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Short Communication

Association Analysis between Exon II of *GH* Gene and Growth Traits in Sheep

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ABSTRACT

SSCP were employed to investigate the genetic polymorphism of sheep *GH* gene and to analyze the correlation of genetic polymorphic sites with growth traits. The results showed that AA, AB and BB genotypes were detected in exon II of *GH* gene in the six sheep populations. The highest frequencies of AB genotype detected in Mongolia sheep, Small-tailed han sheep, Tong sheep, Lanzhou large-tailed sheep and Henan large-tailed Han sheep were 0.375, 0.531, 0.545, 0.350 and 0.596, respectively, and the highest frequency of BB genotype in Yuxi fatty-tailed sheep was 0.378. Exon II of *GH* gene was significantly correlated with body weight, carcass weight, chest width and hip height (P<0.05). Moreover body weight and carcass weight of AB genotype were significantly higher than those of AA and BB genotypes (P<0.05) and chest width and hip height of AB genotype were remarkably higher than those of AA genotype (P<0.05).

s the major gene influencing animal growth traits, GH Agene has functions of improving feed conversion and promoting protein synthesis in muscle. Warwick et al. (1984) cloned GH gene of sheep for the first time and positioned it on chromosome11. The GH gene of sheep consists of five exons (the lengths of which were 13, 161, 117, 162 and 198 bp, respectively) and four introns (the lengths of which were 246, 231, 227 and 273 bp, respectively). Goat GH gene was positioned on chromosome 12, and its length is largely identical to that of sheep GH gene. Afifi et al. (2019) found that intron II, intron III and exon IV of GH gene had significant correlations with milk yield of Najdi sheep. Henan large-tailed han sheep, small-tailed han sheep and Yuxi fatty-tailed sheep are excellent local sheep breeds in Henan Province, especially Henan largetailed han sheep and small-tailed han sheep have the characteristics of multiple lambs (Bai et al., 2014, 2016, 2017, 2020). Hence, the polymorphisms of GH gene in six sheep populations were detected in this study, and further association analysis between GH gene polymorphisms and growth traits were performed, aiming at providing a

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Authors' Contribution JB conceived and designed the study and conducted the lab work. ZD and YC analyzed the data and wrote the article. YL and YY helped in sampling. JL helped in analysis of data.

Key words Sheep, GH gene, Growth traits, SSCP, Association analysis

theoretical basis for marker assisted selection and further variety breeding of sheep.

Materials and methods

Fifty sheep were sampled for each breed, 10 mL of jugular venous blood was collected in the presence of anticoagulant ACD from each sheep and preserved at -20 °C. Genomic DNA was extracted by the wholeblood DNA kit (Shanghai Bioengineering Co., Ltd.). The primer sequences of exon II of GH gene are TCTAGGACACATCTCTGGGG, as follows: F: R: CTCTCCCTAGGGCCCCGGAC (Hu et al., 2007) and the annealing temperature is 57 °C.

Seven μ L of each PCR product was mixed with 13 μ L of loading buffer containing. After denaturation at 94°C for 5 min and snap-cooling on a freeze-block (-20°C), 20 μ L of each sample was loaded onto a 0.5×MDE gel and subjected to electrophoresis in a Mini-Protean 3 Cell (Bio-Rad, USA) at 120 V and 20°C for 5 h using 0.5×TBE as the buffer. After electrophoresis, gels were stained with ethidium bromide for 1 h and photographed using ultraviolettransillumination.

SPSS17.0 statistical software was used to analyze the association between different genotypes and growth traits, and Duncan multiple comparison method was used to make multiple comparison. The final results were expressed in the form of mean value \pm standard error.

