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Mapping Global Research on Reproductive Traits and Molecular Genetics in Small Ruminants: A Bibliometric Study

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Abstract. *Research on the reproductive traits and molecular genetics of small ruminants has grown quickly, yet the field still lacks a quantitative overview of how it has developed. This study applied bibliometric analysis to map the publication dynamics, influential contributors, and thematic structure of the field. A total of 1,312 journal articles published from 2015 to 2025 were retrieved from Scopus and analysed with R-bibliometrix (Biblioshiny) and VOSviewer 1.6.20. The corpus involved 4,570 authors and 308 journals, grew at a compound annual growth rate of 12.49%, and averaged 11.96 citations per document. China produced 48.09% of the articles (n = 631), whereas the United Kingdom showed the highest citation efficiency (21.50 citations per article). The leading journals were* Animals *(MDPI) and* Theriogenology *(Elsevier), and the most influential author was Mingxing Chu (local h-index = 21; 1,221 citations). Cui et al. (2018) received the most citations (TC = 117), while Ruiz-González et al. (2015) reached the highest normalized impact (NTC = 5.07; citations divided by the mean citations of corpus articles published in the same year), reflecting sustained interest in functional markers and maternal–embryo signalling. Keyword co-occurrence revealed three clusters: classical genetics and physiology, transcriptomic regulation including non-coding RNAs, and litter size genomics. Potential gaps suggested by the keyword structure and the literature are inconsistent validation of major fecundity genes (*BMPR1B, BMP15, GDF9*) in tropical breeds, scarce multi-omics integration, and limited attention to male reproductive genomics. These findings offer an evidence base for setting research priorities in small ruminant reproductive genomics. Because only Scopus-indexed, English-language articles were analysed, research published in regional journals and in developing countries may be under-represented.*

Keywords: *Bibliometric analysis, Litter size, Molecular markers, Reproductive genomics, VOSviewer*

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INTRODUCTION

Goats (*Capra hircus*) and sheep (*Ovis aries*) supply meat, milk, fibre, and skins to millions of smallholder households in Africa, Asia, and Latin America. Their tolerance of heat stress and of arid or marginal land allows them to remain productive where larger ruminants perform poorly (Joy et al., 2020). As demand for animal-source food rises with population growth, improving the productive efficiency of small ruminant flocks has become a priority for scientists and policymakers (Sargison, 2020).

Reproductive performance is one of the strongest determinants of this efficiency because it governs flock replacement, the intensity of selection, and farm income. Litter size, fertility, ovulation rate, and age at puberty vary widely within and between breeds, yet most of these traits have low heritability, are expressed in only one sex, and are recorded late in life, so phenotypic selection and crossbreeding have delivered slow progress (Notter, 2012). Breeders have therefore turned to molecular information that reveals the genes behind reproductive performance and allows earlier, more accurate selection (Eggen, 2012).

Over the past decade, falling sequencing costs and improved reference genome assemblies have made such molecular studies far more accessible (Goodwin et al., 2016; Davenport et al., 2022). The literature on small ruminant reproductive genetics has consequently expanded and diversified, covering candidate genes, genome-wide association, transcriptomics, and non-coding RNAs across many breeds and tissues. Yet no global synthesis exists, so the trajectory of the field, its key contributors, and its open questions remain unclear. Bibliometric analysis addresses this by quantifying publication output, citation impact, collaboration, and thematic structure reproducibly (Donthu et al., 2021).

Bibliometric studies in neighbouring areas have had a different scope. Banchi et al. (2022) mapped reproduction research in dogs and cats, Vazquez-Avendaño et al. (2023) examined a single reproductive biotechnology, somatic cell nuclear transfer in sheep, and Martins et al. (2024) mapped genotype × environment interaction across production animals; all three relied on the Web of Science. To our knowledge, no bibliometric study has yet combined reproductive traits with molecular genetic approaches across both sheep and goats, or used such a map to derive research priorities for tropical countries, where many smallholder flocks depend on locally adapted breeds. The novelty of this study

therefore lies in (i) a reproducible, Scopus-based map of this intersection for 2015–2025 that complements the Web of Science-based analyses above, and (ii) research priorities derived from that map for breeding programmes in tropical countries.

