Research Note: Association of *IGF-1R* gene polymorphism with egg quality and carcass traits of quail (*Coturnix japonica*)

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ABSTRACT Insulin-like growth factor 1 receptor (***IGF-1R***) gene is the main effector of insulin-like growth factor (**IGF**), which plays an important role in growth, development and reproduction of the animal organism. This study aimed to investigate the association of *IGF-1R* gene single nucleotide polymorphisms (**SNPs**) with egg quality and carcass traits of quail by direct sequencing. In this study, genomic DNA was extracted from quail blood samples of 46 Chinese yellow (**CY**) quail, 49 Beijing white (**BW**) quail and 48 Korean (**KO**) quail strains. Egg quality and carcass traits were measured and used for *IGF-1R* gene analysis in 3 quail strains. The results showed that 2 SNPs (A57G and A72T) of the *IGF-1R* gene were detected in 3 quail strains. The A57G was significantly associated with yolk width (**YWI**) in BW strain ($P < 0.05$). Whereas A72T was significantly associated with egg shell thickness (**EST**) in BW strain ($P < 0.05$), and significantly associated with egg weight (**EW**), egg long (**EL**), and egg short (**ES**) in KO strain ($P < 0.05$). Haplotypes based on 2 SNPs showed significant effect on EST in 3 quail strains ($P < 0.05$), it also has a significant effect on EW in KO strain ($P < 0.05$). Meanwhile, A72T was significantly associated with liver weight (**LW**) and dressing percentage (**DP**) in 3 strains ($P < 0.05$). Haplotypes showed significant effect on LW ($P < 0.05$). Therefore, the *IGF-1R* gene may be a molecular genetic marker to improve egg quality and carcass traits in quails.

Key words: *IGF-1R*, polymorphism, egg quality, carcass traits, quail

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INTRODUCTION

Quails are small economic poultry widely farmed in China, which has characteristics such as short growth cycle, high reproductive ability, high egg production performance, high nutritional value, low investment and high economic benefits (Bai et al., 2021; Wang et al., 2023). Quails have been loved by consumers around the world in recent years because of its rich minerals, high protein, beneficial fatty acids and other nutrients, and the amount of quail farming has increased rapidly. However, there is little research on quail breeding at home and abroad, especially at the molecular level, which is still in its infancy (Minvielle, 2004; Priti and Satish, 2014). In recent years, marker-assisted selection has replaced traditional breeding methods as the new breeding option used to improve the animal economic traits (Zhang et al., 2014). Studies have revealed that many candidate genes are related to economic traits, among which *IGF2, LEPR*, and *GnRH* genes are well-accepted candidate genes that affect growth and production performance in livestock (Ali et al., 2021; El-Tarabany et al., 2022; Wang et al., 2023).

The insulin-like growth factor 1 receptor (***IGF-1R***) gene was the main effector of insulin-like growth factor (**IGF**). Studies had found that the *IGF-1R* gene played an important role in the animal organism, which not only regulated the vitality of IGFs, but also regulated the cell's own growth cycle, metabolism, proliferation and differentiation, immune regulation and important processes of adulthood have regulatory effects (Cardoso et al., 2021). There are numerous studies indicate that *IGF-1R* gene affects economic traits of animals, different mutation sites and genotypes have different effects on animal growth, carcass and reproduction traits. El-Magd et al. (2017) have proven that 2 SNPs (G64A and G280A) of the *IGF-1* gene had a significant impact on growth traits of buffalo. Szewczuk et al. (2013) purported that the polymorphism of the *IGF-1R* gene was significantly associated with growth-related traits

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weight in Angus cattle. Ding et al. (2022) found 10 SNPs of the *IGF-1* gene were detected in Hulun Buir sheep. Ma et al. (2019) found the *IGF-1R* CNV was significantly associated with body weight and body height of Jinnan cattle and was significantly associated with body height and hucklebone width of Qinchuan cattle. Wu et al. (2017) analyzed the correlation between the *IGF-1* gene of Bian chickens' growth traits, and found that the gene was highly correlated with chicken body weight ($P < 0.05$). Thus, the *IGF-1R* gene has been widely used to evaluate genetic diversity in many regions with different breeds.

Previous genetic studies showed that polymorphisms in the candidate gene were significantly associated with growth, egg production, and meat quality traits in many species (El-Magd et al., 2017; Wu et al., 2017; Ali et al., 2021). However, fewer studies have been conducted on association of polymorphisms with the *IGF-1R* gene with economic traits in poultry (Lei et al., 2008; Pu et al., 2016; Yang et al., 2022). Egg quality and carcass trait are important economic traits in poultry breeding. The objective of this study is to identify the *IGF-1R* gene polymorphism with the egg quality and carcass traits in Chinese yellow (**CY**) quail, Beijing white (**BW**) quail, and Korean (**KO**) quail strains by PCR sequencing, and to provide reference values for the future research of quail breeding.

MATERIALS AND METHODS

Ethics Statement

All experiment procedures in this study were approved by the Institutional Animal Care and Use Committee of College Animal Science, Henan University of Science and Technology (Luoyang, China), and animal experimentation in this study was conducted in strict accordance with the Guidelines for Experimental Animals established by the Ministry of Science and Technology (Beijing, China).

Experimental Animals, Housing Condition, and Phenotypic Measurements

A top of 46 female CY strain, 49 female BW strain, and 48 female KO strain were randomly selected from a commercial hatchery (Henan University of Science and Technology Quail Breeding Co. Ltd., Luoyang, China). All quail individuals were healthy and fed in single cages at the experimental farm of Henan University of Science and Technology under the same conditions. During the whole investigation, all quails were allowed to feed and drink ad libitum. Supplemental heaters were provided first 2 wk of growth. The daily lighting schedule was lights on from 5:00 am to 7:00 pm until 140 d. All 3 strains were fed a diet with 2,900 kcal/Kg of ME and 24% CP from d 1 to 49 (growth periods), ME and CP levels were 2,800 kcal/kg and 20% from d 50 to 140 (laying periods), respectively. One egg from each individual within each quail strain was selected for egg quality measurements at 7 wk of age. The egg quality included egg weight (**EW**), egg long (**EL**), egg short (**ES**), egg shape index (**ESI**), yolk height (**YH**), yolk width (**YWI**), yolk index (**YI**), yolk weight (**YWE**), eggshell thickness (**EST**), and albumen height (**AH**). The carcass traits included body weight (**BOW**), dressed carcass weight (**DCW**), whole net carcass weight (**WNCW**), heart weight (**HW**), liver weight (**LW**), breast muscle weight (**BMW**), leg muscle weight (**LMW**), dressing percentage (**DP**), whole net carcass rate (**WNCR**), heart rate (**HR**), liver rate (**LR**), breast muscle rate (**BMR**), and leg muscle rate (**LMR**) were measured at 20 wk of age in 3 quail strains.

