206.658 (11.067)	230.564 (17.770)	139.254 (6.909)	75.468 (3.363)	43.610 (4.542)	80.908 (3.250)	14.212 (1.714)
	AB(n=23)	153.091 (6.202)	201.818 (7.842)	217.500 (20.581)	135.870 (4.475)	75.435 (3.300)	41.304 (2.619)	80.739 (3.911)	14.130 (1.687)
PE8	AA(n=137)	155.537 (7.868)	206.654 (10.541)	229.985 (17.163)	138.898 (6.548)	74.949 (3.320)	43.401 (4.247)	80.161 (3.339)	14.175 (1.658)
	AE(n=14)	152.538 (6.790)	201.000 (9.899)	215.308 (26.199)	135.214 (5.767)	74.071 (3.222)	40.857 (2.598)	81.214 (3.620)	14.071 (1.817)
	BB(n=14)	157.571 (8.662)	207.071 (10.859)	231.214 (15.278)	139.286 (7.119)	75.571 (2.875)	43.286 (3.561)	81.500 (3.590)	14.286 (2.301)
MYFi2	AA(n=144)	155.437 (7.976)	206.057 (10.203)	228.937 (16.805)	138.264 (6.465)	74.979 (3.354)	42.965 (4.111)	80.194 (3.493)	14.146 (1.681)
	AB(17)	153.167 (6.132)	204.000 (10.930)	228.917 (15.664)	136.667 (7.177)	74.500 (2.844)	45.667 (7.253)	80.667 (3.676)	14.167 (1.337)
dgat1	AB(n=100)	155.180 (7.728)	205.660 (10.348)	228.560 (17.654)	138.510 (6.499)	74.860 (3.207)	43.370 (4.651)	80.480 (3.374)	14.130 (1.745)
	BB(n=29)	158.655 (6.789)	208.621 (9.548)	233.448 (13.876)	140.931 (5.688)	75.483 (3.491)	43.517 (2.959)	81.345 (3.548)	14.276 (1.579)
	CD(n=18)	152.000 (8.066)	203.938 (11.579)	226.938 (14.050)	135.556 (5.575)	74.833 (3.451)	41.778 (4.747)	79.611 (3.274)	13.833 (1.505)

From Table 4, it can be derived that, for PN3, PE8 and dgat1 gene, the population mean value of individuals for 8 important body measurements trait with BB genotype was significantly higher than that with AA or AB or CD genotype.

For MyOD, PI3_SSCP, MYFi2 gene, the mean value of population for 8 important body measurements trait with AA genotype was significantly higher than that with AB genotype.

For PI6_TaqI gene, the mean value of population for 8 important body measurements trait with AB genotype was significantly higher than that with AA genotype.

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-5: Results of stepwise regression analysis for LWBS with other traits

	Traits	CCW	NMW	HQ	BW	HQW	TW	OW	WOW	MOW	KW	DW
	Variables	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}
coefficient	-19.026	0.249	0.596	1.195	1.166	1.846	12.179	0.962	3.901	1.477	38.46	5.341
Sig.	0.067	0	0	0.049	0	0.006	0.008	0	0	0	0	0.001
R square	0.97						F value	518.614(p=0.001)				

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

$$y=-19.026+0.249x_1+3.901x_2+0.596x_{3+}1.846x_4+5.341x_5+1.166x_6+1.477x_7+0.962x_8+38.46x_9+12.179x_{10}+1.195x_{11}$$

LWBS was significantly affected by the eleven traits.

