

Review

# Insulin-Like Growth Factor 1 Gene and Growth Traits Correlations in Sheep: A Systematic Review

<sup>1</sup>Thabang Sako, <sup>1</sup>Thobela Lousi Tyasi and <sup>2</sup>Jones Ng'ambi

<sup>1</sup>Department of Agricultural Economics and Animal Production, School of Agricultural and Environmental Sciences, University of Limpopo, Private Bag X1106, Sovenga, 0727, Limpopo, South Africa

<sup>2</sup>Department of Agriculture and Animal Health, University of South Africa, Florida Science Campus, Private Bag X6, Florida 1710, South Africa

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## Corresponding Author:

Thobela Lousi Tyasi

Department of Agricultural Economics and Animal Production, School of Agricultural and Environmental Sciences, University of Limpopo, Private Bag X1106, Sovenga, 0727, Limpopo, South Africa  
Email: lousi.tyasi@ul.ac.za

**Abstract:** Insulin-like Growth Factor 1 (IGF1) is a growth factor gene of the endocrine that is known for involvement in growth, as well as fetal development and metabolism. The IGF1 is majorly embedded in the animal growth processes and as a result, contributes to the improved output of meat and regulation of somatic cell growth with regards to the dietary conditions. There have been studies that investigated the effect of IGF1 on growth traits. However, as far as we know, there is no study that systematically reviewed the relationship between IGF1 and growth traits in sheep. Therefore, this systematic review aimed to systematically review the Single Nucleotide Polymorphisms (SNPs) of the IGF1 gene and their relationship with growth traits in sheep. Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) were used for identification, screening, eligibility and inclusion and 14 studies were found to be eligible. This systematic review used four search engines (PubMed, web of science, google scholar and science direct) and components of the research question identification of the Population, Exposure and Outcomes (PEO) to gather eligible studies. The results showed that 26 different SNPs were identified with no similar SNPs identified by the included articles. The results indicated that the identified SNPs (G855C, G857A, C271T and A91C) had a relationship with Birth Weight (BWt), Weaning Weight (WW), Body Weight (BW), Average Daily Gain (ADG), Body Length (BL), Withers Height (WH), Heart Girth (HG), Rump Length (RL), Rump Height (RH) and Paunch Girth (PG) in sheep. The IGF1 gene influences growth traits of sheep and as such G855C, G857A, C271T and A91C SNPs might be used as potentially viable genetic indicators for the betterment of performance traits in sheep during breeding programs. Further studies have to confirm the validity of the identified SNPs of the IGF1 gene.

**Keywords:** Body Measurements, Candidate Gene, Polymorphism, Sheep, Systemic Review

## Introduction

Sheep production plays a vital role in meeting the subsistence requirements of rural populations, mostly in developing countries, through the production of milk, wool and meat and important income generation for farmers (Abousoliman *et al.*, 2020; Kumar *et al.*, 2023). In the livestock industry, molecular genetic advances have made allowance for the recognition of genes and sequence variations related to a number of growth traits (Kader Esen and Esen, 2023). There are many developments in molecular technologies including the identification of genetic diversity in genomic regions and the detection of the relationship

between genes and economic traits (Bayraktar and Shoshin, 2021). Economic traits such as growth and development are essential criteria for selection programs in sheep and are considered the most important (Bayraktar and Shoshin, 2021).

Profitability and production in the mutton industry are influenced by meat productivity which is greatly influenced by growth traits such as average daily gain, body size and body weight (Ding *et al.*, 2022). Ding *et al.* (2022) defined Insulin-like Growth Factor 1 (IGF1) as a growth factor endocrine that is involved in animal growth, as well as the metabolism and development of the fetus. The IGF1 is majorly involved in the animal growth processes and as a result contributes to the improved

output of meat and regulation of somatic cell growth in response to the dietary circumstances (Kumar *et al.*, 2023). IGF1 is vital for cellular growth and regulation of metabolism (Al Qasimi *et al.*, 2019). Therefore, it is regarded as a key candidate gene for a lot of the economic and productive traits in sheep (Al Qasimi *et al.*, 2019; Abousoliman *et al.*, 2020; Bayraktar and Shoshin, 2021).

