Association Between Genetic Polymorphisms of Growth Hormone Gene and Egg Production Traits in Chickens: A Systematic Review

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ABSTRACT

Chicken performance traits are affected by the chicken growth hormone (cGH) gene due to its essential part in metabolism and growth, and genetic polymorphisms may be useful as a genetic marker for growth traits. However, no comprehensive review provides information on the cGH polymorphisms and their correlation with egg production traits. The study systematically reviewed the single nucleotide polymorphisms (SNPs) of the growth hormone gene and their association with the chicken's egg production traits. Four databases, Google Scholar, ScienceDirect, PubMed, and Web of Science, were used to search the literature where the keywords 'growth hormone, single nucleotide polymorphisms, genetic variations, genetic effects, egg production traits, and chickens were the keywords during the literature search. The outcomes revealed that four articles published in 2013, 2014, 2015, and 2018 were included. The results indicated that four SNPs (T185G, G662A, T3094C, and C3199T) were identified, with allelic frequencies ranging from 0.020 to 0.964 and genotypic frequencies ranging from 0.007 to 0.930. The findings indicated that some of the articles used more than one breed. The present reveiw revealed that egg number was found to be significantly associated with discovered genotypes six times, while body weight at first egg and egg weight at first egg were found to be significantly related to discovered genotypes four times. However, additional research is required to validate the identified SNPs. Furthermore, identified SNPs could serve as possible molecular markers to genetically improve egg production in chickens.

Keywords: Average egg weight, Body weight, Egg number, Egg weight, Genotype

INTRODUCTION

The poultry industry has a noticeable position as one of the main sources of animal protein for human consumption. Poultry is crucial in genetic research due to breeding practicality, quite short generation intervals, and phenotypic variations. The enhancement of economic traits in chickens has progressively gained attention, and the documentation and use of quantitative trait loci (QTLs) offer the possibility for genetic enhancement in selection programs with no slaughtering (Kazemi et al., 2018). The chicken growth hormone (cGH) gene is one of the highly vital genes that affect chicken performance traits due to its significant role in growth and metabolism, and it has four exons and five introns with an overall length of 4098 bp (Makhsous et al., 2013). Single nucleotide polymorphisms (SNPs) studies help in the identification of gene variants and their possible relationships with the phenotypic expression of useful traits and are a significant aspect of the development of breeding systems that make use of marker-assisted selection (MAS) of traits that influence the economic value of the animal in that breeding program (Kulibaba, 2015). SNPs and their relations with egg production traits has been conducted in different chicken breeds around the world such as Fars Native and

Mazandaran Native fowls in Iran (Makhsous et al., 2013; Kazemi et al., 2018), Recessive White and Qingyuan partridge chicken breeds in China (Su et al., 2014) and Poltavskaya Glinistaya Chickens in Ukraine (Kulibaba, 2015). Based on the authors' knowledge, the literature on SNPs of chicken growth hormone gene and their relationships with egg production traits has not yet been systematically investigated. To address the documented knowledge gap, the study conducted a systematic review of the literature on the impact of single nucleotide polymorphisms in the chicken growth hormone gene on egg production traits. The current study aimed to guide chicken breeders and researchers in identifying potential genetic markers that can be used in the selection of chickens for the improvement of egg production traits during breeding.

MATERIALS AND METHODS

Eligibility criteria

The articles with the word "chicken", "egg production traits", and "single nucleotide polymorphisms" were used for the literature search.

Literature search

The authors searched the research articles using the following databases, including Google Scholar, ScienceDirect, PubMed, and Web of Science up to August 15, 2023, where the keywords used were growth hormone (GH), single nucleotide polymorphisms, genetic variations, genetic effects, egg production traits, and chickens.

Inclusion criteria

The eligibility of all the acquired articles was set to the extent where the following words were fulfilled by the studies: The chickens' GH gene was under investigation, included the polymorphisms of the GH gene, and chickens were included as the animal of interest.

