

Review Article

A Systematic Review of Single Nucleotide Polymorphisms of Caprine Pituitary Transcription Factor 1 Gene and their Association with Economic Important Traits

Masixole Maswana¹, Dikeledi Petunia Malatji¹ and Thobela Louis Tyasi^{2*}

¹Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Florida, South Africa.

²Department of Agricultural Economics and Animal Production, School of Agricultural and Environmental Sciences, University of Limpopo, Sovenga, South Africa.

ABSTRACT

The pituitary transcription factor 1 (POU1F1) plays a crucial role in the transactivation of genes responsible for prolactin, growth hormone, and thyroid-stimulating hormone production. Traditional goat breeding methods have primarily emphasized external characteristics ignoring the internal gene information resulting in that external expression, whereas contemporary techniques utilize marker-assisted selection, which focuses on identifying candidate genes, responsible. To date, there has been no comprehensive review addressing single nucleotide polymorphisms (SNPs) within the *POU1F1* gene in goats. This systematic review aims to investigate the SNPs present in the *POU1F1* gene and to elucidate their relationships with important goat traits. A thorough evaluation of four databases such as Google Scholar, PubMed, ScienceDirect, and Web of Science yielded twelve eligible studies using the search key words. From the reviewed literature, a total of 85 SNPs were identified, with 32 resulting from the T > G transition and 19 from the T > C transition. Among the twelve articles included in this review, 83 % of articles reported associations between their identified SNPs and traits such as cashmere production, litter size, and milk yield, while only 16 % articles did not find any associations. The findings of this study indicate that the SNPs in the *POU1F1* gene are significantly linked to economically important traits in goats. Therefore, *POU1F1* gene might be used as a candidate gene for economically important traits of goats during breeding.

Article Information

Received 20 January 2025

Revised 05 June 2025

Accepted 20 June 2025

Available online 20 February 2026 (early access)

Published 20 June 2026

Authors' Contribution

MM and TLT initial development and designing of the study. MM drafted the initial version of the manuscript. DPM and TLY revised the article. All authors reviewed and approved the final version of the manuscript.

Key words

Goats, Candidate gene, Meat traits, Growth traits, Milk yield, Litter size

INTRODUCTION

The pituitary transcription factor 1 (POU1F1) is a POU-homeo domain transcription factor that is specific to the pituitary gland (Zhang *et al.*, 2019). It is instrumental in the differentiation and proliferation of the lactotroph, somatotroph, and thyrotroph lineages, as well as in the transactivation of the genes for prolactin (*PRL*), growth hormone (*GH*), and the beta subunit of thyroid-stimulating

hormone (*TSHb*) (Zhang *et al.*, 2019). The goat (*Capra hircus*) is recognized as the most prolific of the domesticated ruminants. Its proficiency in surviving within low-input production systems and its adaptability to harsh environmental conditions contribute to its popularity among a wide array of farmers (Olasege *et al.*, 2020).

Conventional approaches to the selection of breeding goats are often inadequate, as breeders primarily rely on phenotypic assessments (Zhu *et al.*, 2019). In contemporary practices, genomic selection employs a comprehensive array of single nucleotide polymorphisms markers that span the entire genome to calculate genomic estimated breeding values (Zhu *et al.*, 2019). To adequately respond to the needs of an ever-growing human population, it is crucial to emphasize high-production breeds. Presently, marker-assisted selection, which entails the selection of candidate genes, is regarded as a precise and efficient technique for advancing the economic traits of livestock (Zhang *et al.*, 2019).

* Corresponding author: louis.tyasi@ul.ac.za
0030-9923/2026/0004-1927 \$ 9.00/0



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This review aids in the identification of single nucleotide polymorphisms as genetic markers and examines their impact on economically significant traits in goat production. Currently, no systematic reviews have been conducted on single nucleotide polymorphisms within the *POU1F1* gene of goats. The objective of this systematic review was to examine single nucleotide polymorphisms found in the *POU1F1* gene and to gain a comprehensive understanding of their correlation with goat traits considered significant in diverse countries. This research seeks to enhance the understanding of genetic markers of *POU1F1* gene in goats and their effect on traits of economic importance. The information will provide the current trend of *POU1F1* gene for goat breeding.

MATERIALS AND METHODS

Eligibility criteria

In accordance with the framework established by Bettany-Saltikov (2010), the identification of the population, exposure, and outcomes (PEO) components relevant to the research question was conducted prior to the systematic review. The population was specified as “goats,” the exposure was identified as “polymorphisms,” and the outcomes were defined as “traits of economic importance.” A preliminary search of these PEO components was performed on the Google Scholar database before the decision to undertake the systematic review.

Literature search

All the authors performed a systematic search for research publications using the databases of Google Scholar, PubMed, ScienceDirect, and Web of Science, with the search period extending from 16 July to October 28, 2024. The keywords employed in this search included: Single nucleotide polymorphisms or polymorphisms or genetic polymorphisms or genetic effects or genetic diversity and pituitary specific transcription factor-1 or *POU1F1* - *POU1F1* - *Pit1* or *Pit-1* and goats or *Capra hircus*.