Several studies, Al Qasimi *et al.* (2019), Bayraktar and Shoshin (2021), Ding *et al.* (2022); Kumar *et al.* (2023) investigated the genetic polymorphisms of IGF1 gene in sheep and their relationship with growth traits. According to Ding *et al.* (2022), in order to evaluate genetic betterment and breeding in sheep, research must be conducted on the identification of genetic variations that are related to growth traits in sheep. There must be establishment of improvement schemes that depend on genetic information aimed at facilitating of selection of breeding stock in order to improve the economically important traits (Abousoliman *et al.*, 2020). Even though some studies have discussed the relationship between IGF1 and growth traits, no conclusive information about the effect of the IGF1 gene on the growth traits of sheep. Therefore, systematically reviewing the research outcomes will add knowledge on the use of IGF1 as the important candidate gene for productive and economic traits in sheep. Thus, this study will add knowledge on the use of IGF1 as one of the candidate genes for performance traits in sheep.

## Materials and Methods

### Eligibility Criteria

Components of the research question known as Identification of Population, Exposure and Outcomes (POE) as explained by Bettany-Saltikov (2010) performed before conducting the study. The population was explained as “sheep”, with the exposure to “polymorphisms” and outcomes of “growth traits /morphological traits/biometric traits/morphometric/body conformation”. A preliminary search of the people on the PubMed database was conducted before deciding to conduct the systematic review.

### Literature Search

The search for publications was performed using search engines such as PubMed, web of Science, google scholar and Science Direct up to August 14, 2023. The following keywords were made use of: ‘IGF1’, ‘polymorphisms/genetic variations’, ‘growth traits/morphological traits/biometric traits/morphometric/ body conformation’ and ‘sheep’.

### Inclusion Criteria

The eligibility of all the acquired articles was set to the extent where the following inclusions were fulfilled by the

studies: (1) The IGF1 gene under investigation; (2) The polymorphisms of the IGF1 gene; (3) Sheep species.

### Exclusion Criteria

The criteria for exclusion involved: (1) Duplicated records; (2) Lacking the association of IGF1 polymorphisms to growth traits/morphological traits/biometric traits/morphometric/body conformation; (3) Studies that inferred association without association analysis with growth traits/morphological traits/biometric traits/morphometric/body conformation.

### Data Extraction

The contents extracted from the articles include the name of the 1<sup>st</sup> author, the year of publication, country, breed, population size, growth traits and observed genotypes.

### Ethical Considerations

Ethical issues including informed consent, similarity, misconduct, data falsification and fabrication were considered by all authors.

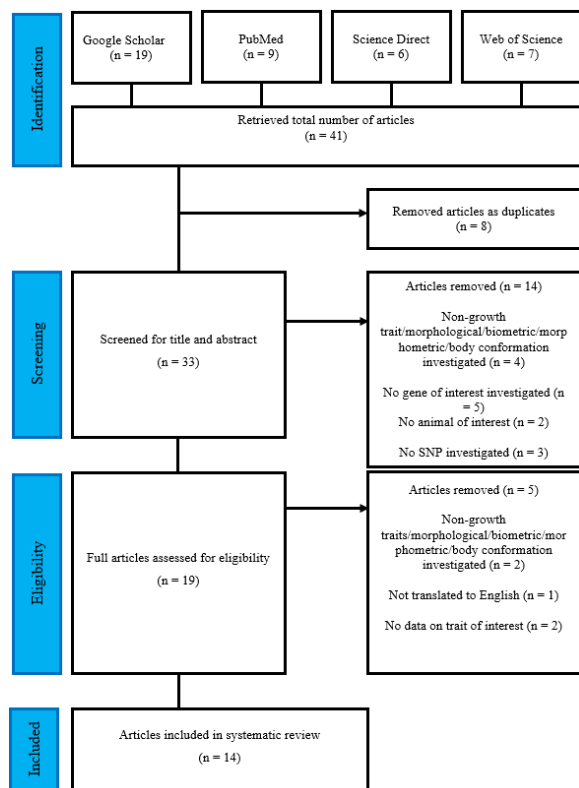
## Results

### Search Results

The articles retrieved for the systematic review amounted to a total of forty-one (n = 41) from the following databases: Google scholar (n = 19), PubMed (n = 9), science direct (n = 6) and web of science (n = 7). The duplicates (n = 8) between the search databases were removed and the remaining were analyzed for inclusion and exclusion criteria. The remaining articles (n = 33) were screened for their title and abstract and the fourteen articles were excluded, followed by the screening of the whole article search which excluded five articles for a total remainder of fourteen (n = 14) articles. The systematic review included a total number of 14 articles (Fig. 1).