Exclusion criteria

The criteria for exclusion involved articles with duplicated records, not published in the English language, other poultry species, such as ducks, and lacking the association of chicken GH polymorphisms to egg production traits.

Data extraction

The authors extracted the articles from databases independently. The information retrieved from the articles included the name of the first author, the chicken breed, the year of publication, population size, the country, egg production traits, and genotyping procedure.

RESULTS

Literature reveiw

A total of 96 articles were retrieved for the systematic review from the following databases, including Google Scholar (n = 37), Web of Science (n = 27), ScienceDirect (n = 16), and PubMed (n = 16), as displayed in Figure 1. The duplicates (n = 21) found in the search databases were eliminated, and the remaining articles were evaluated for inclusion and exclusion criteria. The remaining articles (n = 75) were screened for their title, and sixty-eight (n = 68) were excluded. The screening for the abstract was done, and three (n = 3) were excluded. The study systematically reviewed all the articles searched and excluded articles not eligible for the study, and a total of four articles were included in the systematic review.

Characteristics of included articles

About four studies of the 96 articles were reserved for inclusion in the literature review (Table 1). The included articles all investigated growth hormone (GH) gene single nucleotide polymorphisms (SNPs) and their correlation with egg production traits in chickens. Out of 4 included articles, 3 (75%) of them (Makhsous et al., 2013; Kulibaba, 2015; Kazemi et al., 2018) used PCR-RFLP as a genotyping method, except 1 article (25%) used PCR-LDR genotyping method (Su et al., 2014). All the articles included in the present study used different chicken breeds, however, all used native chicken breeds.

Targeted chicken growth gene genomic regions

The findings displayed that all the reviewed articles targeted the intron 1 region (Table 2). The results showed that one article (Kulibaba, 2015) out of the four articles reviewed targeted intron 1 and intron 4 regions, while the other articles reviewed targeted intron 1 only. Two articles (Makhsous et al., 2013; Su et al., 2014) out of four articles did not identify the regions targeted.

Identified single nucleotide polymorphisms

Table 2 shows the SNPs identified and their positions in the articles involved. The outcomes displayed that one article (Su et al., 2014) out of four involved articles discovered the SNPs and their positions, and 4 similar SNPs (T185G, G662A, T3094C, C3199T) were identified. The findings also revealed that the 4 SNPs were discovered from two different chicken breeds (Qingyuan partridge and Recessive White chickens).

Allelic and genotypic frequencies

Table 2 displays allelic and genotypic frequencies discovered from the included articles. The findings indicated that all four reviewed articles showed the allelic frequencies, while three (Makhsous et al., 2013; Kulibaba, 2015; Kazemi et al., 2018) of the included articles showed the genotypic frequencies. The findings indicated that the allelic frequency ranged from 0.020 to 0.964, while the genotypic frequency ranged from 0.007 to 0.930.