The criteria for the eligibility of all selected articles were established based on the following requirements: (1) the studies must investigate the *POU1F1* gene; (2) they should encompass the polymorphisms associated with any traits of economic importance; and (3) they must involve the species of interest, specifically goats.

The exclusion criteria consisted of (1) duplicate records; (2) studies that did not provide evidence linking *POU1F1* polymorphisms to economically important traits in goats; and (3) research that inferred associations without conducting an association analysis concerning goat traits.

A total of five hundred and ten ($n = 510$) articles were initially retrieved, as illustrated in [Supplementary Figure 1](#). The search was conducted across four databases: Google Scholar ($n = 245$), PubMed ($n = 12$), ScienceDirect ($n = 216$), and Web of Science ($n = 37$). After removing one hundred duplicates, the remaining number of articles for screening was four hundred and ten ($n = 410$). From this pool, three hundred and eighty-six articles were excluded due to their titles not aligning with the research topic of interest. Subsequently, twenty-one articles were screened for their abstracts, resulting in the removal of two articles due to insufficient information. This left nineteen articles ($n = 19$) for eligibility assessment, of which seven ($n = 7$) were excluded after a full-text review, culminating in a final selection of twelve articles for inclusion in this systematic review.

Data extraction

Content extraction was performed independently by the authors. The extracted information from the articles consists of the first author's name, the year of publication, the country, the species, the breed, the population size, and the observed genotypes.

RESULTS

Characterization of included articles

[Table 1](#) presents the characteristics of the articles included for this systematic review. The results showed that all the articles included ($n = 12$) studied *POU1F1* polymorphisms in different traits. Specifically, five articles were related to milk production ([Lan et al., 2008, 2015; Daga et al., 2012; Zhou et al., 2016; Isik and Bilgen, 2019](#)), four articles pertained to cashmere ([Lan et al., 2008, 2009; Li et al., 2016](#)), four articles were linked to litter size ([Feng et al., 2011; Zhang et al., 2019; Zhu et al., 2019; Olasege et al., 2020](#)) two articles focused on growth ([Zhang et al., 2019; Zhu et al., 2019](#)) and one article was associated with meat ([Lan et al., 2008](#)). For population size used, the results indicated that three publications used population (sample sizes) $N > 500$ ([Lan et al., 2008; Li et al., 2016; Zhang et al., 2019; Zhu et al., 2019](#)).

The year 2019 recorded the highest number of published articles, 3 out of the twelve articles ([Isik and Bilgen, 2019; Zhang et al., 2019; Zhu et al., 2019](#)). Only two articles approved each in the year 2008 and 2016.

[Table 1](#) shows that China is the leading contributor, with a total of nine articles ($n = 9$) authored out of twelve included articles. In contrast, only a single article approved from each of the following countries: Turkey, Sardinia, and Nigeria.

Table I. General characteristics of studies included in the review.

Genotyping method	Trait	N	Breed	Country	Authors
PCR-RFLP	Cashmere	847	Inner Mongolia White Cashmere goats	China	Lan <i>et al.</i> , 2008a
PCR-RFLP	Meat, Cashmere and milk	394	Shaanbei white cashmere, Goat, Boer, Haimen goat and Xuhuai Goat/s	China	Lan <i>et al.</i> , 2008b
PCR-RFLP	Litter size	183	Jining grey, Guizhou White, Boer, Wendeng Dairy, and Liaoning Cashmere goat/s	China	Feng <i>et al.</i> , 2011
PCR-RFLP	Milk	349	Xinong Sannen, Guanzhong dairy, Laoshan, Leizhou, Guizhou black, Guizhou white, Banjiao and Matou goat/s	China	Lan <i>et al.</i> , 2015
PCR-RFLP	Cashmere	709	Nanjiang, Xinjiang, Shaanbei White, Boer goat, Haimen and Xuhuai goat/s	China	Li <i>et al.</i> , 2016
PCR-RFLP	Milk	235	Guanzhong goat/s	China	Zhou <i>et al.</i> , 2016
PCR-RFLP	Milk	108	Saanen	Turkey	Isik and Bilgen, 2019
PCR-RFLP	Litter size and growth	653	Shaanbei white cashmere goat/s	China	Zhang <i>et al.</i> , 2019
PCR-RFLP	Litter size and growth	609	SBWC goat/s	China	Zhu <i>et al.</i> , 2019
PCR-RFLP	Litter size	366	West African Dwarf, Kalahari red and Red Sokoto	Nigeria	Olasege <i>et al.</i> , 2020
PCR-SSCP	Cashmere	452	Inner Mongolia White Cashmere goat	China	Lan <i>et al.</i> , 2009
CR-SSCP	Milk	129	Sarda goat/s	Sardinia	Daga <i>et al.</i> , 2012

PCR, polymerase chain reaction; SSCP, single strand conformation polymorphism; RFLP, restriction fragment length polymorphism.

