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RESEARCH ARTICLE

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Correlation analysis of relationships between polymorphisms of high quality chicken *myogenin* gene and slaughter and meat quality traits

Abstract In this study, PCR-SSCP technique was designed to investigate the effect of the *myogenin* (*MyoG*) gene on quality of chicken meat (developed by Sichuan Dahen Poultry Breeding Company using local breeds). Four mutations at base position in the promoter region were detected among individuals in each line, i.e. T/C in locus A, and T/A, T/C and A/G in locus B. Least squares analysis showed that there was a significant difference between genotype and breast muscle percentage and some carcass traits ($P < 0.05$) for locus A. There were significant differences ($P < 0.05$) in breast muscle weight between AC, AA and AB genotypes; a significant difference ($P < 0.05$) in leg muscle percentage between CC and AC for locus B, and an extremely significant difference ($P < 0.01$) in the frequency of genotype muscle fiber density for both locus A and locus B. Nonsignificant difference ($P > 0.05$) was detected in the other traits. It was concluded that the *MyoG* gene is the major gene affecting the muscle fiber traits of chicken or it links with the candidate gene, and the mutation can be used as the molecular genetic marker to select the chickens for meat quality traits.

Keywords chicken, *MyoG* gene, PCR-SSCP, carcass traits, meat traits, correlation analysis

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1 Introduction

The development of muscle fiber in animals completed during formation of the embryo is regulated by the *MyoD* gene family. As a result, this study about muscle fiber focuses more on the *MyoD* gene. The family of the *MyoD* gene has four kinds of genes correlated in constitution, i.e., *MyoD1* (myogenic determination factor 1), *myogenin* (*MyoG*), *myofactar-5* (*Myf-5*) and *myofactar-6* (*Myf-6*). These genes, encoding *basic-helix-loop-helix* (*bHLH*), participate in the determination and differentiation of myocytes by regulating the expression of specific proteins during muscle differentiation (Olson, 1990; Weintraub et al., 1991; Fujisawa-Sehara et al., 1992; Dechesne et al., 1994; Malik et al., 1995; Rudnicki and Jaenisch, 1995; Ordahl and Williams, 1998; Barbut, 1993). Among them, *Myf-5* and *MyoD1* are expressed in myoblast generation while *MyoG* reacts in the development of the fetus and is expressed during the late stages of differentiation. *Myf-6* is expressed mainly after the birth of the fetus, and participates in the formation of muscle in majority of animals. The growth rate and time of the myoblast, and the time of priming differentiation have an effect on the quantity of muscle fiber, which is that they have an effect on the maximum potency of the lean meat growth (te Pas and Visscher, 1994). The polymorphism of *MyoD1* relates to the process of muscle reparation (Key et al., 1993), delay in priming differentiation, and muscle fiber hypertrophy as seen in quails (Coutinho et al., 1993).

The result of the study on the *MyoD* gene in pigs (te Pas et al., 1998) indicates that the mutations on the *MyoD* locus are concerned with the amount of muscle fiber, the growth rate, and the carcass weight (te Pas et al., 1996). Therefore, we further study *MyoG*, which is correlated intimately to the meat trait as a candidate gene affecting muscle development in poultry. By incorporating traditional and modern molecular genetics and applying them to domestic and poultry breeding practices, this will

largely elevate selection efficiency and further efficiently enlarge domestic and poultry production.

2 Materials and methods

2.1 Materials

In this study, high quality chicken populations were purchased from Sichuan Institute of Animal Science, and Sichuan Dahen Poultry Breeding Company, including five pure lines named S01, S02, S03, S05 and D99, and three hybrid combinations named S01 × D99, S01 × S10, and S01 × S05. From each population, 15 males and 15 females were randomly chosen, which were then managed specially, fed in a single cage with equal management and nutrition levels, allowed to forage freely, and slaughtered when reaching the market weight and age. Samples were collected by slaughtering determination, with blood samples collected from the wing vein, anticoagulated with EDTA, and conserved at a temperature of −20°C after coding. After the full pectoral muscle was chosen, it was frozen after coding, conserved, and quickly sent to the Animal Nutrition Institute, Sichuan Agricultural University for analysis of meat quality. Finally, we chose the pectoral muscle by a bulk of 1 cm × 2 cm × 3 cm, conserved it with formalin after coding and fixed it for slicing.