This study therefore maps global research on reproductive traits and molecular genetics in small ruminants published between 2015 and 2025 by answering six research questions (RQs): (RQ1) How did publication output develop over this period? (RQ2) Which articles had the greatest citation impact? (RQ3) Which journals were the most productive? (RQ4) Which countries contributed most? (RQ5) Who were the most influential authors? (RQ6) What are the dominant topics and remaining research gaps? The results are intended to guide researchers, funders, and breeding programmes, particularly in tropical countries such as Indonesia, toward evidence-based priorities.

LITERATURE REVIEW

Prolificacy in sheep and goats depends on a few genes of large effect together with many loci of small effect. The best-known major genes, *BMPR1B* (*FecB*), *BMP15* (*FecX*), and *GDF9*, belong to the transforming growth factor-β (TGF-β) superfamily and carry mutations that raise ovulation rate and litter size in several prolific breeds (Notter, 2012). Beyond this pathway, a review of goat studies lists further candidates for litter size, such as *AMH*, *KITLG*, *PRLR*, *KISS1*, and SMAD family genes (W. Chen et al., 2025). The effects of these genes are not always consistent across populations, so validation in local breeds is an essential step before they are used in selection (Budiyanto et al., 2023).

Methods for studying these traits have changed considerably: quantitative trait loci (QTL) mapping and candidate-gene studies were followed by single nucleotide polymorphism (SNP) arrays, genome-wide association studies (GWAS), and next-generation sequencing (NGS), which now allow genome-wide scans at steadily falling cost (Goodwin et al., 2016). Marker choice has also diversified: insertion/deletion (InDel) polymorphisms remain attractive because they can be genotyped with simple PCR assays (Vignal et al., 2002), whereas genomic selection uses thousands of markers simultaneously and has become a new breeding paradigm (Eggen, 2012). More recently, RNA sequencing has shifted attention from DNA variants to the regulation of gene expression, including the roles of microRNAs and long non-coding RNAs in the ovary (Miao et al., 2016). Because such technological shifts can change both the volume of

publications and the studies that attract citations, they provide the context for interpreting publication growth (RQ1) and citation impact (RQ2).

These developments make three topics particularly important for tropical production systems. First, validation in tropical and indigenous breeds is a priority because the frequency and effect of fecundity mutations differ between populations, so a marker that is useful in one breed cannot be assumed to work in another (Notter, 2012; Budiyanto et al., 2023). Second, multi-omics integration is needed because single-locus associations explain only part of the genetic variation in prolificacy, whereas transcriptomic studies show that microRNAs and long non-coding RNAs regulate ovarian function (Miao et al., 2016; Yousuf et al., 2025); combining genomic, transcriptomic, and epigenomic layers is required to move from associated markers to causal mechanisms (Cao, 2026). Third, male reproductive genomics deserves attention because a single ram or buck mates many females, so its fertility affects the reproductive output of the whole flock, and major prolificacy genes have also been shown to influence sperm biology (Zhang et al., 2025). Whether these topics are reflected in the literature is examined through the keyword analysis (RQ6).

Bibliometrics applies quantitative techniques to publication records to describe how a research field is structured and how it evolves. Its two main components are performance analysis, which measures the productivity and impact of authors, journals, and countries, and science mapping, which reveals the conceptual and social structure of a field through citation, collaboration, and keyword co-occurrence networks (Donthu et al., 2021; Zupic & Čater, 2015). Indicators such as the h-index summarise both the quantity and the citation impact of a researcher's output (Hirsch, 2005), while software such as bibliometrix and VOSviewer makes these analyses reproducible. In this study, performance analysis is used to answer RQ1–RQ5, and science mapping through keyword co-occurrence is used to answer RQ6. Nevertheless, no bibliometric study has yet focused on the intersection of reproductive traits and molecular genetics in small ruminants, which is the gap addressed here.