DNA Samples, Primer Designing, PCR Amplification, and DNA Sequencing

Blood samples (5 mL) were taken from the wings of 143 quails (46 CY, 49 BW, and 48 KO) into a syringe containing 2% EDTA used as an anticoagulant and stored at −80°C for further experiment. Genomic DNA was isolated from venous blood samples using a poultry whole DNA extraction kit (Dingguo Changsheng Biotechnology Company, Beijing, China). Based on the potential SNPs of *IGF-1R* gene published in the NCBI database (https://www.ncbi.nlm.nih.gov/), the primer pairs were designed using Primer Premier 5.0 software (Premier Biosoft International, Palo Alto, CA), which were F-AACGCCTGGAGAACTGTACG and R-ATCGCTGAGGCTTTCCAAG. The primer specificity was verified by BLAST at NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The expected amplified segment size was 155 bp. PCR was performed in a total volume of 20 μL, which included 10 μL of the 2 × Taq PCR Master Mix, 0.7 μL of each primer, 1 μL genomic DNA, and 7.6 μL double-distilled water. The reaction conditions were as follows: initial denaturation at 95°C for 5 min, followed by 35 cycles of 95°C for 40 s, annealing for 56°C for 45 s, extension at 72°C for 35 s, and a final extension at 72°C for 10 min. The reaction system was stored under 4°C (Lei et al., 2008). Then, the amplified samples of the *IGF-1R* gene were sent to Beijing Tsingke Biological Co., Ltd. for sequencing.

Statistical Analysis

Sequence alignment and SNP identification were conducted via MegAlign program (version 5.0; DNAstar, Madison, WI). Chromas software (version 2.2.2; Technelysium, Queensland, Australia) was used to conduct sequence analyses. Genotypes and alleles were recorded using Excel (version 2016; Microsoft, Redmond, WA). The population genetic information was statistically analyzed using the Popgene version 1.32 (Yeh and Boyle, 1997). Finally, association analysis of polymorphisms was accomplished with the measured egg quality and carcass traits using Duncan's multiple range test in SPSS (version 26.0; IBM Corp., Armonk, NY) and

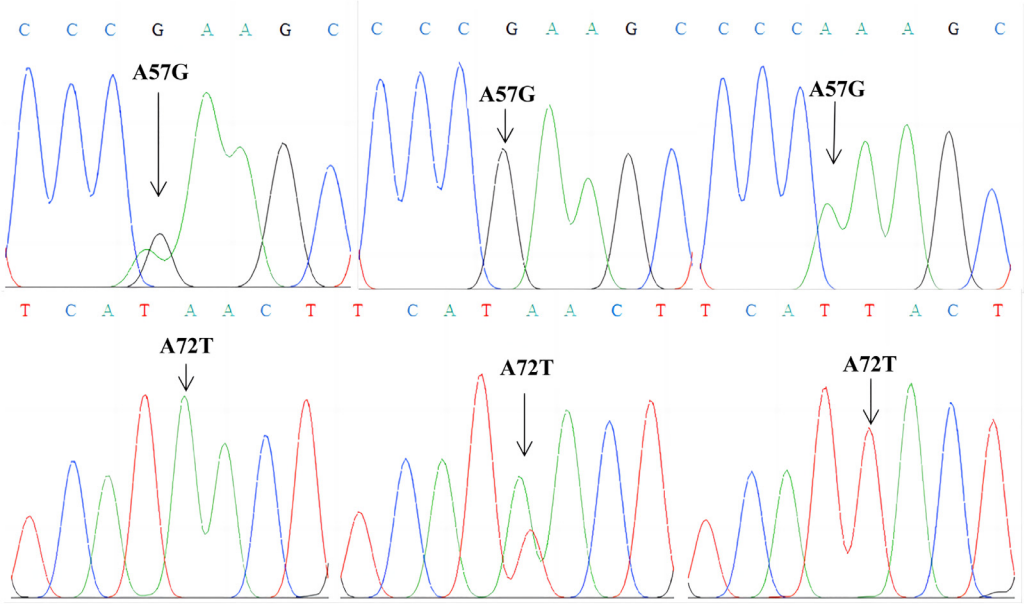

Figure 1. Sequencing results of A57G and A72T site of *IGF-1R* gene.

expressed as means ± standard error (**SE**). Differences were considered highly significant or significant at $P \leq 0.01$ or $P \leq 0.05$, respectively. The association analysis model of egg quality was as follows:

$$Y_{ij} = \mu + G_i + e_{ij}. \quad (1)$$

Y_{ij} is the phenotype value, μ is the total mean value, G_i is the effect of genotype, and e_{ij} is the random error. The association analysis model of carcass traits was as follows:

$$Y_{ijk} = \mu + S_i + G_j + e_{ijk}. \quad (2)$$

Y_{ijk} is the phenotype value, μ is the total mean value, S_i is the effect of strain, G_j is the effect of genotype, and e_{ijk} is the random error.