Results and discussion

The PCR amplification results of exon II of GH gene

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Population	ulation Genotype frequency		ency	Gene frequency		Population genetic polymorphism		
	AA	AB	BB	A	В	Heterozy- gosity	Polymorphism in- formation content	Number of ef- fective alleles
Mongolia sheep	0.313	0.375	0.312	0.500	0.500	0.500	0.375	2.000
Small-tailed han sheep	0.281	0.531	0.188	0.547	0.453	0.496	0.373	1.982
Tong sheep	0.364	0.545	0.091	0.636	0.364	0.463	0.356	1.862
Yuxi fatty-tailed sheep	0.311	0.311	0.378	0.467	0.533	0.498	0.374	1.991
Lanzhou large-tailed sheep	0.350	0.350	0.300	0.525	0.475	0.499	0.374	1.995
Henan large-tailed han sheep	0.213	0.596	0.191	0.511	0.489	0.500	0.375	1.999

Table I.	Genetic	polymor	phism	of exon	П	of GH	gene in	sheep.
							A	

in five sheep populations are shown in Figure 1. PCR product was subjected to SSCP. According to Figure 2 three genotypes were detected by exon II of *GH* gene in sheep, being AA, AB and BB, respectively.



Fig. 1. PCR product detection of exon II of GH gene. Note: 1, 2, 3, 4 and 5 are Mongolia sheep, Small-tailed Han sheep, Tong sheep, Lanzhou large-tailed sheep and Henan large-tailed Han sheep, respectively.



Fig. 2. Detection of exon II polymorphism of *GH* gene in sheep.

Note: Lanes 1, 4, 6, 7, 11, 12 are AB genotype, 2,3,8,9 are BB genotype and 5,10,13 are AA genotype.

Table I shows that the highest AB genotype frequencies in Mongolia sheep, small-tailed han sheep, Tong sheep, Lanzhou large-tailed sheep and Henan large-tailed han sheep were 0.375, 0.531, 0.545, 0.350 and 0.596, respectively, and the BB genotype frequency was the highest in Yuxi fatty-tailed sheep (0.378). The genetic heterozygosity values were the same in Mongolia sheep

and Henan large-tailed han sheep, both being 0.500, and the polymorphic information contents in the two sheep populations were also the highest (0.375), namely genetic diversity of Mongolia sheep and Henan large-tailed han sheep was quite abundant.

As an important candidate gene, GH gene has been reported largely. Zhou et al. (2009) found that $G \rightarrow C$ mutation occurred at the 11th site of exon II of GH gene in Hainan black goat, which led to change of coding amino acid, three genotypes including AA, AB and BB were detected in exon II of GH gene. Li (2007) found that AA and AB genotypes of exon II of GH gene could be detected in three goat populations. Marques et al. (2003) found that A/B genotype was detected from exon II of GH gene in Jarlnelistae goat population. Hu et al. (2007) detected AB and BB genotypes from exon II of GH gene in five goat populations. Han (2016) detected three genotypes from exon II of GH gene in China Tibetan sheep, and found a g.498G>C mutation site. In this study, AA, AB and BB genotypes were detected from exon II of GH gene in the three sheep populations, and the sequencing results indicated that exon II of GH gene experienced $G \rightarrow C$ mutation, which was according to the study result of Han (2016).

It can be seen from Table II that body weight and carcass weight of AB genotype were significantly higher than those of AA and BB genotypes (P<0.05), and AA and BB genotypes had no significant differences in the body weight and carcass weight (P>0.05). Chest width and hip height of AB genotype were remarkably higher than those of AA genotype (P<0.05), but AB genotype and BB genotype had insignificant differences in the aspect of chest width and hip height (P>0.05). Therefore, exon II of GH gene had no significant influence on other growth traits (P>0.05). Abdelmoneim *et al.* (2017) indicated that intron II, intron IV and exon IV of GH gene had significant correlations with 120d body weight and daily weight gain of Harri sheep. The study by Han (2016) manifested

that exon II (g.498G>C) of *GH* gene was significantly correlated with sheep body weight in all of the three sheep populations. The study by Yousefi *et al.* (2012) showed that exon V of *GH* gene had no remarkable influence on one-year-old body weight of Zel sheep. The study by Hu *et al.* (2007) indicated that exon II of *GH* gene had no significant correlation with body weight, body height and chest circumference of Xinong Saanen dairy goat. This study pointed out that exon II of *GH* gene had significant correlations with body weight, carcass weight, chest width and hip height of sheep (P<0.05), and AB genotype showed certain advantages, and this study result was similar to that of Han (2016).