2.2 Methods

DNA was extracted with an automatic nucleic acid extraction equipment. The PCR primers were designed to amplify the target fragments in the *MyoD* gene using primer5 and OLIGO 6.0 according to the chicken genomic sequence in the GenBank database (Accession No: AF487518). Primer synthesis was completed by TaKaRa Biotechnology (Dalian) Co., Ltd., China. The primer pairs were designed to detect the polymorphic regions. One pair of primer F5′- ggt ggg tgt ggg gaa tgg tgc t -3′ and R5′- ccg gct ttg tct cta atc ct -3′ (locus A) was used to amplify a 203-bp fragment in *MyoD* gene CDs. Another pair of primer F5′- aaa ccc atc cca ttg tgc -3′ and R5′- cat cat ctg gtc cct tca gtt -3′ (locus B) was used to amplify a 236-bp fragment.

The PCR conditions were as follows: at 95°C for 4 min, 33 cycles at 95°C for 40 s, at 56°C for 45 s, at 72°C for 55 s, and an extension at 72°C for 10 min.

A total of 3 μL of PCR products were mixed with 0.5 μL of 6 × loading buffer. The mixture was denatured at 95°C for 15 min, and then placed on ice for 5 min. Electrophoresis was run at 160 V·cm^{-1} on a 10% PAGE for 8 h at 20°C. Gels were stained using silver staining. Individual PCR-SSCP banding patterns were determined under visible light.

The PCR products were purified. The homozygous individuals of different genotypes were sequenced by TaKaRa Biotechnology (Dalian) Co., Ltd., China.

3 Statistical analysis

Marker gene polymorphisms were analyzed using Polymorphism Information Content (*PIC*). According to the experimental results, the distribution of the genotypic frequency and gene frequency of each strain tested was calculated, which showed high polymorphism when $PIC > 0.5$, midrange polymorphism when $0.25 < PIC < 0.5$, and low polymorphism when $PIC < 0.25$.

$$PIC = 1 - \left(\sum_{i=1}^{n} P_i^2\right) - \left(\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} 2P_i^2 P_j^2\right),$$

where i and j are the allelomorphs, P_i and P_j are the allele frequencies, and n is the number of allelomorphs.

DBF database was established with the routine line linearity model of SAS (SAS Institute Inc, SAS 6.12, 1996) to analyze the differences in the genotypic frequency and gene frequency among the breeds at each locus.

The results were analyzed by Aniso-duplication analysis of variance with SAS, and hereditary effect in each locus was found to exist. The following model was used:

$$Y_{ijk} = \mu + A_i + B_j + G_k + E_{ijkl} + b_{jk}X,$$

where Y_{ijk} is the individual abatage meat traits measured on chickens, μ is the population mean, A_i is the strain effect, B_j is the sexual effect, G_k is the genotype effect, E is the random error, b_{jk} is the fixed effects of breed, and X is the carcass weight or the concomitant variable. The carcass weight should be taken as a concomitant variable in the mode for the weight and percentage of breast muscle, leg muscle and abdominal fat because it has some effect on them. However, our experimental materials all come from the same breeding field, and we made a choice and omitted parts of the equation based on them, i.e., all the chickens had high regularity with almost all having equal carcass weights, therefore X was ignored in the model.

The Least Square means (LS means) of butcher and meat traits of the different genotypes were measured by GLM with concurrent significance testing.

4 Results

4.1 PCR-SSCP analysis

The PCR-SSCP method was used for the detection of nucleotide sequence polymorphism in the 5′UTR of the

chicken *MyoG* gene, and 3 genotypes in site A and 6 in site B were found.

4.2 The sequencing result

The PCR products were sequenced directly and the results showed T-C(154) at the first site in 5′UTR and T-A(348), T-C(425), and A-G(428) in the second site, contrasted by DNASTAR6.0.