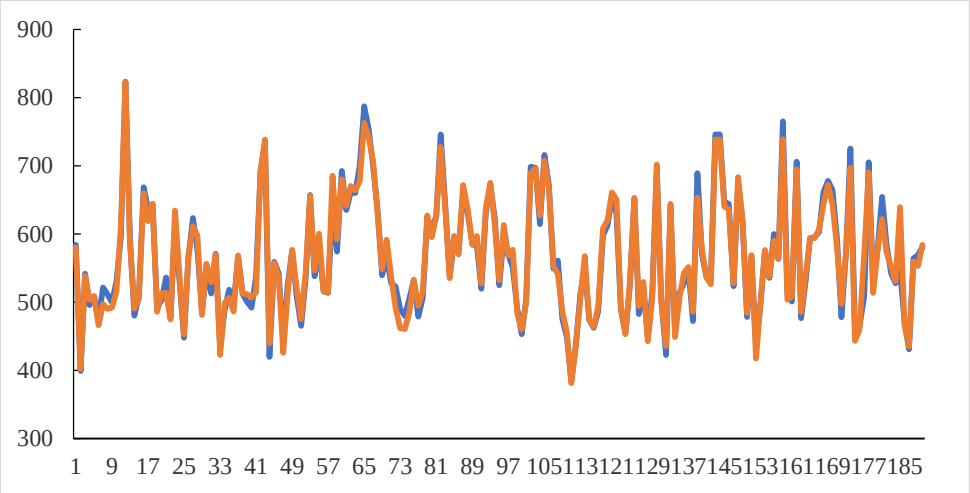

Fig-1: The prediction results of LWBS with 11 traits were described by stepwise regression analysis

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-6: 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	8.347	52.169	52.169	8.347	52.169	52.169
2	1.794	11.209	63.378	1.794	11.209	63.378
3	1.041	6.508	69.886	1.041	6.508	69.886
4	0.770	4.815	74.700			
5	0.647	4.041	78.741			
6	0.622	3.887	82.629			
7	0.583	3.644	86.273			
6	0.537	3.359	89.632			
8	0.484	3.025	92.656			
9	0.299	1.869	94.525			
10	0.255	1.595	96.120			
11	0.210	1.311	97.432			
12	0.157	0.9079	98.410			
13	0.106	0.664	99.074			
14	0.092	0.574	99.648			
15	0.056	0.352	100.000			

Table-7: coefficient derived by the principal component analysis

Traits / PC	CCW	NMW	HQ	IMF	BW	HQW	FW	ROW
PC1	0.322	0.312	0.285	-0.119	0.316	0.307	0.303	0.204
PC2	0.072	0.118	0.146	0.469	-0.11	-0.066	-0.167	0.055
PC3	0.004	-0.004	0.099	-0.241	0.025	0.034	0.011	-0.183
Traits / PC	PW	TW	OW	WOW	MOW	LF	KW	DW
PC1	0.227	0.215	0.301	0.231	0.039	-0.019	0.288	0.223
PC2	-0.251	-0.014	-0.141	0.34	0.644	0.203	0.031	0.189
PC3	0.019	0.155	0.028	-0.211	-0.001	0.88	-0.184	0.139

Table-8: Prediction of LWBS trait by principal component analysis

	constant	F1	F2
coefficient	-5.7295E-15	0.332	0.148
Sig.	0	0	0
R square	0.961		
F value	0.000		

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

$$y=0.332*F1+0.148*F2$$

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.