RESULTS AND DISCUSSION

Polymorphisms of IGF-1R Gene in Quail

The egg quality traits and carcass traits are important economic traits in poultry breeding, which are controlled by genetic, environmental, and nutritional factors (Ye et al., 2017). The *IGF-1R* gene is well known to play an important role in economic traits of animals. It is reported that 10 SNPs of the *IGF-1* gene were detected in Hulun Buir sheep. SNP8, haplotype combinations H5H5 and H5H6 of the *IGF-1R* gene showed superior growth traits during the early stage (Ding et al., 2022). In this study, we have detected polymorphisms of the *IGF-1R* gene in quails. Two SNPs (A57G and A72T) identified in the 3 quail strains of *IGF-1R* gene were genotyped by sequencing technology (Figure 1). It can be seen from Table 1 that 3 genotypes (AA, AG, and GG) were detected at the A57G site. Three genotypes (AA, AT, and TT) were detected at the A72T site. The AA, AG, and GG genotype frequencies were 2.2, 19.6, and 78.2% at the A57G site in CY strain, respectively (Figure 2A). The AA, AG, and GG genotype frequencies were 16.3, 65.3, and 18.4% at the A57G site in BW strain, respectively (Figure 2B). The AA, AG, and GG genotype frequencies were 2.1, 37.5, and 60.4% at the A57G site in KO strain, respectively (Figure 2C). Furthermore, allele G was the dominant gene in 3 strains (Figure 2D). The AA, AT, and TT genotype frequencies were 30.4, 43.5, and 26.1% at the A72TG site in CY strain, respectively (Figure 2E). The AA, AT, and TT genotype frequencies were 14.3, 73.5, and 12.2% at the

Table 1. Genotype frequency, allele frequency, and Hardy-Weinberg's law data of SNPs of *IGF-1R* gene in quail.

SNP[1]	S[2]	Genotypic frequency			Allelic frequency		HWE[3]					
					Major	Minor	Chi-square	*P*	*Ho*[4]	*He*[5]	*PIC*[6]	*Ne*[7]
A57G	CY(46)	0.022(AA)	0.196(AG)	0.782(GG)	0.880	0.120	0.230	0.632	0.789	0.211	0.188	1.267
	BW(49)	0.163(AA)	0.653(AG)	0.184(GG)	0.510	0.490	4.608	0.032	0.500	0.500	0.375	1.999
	KO(48)	0.021(AA)	0.375(AG)	0.604(GG)	0.792	0.208	0.899	0.343	0.670	0.330	0.275	1.492
A72T	CY(46)	0.304(AA)	0.435(AT)	0.261(TT)	0.522	0.478	0.763	0.382	0.501	0.499	0.375	1.996
	BW(49)	0.143(AA)	0.735(AT)	0.122(TT)	0.510	0.490	10.824	0.001	0.500	0.500	0.375	1.999
	KO(48)	0.188(AA)	0.479(AT)	0.333(TT)	0.573	0.427	0.021	0.885	0.511	0.489	0.370	1.958

Abbreviations: BW, Beijing white quail; CY, Chinese yellow quail; *He*[5], heterozygosity; *Ho*[4], homozygosity; HWE[3], Hardy-Weinberg equilibrium test; KO, Korean quail; *Ne*[7], effective allele numbers; *PIC*[6], polymorphism information content; S[2], strain; SNP[1], single nucleotide polymorphism.

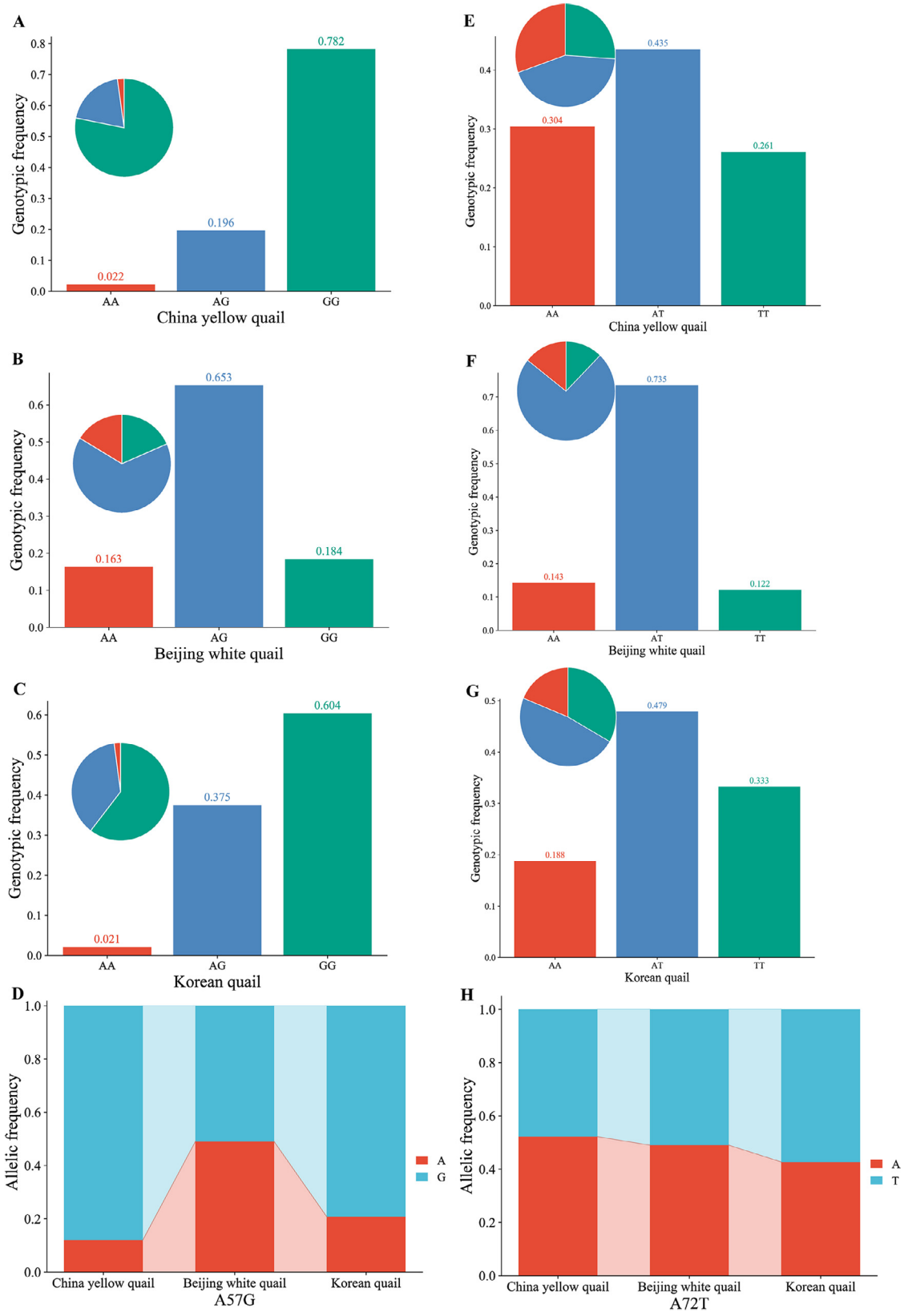

Figure 2. The number of genotypes and frequencies of allelotypes in *IGF-1R* gene.