4.3 PCR-SSCP genetic polymorphism analysis in the 5′UTR of the chicken *MyoG* gene

The tested individualities of the eight colonies were analyzed by heredity index including *Ho, He, Ne, PIC*; the independence test results among the different strains at locus A and locus B are shown in Fig. 1, Fig. 2, Table 1 and Table 2. Their differences were significant ($P < 0.05$). The allelomorphic gene frequency prevailed at *B* except for S03, and the site at $0.25 < PIC < 0.5$ showed midrange polymorphism. *PIC* at the same site in each colony showed relative equality, with the maximum at S01 × S05, where *PIC* was 0.4286, and the minimum at S01 × D99, where *PIC* was 0.3198. As for site B, the independence test results among different stains showed that the distribution differences of these eight stains were extremely significant ($P > 0.01$) with high polymorphism (where $PIC > 0.5$). The *PIC* contents of every colony at site B were fundamentally equal, with the maximum at S01 × S10, where *PIC* was 0.662, and the minimum at S05 and S03, where *PIC* was 0.563. It was revealed that the rate of polymorphism among the eight stains at site B was relatively large.

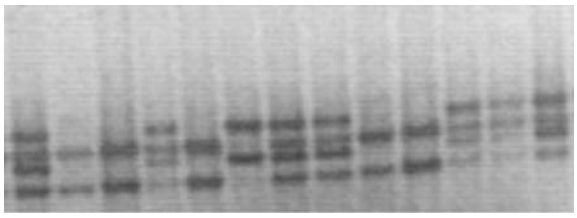

Fig. 1 Electrophoresis results of PCR-SSCP in region locus A

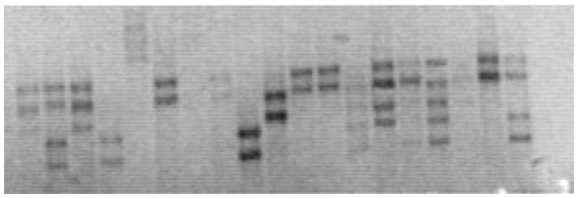

Fig. 2 Electrophoresis results of PCR-SSCP in region locus B

4.4 PCR-SSCP polymorphism and butcher traits correlation analysis in the 5′UTR of the chicken *MyoG* gene

The genotypes and butcher traits at A site of the *MyoG* gene were analyzed with Least Squares analysis, and the results are shown in Fig. 3, Fig. 4, Table 3 and Table 4.

Table 1 The genotypes, allele frequencies and genetic parameters of *MyoG* gene 5′control region site A in eight populations of chickens

strain	genotype frequency			allele frequency		polymorphism index			
	AA	*AB*	*BB*	*A*	*B*	*Ho*	*He*	*ENA*	*PIC*
S03(27)	0.185(5)	0.741(20)	0.074(2)	0.056	0.444	0.506	0.494	1.976	0.372
S02(29)	0.103(3)	0.414(12)	0.483(14)	0.310	0.690	0.572	0.428	1.749	0.337
D99(27)	0.111(3)	0.370(10)	0.519(14)	0.296	0.704	0.583	0.417	1.175	0.330
S01(29)	0.035(1)	0.690(20)	0.276(8)	0.379	0.621	0.529	0.471	1.890	0.360
S01 × D99(29)	0.690(2)	0.414(12)	0.517(15)	0.276	0.724	0.600	0.400	1.666	0.320
S01 × S10(29)	0.211(7)	0.483(14)	0.276(8)	0.483	0.517	0.501	0.499	1.998	0.375
S05(28)	0.286(8)	0.357(10)	0.357(10)	0.464	0.536	0.503	0.498	1.990	0.374
S01 × S05(28)	0.179(5)	0.500(14)	0.321(9)	0.429	0.571	0.451	0.549	2.215	0.429

Note: $PIC > 0.5$ for high polymorphism; $0.25 < PIC < 0.5$ for medium polymorphism; $PIC < 0.25$ for low polymorphism. The numbers in brackets are the individuals that belong to the respective genotypes.