Figure 1 shows that ten articles (n = 10) out of the twelve articles used the PCR-RFLP method while only two articles (n = 2) used PCR-SSCP (Table I).

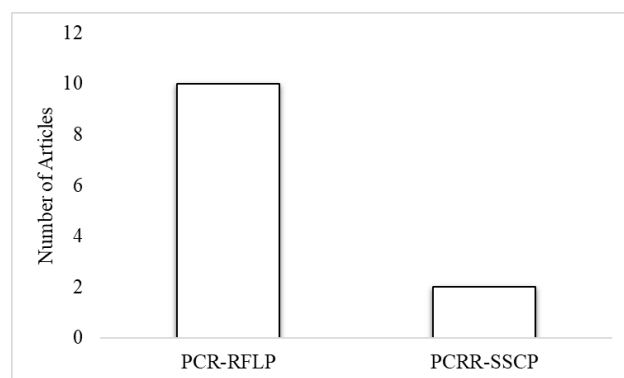


Fig. 1. Publication by genotyping method.

Identified SNPs and their positions

Table II shows presents the SNPs variations of the *POUIF1* gene along with their respective positions. All the included articles (n = 12) reported SNPs of *POUIF1* gene and their positions. A total of 85 SNPs were identified from the reviewed literature, with 32 occurring at the T > G transition, followed by 19 at the T > C transition. The position with the highest frequency of SNPs was position 102, which recorded 14 occurrences.

Table II shows that the genotypic frequencies of SNPs varied from 0.008 to 1.00 with the maximum value reported in three articles (Feng *et al.*, 2011; Lan *et al.*, 2015; Zhu *et al.*, 2019). A cumulative total of 134 alleles were identified in the reviewed articles. The lowest (0.024) and highest (1.00) frequency of alleles were identified in one article each (Lan *et al.*, 2009; Feng *et al.*, 2011).

All the included articles (n = 12) showed the ages of the used goats which ranged from two to five years. Three articles used goats that were two years old (Lan *et al.*, 2008; Lan *et al.*, 2009; Olasege *et al.*, 2021), while nine articles used animals that were older than two years (Fig. 2).

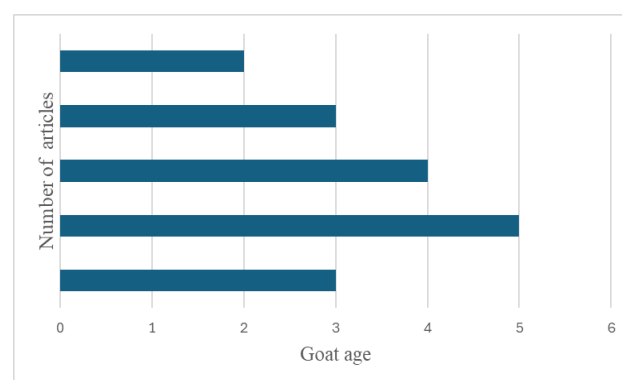


Fig. 2. The different goat ages used in the samples used by the articles.

Table II. Single nucleotide polymorphisms (SNPs), genotypic and allelic frequencies.