### Characteristics of Included Studies

About fourteen (n = 14) studies of the forty-one analyzed were retained and included in the literature review (Table 1). All authors had one (n = 1) article in each of the 18 included studies. The retained articles had a range from the year 2014-2023. Studies were from 13 different countries. The number of animals used ranged from 15-848, with 35.718%, (n = 5), of studies ranging from 100-200 animals. The included articles all investigate the IGF1 association with traits in sheep with the Barki breed probing most, being investigated in 11.11% of the included studies. Polymerase Chain Reaction-Restricted Fragment Length Polymorphism (PCR-RFLP) was the most genotyping method used, with 50% of the studies that were included.



**Fig. 1:** Study selection flow diagram

BWt, birth weight; ADG, average daily gain; ADG1, average daily gain from birth to one month; ADG1w, average daily gain from one month to weaning; ADGw,

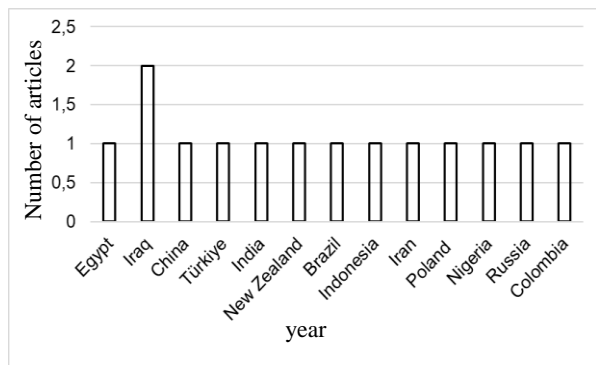
average daily gain from birth to weaning; ADG5, average daily gain at five months; ADGpw, average daily gain post-weaning; ADG6, average daily gain from birth to six months; ADGw6, average daily gain from weaning to six months; WW, weaning weight; BW, body weight; BW1, birth weight at one month; BW5, body weight at five months; BW6, body weight at six months; BW7, body weight at seven months; BW12, body weight at one year; BL, body length; BLb, body length at birth; BLw, body length at weaning; BL6 body length at six months; BH, body height; HG, heart girth; HGb, heart girth at birth; HGw, heart girth at weaning; HG6, heart girth at six months; RH, rump height; RHb, rump height at birth; RHw, rump height at weaning; RH6, rump height at six months; RW, rump width; RL, rump length; WH, withers height; WHb, withers height at birth; WHw, withers height at weaning; WH6, withers height at six months; PG, paunch girth; PGb, paunch girth at birth; PGw, paunch girth at weaning; PG6, paunch girth at six months; PCR, polymerase chain reaction; SSCP, single strand conformation polymorphism; RFLP, restriction fragment length polymorphism.

### Publication by Country

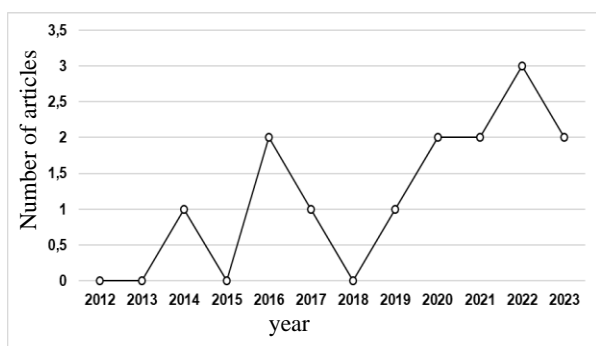
Figure 2 displays the publication by country of the included studies. The results indicated that fourteen studies were published in different countries worldwide. These studies were from thirteen different countries. No country had more than two articles, there were two articles in Iraq (Al Qasimi *et al.*, 2019; Bayraktar and Shoshin, 2021) and 12 countries (China; Egypt; Iran; India; Türkiye; New Zealand; Brazil; Indonesia; Poland; Nigeria; Russia; Colombia) had one study each out of 14 studies.