A72TG site in BW strain, respectively (Figure 2F). The AA, AT, and TT genotype frequencies were 18.8, 47.9, and 33.3% at the A72TG site in KO strain, respectively (Figure 2G). Furthermore, allele A was the dominant gene of CY and BW strains, while allele T was the dominant gene of KO strain (Figure 2H). The PIC analysis results showed that all SNPs were in moderate polymorphism ($0.25 < PIC < 0.50$) except A57G site of CY quail that showed a low polymorphism ($PIC < 0.25$). The A57G and A72TG of CY and KO strains were in

Table 2. Association analysis of A57G and A72T site with egg quality of quail.

		A57G (mean ± SE)			A72T (mean ± SE)		
S	EQ	AA	AG	GG	AA	AT	TT
CY(46)	EW	10.900 ± 0.112	10.733 ± 0.131	10.706 ± 0.141	10.929 ± 0.211	10.568 ± 0.173	10.700 ± 0.203
	EL	32.490 ± 0.172	32.142 ± 0.314	31.987 ± 0.207	32.391 ± 0.307	32.007 ± 0.287	31.642 ± 0.27
	ES	24.950 ± 0.094	24.914 ± 0.105	25.009 ± 0.118	25.121 ± 0.160	24.822 ± 0.149	25.098 ± 0.182
	ESI	1.302 ± 0.007	1.290 ± 0.014	1.279 ± 0.008	1.289 ± 0.009	1.290 ± 0.012	1.261 ± 0.011
	YH	8.000 ± 0.103	8.067 ± 0.133	7.991 ± 0.129	7.943 ± 0.174	8.011 ± 0.146	8.075 ± 0.250
	YWI	25.870 ± 0.199	24.437 ± 0.463	24.611 ± 0.227	24.486 ± 0.360	24.431 ± 0.312	25.018 ± 0.380
	YI	0.309 ± 0.005	0.331 ± 0.009	0.326 ± 0.007	0.326 ± 0.010	0.329 ± 0.008	0.324 ± 0.012
	YWE	3.600 ± 0.041	3.478 ± 0.072	3.429 ± 0.049	3.407 ± 0.062	3.389 ± 0.056	3.567 ± 0.099
	EST	0.208 ± 0.002	0.175 ± 0.004	0.176 ± 0.002	0.170 ± 0.004	0.179 ± 0.003	0.179 ± 0.004
	AH	1.570 ± 0.073	1.754 ± 0.156	1.725 ± 0.086	1.704 ± 0.105	1.663 ± 0.138	1.855 ± 0.113
BW(49)	EW	10.514 ± 0.222	10.410 ± 0.163	10.757 ± 0.360	10.400 ± 0.497	10.432 ± 0.146	10.833 ± 0.246
	EL	31.499 ± 0.241	31.684 ± 0.286	32.211 ± 0.695	31.565 ± 0.802	31.639 ± 0.266	32.435 ± 0.295
	ES	25.094 ± 0.322	24.807 ± 0.133	25.033 ± 0.266	24.773 ± 0.404	24.839 ± 0.122	25.273 ± 0.284
	ESI	1.257 ± 0.022	1.277 ± 0.010	1.287 ± 0.027	1.275 ± 0.032	1.274 ± 0.010	1.284 ± 0.020
	YH	7.886 ± 0.240	7.924 ± 0.130	7.814 ± 0.202	7.683 ± 0.294	7.935 ± 0.122	7.933 ± 0.198
	YWI	25.224 ± 0.393^{ab}	24.569 ± 0.227^{b}	26.250 ± 0.892^{a}	24.030 ± 0.792	25.065 ± 0.270	25.270 ± 0.431
	YI	0.313 ± 0.011	0.312 ± 0.013	0.301 ± 0.018	0.322 ± 0.019	0.307 ± 0.012	0.315 ± 0.011
	YWE	3.486 ± 0.055	3.362 ± 0.058	3.543 ± 0.181	3.267 ± 0.201	3.426 ± 0.057	3.483 ± 0.065
	EST	0.167 ± 0.006	0.159 ± 0.002	0.160 ± 0.005	0.151 ± 0.007^{b}	0.164 ± 0.002^{a}	0.153 ± 0.005^{ab}
	AH	1.997 ± 0.199	1.883 ± 0.077	1.683 ± 0.133	1.778 ± 0.193	1.870 ± 0.071	1.955 ± 0.237
KO(48)	EW	10.307 ± 0.301	10.417 ± 0.172	10.380 ± 0.151	10.100 ± 0.287^{b}	10.045 ± 0.218^{b}	10.993 ± 0.225^{a}
	EL	31.913 ± 0.457	31.839 ± 0.240	31.864 ± 0.219	31.457 ± 0.511^{b}	31.489 ± 0.281^{b}	32.609 ± 0.373^{a}
	ES	24.771 ± 0.224	24.834 ± 0.145	24.813 ± 0.121	24.626 ± 0.225^{b}	24.542 ± 0.167^{b}	25.287 ± 0.198^{a}
	ESI	1.288 ± 0.014	1.282 ± 0.008	1.284 ± 0.007	1.277 ± 0.016	1.283 ± 0.009	1.290 ± 0.015
	YH	6.593 ± 0.239	6.428 ± 0.105	6.484 ± 0.106	6.767 ± 0.112	6.380 ± 0.153	6.453 ± 0.224
	YWI	26.339 ± 0.466	26.876 ± 0.342	26.693 ± 0.276	26.446 ± 0.820	26.274 ± 0.406	27.399 ± 0.318
	YI	0.252 ± 0.012	0.241 ± 0.006	0.245 ± 0.006	0.258 ± 0.010	0.245 ± 0.009	0.237 ± 0.010
	YWE	3.440 ± 0.144	3.576 ± 0.073	3.530 ± 0.069	3.456 ± 0.176	3.450 ± 0.106	3.680 ± 0.095
	EST	0.169 ± 0.007	0.180 ± 0.003	0.176 ± 0.003	0.190 ± 0.006	0.172 ± 0.005	0.174 ± 0.004
	AH	1.375 ± 0.110	1.382 ± 0.088	1.380 ± 0.068	1.430 ± 0.134	1.334 ± 0.103	1.411 ± 0.127

^{ab}The difference between genotypes with different lowercase letters were significant ($P < 0.05$).Abbreviations: AH, albumen height; BW, Beijing white quail; CY, Chinese yellow quail; EL, egg long; EQ, egg quality; ES, egg short; ESI, egg shape index; EST, egg shell thickness; EW, egg weight; KO, Korean quail; S, Strain; YH, yolk height; YI, yolk index; YWE, yolk weight; YWI, yolk width.