Table 2 The genotypes, allele frequencies and genetic parameters of *MyoG* gene 5′control region site B in eight populations of chickens

strain	genotype frequency						allele frequency			polymorphism index			
	AA	*AB*	*AC*	*BB*	*BC*	*CC*	*A*	*B*	*C*	*Ho*	*He*	*ENA*	*PIC*
S03(27)	0.482(13)	0.222(6)	0.037(1)	0.185(5)	0.370(1)	0.370(1)	0.580	0.284	0.136	0.436	0.564	2.295	0.563
S02(27)	0.370(1)	0.259(7)	0.370(1)	0.741(2)	0.482(13)	0.111(3)	0.296	0.333	0.370	0.336	0.664	2.975	0.661
D99(29)	0.000(0)	0.690(2)	0.275(8)	0.345(1)	0.517(15)	0.103(3)	0.287	0.332	0.391	0.339	0.661	2.972	0.659
S01(30)	0.167(5)	0.200(6)	0.667(2)	0.133(4)	0.200(6)	0.233(7)	0.322	0.289	0.389	0.339	0.661	2.953	0.659
S01 × S10(30)	0.133(4)	0.333(1)	0.400(12)	0.100(3)	0.167(5)	0.167(5)	0.333	0.300	0.367	0.336	0.664	2.980	0.662
S05(30)	0.533(16)	0.100(3)	0.067(2)	0.200(6)	0.000(0)	0.100(3)	0.589	0.265	0.156	0.436	0.564	2.292	0.563
S01 × S05(28)	0.000(0)	0.429(12)	0.179(5)	0.143(4)	0.143(4)	0.107(5)	0.250	0.393	0.357	0.344	0.656	3.904	0.653

Note: $PIC > 0.5$ for high polymorphism; $0.25 < PIC < 0.5$ for medium polymorphism; $PIC < 0.25$ for low polymorphism. The numbers in brackets are the individuals that belong to the respective genotypes.

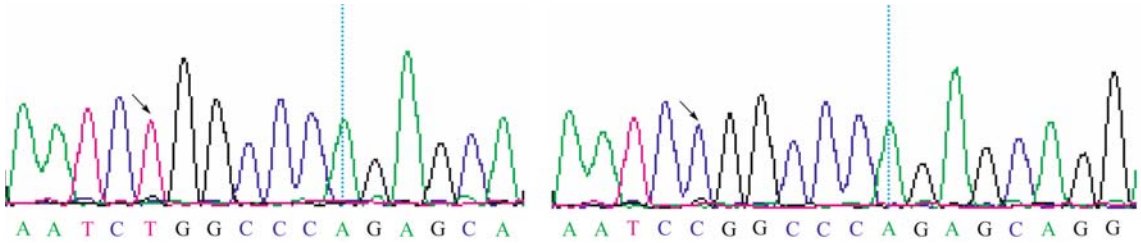

Fig. 3 The sequencing result of T/T homozygote and G/G homozygote at the 154 site in the 5′control region of *MyoG*
Note: The arrow indicates the 154 site.

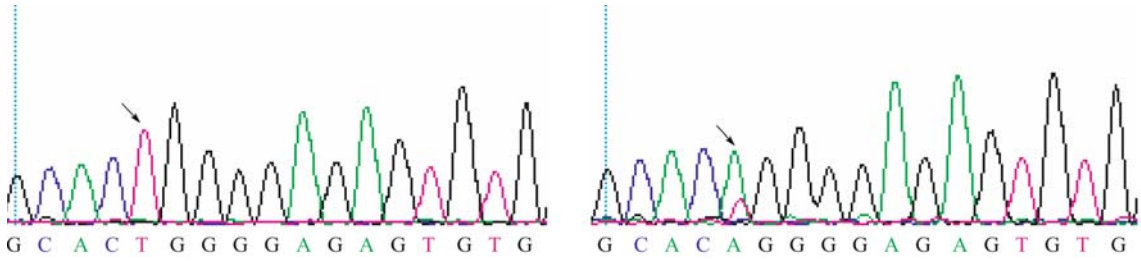

Fig. 4 The sequencing result of T/T homozygote and A/T heterozygosis at the 348 site in 5′control region of *MyoG*
Note: The arrow indicates the 348 site.