**Table 1.** General characteristics of the included studies of the review

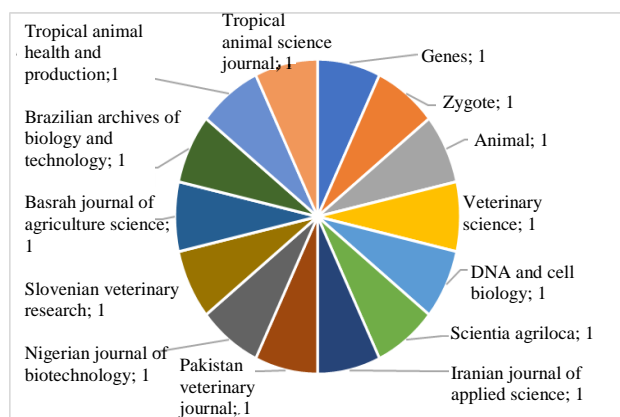
Author	Year	Country	Breed	N	Trait	Genotypic method
Abousoleman <i>et al.</i> (2020)	2020	Egypt	Barki	251	BWt, WW, ADG	PCR Assay
Al Qasimi <i>et al.</i> (2019)	2019	Iraq	Awassi	68	BWt, BL, WH, RH, HG, AC, BW6, GRbw, GRB6, GRw6	PCR Assay
Bayraktar and Shoshin (2021)	2021	Iraq	Hamdani	65	BWt, WW, BW6, ADGw, ADG6, ADGw, ADGw9, ADG9, BHW,	PCR-RFLP
Ding <i>et al.</i> (2022)	2022	China	Hulun buir	229	BH9, BLw, BL9, HGw, HG9	PCR-RFLP
Kader Esen and Esen (2023)	2023	Türkiye	German blackhead Mutton × Kivircik, Hampshire own x merino, Kivircik, Karacabey Merino and ramlic	202	BWt, WW, BW6, BW9, BW12, BL, BkH, RH, WH, HG, CBP	PCR-SSCP
Kumar <i>et al.</i> (2023)	2023	India	Munjal	50	BWt, WW, BW6, BW, BL, BH, HG, PG	PCR-RFLP
Li <i>et al.</i> (2021)	2021	New Zealand	NZ Romney	848	BWt, ADGw	PCR-SSCP
Machado <i>et al.</i> (2021)	2021	Brazil	Santa Inês	192	WH, RH, BL, HG, ADG, WW, BW6, RW, CW	PCR-SSCP
Malewa and Awaluddin (2022)	2022	Indonesia	Palu	60	BW, WH, BL, RH	PCR-RFLP
Nazari <i>et al.</i> (2016)	2016	Iran	Zandi	120	BWt, BW5, ADG5	PCR-RFLP
Proskura and Szewczuk (2014)	2014	Poland	Pomeranian coarsewool	100	BWt, BW1, WW, ADG1, ADGbw, ADG1w	PCR-RFLP
Raji <i>et al.</i> (2017)	2017	Nigeria	Balami, uda and Yankasa	150	BW, BL, HG, WH	PCR-RFLP
Trukhachev <i>et al.</i> (2016)	2016	Russia	Soviet merino	15	BW, WH, RH, RL, RW	emPCR HGVS
Valencia <i>et al.</i> (2022)	2022	Colombia	OPC	142	BWt, WW, ADG, BW, BW6, ADG6	PCR-SSCP



**Fig. 2:** Publication by country



**Fig. 3:** Publication by year



**Fig. 4:** Distribution of articles by journal

### Publication by Year

Figure 3 indicates the publication by year of included studies ( $n = 14$ ). The findings showed that included studies were published from the year 2014-2023. The majority of the studies were published in 2022 with three articles out of 14 (Ding *et al.*, 2022; Malewa and Awaluddin, 2022; Valencia *et al.*, 2022), 3 years (2016; 2020; 2021;

2023) included two studies each out of 14 and four years (2014; 2017; 2019) included one study each out of 14.

### Distribution of Articles by Journal

Figure 4 indicates the publication by the journal of included articles. The findings showed that included articles were published in different journals worldwide including Animals, Basrah journal of agricultural sciences, Basrah journal agricultural sciences, Brazilian Archives of biology and Technology, genes, veterinary sciences, zygote, DNA and cell biology, scientia agriloca, tropical animal science journal, Iranian journal of applied animal science, Pakistan veterinary journal, Nigerian journal of biotechnology, Slovenian veterinary research and tropical animal health and production. Each journal contributed 7% to the 14 included studies.

### Identified Single Nucleotide Polymorphisms (SNPs) and Targeted Genomic Regions

The identified SNPs as well as their genomic regions are presented in Table 2. The findings showed that 6 out of 14 reviewed articles identified the SNPs and their targeted regions. The results revealed that the total number of SNPs identified was 26 in 28 targeted genomic regions. About 12 (46.16%) out of 26 identified SNPs were found on Intron variant regions. A total of 5 articles (62.5%) out of the 8 found SNPs on exon 1. The results indicated that there were no similar SNPs identified from the included articles.