Hardy-Weinberg equilibrium (**HWE**) based on the chi-square test ($P > 0.05$). The A57G site of BW strain has deviated from the HWE ($P < 0.05$), the A72T site of BW strain has significantly deviated from the HWE ($P < 0.01$), which was not statistically significant (Table 1).

Association Analysis of IGF-1R Gene With Egg Quality in Quail

The present study was conducted to correlate the egg quality of quail at 7 wk of age (Table 2). The results showed that there was no significant association between the A57G site of *IGF-1R* gene with egg quality in CY strain ($P > 0.05$). The A57G site was significantly associated with the YWI in BW strain, and individuals with the GG genotype had significantly higher YWI than that of AG genotype ($P < 0.05$). In addition, there was no significant association between A57G site with egg quality in KO strain ($P > 0.05$). The results showed that A57G site had less effect on the egg quality in CY and KO quail strains.

For the A72TG site, there was no significant association with egg quality in CY strain ($P > 0.05$). However, there was significantly associated with the EST in BW strain, and individuals with the AT genotype had significantly higher EST than that of AA genotype ($P < 0.05$). In addition, the A72TG site was significantly associated with the EW, ES, and EL in KO strain ($P < 0.05$), and individuals with the TT genotype had better performance on EW, ES, and EL ($P < 0.05$). The results showed that A72T site had less effect on the egg quality in CY quail strain.

In the linkage between 2 SNPs (A57G and A72T), there were 6, 8, and 6 haplotype combinations (combinations with the number of individuals higher than or equal to 3) in CY, BW, and KO quail strains, respectively (Table 3). The result showed that haplotype combination AAAA had significantly higher EST than AGAA in CY strain ($P < 0.05$). AAAA and AAAT combinations had significantly higher EST than AATT, AGAA and GGAA in BW strain ($P < 0.05$). AGTT and GGTT combinations had significantly higher EW than AGAT in KO strain ($P < 0.05$). AGAT combination had significantly lower EST than the other 5 haplotype combinations in KO strain ($P < 0.05$). Similar to this study, a previous study in Japanese quail showed that a SNP (c.2293G>A) of the *IGF-1R* gene was significantly associated with growth traits (Moe et al., 2007). Jin et al. (2014) showed that based a haplotype comprising of 3-SNP (rs14011783, rs14011780, and rs14011776) of *IGF-1R* gene was significantly associated with BW49, BW70, and FCR ($P < 0.05$), which similar to this study. It can be seen that there was a significant correlation between *IGF-1R* gene and economic traits of animals.

Table 3. Correlation analysis of *IGF-1R* gene haplotype combinations with egg quality of quail.