Identified SNPs' genotypes and their relationship with the egg production traits

Identified genotypes and their correlation with egg production traits of included articles are presented in Table 3. Five chicken breeds (Recessive White, Qingyuan partridge, Mazandaran native, Poltavskaya Glinistaya, and Fars Native) were used to study the relationship between identified SNPs' genotypes and egg production traits. The article studied in Recessive White and Qingyuan partridge chicken breeds found that the genotypes of SNPs T185G and T3094C were associated with BFE, EWFE, and EN (Su et al., 2014). The article investigated the Poltavskaya Glinistaya chicken breed and found that the genotypes were associated with EN and WE (Kulibaba, 2015), while the article examined the Fars Native chicken breed and found that identified genotypes were associated with EN and ELR (Makhsous et al., 2013). These results found that EN was significantly related to genotypes six times, while BFE and EWFE were found to be significantly related to genotypes four times.
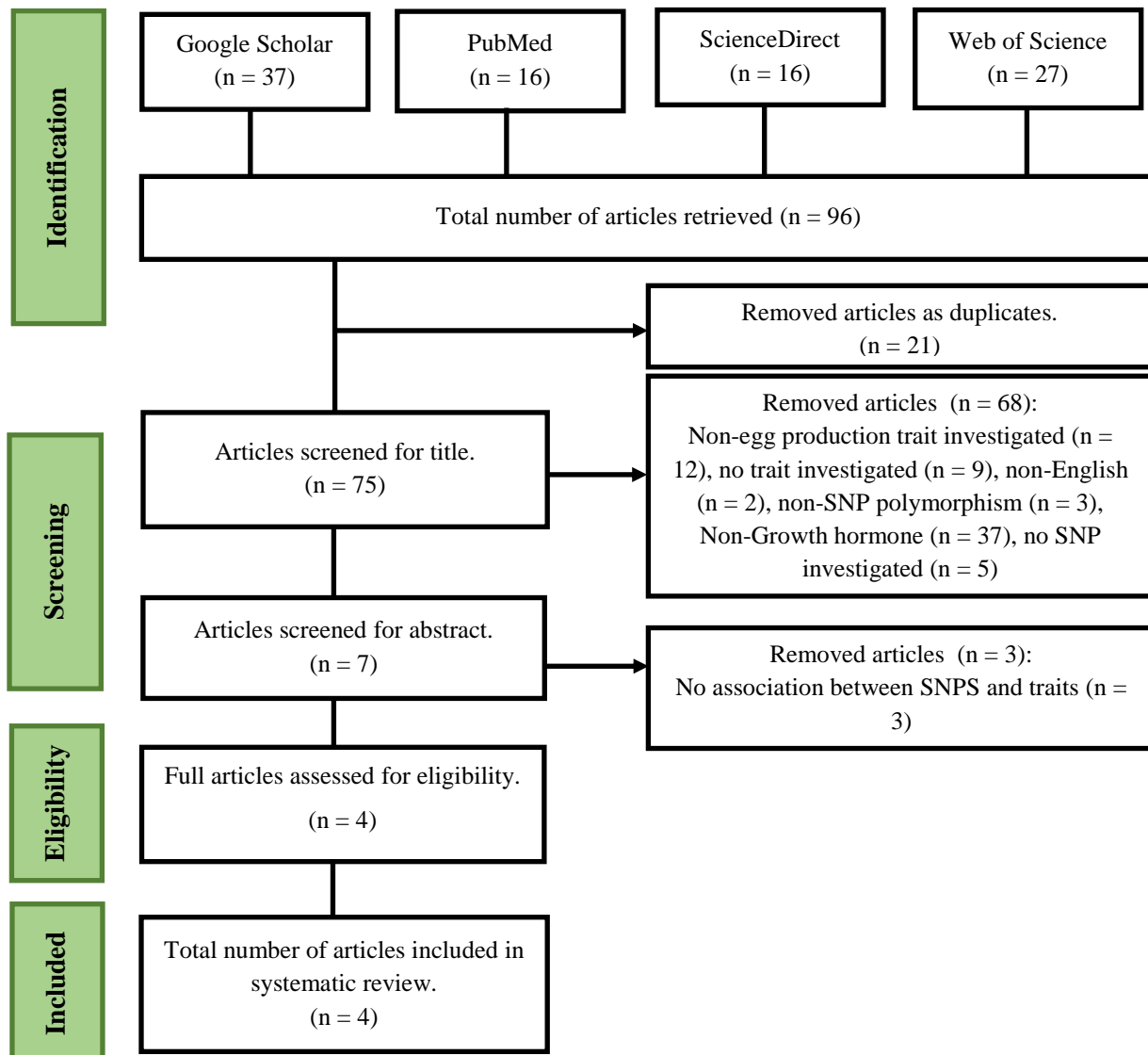

Figure 1. The process of article selection in the present study

Table 1. Characterization of the articles included for the present systematic review