### Genotypic Frequencies

All the reviewed articles detailed the genotypic frequencies as presented in Table 3. A total of 96 discovered genotypes were recognized throughout the included articles. Out of 10 reviewed articles, there were 32 genotypic frequencies associated with the identified SNPs. The results indicated that out of 32 identified genotypes, 20 (68.75%) of them identified 3 genotypes per SNP, whereas 10 (31.25%) SNPs found 2 genotypes per SNP. The genotypic frequencies of the included articles ranged from 0.016-0.984, with Ding *et al.* (2022) showing the highest genotypic frequency (0.940) and the lowest genotypic frequency (0.016).

### Allelic Frequencies

The allele frequencies of the included articles are detailed in Table 4. A total of 74 discovered alleles were observed throughout all the included articles. The results showed that 12 out of 14 collected reviewed articles were clear about allelic frequencies, whereas 10 were not. The lowest (0.008) and highest allelic frequency (0.992) were observed in Ding *et al.* (2022).

**Table 2:** SNPs and genomic region

Author	Breed	N	Region	SNP
Abousoliman <i>et al.</i> (2020)	Barki	251	Exon 3	N/A
Bayraktar and Shoshin (2021)	Hamdani	65	5' regulatory region	N/A
Ding <i>et al.</i> (2022)	Hulun Buir	229	Exon 2 Exon 2 Exon 5	144G>A 150T>C 495G>A
Kader Esen and Esen (2023)	German blackhead mutton x Kivircik, hampshire own x merino, kivircik, karacabey merino and ramlic	202	Exon 1	N/A
Kumar <i>et al.</i> , 2023	Munjhal	50	5' flanking region 5' flanking region	855G>C 857G>A
Li <i>et al.</i> (2021)	New Zealand romney	848	5' flanking region Exon 3 Exon 4	153T>C
Machado <i>et al.</i> (2021)	Santa Inês	192	Intron 1	171110428C > T
Malewa and Awaluddin (2022)	Palu	60	5' flanking region	N/A
Nazari <i>et al.</i> (2016)	Zandi	120	Exon 1	N/A
Proskura and Szewczuk (2014)	Pomeranian coarsewool	100	Exon 3	271C>T
Raji <i>et al.</i> (2017)	Balami, uda and yankasa	150	Exon 1	N/A
Trukhachev <i>et al.</i> (2016)	Soviet merino	15	Upstream gene variant, Upstream gene variant, 5'UTR variant, 5' UTR variant, Intron variant, Intron variant, Intron variant, synonymous variant, intron variant, Intron variant, intron variant, intron variant, Intron variant, intron variant, intron variant, Intron variant, intron variant, UTR variant 3 prime	-5412A>G, -5363C>T, -5188G>C, -5186G>A, -4088G>A, -4032G>A, -91A>C, 81T>C, 151+199G>A, 151+463A>C, 152-159G>A, 152-47C>A, 333+7C>T, 333+88T>C, 333+164C>T, 333+259T>A, 333+435A>G, *72C>G
Valencia <i>et al.</i> (2022)	OPC	142	Exon 1	N/A

N: Sample size, N/A: Not available

**Table 3:** Genotypic frequencies

Author	Breed	N	Genotypic frequency
Abousoliman <i>et al.</i> (2020)	Barki	251	GG (0.47), AG (0.43), AA (0.10) GG (0.51), AG (0.39), AA (0.10)
Bayraktar and Shoshin (2021)	Hamdani	65	AA (0.71), AB (0.15), BB (0.14)
Ding <i>et al.</i> (2022)	Hulun Buir	229	AA (0.984), AB (0.016) AA (0.49), AB (0.436), BB (0.074) AA (0.646), AB (0.329), BB (0.025)
Kumar <i>et al.</i> (2023)	Munjhal	50	AA (0.26), GA (0.66), GG (0.08)
Malewa and Awaluddin (2022)	Palu	60	CC (0.10), GC (0.68), GG (0.22)
Nazari <i>et al.</i> (2016)	Zandi	120	AA (28.33), AB (37.50), BB (34.17)
Proskura and Szewczuk (2014)	Pomeranian coarsewool	100	CC (0.05), CT (0.31), TT (0.64)
Raji <i>et al.</i> (2017)	Balami	50	AA (0.33), AB (0.56), BB (0.11)
	Uda	50	AA (0.21), AB (0.29), BB (0.50)
	Yankasa	50	AA (0.21), AB (0.46), BB (0.33)
Trukhachev <i>et al.</i> (2016)	Soviet merino	15	TT (0.83), TC (0.07), CC (0.13) GG (0.8), GA (0.2) CC (0.73), CG (0.27) CC (0.73), CT (0.27) CC (0.8), CT (0.2) CC (0.93), CT (0.07) TT (0.47), TG (0.47), GG (0.06) AA (0.20), AG (0.60), GG (0.20) CC (0.40), CT (0.60)