SNP	Region	Genotypic frequencies	Gene frequencies	Breed	Author
110 T>C	Exon 3	CT (0.041-0.959)		Inner Mongolia white Cashmere goats	Lan <i>et al.</i> , 2008a
102 T>G	Exon 6	TT/TC/CC (0.718/0.282/0.000)	T (0.859)	Shaanbei white cashmere goat	Lan <i>et al.</i> , 2008b
102 T>G	Exon 6	TT/TC/CC (0.952/0.048/0.00)	T (0.976)	Boer goat	Lan <i>et al.</i> , 2008b
102 T>G	Exon 6	TT/TC/CC (0.572/0.371/ 0.057)	T (0.757)	Xuhuai goats	Lan <i>et al.</i> , 2008b
102 T>G	Exon 6	TT/TC/CC (0.820/0.131/0.049)	T (0.885)	Haimen goat	Lan <i>et al.</i> , 2008b
+ 10 G > T	IVS	GG (0.409)	G (0.690), T (0.310)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
113 G> T	Exon 3	GG (0.847)	G (0.920), T (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
114 G> T	Exon 3	GG (0.847)	G (0.920), T (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
+ 8 C > T	IVS3	CC (0.847)	C (0.920), T (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
+ 41 T >G	IVS3	TT (0.847)	T (0.920), G (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
+41_ 42insT	IVS3	TT (0.847)	T (0.920), G (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
+ 175 T >A	IVS3	TT (0.847)	T (0.920), G (0.024)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
53 del A	Exon 4	AA (0.668)	A (0.834), (0.166)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
+ 710 T >A	IVS4	TT (0.774)	T (0.887), A (0.113)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
14 G>A	Exon 5	GG (0.774)	T (0.887), A (0.113)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
34 G>A	Exon 5	GG (0.774)	T (0.887), A (0.113)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
59 G>A	Exon 5	GG (0.774)	T (0.887), A (0.113)	Inner Mongolia white Cashmere goat	Lan <i>et al.</i> , 2009
256 C >T	Exon 3	CC (0.896) and CT (0.104)	C (0.948), T (0.052)	Jining grey goat	Feng <i>et al.</i> , 2011
53 T>C	Intron 3	CC (0.011), TC (0.415) and TT (0.57)	C (0.219), T (0.781)	Jining grey goat	Feng <i>et al.</i> , 2011
123 T>G	Intron 3	TT (0.574), TG (0.415) and GG (0.011)	T (0.781), G 0.219	Jining grey goat	Feng <i>et al.</i> , 2011
682 G>T	Exon 6	GG (0.914) and GT 0.086	G (0.957), T (0.043)	Jining grey goat	Feng <i>et al.</i> , 2011
723 T >G	Exon 6	TT (0.632), TG (0.331) and GG (0.037)	T (0.798), G (0.202)	Jining grey goat	Feng <i>et al.</i> , 2011
837 T >C	Exon 6	CC (0.242), CT (0.511) and TT (0.247)	C (0.497), T 0.503	Jining grey goat	Feng <i>et al.</i> , 2011
256 C >T	Exon 3	CC (0.967) and CT (0.033)	C (0.983), T (0.017)	Guizhou white goat	Feng <i>et al.</i> , 2011
53 C >T	Intron 3	TC (0.133) and TT (0.867)	C (0.067), T (0.933)	Guizhou white goat	Feng <i>et al.</i> , 2011
123 T>G	Intron 3	TT (0.867) and TG (0.133)	T (0.933), G (0.067)	Guizhou white goat	Feng <i>et al.</i> , 2011
682 G>T	Exon 6	GG (1.000)	G (1.000)	Guizhou white goat	Feng <i>et al.</i> , 2011
723 T >G	Exon 6	TT (0.712) and TG (0.288)	T (0.856), G (0.144)	Guizhou white goat	Feng <i>et al.</i> , 2011
837 T >C	Exon 6	CC (0.224), CT (0.569) and TT (0.207)	C (0.509), T (0.491)	Guizhou white goat	Feng <i>et al.</i> , 2011

Table continues on next page.....

SNP	Region	Genotypic frequencies	Gene frequencies	Breed	Author
256 C>T	Exon 3	CC (0.957) and CT (0.043)	C (0.978), T (0.022)	Boer goat	Feng <i>et al.</i> , 2011
53 C>T	Intron 3	TC (0.435), TC (0.304) and TT (0.261)	C (0.587), T (0.413)	Boer goat	Feng <i>et al.</i> , 2011
123 T>G	Intron 3	TT (0.261), TG (0.304) and GG (0.435)	T (0.413), G (0.587)	Boer goat	Feng <i>et al.</i> , 2011
682 G>T	Exon 6	GG (1.000)	G (1.000)	Boer goat	Feng <i>et al.</i> , 2011
723 T>G	Exon 6	TT (0.734), TG (0.133) and GG (0.133)	T (0.800), G (0.200)	Boer goat	Feng <i>et al.</i> , 2011
837 T>C	Exon 6	TT (1.000)	T (1.000)	Boer goat	Feng <i>et al.</i> , 2011
256 C>T	Exon 3	CC (1.000)	C (1.000)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
53 C>T	Intron 3	CC (0.146) TC (0.479) and TT (0.375)	C (0.385), T (0.615)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
123 T>G	Intron 3	TT (0.375), TG (0.479) GG (0.146)	T (0.615), G (0.385)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
682 G>T	Exon 6	GG (0.750) and GT (0.250)	G (0.875), T (0.125)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
723 T>G	Exon 6	TT (0.775), TG (0.125) and GG (0.100)	T (0.838), G (0.162)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
837 T>C	Exon 6	CC (0.064), CT (0.468) and TT (0.468)	C (0.298), T (0.702)	Wendeng dairy goats	Feng <i>et al.</i> , 2011
256 C>T	Exon 3	CC (0.896) and CT (0.104)	C (0.948), T (0.052)	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
53 T>C	Intron 3	CC (0.011), TC (0.415) and TT (0.57)	C (0.219), T (0.781)	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
123 T>G	Intron 3	TT (0.574), TG (0.415) and GG (0.011)	T (0.781), G 0.219	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
682 G>T	Exon 6	GG (0.914) and GT 0.086	G (0.957), T (0.043)	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
723 T>G	Exon 6	TT (0.632), TG (0.331) and GG (0.037)	T (0.798), G (0.202)	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
837 T>C	Exon 6	CC (0.242), CT (0.511) and TT (0.247)	C (0.497), T 0.503	Liaoning Cashmere goats	Feng <i>et al.</i> , 2011
61 G>C	Exon 1	GG (0.992) and GC (0.008)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
108 G>A	Exon 1	GG (0.016) and GA (98.4)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
42 C>T	Exon 3	CC (0.992) and CT (0.008)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
92 C>T	Exon 3	CC (0.705), CT (0.248) and TT (0.047)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
110 A>G	Exon 4	AA (0.729), AG (0.225) and GG (0.047)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
34G>A	Exon 5	GG (0.977) and GA (0.023)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
17 G>T	Exon 6	GG (0.713), GT (0.256) and TT (0.31)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
58 G>T	Exon 6	GG (0.550), GT (0.411) and TT (0.039)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
172 T>C	Exon 6	TT (0.891) and CT (0.109)	Not mentioned	Sarda goat	Daga <i>et al.</i> , 2012
102 T>G	Exon 6	D ₁ D ₁ (0.770), D ₁ D ₂ (0.230)	D ₁ (0.885)	Xinong Sannen dairy	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.200), D ₁ D ₂ (0.800)	D ₁ (0.600)	Guanzhong dairy	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.694), D ₁ D ₂ (0.306)	D ₁ (0.847)	Laoshan dairy	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (1.00)	D ₁ (1.00)	Leizho	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.455), D ₁ D ₂ (0.545)	D ₁ (0.727)	Guizhou black	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.840), D ₁ D ₂ (0.016)	D ₁ (0.920)	Guizhou white	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.355), D ₁ D ₂ (0.645)	D ₁ (0.706)	Banjiao	Lan <i>et al.</i> , 2015
102 T>G	Exon 6	D ₁ D ₁ (0.418), D ₁ D ₂ (0.588)	D ₁ (0.777)	Matou	Lan <i>et al.</i> , 2015
174 T>C	Exon 6	TT (0.336), TC (0.524), CC (0.030)	T (0.708), C (0.292)	Guanzhong goat/s	Zhou <i>et al.</i> , 2016
174 T>C	Exon 6	TT (0.716), TC (0.265), CC (0.019)	T (0.848), C (0.152)	Guanzhong goat/s	Zhou <i>et al.</i> , 2016
174 T>C	Exon 6	TT (0.953), TC (0.047),	T (0.977), C (0.023)	Guanzhong goat/s	Zhou <i>et al.</i> , 2016
102 T>G	Exon 6	P _{D₁D₁} (0.324), P _{D₁D₂} (0.514), P _{D₂D₂} (0.162)	D ₁ (0.561) D ₂ (0.419)	Nanjiang	Li <i>et al.</i> , 2016
102 T>G	Exon 6	P _{D₁D₁} (0.663), P _{D₁D₂} (0.262), P _{D₂D₂} (0.074)	D ₁ (0.794). D ₂ (0.206)	Xinjiang	Li <i>et al.</i> , 2016