Table 3 Effect of different genotypes of PCR-SSCP in the 5′control region of *MyoG* A locus on slaughter traits

trait	locus A	*LSM* ± *SE*		additive effect	dominance effect
	AA(37)	*AB*(113)	*BB*(76)		
live weight (BW)/g	1897 ± 38.94	1839 ± 21.95	1815 ± 21.33	−41	−17
carcass weight (CW)/g	1690 ± 36.46	1636 ± 20.56	1609 ± 25.59	−40.5	−13.5
percentage of half-eviscerated yield (SEP)/%	92.52 ± +0.40	93.04 ± 0.23	92.84 ± 0.29	0.16	0.36
percentage of eviscerated yield (EP)/%	77.59 ± 0.42	76.94 ± 0.24	77.39 ± 0.30	0.10	−0.54
breast muscle weight (BMW)/g	208.17 ± 5.90	194.24 ± 3.32	195.75 ± 4.14	−6.21	−7.72
percentage of breast muscle (BMP)/%	12.35^{a} ± 0.22	11.85^{b} ± 0.13	12.15^{ab} ± 0.16	−0.10	−0.40
leg muscle weight (LMW)/g	302.76 ± 8.23	286.08 ± 4.64	276.67 ± 5.77	−13.04	−3.62
percentage of leg muscle (LMP)/%	17.75 ± 0.24	17.34 ± 0.14	17.06 ± 0.17	−0.34	−0.06
abdominal fat weight (AW)/g	39.01 ± 3.39	42.16 ± 1.91	39.42 ± 2.48	0.21	2.96
percentage of abdominal fat (AP)/%	2.37 ± 0.19	2.60 ± 0.11	2.51 ± 0.14	0.07	0.16
thickness of subcutaneous fat (SFT)/mm	3.92 ± 0.13	3.75 ± 0.08	3.88 ± 0.09	−0.02	−0.14

Note: Different superscripts indicate significant difference ($P < 0.05$), and the same superscripts indicate not significant difference ($P > 0.05$). The numbers in brackets are the individuals that belong to the respective genotypes. Additive effect = $(BB - AA)/2$, dominance effect = $AB - (AA + BB)/2$.

Table 4 Effect of different genotypes at the PCR-SSCP control region of the *MyoG* B locus on slaughter traits

trait	locus B			*LSM* ± *SE*			additive effect			dominance effect		
	AA(39)	*AB*(37)	*AC*(31)	*BB*(25)	*BC*(44)	*CC*(25)						
BW/g	1883 ± 56.65	1810 ± 52.24	1898 ± 58.67	1783 ± 62.27	1872 ± 50.95	1884 ± 62.07	50	−0.5	0.5	−23	14.5	38.5
CW/g	1666 ± 52.90	1613 ± 48.78	1686 ± 54.79	1584 ± 58.15	1663 ± 47.58	1663 ± 57.96	41	1.5	39.5	−12	21.5	39.5
SEP/%	92.75 ± 0.41	92.36 ± 0.38	92.30 ± 0.43	93.03 ± 0.45	93.08 ± 0.37	93.56 ± 0.45	−0.11	−0.4	0.27	−0.54	−0.86	−0.22
EP/%	77.43^{ab} ± 0.47	76.77^{b} ± 0.44	77.16^{b} ± 0.49	76.72^{ab} ± 0.52	77.06^{b} ± 0.42	77.37^{a} ± 0.52	0.36	0.03	0.33	−0.27	−0.24	0.02
BMW/g	196.69^{b} ± 7.85	192.05^{b} ± 7.24	210.64^{a} ± 8.13	191.25^{ab} ± 8.63	201.12^{ab} ± 7.06	196.37^{ab} ± 8.60	2.27	0.16	2.65	−3.86	14.1	7.31
BMP/%	11.82^{b} ± 0.25	11.92^{ab} ± 0.23	12.49^{a} ± 0.25	11.98^{ab} ± 0.27	12.04^{ab} ± 0.22	11.73^{b} ± 0.27	−0.08	0.06	−0.13	0.02	0.73	0.18
LMW/g	292. ± 11.99	278. ± 11.06	288. ± 12.42	275.00 ± 13.18	293.45 ± 10.78	298.63 ± 13.14	8.8	−3.02	11.8	−5.14	−7.39	6.6
LMP/%	17.40^{ab} ± 0.29	17.13^{ab} ± 0.27	17.05^{b} ± 0.30	17.13^{ab} ± 0.32	17.58^{ab} ± 0.58	17.80^{a} ± 0.32	0.13	−0.2	−0.34	−0.14	−0.55	0.11
AW/g	37.10 ± 3.81	40.07 ± 3.51	40.76 ± 3.94	33.89 ± 4.18	42.67 ± 4.32	37.81 ± 4.17	1.6	−0.36	−1.96	4.57	3.3	6.82
AP/%	2.24 ± 0.23	2.56 ± 0.21	2.46 ± 0.24	2.22 ± 0.25	2.58 ± 0.21	2.29 ± 0.25	0.01	−0.02	0.03	0.33	0.20	0.32
SFT/mm	3.65^{bc} ± 0.16	3.81^{bac} ± 0.15	4.07^{a} ± 0.16	3.49^{c} ± 0.17	4.16^{ba} ± 0.14	3.71^{bc} ± 0.17	0.08	−0.03	0.11	−0.07	0.39	0.56