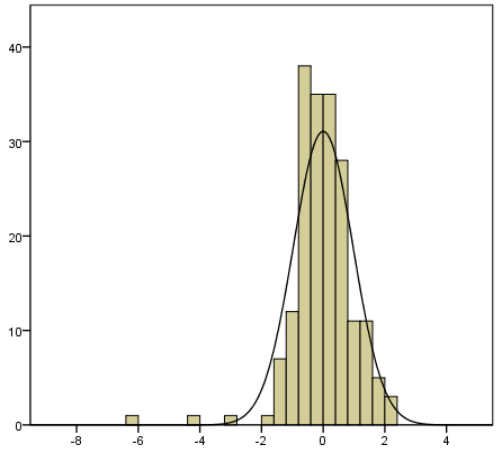

Fig-2: Histogram of regression residuals

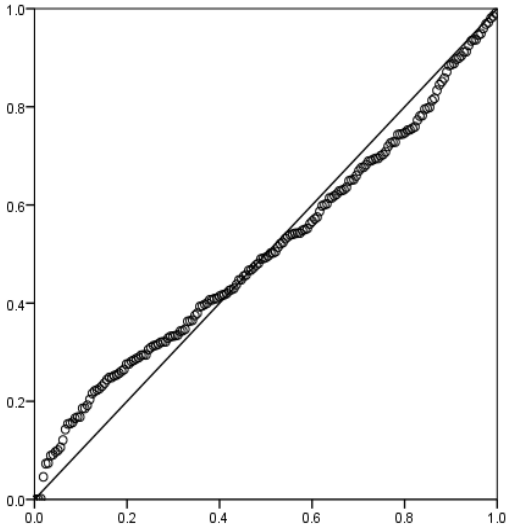

Fig-3: Residual normal graph of regression

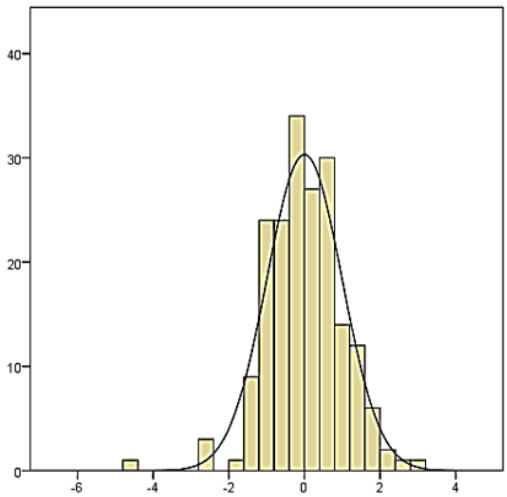

Fig-4: Histogram of PCA residuals

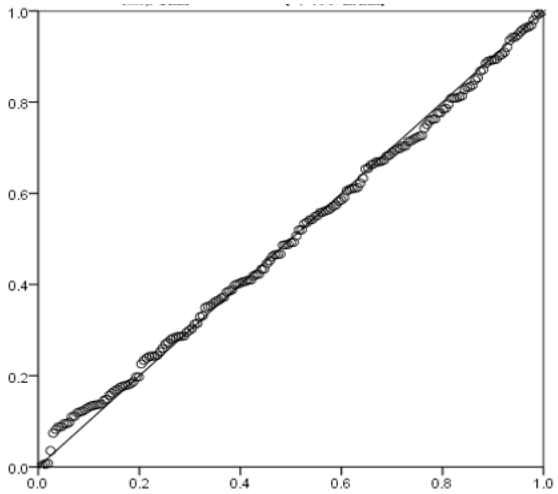

Fig-5: Residual normal graph of PCA

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 1.844 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.

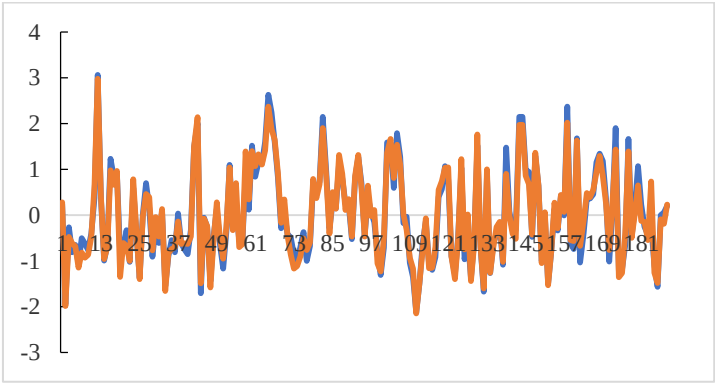

Fig-6: The prediction results of LWBS with 16 traits were described by PCA (standardized data)

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

CONCLUSIONS

The improvement of beef meat quality is always an important topic in beef breeding. It is important 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. Totally 23 of 28 traits are significantly affected by the 10 genes concluded from the significant tests of each gene and important economic traits of beef cattle.

It can be concluded that 13 are significantly affected by the 10 genes with the significant tests of each gene and important allometric traits of beef cattle. Also, it can be derived that, for PN3, PE8 and dgat1 gene, the population mean value of individuals for 8 important body measurements trait with BB genotype was significantly higher than that with AA or AB or CD genotype. For MyOD, PI3_SSCP, MYFi2 gene, the mean value of population for 8 important body measurements trait with AA genotype was significantly higher than that with AB genotype. For PI6_TaqI gene, the mean value of the population for 8 important body measurements trait with AB genotype was significantly higher than that with AA genotype.

We adopt the stepwise regression analysis for LWBS with the important economic traits and the

results demonstrated that LWBS was significantly affected by the eleven traits. Last, comparison between stepwise regression analysis and principal component analysis was studied, and 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.

However, due to the high allometric 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.

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