Table continues on next page.....

SNP	Region	Genotypic frequencies	Gene frequencies	Breed	Author
102 T>G	Exon 6	P _{D₁D₁} (0.460) P _{D₁D₂} (0.140), P _{D₂D₂} (0.140)	D ₁ (0.660), D ₂ (0.340)	Shaanbei	Li <i>et al.</i> , 2016
102 T>G	Exon 6	P _{D₁D₁} (0.774), P _{D₁D₂} (0.226)	D ₁ (0.887), D ₂ (0.113)	Boer	Li <i>et al.</i> , 2016
102 T>G	Exon 6	P _{D₁D₁} (0.576), P _{D₁D₂} (0.333), P _{D₂D₂} (0.091)	D ₁ (0.758), D ₂ (0.242)	Haimen	Li <i>et al.</i> , 2016
102 T>G	Exon 6	P _{D₁D₁} (0.700), P _{D₁D₂} (0.300)	D ₁ (0.850), D ₂ (0.150)	Xuhuai	Li <i>et al.</i> , 2016
172 T>C	Exon 6	TT (0.494), TC (0.419) CC (0.087)	T (0.70), C (0.30)	Saanen	Isik and Bilgen, 2019
110 C>T	Exon 6	TT (0.648), TC (0.306) CC (0.037)	T (0.80), C (0.20)	Saanen	Isik and Bilgen, 2019
838 T>G	Exon 6	TT (0.933), TG (0.067),	T (0.966), G (0.034)	Shaanbei white cashmere	Zhang <i>et al.</i> , 2019
682 G>T	Exon 6	GG (0.884), GT (0.108), TT (0.008)	G (0.938), T (0.062)	Shaanbei white cashmere	Zhu <i>et al.</i> , 2019
723 T>G	Exon 6	TT (0.581), TG (0.371), GG (0.048)	T (0.767), C (0.233)	Shaanbei white cashmere	Zhu <i>et al.</i> , 2019
837 T>C	Exon 6	TT (0.750), TC (0.220), CC (0.030)	T (0.860), C (0.140)	Shaanbei white cashmere	Zhu <i>et al.</i> , 2019
876 + 110 T>C	Exon 6	TT (1.00)	T (1.00)	Shaanbei white cashmere	Zhu <i>et al.</i> , 2019
306 G>A	Intron 1	GG (0.01) GA (0.29) AA (0.70)	A (0.84), G (0.16)	West African Dwarf	Olasege <i>et al.</i> , 2020
306 G>A	Intron 1	GG (0.12) GA (0.31) AA (0.58)	A (0.73), G (0.27)	Red Sokoto	Olasege <i>et al.</i> , 2020
11236 C>T	Intron 3	CC (0.67) CT (0.28) TT (0.04)	C (0.81), T (0.19)	West African Dwarf	Olasege <i>et al.</i> , 2020
11236 C>T	Intron 3	CC (0.33) CT (0.41) TT (0.26)	C (0.54), T (0.46)	Red Sokoto	Olasege <i>et al.</i> , 2020
11236 C>T	Intron 3	CC (0.67), CT (0.23)	C (0.83), T (0.17)	Kalahari red	Olasege <i>et al.</i> , 2020