Note: Different superscripts indicate significant difference ($P < 0.05$), and the same superscripts indicate not significant difference ($P > 0.05$). The numbers in brackets are the individuals that belong to the respective genotypes.

The differences among all traits were not significant ($P > 0.05$) except for *AA*, *BB* and the percentage of breast muscle of *AB* ($P < 0.05$). Allele A had a positive additive effect on the carcass weight, live weight, breast muscle weight, percentage of breast muscle, leg muscle weight, percentage of leg muscle and the thickness of subcutaneous fat, with additive effect values being 41 g, 40.5 g, 6.21 g, 0.10%, 13.04 g, 0.34% and 0.02 mm, respectively, but had a negative additive effect on the percentage of half-eviscerated yield, percentage of eviscerated yield, abdominal fat weight, and percentage of abdominal fat, with additive effect values of 0.16%, 0.10%, 0.21 g and 0.07%, respectively. As for site B, there existed significant individual differences among *CC*, *AB*, *AC* and *BC* in the percentage of eviscerated yield ($P < 0.05$); among *AC*, *AA* and *CC* in the percentage of breast muscle ($P < 0.05$); and between *CC* and *AC* in the percentage of leg muscle ($P < 0.05$). According to the results mentioned above, the two polymorphism sites in the 5′UTR of the chicken *MyoG* gene had significant effects on breast muscle weight, percentage of breast muscle, leg weight and percentage of leg muscle. Therefore, we can presume that the gene has an important relevance in the growth and development of poultry muscle fiber.

4.5 PCR-SSCP polymorphism and meat trait correlation analysis in the 5′UTR of chicken *MyoG* gene

The different genotypes and meat traits in the 5′UTR of the *MyoG* gene were analyzed by Least Squares analysis and the results are shown in Fig. 5, Table 5 and Table 6. According to the tables, at site A in 5′UTR of the *Myo*G gene, there was a significant difference ($P < 0.05$) in the dry matter content between *AB* and *BB*, an extreme difference in the muscle fiber density ($P < 0.01$), but no significant difference among other meat traits ($P > 0.05$). *BB* was bigger than *AA* in muscle fiber density, which was reversed in the muscle fiber diameter. There was a positive additive effect on the muscle fiber density in an allele at site A, and a negative additive effect at site B, where an extremely significant difference ($P < 0.01$) was found in the muscle fiber densities among *BB*, *CC* and *AC*, and a significant difference ($P < 0.05$) in crude protein content between *AA* and *BB*, *BC* and *CC* was also seen. *BB* was extremely significantly larger than *CC* in the muscle fiber density. There was a significant and positive additive effect in the muscle fiber density in allele A, not seen in other traits ($P > 0.05$). Therefore, we can further presume that there is a positive correlation between *MyoG* gene and the growth and development of chicken muscle fiber.