**Table 3:** Continue

			TT (0.87), TG (0.13) CC (0.67), CT (0.27), TT (0.06) GG (0.67), GT (0.27), TT (0.06) GG (0.73), GA (0.20), AA (0.07) AA (0.73), AG (0.20), GG (0.07) GG (0.80), GA (0.13), AA (0.07) AA (0.73), AT (0.27) TT (0.73), TC (0.20), CC (0.07) GG (0.93), GC (0.07) AA (0.36), AG (0.15), GG (0.49)
Valencia <i>et al.</i> (2022)	OPC	142	

N: Sample size

**Table 4:** Allelic frequencies

Author	Breed	N	Allelic frequencies
Abousoliman <i>et al.</i> (2020)	Barki	251	G (0.69) A (0.31) G (0.70) A (0.30)
Bayraktar and Shoshin (2021)	Hamdani	65	A (0.79) B (0.21)
Ding <i>et al.</i> (2022)	Hulun Buir	229	A (0.992) B (0.008) A (0.708) B (0.292) A (0.811) B (0.189)
Kumar <i>et al.</i> (2023)	Munjal	50	A (0.59) G (0.41)
Li <i>et al.</i> (2021)	NZ Romney	848	A (0.04) B (0.956) A (0.472) B (0.528) A (0.144) B (0.856)
Malewa and Awaluddin (2022)	Palu	60	C (0.44) G (0.56)
Nazari <i>et al.</i> (2016)	Zandi	120	A (47.08) B (52.92)
Proskura and Szweczuk (2014)	Pomeranian coarse wool	100	C (0.205) T (0.795)
Raji <i>et al.</i> (2017)	Balami	50	A (0.61) B (0.39)
	Uda	50	A (0.36) B (0.64)
	Yankasa	50	A (0.44) B (0.56)
	Rampur-Bushair	N/A	A (0.59) B (0.41)
Trukhachev <i>et al.</i> (2016)	Soviet Merino	15	T (0.83), C (0.17) G (0.9), A (0.1) C (0.87), G (0.13) C (0.87), G (0.13) C (0.9), T (0.1) C (0.97), T (0.03) T (0.7), G (0.30) A (0.5), G (0.5) C (0.7), T (0.3) T (0.93), G (0.07) C (0.80), T (0.20) G (0.80), T (0.20) G (0.83), A (0.17) A (0.83), G (0.17) G (0.87), A (0.13) A (0.87), T (0.13) T (0.83), C (0.17) G (0.97), C (0.03) A (0.44) G (0.56)
Valencia <i>et al.</i> (2022)	OPC	142	

N: Sample size, N/A: Not available

*Single Nucleotide Polymorphisms (SNPs) and their Associations with Growth Traits*

The SNPs and their relationship with growth traits are presented in Table 5. The results showed that 14 included articles studied 11 growth traits including BWt, BW, WW, BL, RH, HG, WH, RL, BH, PG and ADG and their association with genotypes of the identified SNPs. Out of a total of 14 included articles, 6 articles observed a significant difference between identified genotypes of the IGF1 gene identified SNPs in more than one growth trait. Reviewed articles showed a significant relationship between identified genotypes and traits. Six out of 14 articles observed a significant relationship between genotypes and BW followed by WW in 4 articles and HG in 3 articles. Birth weight, ADG, WH, PG and RH showed significant ( $p < 0.05$ ) associations in 2 articles. A significant association was observed in one article each for RL and BL.