Sequences of the primers used, product size and annealing temperatures

Table III shows different primer sequences, product sizes, and the annealing temperatures. The primer sequence pair F: 5'-CCATCATCTCCCTTCTT-30 and R: 50-AATGTACAATGTGCCTTCTGAG-3' was used in two articles (Lan *et al.*, 2008), while different sequences were used by all other articles. The product size results indicated that the minimum size recorded was 106 bp in the research conducted by Feng *et al.* (2011) and the maximum size was 943 bp as indicated by Olasege *et al.* (2020). The annealing temperatures in these studies spanned from 50 °C being the lowest used in the article by Zhang *et al.* (2019) and the highest was 63 °C (Lan *et al.*, 2009).

Targeted genomic regions

The genomic regions associated with the polymorphisms of the *POU1F1* gene are shown in Figure 3. The results of all the twelve included articles showed the genomic regions that were located in the fifty-six experiments. Twenty-three experiments, derived from the 56 experiments identified the polymorphisms within exon 6, while eight experiments pinpointed their location to

intron 3. Additionally, only two experiments were found to occur in intron 1, both of which were part of the research conducted by Olasege *et al.* (2020).

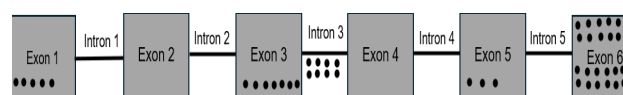


Fig. 3. Genomic regions of *POU1F1* gene. Black dots represent the experiments that located SNPs that genomic region.

SNPs of *POU1F1* gene and its association with traits

The associations between SNPs and various traits are comprehensively presented in Table IV. Out of twelve included articles, ten articles associated their identified SNPs with traits such as cashmere, litter size and milk yield, and only two articles did not associate their SNPs with any traits. The *POU1F1* genotype association was found to be statistically significant with cashmere traits in two articles (Lan *et al.*, 2008, 2009), also in three articles associations with milk yield were found (Lan *et al.*, 2015; Zhou *et al.*, 2016; Daga *et al.*, 2017) and then other three articles found association in litter size (Feng *et al.*, 2011; Zhang *et al.*, 2019; Zhu *et al.*, 2019).

Table III. Primer sequence, product size, amplified region and annealing temperature used in analyses of the goat *POU1F1* gene.