		Traits (mean ± SE)									
S	D	EW	EL	ES	ESI	YH	YWI	YI	YWE	EST	AH
CY											
(46)	AAAA	10.900 ± 0.112	32.490 ± 0.172	24.950 ± 0.094	1.302 ± 0.007	8.000 ± 0.103	25.870 ± 0.199	0.309 ± 0.005	3.600 ± 0.041	0.208 ± 0.002[a]	1.570 ± 0.073
	AGAA	10.850 ± 0.250	32.255 ± 0.025	25.160 ± 0.180	1.282 ± 0.010	7.650 ± 0.050	23.925 ± 0.145	0.320 ± 0.000	3.400 ± 0.000	0.169 ± 0.011[b]	1.615 ± 0.285
	AGAT	10.717 ± 0.189	32.220 ± 0.467	24.758 ± 0.093	1.301 ± 0.019	8.200 ± 0.165	24.172 ± 0.504	0.340 ± 0.011	3.450 ± 0.092	0.175 ± 0.005[ab]	1.815 ± 0.225
	AGTT	10.600 ± 0.112	31.450 ± 0.172	25.360 ± 0.094	1.240 ± 0.007	8.100 ± 0.103	27.050 ± 0.199	0.299 ± 0.005	3.800 ± 0.041	0.186 ± 0.002[ab]	1.670 ± 0.073
	GGAT	10.500 ± 0.240	31.908 ± 0.369	24.852 ± 0.216	1.285 ± 0.016	7.923 ± 0.199	24.551 ± 0.401	0.324 ± 0.010	3.362 ± 0.071	0.182 ± 0.004[ab]	1.593 ± 0.175
	GGTT	10.709 ± 0.223	31.659 ± 0.295	25.074 ± 0.198	1.263 ± 0.012	8.073 ± 0.274	24.833 ± 0.364	0.326 ± 0.013	3.545 ± 0.106	0.178 ± 0.004[ab]	1.872 ± 0.123
BW(49)	AAAA	11.100 ± 0.128	30.290 ± 0.225	26.160 ± 0.111	1.158 ± 0.009	8.300 ± 0.100	23.930 ± 0.233	0.347 ± 0.009	3.500 ± 0.050	0.182 ± 0.002[a]	1.870 ± 0.065
	AAAT	10.075 ± 0.085	31.628 ± 0.237	24.495 ± 0.229	1.292 ± 0.020	7.650 ± 0.393	25.050 ± 0.474	0.306 ± 0.017	3.425 ± 0.085	0.173 ± 0.004[a]	1.820 ± 0.233
	AATT	11.100 ± 0.300	31.845 ± 0.005	25.760 ± 0.370	1.236 ± 0.018	8.150 ± 0.150	26.220 ± 0.080	0.311 ± 0.007	3.600 ± 0.000	0.147 ± 0.002[b]	2.415 ± 0.515
	AGAA	9.900 ± 0.351	31.660 ± 0.802	24.173 ± 0.192	1.310 ± 0.033	7.433 ± 0.484	23.527 ± 0.477	0.317 ± 0.025	3.100 ± 0.100	0.142 ± 0.004[b]	1.777 ± 0.384
	AGAT	10.427 ± 0.199	31.497 ± 0.348	24.853 ± 0.156	1.267 ± 0.011	8.009 ± 0.150	24.670 ± 0.271	0.311 ± 0.017	3.386 ± 0.072	0.162 ± 0.002[ab]	1.926 ± 0.083
	AGTT	10.700 ± 0.344	32.730 ± 0.362	25.030 ± 0.346	1.308 ± 0.019	7.825 ± 0.287	24.795 ± 0.488	0.317 ± 0.017	3.425 ± 0.085	0.156 ± 0.007[ab]	1.725 ± 0.208
	GGAA	10.800 ± 1.600	32.060 ± 2.580	24.980 ± 0.890	1.281 ± 0.058	7.750 ± 0.550	24.835 ± 2.775	0.319 ± 0.058	3.400 ± 0.700	0.148 ± 0.005[b]	1.735 ± 0.335
	GGAT	10.740 ± 0.125	32.272 ± 0.589	25.054 ± 0.262	1.289 ± 0.034	7.840 ± 0.234	26.816 ± 0.787	0.294 ± 0.018	3.600 ± 0.130	0.165 ± 0.005[ab]	1.662 ± 0.160
KO											
(48)	AGAA	9.933 ± 0.865[ab]	30.987 ± 1.435	24.507 ± 0.598	1.263 ± 0.032	6.800 ± 0.153	26.270 ± 0.822	0.259 ± 0.002	3.467 ± 0.406	0.186 ± 0.006[a]	1.200 ± 0.058
	AGAT	9.640 ± 0.491[b]	31.134 ± 0.607	24.316 ± 0.377	1.281 ± 0.027	6.320 ± 0.437	25.404 ± 1.102	0.253 ± 0.027	3.060 ± 0.252	0.150 ± 0.015[b]	1.240 ± 0.084
	AGTT	10.943 ± 0.316[a]	32.866 ± 0.540	25.210 ± 0.267	1.304 ± 0.021	6.700 ± 0.421	27.036 ± 0.474	0.249 ± 0.018	3.700 ± 0.148	0.175 ± 0.006[a]	1.547 ± 0.216
	GGAA	10.183 ± 0.209[ab]	31.692 ± 0.426	24.685 ± 0.220	1.284 ± 0.019	6.750 ± 0.159	26.533 ± 1.214	0.258 ± 0.016	3.450 ± 0.205	0.192 ± 0.009[a]	1.545 ± 0.186
	GGAT	10.180 ± 0.240[ab]	31.607 ± 0.323	24.617 ± 0.188	1.284 ± 0.009	6.400 ± 0.156	26.563 ± 0.398	0.242 ± 0.009	3.580 ± 0.096	0.179 ± 0.004[a]	1.365 ± 0.135
	GGTT	11.038 ± 0.338[a]	32.384 ± 0.536	25.354 ± 0.304	1.278 ± 0.023	6.238 ± 0.201	27.718 ± 0.423	0.226 ± 0.009	3.663 ± 0.132	0.173 ± 0.006[a]	1.291 ± 0.146

[ab]The difference between genotypes with different lowercase letters were significant ($P < 0.05$).Abbreviations: AH, albumen height; BW, Beijing white quail; CY, Chinese yellow quail; D, diplotype; EL, egg long; EQ, egg quality; ES, egg short; ESI, egg shape index; EST, egg shell thickness; EW, egg weight; KO, Korean quail; S, strain; YH, yolk height; YI, yolk index; YWE, yolk weight; YWI, yolk width.

Table 4. Association of between A57G and A72T site with carcass traits of quail.

	A57G (mean ± SE)			A72T (mean ± SE)		
CT	AA	AG	GG	AA	AT	TT
BOW	142.643 ± 3.615	140.546 ± 2.002	140.963 ± 2.146	141.493 ± 2.982	139.635 ± 1.921	143.461 ± 2.646
DCW	137.186 ± 3.516	135.524 ± 2.024	136.341 ± 2.164	136.367 ± 2.971	134.565 ± 1.909	139.283 ± 2.747
WNCW	86.086 ± 3.417	87.130 ± 1.566	90.574 ± 1.646	90.147 ± 2.579	87.706 ± 1.489	90.430 ± 2.104
HW	1.071 ± 0.102	1.054 ± 0.033	1.070 ± 0.028	1.160 ± 0.052	1.031 ± 0.023	1.074 ± 0.052
LW	4.157 ± 0.532	4.165 ± 0.125	3.943 ± 0.145	4.073 ± 0.288[ab]	3.879 ± 0.087[b]	4.426 ± 0.264[a]
BMW	27.886 ± 1.648	27.789 ± 0.655	28.635 ± 0.650	28.427 ± 1.213	27.844 ± 0.563	28.97 ± 0.896
LMW	7.600 ± 0.307	7.324 ± 0.138	7.517 ± 0.145	7.600 ± 0.228	7.340 ± 0.140	7.578 ± 0.137
DP	96.179 ± 0.457	96.399 ± 0.153	96.682 ± 0.128	96.358 ± 0.145[b]	96.348 ± 0.134[b]	97.039 ± 0.179[a]
WNCR	60.318 ± 1.624	62.005 ± 0.714	64.239 ± 0.538	63.669 ± 1.173	62.815 ± 0.564	63.044 ± 0.897
HR	1.263 ± 0.138	1.214 ± 0.034	1.189 ± 0.030	1.295 ± 0.055	1.185 ± 0.028	1.190 ± 0.052
LR	4.969 ± 0.802	4.816 ± 0.149	4.377 ± 0.149	4.589 ± 0.359	4.467 ± 0.110	4.922 ± 0.298
BMR	32.338 ± 1.198	31.895 ± 0.495	31.606 ± 0.423	31.482 ± 0.892	31.773 ± 0.392	31.997 ± 0.602
LMR	17.703 ± 0.573	16.850 ± 0.219	16.626 ± 0.190	16.917 ± 0.395	16.744 ± 0.176	16.857 ± 0.297

[ab]The difference between genotypes with different lowercase letters were significant ($P < 0.05$).Abbreviations: BMR, breast muscle rate; BMW, breast muscle weight; BOW, body weight; CT, carcass trait; DCW, dressed carcass weight; DP, dressing percentage; HR, heart rate; HW, heart weight; LMR, leg muscle rate; LMW, leg muscle weight; LR, liver rate; LW, liver weight; WNCR, whole net carcass rate; WNCW, whole net carcass weight.