Table II. Correlation analysis between exon II of *GH* gene and growth traits in sheep.

Growth traits	AA	AB	BB
Body weight (g)	$46.25\underline{+}11.25^{\mathtt{b}}$	54.003 <u>+</u> 1.78 ^a	$46.769\underline{+}1.20^{\mathrm{b}}$
Body height (cm)	$69.00{\underline{+}}11.00^a$	69.50 ± 2.08^{a}	65.00 <u>+</u> 3.21ª
Body length (cm)	$68.00\underline{+}14.00^a$	$69.47\underline{+}1.76^{a}$	66.62 ± 1.64^{a}
Chest width (cm)	22.50 <u>+</u> 3.50 ^b	29.24 <u>+</u> 1.23ª	26.92 <u>+</u> 1.179ab
Rump height (cm)	71.00 ± 9.00^{a}	71.03 ± 3.24^{a}	68.92 ± 1.87^{a}
Hip height (cm)	57.00 <u>+</u> 6.00 ^b	69.06 <u>+</u> 1.76 ª	$64.23\underline{+}2.27^{ab}$
Foreleg height(cm)	22.50 <u>+</u> 4.50 ^a	26.06 <u>+</u> 2.33ª	26.08 <u>+</u> 3.01ª
Head length (cm)	18.00 ± 2.00^{a}	21.35 <u>+</u> 0.69 ^a	19.31 ± 0.83^{a}
Chest circumfer- ence (cm)	88.50 <u>+</u> 16.50 ^a	90.68 <u>+</u> 2.14ª	91.54 <u>+</u> 2.29ª
Circumference of cannon bone (cm)	9.50 <u>+</u> 1.50 ª	10.12 <u>+</u> 0.36ª	9.23 <u>+</u> 0.34ª
Rump length (cm)	22.00 ± 1.00^{a}	23.94 ± 1.02^{a}	22.54 <u>+</u> 0.93ª
Neck length (cm)	22.50 <u>+</u> 3.50ª	33.03 ± 3.18^{a}	31.54 <u>+</u> 3.02 ^a
Waist width (cm)	22.50 <u>+</u> 5.50ª	20.47 <u>+</u> 3.01ª	27.08 ± 2.88^{a}
Hip width (cm)	21.50 <u>+</u> 2.50 ^a	20.77 <u>+</u> 0.83ª	19.39 <u>+</u> 1.05ª
Chest depth (cm)	32.50 ± 5.50^{a}	33.94 <u>+</u> 1.11ª	33.08 ± 0.85^{a}
Head depth (cm)	18.50 ± 4.50^{a}	17.35 ± 0.69^{a}	16.50 <u>+</u> 0.75 ^a
Back height (cm)	68.00 ± 8.00^{a}	72.79 <u>+</u> 1.62ª	70.00 <u>+</u> 1.63ª
Carcass weight (cm)	21.00 <u>+</u> 5.50 ^b	24.41 <u>+</u> 0.86ª	20.64 <u>+</u> 1.42 ^b
Hip circumference (cm)	92.00 <u>+</u> 8.00 ^a	93.88 <u>+</u> 1.91ª	89.46 <u>+</u> 3.74ª
Abdomen circum- ference (cm)	98.00 <u>+</u> 17.00 ^a	$97.47\underline{+}3.08^{a}$	97.62 <u>+</u> 2.72 ^a

Note: different letters showed significant difference (P<0.05); the same letter showed no significant difference (P>0.05).

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Statement of conflict of interest

The authors have declared no conflict of interest.

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