Author	Year	Country	Breed	N	Egg production traits	Genotyping method
Kazemi et al.	2018	Iran	Mazandaran native Fowls	380	EN, LI, EW, AEW, PH	PCR-RFLP
Kulibaba	2015	Ukraine	Poltavskaya Glinistaya chickens	98	EN, EW	PCR-RFLP
Makhsous et al.	2013	Iran	Fars Native Chickens	142	EW, AFE, ELR	PCR-RFLP
Su et al.	2014	China	Recessive White chickens and Qingyuan partridge chickens	136; 187	EN, BWFE, EWFE, AFE	PCR-LDR

N: Sample size, EN: Egg number, LI: Laying intensity, EW: Egg weight, AEW: Average egg weight, PF: Percentage fertility, PH: Percentage hatchability, AFE: Age at first egg, ELR: Egg laying rate, BWFE: Body weight at first egg, EWFE: Egg weight at first egg, PCR-LDR: Polymerase chain reaction-ligase detection reaction, PCR-RFLP: Polymerase chain reaction-restriction fragment length polymorphism.

Table 2. Identified single nucleotide polymorphisms and their positions in the included articles

Breed	SNP	Region	Allelic frequencies	Genotypic frequencies	Author
Recessive White chickens	T185G	Not identified	T (0.812), G (0.188)	Not identified	Su et al. (2014)
Recessive White chickens	G662A	Not identified	G (0.435), A (0.565)	Not identified	Su et al. (2014)
Recessive White chickens	T3094C	Not identified	T (0.200), C (0.800)	Not identified	Su et al. (2014)
Recessive White chickens	C3199T	Not identified	C (0.713), T (0.287)	Not identified	Su et al. (2014)
Qingyuan Partridge chickens	T185G	Not identified	T (0.951), G (0.049)	Not identified	Su et al. (2014)
Qingyuan Partridge chickens	G662A	Not identified	G (0.287), A (0.713)	Not identified	Su et al. (2014)
Qingyuan Partridge chickens	T3094C	Not identified	T (0.122), C (0.878)	Not identified	Su et al. (2014)
Qingyuan Partridge chickens	C3199T	Not identified	C (0.831), T (0.169)	Not identified	Su et al. (2014)
Mazandaran Native fowls	Not identified	Intron 1	A (0.305), B (0.098), C (0.597)	AA (0.10), BB (0.01), CC (0.36), AB (0.07), AC (0.34), BC (0.12)	Kazemi et al. (2018)
Poltavskaya Glinistaya chickens	Not identified	Intron 1	A (0.908), B (0.020), C (0.072)	AA (0.820), AB (0.040), AC (0.140)	Kulibaba (2015)
Poltavskaya Glinistaya chickens	Not identified	Intron 4	A (0.036), B (0.964)	AB (0.070), BB (0.930)	Kulibaba (2015)
Fars Native Chickens	Not identified	Not identified	A (0.599), B (0.102), C (0.299)	AA (0.338), AB (0.113), AC (0.409), BB (0.007), BC (0.070), CC (0.063)	Makhsous et al. (2013)

Table 3. Identified single nucleotide polymorphisms and their association with egg production traits

Author	Breed	SNP	Egg production traits	Genotypes			Sig
Su et al. (2014)	Recessive white chickens	T185G	AFE	TT	TG	GG	ns
		T185G	BFE	TT	TG	GG	*
		T185G	EWFE	TT	TG	GG	*
		T185G	EN	TT	TG	GG	*
		T3094C	AFE	TT	TC	CC	*
		T3094C	BFE	TT	TC	CC	*
		T3094C	EWFE	TT	TC	CC	*
		T3094C	EN	TT	TC	CC	*
Su et al. (2014)	Qingyuan partridge chickens	T185G	AFE	TT	TG	GG	ns
		T185G	BFE	TT	TG	GG	*
		T185G	EWFE	TT	TG	GG	*
		T185G	EN	TT	TG	GG	*
		T3094C	AFE	TT	TC	CC	*
		T3094C	BFE	TT	TC	CC	*
		T3094C	EWFE	TT	TC	CC	*
		T3094C	EN	TT	TC	CC	*
Kazemi et al. (2018)	Mazandaran native fowls	Not identified	BFE	AA	BB	CC	ns
			EW	AA	BB	CC	ns
			EN	AA	BB	CC	ns
			LI	AA	BB	CC	ns
			PH	AA	BB	CC	ns
			AEW	AA	BB	CC	ns
Kulibaba (2015)	Poltavskaya Glinistaya chickens	Not identified	EW	AA	BB	AB	*
			EN	AA	BB	AB	*
Makhsous et al. (2013)	Fars native chickens	Not identified	EN	AA	BB	CC	*
			EW	AA	BB	CC	ns
			ELR	AA	BB	CC	*