Table 5. Correlation analysis of *IGF-1R* gene haplotype combinations with carcass traits of quail.

Traits	AAAA	AAAT	AATT	AGAA	AGAT	AGTT	GGAA	GGAT	GGTT
BOW	138.200 ± 1.388	148.167 ± 6.996	138.600 ± 3.980	139.833 ± 13.471	139.092 ± 2.221	145.538 ± 3.744	142.245 ± 2.618	139.135 ± 3.460	143.292 ± 4.401
DCW	134.300 ± 1.400	141.567 ± 7.626	133.767 ± 3.398	134.633 ± 13.165	133.831 ± 2.203	141.363 ± 4.033	137.027 ± 2.690	134.483 ± 3.443	139.275 ± 4.534
WNCW	92.300 ± 1.098	90.267 ± 6.636	79.833 ± 1.729	81.633 ± 11.341	87.027 ± 1.617	89.525 ± 3.427	92.273 ± 1.791	88.139 ± 2.768	93.683 ± 2.879
HW	1.200 ± 0.021	0.967 ± 0.088	1.133 ± 0.233	1.233 ± 0.186	1.046 ± 0.035	1.013 ± 0.072	1.136 ± 0.054	1.022 ± 0.033	1.100 ± 0.072
LW	3.200 ± 0.098	3.500 ± 0.265	5.133 ± 1.033	4.800 ± 0.458	3.969 ± 0.131	4.563 ± 0.298	3.955 ± 0.352	3.826 ± 0.122	4.158 ± 0.401
BMW	27.600 ± 0.444	29.433 ± 3.147	26.433 ± 2.617	23.600 ± 3.143	27.538 ± 0.702	30.175 ± 1.285	29.818 ± 1.198	27.983 ± 0.943	28.800 ± 1.353
LMW	7.900 ± 0.096	8.033 ± 0.371	7.067 ± 0.521	6.833 ± 0.696	7.358 ± 0.172	7.400 ± 0.208	7.782 ± 0.230	7.230 ± 0.245	7.825 ± 0.166
DP	97.178 ± 0.098	95.489 ± 0.641	96.536 ± 0.764	96.258 ± 0.183	96.204 ± 0.182	97.085 ± 0.291	96.311 ± 0.177	96.623 ± 0.195	97.134 ± 0.231
WNCR	66.787 ± 0.440	60.835 ± 2.523	57.644 ± 1.192	57.981 ± 2.711	62.642 ± 0.845	61.443 ± 1.394	64.938 ± 1.045	63.268 ± 0.799	65.462 ± 0.921
HR	1.300 ± 0.023	1.097 ± 0.175	1.416 ± 0.278	1.507 ± 0.035	1.206 ± 0.040	1.129 ± 0.060	1.237 ± 0.064	1.173 ± 0.040	1.174 ± 0.063
LR	3.467 ± 0.116[b]	3.947 ± 0.547[b]	6.492 ± 1.464[a]	5.946 ± 0.256[a]	4.596 ± 0.169[ab]	5.108 ± 0.293[a]	4.322 ± 0.417[ab]	4.388 ± 0.144[ab]	4.406 ± 0.354[ab]
BMR	29.903 ± 0.308	32.490 ± 1.391	32.998 ± 2.625	28.975 ± 0.929	31.679 ± 0.614	33.691 ± 0.643	32.309 ± 1.099	31.785 ± 0.544	30.618 ± 0.727
LMR	17.118 ± 0.141	17.879 ± 0.634	17.723 ± 1.351	16.947 ± 1.163	16.915 ± 0.272	16.603 ± 0.366	16.891 ± 0.472	16.403 ± 0.218	16.811 ± 0.422

[ab]The difference between genotypes with different lowercase letters were significant ($P < 0.05$).Abbreviations: BMR, breast muscle rate; BMW, breast muscle weight; BOW, body weight; DCW, dressed carcass weight; DP, dressing percentage; HR, heart rate; HW, heart weight; LMR, leg muscle rate; LMW, leg muscle weight; LR, liver rate; LW, liver weight; WNCR, whole net carcass rate; WNCW, whole net carcass weight.

Association Analysis of IGF-1R Gene With Carcass Traits in Quail

The present study was conducted to correlate the carcass traits of quail at 20 wk of age (Table 4). The result showed that A57G site was not significantly related to carcass traits in 3 quail strains ($P > 0.05$). The A72T site was significantly associated with the LW in 3 quail strains, and individuals with the TT genotype had significantly higher LW than that of AT genotype ($P < 0.05$). The A72T site was significantly associated with the DP in 3 quail strains, and individuals with the TT genotype had significantly higher DP than that of AA and AT genotype ($P < 0.05$). In the linkage between 2 SNPs (A57G and A72T), 9 haplotype combinations (combinations with the number of individuals higher than or equal to 3) were formed in 3 strains (Table 5). The result showed that haplotype combination AATT, AGAA and AGTT had significantly higher LR than of AAAA and AAAT combination ($P < 0.05$). Similar to this study, a previous study in chicken showed that A17299834G SNP of the *IGF-1R* gene was significantly associated with carcass traits, and a haplotype based on 2 SNPs (A17299834G and C17293932T) showed significant correlation with most of the early growth traits and carcass traits (Lei et al., 2008). The *IGF-1R* gene may be used as the major gene affecting quail carcass traits. These studies suggest that the associations of the SNP or haplotype with economic traits in the present study were reliable.