5 Discussion

Quantitative traits of chicken, including muscle fiber density, muscle fiber diameter, and muscle fiber number play a crucial role in meat indexes of chicken (fatty acid-binding protein, body fat content, tenderness and meat color), and the relatively high inheritability can improve meat

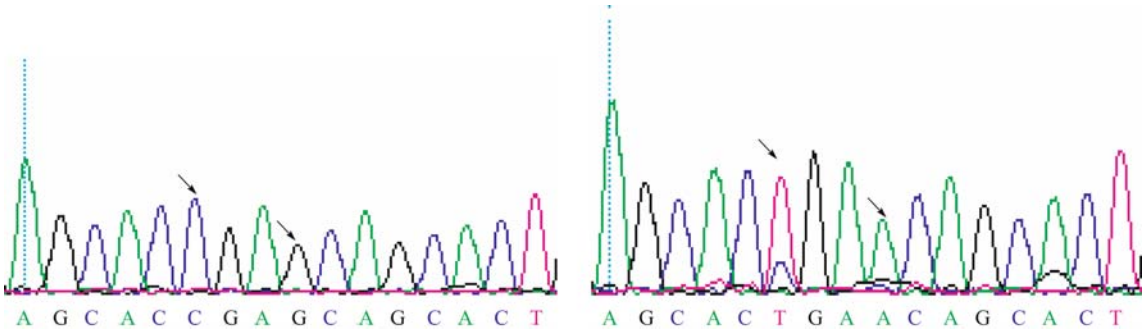

Fig. 5 The sequencing result of T/T homozygote and C/T heterozygosis at the 425 and 428 sites in 5′control region of *MyoG*
Note: The arrow indicates the mutable point.

Table 5 Effect of different genotypes of PCR-SSCP 5′control region of the *MyoG* A locus on meat traits

trait	locus A	*LSM* ± *SE*		additive effect	dominance effect
	AA(15)	*AB*(37)	*BB*(28)		
matter/%	$91.61^{ab} \pm 2.08$	$91.91^{a} \pm 1.36$	$85.95^{b} \pm 2.35$	−2.83	3.13
protein/%	84.14 ± 0.51	83.30 ± 0.33	83.93 ± 0.57	−0.11	−0.74
ash/%	4.33 ± 0.05	4.31 ± 0.03	4.34 ± 0.05	0.005	−0.025
inosinic acid/mg	1.54 ± 0.04	1.46 ± 0.02	1.48 ± 0.04	−0.03	−0.05
fat/mg	4.88 ± 0.42	5.37 ± 0.37	4.98 ± 0.49	0.05	0.44
muscle fiber density/fiber number·mm^{-2}	$724.03^{B} \pm 74.12$	$826.99^{AB} \pm 48.43$	$950.19^{A} \pm 83.34$	113.08	−10.12
muscle fiber diameter/μm	3.27 ± 0.23	3.30 ± 0.15	3.24 ± 0.26	−0.02	0.05

Note: Different capital superscripts indicate extremely significant difference ($P < 0.01$), and different small superscripts indicate significant difference ($P < 0.05$).

Table 6 Effect of different genotypes of PCR-SSCP 5′control region of the *MyoG* B locus on meat traits