Primer sequence	Product position	Product size	Annealing temperature	Author
F: 5'-CCATCATCTCCCTTCTT-3' R: 5''- AATGTACAATGTGCCTTCTGAG-3''	Exon 6	450 bp	54.5 °C	Lan <i>et al.</i> , 2008
F: 5'-CCATCATCTCCCTTCTT-3'' R: 5''-AATGTACAATGTGCCTTCTGAG-3''	Exon 6	450 bp	54.5 °C	Lan <i>et al.</i> , 2008
F:5'-TGAAAGTAGAAACACTCGCTAT-3' R: 5'-GCAACTCATTCCCACAA-3'	5'-UTR	292 bp	52.0 °C	Lan <i>et al.</i> , 2009
F:5'-GATGAGTTGCCAACCTTTTAC-3' R:5'-CAAAGCACCCATCCTGAC-3'	Exon 1 and partial intron 1	204 bp	60 °C	Lan <i>et al.</i> , 2009
F: 5'-CTT ACC AGT CCC GTC TAT T-3' R: 5'-TTC TTA CCT GCC ATC ACG-3'	Exon 2 and partial 1 and 2	165 bp	51.3 °C	Lan <i>et al.</i> , 2009
F:5'-TTCTTGTTGTTACAGGGAGC-3' R: 5'-AAGGATAAGCAGAGGGA-3'	Exon 3 and partial intron 3	567 bp	54.0 °C	Lan <i>et al.</i> , 2009
F:5'-AGGATACACCCAGACAAATG-3' R:5'-TACTGATTGTTGTTCTCCGT-3'	Exon 4 and intron 4	326 bp	58.9 °C	Lan <i>et al.</i> , 2009
F: 5'-AGT GTA GCC AGA CCA TTC G-3' R:5'-TACTGATTGTTGTTCTCCGT-3'	Exon 5 and partial intron 4	455 bp	53.4 °C	Lan <i>et al.</i> , 2009
F:5'-CCTCTGTCCATGGGATTTTC-3' R: 5'-CCATCATCTCCCTTCTT-3'	Partial intron 5	341 bp	63.0 °C	Lan <i>et al.</i> , 2009
F: TGAAAGTAGAAACACTCGCTAT R: GCAACTCATTCCCACAA	Promoter region ^a	292 bp	52.0 °C	Feng <i>et al.</i> , 2011
F: ATGAGTTGCCAACCTTTTAC R: CAAAGCACCCATCCTGAC	Partial exon 1 and flanking	204 bp	55.0 °C	Feng <i>et al.</i> , 2011
F: CTTACCACTCCCGTCTATT R: TTCTTACCTGCCATCACG	Exon 2 and flanking	106 bp	53.0 °C	Feng <i>et al.</i> , 2011
F: TTCTTGTTGTTACAGGGAGC R: AAGGATAAGCAGAGGGA	Exon 3 and flanking	563 bp	55.0 °C	Feng <i>et al.</i> , 2011
F: AGGATACACCCAGACAAATG R: CACTTTCGCTGGCCTTGC	Exon 4 and flanking	343 bp	62.0 °C	Feng <i>et al.</i> , 2011
F: AGTGTAGCCAGACCATTCG R: CTGATTGTTGTTCTCCGT	Exon 5 and flanking	455 bp	60.0 °C	Feng <i>et al.</i> , 2011
F: CCATCATCTCCCTTCTT R: AATGTACAATGTGCCTTCTGAG	Partial exon 6 and flanking	450 bp	54.0 °C	Feng <i>et al.</i> , 2011
F: 5'-CCATCATCTCCCTTCTT-3' R: 5'-AATGTACAATGTGCCTTCTGAG-3'	Exon 6	450 bp	54.5 °C	Lan <i>et al.</i> , 2015
F: 5'-CCATCATCTCCCTTCTT-3' R: 5'-AATGTACAATGTGCCTTCTGAG-3'	Exon 6	450 bp	54.5 °C	Li <i>et al.</i> , 2016
F: 5'-CCATCATCTCCCTTCTT-3' R: 5'-AATGTACAATGTGCCTTCTGAG-3'	Exon 3 and partial intron 3	450 bp	54.0 °C	Zhou <i>et al.</i> , 2016
F:5'-ATGTGGTCTGGGATGGATG-3' R:5'-CTGGTGAAGGTTTGGGTTAG-3'	Exon 4 and intron 4	414 bp	58.9 °C	Zhou <i>et al.</i> , 2016
F:5'-CCAAGCGTGAGACAGAATAC-3' R:5'-AGGAGGGATAGGAGCAAGTT-3'	Exon 5 and partial intron 4	655 bp	53.4 °C	Zhou <i>et al.</i> , 2016
F:5'-CCATCATCTCCCTTCTT-3' R:5'-AATGTACAATGTGCCTTCTGAG-3'	Exon 6	450 bp	54.0 °C	Isik and Bilgen 2019

Table continues on next page.....

Primer sequence	Product position	Product size	Annealing temperature	Author
F:5'-AGGAGCCTACATGAGACAAGC-3' R: 5'-AATGTACAATATGCCTTCTGAG-3'	partial intron 5 and whole exon 6	600 bp	50.0 °C	Zhang <i>et al.</i> , 2019
F:5'-CGATCATCTCCCTTCTT-3' R: 5'-AATGTACAATATGCCTTCTGAG-3'	Exon 6 and 3'UTR.	450 bp	54.0 °C	Zhu <i>et al.</i> , 2010
TTGCCTTCATTCCCTACCCA	Promoter region and exon 1	837 bp	58.62 °C	Alasege <i>et al.</i> , 2020
ACGAATGTGTCTTGAATCCTCAT	Exon 2 + introns	493 bp	58.93 °C	Alasege <i>et al.</i> , 2020
GCTTCAGAAAACCGAATGTC	Exon 3 + introns	943 bp	59.50 °C	Alasege <i>et al.</i> , 2020
TGAATGGCAGATGTTCTATCTG	Exon 4 + introns	682 bp	58.29 °C	Alasege <i>et al.</i> , 2020
GGAAACGGAGAACAATATC	Exon 5 + introns	802 bp	57.52 °C	Alasege <i>et al.</i> , 2020
GCTTGAAGGTGTTTGCAGA	Exon 6 + introns	788 bp	59.89 °C	Alasege <i>et al.</i> , 2020

Table IV. Association between *POU1F1* gene SNPs and traits.