In conclusion, 2 SNPs (A57G and A72T) or haplotype combination of *IGF-1R* gene which were significantly correlated to egg quality and carcass traits. Therefore, *IGF-1R* gene could be a molecular genetic marker to improve economic traits with quail breeding. However, due to limitation of the number of quail population, further studies in large populations with different quail strains are required to further assess associations of the *IGF-1R* gene polymorphisms with egg quality, carcass traits, and other economic traits.

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I declare that research on live animals is in line with the guidelines approved by the institutional animal care and use Committee (IACUC) through the use of appropriate management and laboratory techniques to avoid unnecessary discomfort of animals.

DISCLOSURES

The authors declare no conflicts of interest.

REFERENCES

Ali, D. A., M. B. S. Al-Shuhaib, G. Farhadi, F. R. Al-Kafajy, T. M. Al-Thuwaini, and A. Esmailizadeh. 2021. Detection of a novel single nucleotide polymorphism in IGF2 gene with a negative impact on egg production and body weight in Japanese quail (Coturnix japonica). J. Genet. Eng. Biotechnol. 19:170.

Bai, J. Y., Z. H. Dong, Y. Lei, Y. B. Yang, X. P. Jia, and J. Y. Li. 2021. Association analysis between polymorphism of gonadotrophin releasing hormone genes and growth traits of quail (Coturnix Coturnix). Braz. J. Poult. Sci. 23:eRBCA-2020-1314.

Cardoso, S., I. P. López, S. Piñeiro-Hermida, J. G. Pichel, and P. I. Moreira. 2021. IGF1R deficiency modulates brain signaling pathways and disturbs mitochondria and redox homeostasis. Biomedicines 9:158.

Ding, N., D. Tian, X. Li, Z. Zhang, F. Tian, S. Liu, B. Han, D. Liu, and K. Zhao. 2022. Genetic polymorphisms of IGF1 and IGF1R genes and their effects on growth traits in Hulun Buir sheep. Genes. 13:666.

El-Magd, M. A., A. A. Saleh, A. A. Nafeaa, S. M. El-Komy, and M. A. Afifi. 2017. Polymorphisms of the IGF1 gene and their association with growth traits, serum concentration and expression rate of IGF1 and IGF1R in buffalo. J. Zhejiang. Univ. Sci. B 18:1064–1074.

El-Tarabany, M. S., A. A. Saleh, I. E. El-Araby, and M. A. El-Magd. 2022. Association of LEPR polymorphisms with egg production and growth performance in female Japanese quails. Anim. Biotechnol. 33:599–611.

Jin, S., S. Chen, H. Li, Y. Lu, G. Xu, and N. Yang. 2014. Associations of polymorphisms in GHRL, GHSR, and IGF1R genes with feed efficiency in chickens. Mol. Biol. Rep. 41:3973–3979.

Lei, M., X. Peng, M. Zhou, C. Luo, Q. Nie, and X. Zhang. 2008. Polymorphisms of the IGF1R gene and their genetic effects on chicken early growth and carcass traits. BMC Genet. 9:70.

Ma, Y. L., Y. F. Wen, X. K. Cao, J. Cheng, Y. Z. Huang, Y. Ma, L. Y. Hu, C. Z. Lei, X. L. Qi, H. Cao, and H. Chen. 2019. Copy number variation (CNV) in the IGF1R gene across four cattle breeds and its association with economic traits. Arch. Anim. Breed. 62:171–179.

Minvielle, F. 2004. The future of Japanese quail for research and production. World's Poult. Sci. J. 60:500–507.

Moe, H. H., T. Shimogiri, W. Kamihiraguma, H. Isobe, K. Kawabe, S. Okamoto, F. Minvielle, and Y. Maeda. 2007. Analysis of polymorphisms in the insulin-like growth factor 1 receptor (IGF1R) gene from Japanese quail selected for body weight. Anim. Genet. 38:659–661.

Priti, M., and S. Satish. 2014. Quail farming: an introduction. Int. J. Life Sci. 2:190–193.

Pu, Y. J., Y. Wu, X. J. Xu, J. P. Du, and Y. Z. Gong. 2016. Association of VIPR-1 gene polymorphisms and haplotypes with egg production in laying quails. J. Zhejiang Univ. Sci. B 17:591–596.

Szewczuk, M., S. Zych, J. Wójcik, and E. Czerniawska-Piątkowska. 2013. Association of two SNPs in the coding region of the insulin-like growth factor 1 receptor (IGF1R) gene with growth-related traits in Angus cattle. J. Appl. Genet. 54:305–308.

Wang, X. L., J. Y. Li, J. Y. Bai, L. W. Wang, H. D. Fan, M. K. Chen, F. L. Zeng, X. N. Lu, and Y. H. He. 2023. Research Note: Polymorphisms of gonadotrophin-releasing hormone gene and their association with growth traits in quail (Coturnix Coturnix). Poult. Sci. 102:102439.

Wu, P. F., D. Wang, C. F. Jin, X. Q. Zhang, H. Q. Wu, L. Zhang, F. X. Ding, K. Z. Xie, and G. X. Zhang. 2017. Polymorphisms of AluI and Hin1I loci of the IGF-1R gene and their genetic effects on growth traits in Bian chickens. Genet. Mol. Res. 16:10.4238.

Yang, C., J. Teng, C. Ning, W. Wang, S. Liu, Q. Zhang, D. Wang, and H. Tang. 2022. Effects of growth-related genes on body measurement traits in Wenshang barred chickens. J. Poult. Sci. 59:323–327.

Ye, M., F. Ye, L. He, Y. Liu, X. Zhao, H. Yin, D. Li, H. Xu, Q. Zhu, and Y. Wang. 2017. Molecular cloning, expression profiling, and marker validation of the chicken Myoz3 gene. Biomed. Res. Int. 2017:5930918.

Yeh, F. C., and T. J. B. Boyle. 1997. Population genetic analysis of co-dominant and dominant markers and quantitative traits. Belg. J. Bot. 129:157.

Zhang, Y. R., Y. K. Li, C. Z. Fu, J. L. Wang, H. B. Wang, and L. S. Zan. 2014. Effects of bovine SMO gene polymorphisms on the body measurement and meat quality traits of Qinchuan cattle. Genet. Mol. Res. 13:8105–8117.