trait	locus B			*LSM* ± *SE*			additive effect			dominance effect		
	AA(20)	*AB*(11)	*AC*(14)	*BB*(14)	*BC*(20)	*CC*(5)						
matter/%	91.31 ± 2.58	90.09 ± 2.88	93.46 ± 2.65	91.56 ± 2.54	87.50 ± 2.21	91.77 ± 4.21	−0.12	0.22	−0.11	−1.35	1.91	−4.16
protein/%	84.24^{a} ± 0.61	83.62^{a} ± 0.68	82.53^{ba} ± 0.63	83.86^{bac} ± 0.60	83.48^{c} ± 0.53	84.88^{c} ± 1.00	0.19	0.32	−0.51	−0.43	−2.03	−0.89
ash/%	4.31 ± 0.06	4.32 ± 0.06	4.30 ± 0.06	4.31 ± 0.06	4.37 ± 0.06	4.31 ± 0.09	0.00	0.00	0.00	0.01	−0.01	0.06
inosinic acid/mg	1.52 ± 0.05	1.48 ± 0.05	1.41 ± 0.05	1.54 ± 0.05	1.45 ± 0.04	1.48 ± 0.07	−0.01	−0.02	0.03	0.01	−0.09	−0.06
fat/mg	4.84 ± 0.50	4.74 ± 0.56	6.00 ± 0.52	5.23 ± 0.50	5.04 ± 0.43	5.18 ± 0.82	−0.20	0.17	0.03	−0.30	0.99	−0.17
muscle fiber density/fiber number·mm^{-2}	883.4^{ab} ± 89.24	792.8^{ab} ± 99.59	932.9^{A} ± 91.61	654.1^{B} ± 87.68	878.7^{ab} ± 76.44	684.1^{B} ± 145.61	114.65	−99.65	−15.04	20.08	209.6	149.15
muscle fiber diameter/μm	3.22 ± 0.3	3.48 ± 0.3	2.56′ ± 0.3	3.65 ± 0.3	3.35 ± 0.2	3.50 ± 0.4	0.04	0.00	−0.04	0.01	0.01	0.03

Note: Different capital superscripts indicate extremely significant difference ($P < 0.01$), and different small superscripts indicate significant difference ($P < 0.05$).

traits. The muscle fiber diameter regulated by the *MyoD* gene in the process of development can affect meat tenderness. Soumillion et al. (1997) studied Myogenin gene locus mutation and found its effect on muscle fiber number in relation to birth weight, growth rate and carcass weight. Lin et al. (2002) detected the *MyoD* gene variations of Erhualian pigs in different clutches by *Msp1*-PCR-RFLP, and found that the *MyoD* gene can affect birth weight and muscle fiber number to some extent. Zhu and Li (2005) analyzed the different genotypes, correlation of relative traits, and genetic effects of different alleles by the same method in the 3′UTR of the *MyoG* gene *Msp*1 site in the Ya-nan Pig, and found that allele N has a genetic effect that can make the fiber growth more sufficient, the diameter thicker, and the area larger; it can also significantly elevate the naked body lean meat rate and the longissimus dorsi area, improve the production of naked body meat, and elevate the quality of the naked body. Malik et al. (1995) studied the *MyoG* gene of chicken and discovered that there was a 131-bp fragment in the upstream 5′UTR control region including an E-box and *myocyte-enhencer-binding-factor-2* (*MEF-2*), which was a complete promoter whose functions were: (a) to regulate the *MyoD* gene activation by *MyoD* protein itself, and (b) to regulate *PKC* gene closure by blocking the activation of *MEF-2*. In our study, we took the *MyoG* gene of the chicken as a candidate gene affecting muscle fiber number and muscle fiber diameter, analyzed the mutation of the 5′UTR control region in the gene, and then analyzed live weight, carcass weight, percentage of half-eviscerated yield, percentage of eviscerated yield, breast muscle weight, percentage of breast muscle, leg muscle weight, percentage of leg muscle, abdominal fat weight, percentage of abdominal fat, and thickness of subcutaneous fat by Least Squares analysis. The results indicated that there was a significant difference ($P < 0.05$) among different genotypes of the two sites in breast muscle weight, percentage of breast muscle, and percentage of leg muscle; extreme significance ($P < 0.01$) was found in muscle fiber density. Individual significant differences ($P < 0.05$) among different genotypes with regard to percentage of eviscerated yield was found at site B. Therefore, we can conclude that the *MyoG* gene is related to the growth and development of chicken muscle, and the mutation of the gene may be related to the muscle fiber. So it is necessary to conduct further studies on the gene as a candidate gene related to meat traits of chicken.

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