EN: Egg number, LI: Laying intensity, EW: Egg weight, AEW: Average egg weight, PF: Percentage fertility, PH: Percentage hatchability, AFE: Age at first egg, ELR: Egg laying rate, BFE: Body weight at first egg, EWFE: Egg weight at first egg, Sign: Significant, *: Significant at $p < 0.05$, ns: Non-significant.

DISCUSSION

Egg production traits are economically important in poultry production, and they can be affected by the genetic makeup of the birds (Su et al., 2014). Enhancing the economic traits in chickens has progressively gained attention, and the documentation and exploitation of QTLs offer a possibility for genetic enhancement in selection programs without slaughtering (Kazemi et al., 2018). The findings indicated that out of the 4 articles included in the study, only 1 article identified four similar SNPs (T185G, G662A, T3094C, C3199T) in the two chicken breeds, namely, Recessive White chickens and Qingyuan partridge (Su et al., 2014). The findings further displayed that out of the four SNPs identified, only two SNPs showed significant association with the egg production traits. Su et al. (2014) indicated the T185G SNP and discovered that it is associated with three egg production traits: Egg weight at first egg, body weight at first egg, and egg number, however, there was no significant association with age at first egg laying. In addition, T3094C SNP was associated with body weight at first egg laying, age at first laying, egg weight at first laying, and egg number in Recessive White chickens and Qingyuan partridge chickens. Kazemi et al. (2018) reported that the SNP found in the study had no significant association with all the studies' egg production traits, namely egg weight, body weight at first egg, laying intensity, egg number, percentage hatchability, and average egg weight in Mazandaran native fowls. Kulibaba (2015) found that the SNP linked significantly with egg weight and egg number in Poltavskaya Glinistaya chickens, while Makhsous et al. (2013) reported that the SNP was found to correlate with egg number and egg laying rate, but no significant association with egg weight in Fars Native Chickens. The present systematic review confirms the influence of the chicken growth hormone gene on egg production traits. Kazemi et al. (2018) targeted the intron 1 genomic region during the study, while Kulibaba (2015) targeted intron 1 and 4 genomic regions. According to Su et al. (2014), the chicken growth hormone gene intron is highly polymorphic. According to the knowledge of the authors, this systematic review is one

of the first studies on the relationship of the growth hormone gene SNPs with egg production traits. Thus, the current study does not compare with other systematic review findings.

CONCLUSION

Two SNPs associated with egg production traits can be used as genetic markers to improve egg weight at first laying, body weight at first laying egg, and egg number. According to the present systematic review, there is insufficient information on the identified SNPs of the growth hormone gene and their relationship with egg production traits. The growth hormone gene influences the egg production traits, and the T185G and T3094C SNPs may be employed as possible genetic markers for improving the egg production traits in chickens during breeding.

DECLARATIONS

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Availability of data and materials
All data are presented in this article but the prepared data are available upon reasonable request from authors.

Ethical considerations
The ethical issues considered by all authors while this review results were checked for plagiarism, informed consent, misconduct, and data manipulation.

Authors' contributions
The conceptualization of the study was done by Victoria Rankotsane Hlokoe and Thobela Louis Tyasi. Victoria Rankotsane Hlokoe was responsible for the methodology and original draft preparation, and Victoria Rankotsane Hlokoe and Thobela Louis Tyasi were responsible for reviewing and editing the manuscript. The manuscript's final edition has been read and agreed upon by all authors.

Competing interests
The authors state that there is no conflict of interest.

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