BWt, birth weight; WW, weaning weight; ADG, average daily gain; ADG1, average daily gain from birth

to one month; ADG1w, average daily gain from one month to weaning; ADGw, average daily gain from birth to weaning; ADG5, average daily gain at five months; ADGpw, average daily gain post-weaning; ADG6, average daily gain from birth to six months; ADGw6, average daily gain from weaning to six months; BW, body weight; BW1, birth weight at one month; BW5, body weight at five months; BW6, body weight at six months; BW7, body weight at seven months; BW12, body weight at one year; BL, body length; BLb, body length at birth; BLw, body length at weaning, BL6 body length at six months; BH, body height; HG, heart girth; HGb, heart girth at birth; HGw, heart girth at weaning; HG6, heart girth at six months; RH, rump height; RHb, rump height at birth; RHw, rump height at weaning; RH6, rump height at six months; RW, rump width; RL, rump length; WH, withers height; WHb, withers height at birth; WHw, withers height at weaning; WH6, withers height at six months; PG, paunch girth; PGb, paunch girth at birth; PGw, paunch girth at weaning; PG6, paunch girth at six months.

**Table 5:** Single nucleotide polymorphisms (SNPs) and their associations with growth traits

Author	Breed	Growth traits	Genotypes			Significance
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Abousoliman <i>et al.</i> (2020)	Barki	BWt	GG	AG	AA	ns
		WW	GG	AG	AA	ns
		ADG	GG	AG	AA	ns
Al Qasimi <i>et al.</i> (2019)	Awassi	BWt	AG	CC	GC	ns
		BLb	AG	CC	GC	ns
		WHb	AG	CC	GC	ns
		RHb	AG	CC	GC	ns
		HGb	AG	CC	GC	ns
		PGb	AG	CC	GC	ns
		BWw	AG	CC	GC	*
		BLw	AG	CC	GC	ns
		WHw	AG	CC	GC	*
		RHw	AG	CC	GC	*
		HGw	AG	CC	GC	ns
		PGw	AG	CC	GC	*
		ADGw	AG	CC	GC	*
		BW6	AG	CC	GC	*
		BL6	AG	CC	GC	ns
WH6	AG	CC	GC	ns		
RH6	AG	CC	GC	ns		
HG6	AG	CC	GC	*		
PG6	AG	CC	GC	*		
ADGw6	AG	CC	GC	*		
ADG6	AG	CC	GC	*		
Bayraktar and Shoshin (2021)	Hamdani	BWt	AA	AB	BB	*
		WW	AA	AB	BB	*
		BW6	AA	AB	BB	*
		ADGw	AA	AB	BB	ns
		ADG6	AA	AB	BB	*
Kumar <i>et al.</i> (2023)		BWt	GG	GA	AA	ns
		WW	GG	GA	AA	*
		BW6	GG	GA	AA	*

**Table 5:** Continue

		BWy	GG	GA	AA	*
		BL	GG	GA	AA	ns
		BH	GG	GA	AA	ns
		HG	GG	GA	AA	*
		PG	GG	GA	AA	*
Li <i>et al.</i> (2021)	NZ Romney	BWt	AA	AB	BB	ns
		ADGw	AA	AB	BB	ns
Malewa and Awaluddin (2022)	Palu	BW	CC	GC	GG	ns
		BL	CC	GC	GG	ns
		WH	CC	GC	GG	ns
Nazari <i>et al.</i> (2016)	Iranian zandi	RH	CC	GC	GG	ns
		BWt	AA	AB	BB	ns
		BW5	AA	AB	BB	ns
		ADG5	AA	AB	BB	ns
Proskura and Szewczuk (2014)	Pomeranian coarse wool	Bwt	CC	CT	TT	*
		BW1	CC	CT	TT	*
		WW	CC	CT	TT	*
		ADG1	CC	CT	TT	*
		ADG1w	CC	CT	TT	*
		ADGw	CC	CT	TT	*
Raji <i>et al.</i> (2017)	Balami	BW	AA	AB	BB	*
		BL	AA	AB	BB	*
		HG	AA	AB	BB	*
		WH	AA	AB	BB	ns
	Yankasa	BW	AA	AB	BB	ns
		BL	AA	AB	BB	ns
		HG	AA	AB	BB	ns
		WH	AA	AB	BB	*
	Uda	BW	AA	AB	BB	ns
		BL	AA	AB	BB	ns
		HG	AA	AB	BB	ns
Trukhachev <i>et al.</i> (2016)	Russian	WH	AA	AB	BB	ns
		BW	CC	CT		*
		WH	CC	CT		ns
		HG	CC	CT		ns
		RH	CC	CT		ns
		RL	CC	CT		ns
		RW	CC	CT		ns
		BW	TT	TG	GG	*
		WH	TT	TG	GG	*
		HG	TT	TG	GG	ns
		RH	TT	TG	GG	*
		RL	TT	TG	GG	*
		RW	TT	TG	GG	*
Valencia <i>et al.</i> (2022)	Colombian hair	BWt	AA	AG	GG	ns
		WW4	AA	AG	GG	ns
		BW7	AA	AG	GG	ns
		ADGw	AA	AG	GG	ns
		ADGpw	AA	AG	GG	ns