Traits	Breed	SNP	Genotypes				Significant	Authors
Cashmere	Inner Mongolia white Cashmere goats	110 T>C	TT	TC	-	*		Lan <i>et al.</i> , 2008
Cashmere	Inner Mongolia white Cashmere goats	113 G>T	GG	GH	-	*		Lan <i>et al.</i> , 2009
Milk yield	Sarda goat	61 G>C	GG	GA	-	ns		Daga <i>et al.</i> , 2012
		108 G>A	GG	GC	-	ns		
		42 C>T	CC	CT	-	ns		
		92 C>T	CC	CT	-	*		
		110 A>G	AA	AG	-	*		
		34 G>A	GG	GA	-	ns		
		17 G>T	GG	GT	-	ns		
		58 G>T	GG	GT	-	ns		
		172 T>C	TT	CT	-	ns		
Milk yield	Xinong Sannen dairy	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		Lan <i>et al.</i> , 2015
	Guanzhong dairy	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		
	Laoshan dairy	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		
	Leizho	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		
	Guizhou black	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		
	Guizhou	102 T>G	D ₁ D ₁	D ₁ D ₂	-	*		
	White							
	Banjiao							
Milk yield	Matou							Zhou <i>et al.</i> , 2016
	Gauzhong goat	174 T>C	TT	TC	-	*		
Litter size	Shaanbei white cashmere	682 G>T	GG	GT	TT	ns		Zhu <i>et al.</i> , 2019
		723 T>G	TT	TG	GG	ns		
		837 T>C	TT	TC	CC	*		
Growth traits	Shaanbei white cashmere	838 T>G	TT	TG	-	*		Zhang <i>et al.</i> , 2019
Milk yield	Sannen	172 T>C	TT	TC	CC	*		Isik and Billgen 2019
Growth		172 T>C	TT	TC	CC	ns		
Litter size	West African Dwarf	306 G>A	GG	GA	AA	ns		Alasege <i>et al.</i> , 2020
	Red Sokoto	11236C>T	GG	GA	AA	ns		
	West African Dwarf		CC	CT	TT	ns		
	Red Sokoto		CC	CT	-	ns		
	Kalahari Red		TT	CC	CT	ns		

DISCUSSION

Comprising six exons and five introns, the *POU1F1*

gene encodes a protein that is 291 amino acids in length and variations in this gene have been correlated with traits that hold considerable economic importance in the field of

livestock production (Olasege et al., 2020). The objective of this systematic review was to review articles that identified single nucleotide polymorphisms (SNPs) in the *POUIF1* gene and their association with traits of economic importance in goats. During this systematic review, twelve articles were identified and the majority of them were originating from China (n = 9) and most (25%) of them were published in 2019 (Isik and Bilgen, 2019; Zhang et al., 2019; Zhu et al., 2019), while the least of them were published in 2009, 2011, 2012, 2015 and 2020 (8 %) (Lan et al., 2009, 2015; Feng et al., 2011; Daga et al., 2012; Olasege et al., 2020). Approximately thirty-three SNPs in the *POUIF1* gene were discovered through the experiments detailed in the twelve reviewed articles, with the majority situated in exon 6 (n = 23), followed by a smaller number in intron 3 (n = 8). The genotypes of the identified SNPs were found to influence cashmere production, litter size, and milk yield and the greater emphasis on milk yield was observed in four articles (Daga et al., 2012; Lan et al., 2015; Zhou et al., 2016; Isik and Bilgen, 2019). The goat milk has superior benefits over the milk of other species in relation to various parameters, highlighting its particular significance for human nutrition and food security (Zhou et al., 2016). The systematic review confirms the influence of *POUIF1* gene on goat traits of economic importance. Based on authors' knowledge, there is not systematic review of SNPs in the *POUIF1* gene for the comparison of the present results. The strength of this review is to showcase the limitations of literature around the SNPs of *POUIF1* in traits of economic important in goats. The review contributes to the identification of SNPs as genetic markers and their influence in traits of economic importance in goat production. Among the reviewed literature, only a single study represents the African continent (Olasege et al., 2020), which makes it difficult to conclude for the continent. The systematic review suggests that there is insufficient evidence on SNPs of *POUIF1* gene and their effects on traits of economic importance of goats for meta-analysis. It is recommended that African continent conduct studies in SNPs of *POUIF1* gene in goats and their association with traits of economic importance in the African context.

CONCLUSION

This study concludes that single nucleotide polymorphisms of the *POUIF1* gene were located at more than three regions and were found to be associated significantly with traits of economic importance in goats coming from different countries. A further conclusion is that exon 6 is the mostly identified region where *POUIF1* gene polymorphism occurs.

DECLARATIONS

Acknowledgement

The authors wish to express their gratitude to Tutimomo Farm for supplying the tools necessary for the formulation of this research, as well as to the University of South Africa for granting the permission to conduct the study.

Funding

Funding was provided by University of South Africa Doctoral bursary 2025 and TUTIMOMO Farm Continuous Development.

Ethical considerations

The authors examined a range of ethical issues, specifically focusing on plagiarism, misconduct, informed consent, data falsification, and fabrication.

Supplementary material

There is supplementary material associated with this article. Access the material online at: <https://dx.doi.org/10.17582/journal.pjz/20250120133106>

Statement of conflict of interest

The authors have declared no conflict of interest.

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