\*- Significant at  $p < 0.05$ , ns non-significant

## Discussion

The associations of the IGF1 gene with cell differentiation, embryogenesis, metabolism, reproduction and fetal development make it a key candidate gene for a lot of the economic and productive traits in sheep (Abousoliman *et al.*, 2020). This systematic review was conducted to establish the impact of the IGF1 gene on the

performance traits in sheep. According to Ding *et al.* (2022), to improve sheep growth performance, genetic polymorphisms of the IGF1 gene and their associations with growth traits require investigation. The results of this systematic review indicated that out of 14 articles reviewed, there were 26 different Single Nucleotide Polymorphisms (SNPs) found with the Intron variant region being the most targeted region of the 28 targeted



genomic regions. Al Qasimi *et al.* (2019) discovered an unidentified SNP that was associated with BW, WH, RH, PG and ADG at weaning as well as association with BW, HG, PG and ADG at six months in Awassi sheep. Bayraktar and Shoshin (2021) also reported unidentified SNP in the 5' regulatory region that was associated with BWt, WW, BW6 and ADG6 in Hamdani sheep. Unidentified SNP in a study by Raji *et al.* (2017) indicated a relationship with BW, BL and HG in Balami sheep and an association with WH in Yankasa sheep. Four SNPs, C5363T, G5188C, G5186C and G4088A, were associated with BW in the study by Trukhachev *et al.* (2016) in Soviet Merino sheep. The study found an association between SNP A91C in the Intron variant and BW, WH, RH, RL and RW. Kumar *et al.* (2023) revealed that two SNPs; G855C and G857A in the 5' flanking region were associated with WW, BW6, BWy, HG and PG in Munjal sheep. Proskura and Szewczuk (2014) discovered that SNP C271T in exon 3 was associated with BWT, BW1, WW, ADG1, ADG1w and ADGw in Pomeranian Coarse wool sheep. Studies by Abousoliman *et al.* (2020) in Barki sheep, Ding *et al.* (2022) in Hulun Buir sheep, Kader Esen and Esen (2023) in German Blackhead mutton x Kivircik, Hampshire own x Merino, Kivircik, Karacabey Merino and Ramlic sheep, Li *et al.* (2021) in New Zealand Romney sheep, Machado *et al.* (2021) in Santa Inês sheep, Malewa and Awaluddin (2022) in Palu sheep, Nazari *et al.* (2016) in Zandi sheep and Valencia *et al.* (2022) in OPC sheep found no relationship between SNPs that were identified and the growth traits. The contribution of this systematic review to the body of knowledge is that there are four identified SNPs (G855C, G857A, C271T and A91C) that are associated with growth traits in sheep. These SNPs are found in different genomic regions, namely, the 5' flanking region, Exon 3 and intron variant. Based on our knowledge, this is the first systematic review reporting on the association between SNPs of the IGF1 gene in sheep and growth traits. Therefore, there were no comparisons of the other systematic review findings in this field. The limitations of this systematic review are that (1) Some articles did not disclose the identified SNPs and their relationship with production traits and (2) The identified SNPs in the included articles are not similar which makes it not possible to do a meta-analysis. It is concluded that the IGF1 gene of sheep influences BW, WW, ADG, BW, BL, HG, WH, RH, RL, RW and PG. Therefore G855C, G857A, C271T and A91C might be utilized as potential molecular indicators favorable to the genetic improvement of growth traits during sheep breeding.

## Conclusion

The IGF1 gene has an effect on the growth traits of sheep and as such, G855C, G857A, C271T and A91C SNPs might be used as potentially viable genetic

indicators for the betterment of growth traits in sheep during breeding programs.

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## Author's Contributions

All authors equally contributed to this study.

## Ethics

Ethical issues including similarities, informed consent, misconduct, data falsification and fabrication were regarded by all the authors.

## Conflict of Interest

The authors declared that there is no conflict of interest.

## Data Availability

All data generated during the course of this study are available from the corresponding author through a request.

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