RESEARCH METHODS

Data Source and Search Strategy

Scopus was used as the data source because of its broad and curated coverage, which is evaluated by an independent Content Selection and Advisory Board (Baas et al.,

2020). The query combined three blocks of terms, joined internally with OR and linked to each other with AND, in titles, abstracts, and keywords (Table 1) and was limited to English-language journal articles published from 2015 to 2025. The blocks covered (i) both sheep and goats (small ruminant*, sheep, goat*, caprine, and ovine); (ii) the reproductive traits examined (reproductive trait*, fertility, fecundity, prolificacy, lambing interval, kidding, estrous cycle, sexual maturity, breeding season, reproductive performance, and litter size); and (iii) molecular genetic approaches (molecular genetic*, genomic*, DNA marker*, SNP, gene expression, quantitative trait loci, QTL, and GWAS). These filters were applied within Scopus, and all retrieved records were exported with full bibliographic information and cited references. Because all records came from one database and each carried a unique Scopus EID, no cross-database duplicates could arise. No additional title–abstract relevance screening was performed, so the corpus includes a few articles in which reproduction is a secondary topic (e.g., Guo et al., 2016; Bérénos et al., 2016); this is acknowledged as a limitation. The search, run on 1 June 2026, returned 1,312 articles.

Table 1. Search string used in the Scopus database (complete query as executed on 1 June 2026; the OR-linked terms of each block are enclosed in parentheses, and the three blocks are combined with AND)

Database	Search string
Scopus	(TITLE-ABS-KEY (small ruminant*) OR TITLE-ABS-KEY (sheep) OR TITLE-ABS-KEY (goat*) OR TITLE-ABS-KEY (caprine) OR TITLE-ABS-KEY (ovine)) AND (TITLE-ABS-KEY (reproductive trait*) OR TITLE-ABS-KEY (fertility) OR TITLE-ABS-KEY (fecundity) OR TITLE-ABS-KEY (prolificacy) OR TITLE-ABS-KEY (lambing interval) OR TITLE-ABS-KEY (kidding) OR TITLE-ABS-KEY (estrous cycle) OR TITLE-ABS-KEY (sexual maturity) OR TITLE-ABS-KEY (breeding season) OR TITLE-ABS-KEY (reproductive performance) OR TITLE-ABS-KEY (litter size)) AND (TITLE-ABS-KEY (molecular genetic*) OR TITLE-ABS-KEY (genomic*) OR TITLE-ABS-KEY (DNA marker*) OR TITLE-ABS-KEY (SNP) OR TITLE-ABS-KEY (gene expression) OR TITLE-ABS-KEY (quantitative trait loci) OR TITLE-ABS-KEY (QTL) OR TITLE-ABS-KEY (GWAS)) AND PUBYEAR > 2014 AND PUBYEAR < 2026 AND (LIMIT-TO (SRCTYPE , "j")) AND (LIMIT-TO (DOCTYPE , "ar")) AND (LIMIT-TO (LANGUAGE , "English"))

Data Analysis

Performance indicators were computed with the bibliometrix R package version 14.5.1 through Biblioshiny: annual growth rate, total citations (TC), normalized total citations (NTC), journal and country productivity, and the local h-, g-, and m-indices of authors within the corpus. The annual growth rate (AGR) is the compound annual growth

rate, AGR = $[(N_{2025}/N_{2015})^{1/10} - 1] \times 100$, where N_{2015} and N_{2025} are the numbers of articles published in 2015 and 2025, respectively. NTC divides the citations of an article by the mean citations of corpus articles from the same year, so that older and newer papers can be compared fairly. All citation counts are those recorded in Scopus on the search date. The h-index is the largest number h such that h of an author's articles have at least h citations each (Hirsch, 2005); the g-index is the largest number g such that the g most cited articles together have at least g^2 citations (Egghe, 2006); and the m-index is the h-index divided by the number of years from the author's first article in the corpus up to 2026, the year of analysis (Hirsch, 2005). These author indices are local because they are computed only from the authors' articles in the corpus and the Scopus citation counts of those articles, and Scopus Author Identifiers are reported to distinguish authors with similar names. Each article was assigned to the country of its corresponding author, so that country counts do not overlap. VOSviewer 1.6.20 was used to map keyword co-occurrence clusters and to overlay the average publication year of each keyword. The co-occurrence map used all keywords (author keywords and Scopus index keywords) with full counting; after generic indexing terms without topical meaning (e.g., "female", "animal", and "nonhuman") were excluded, 61 keywords were retained. Links were normalized by association strength, and clustering used the default settings (resolution 1.00; minimum cluster size 1), which produced three clusters of 28, 24, and 9 keywords. Synonyms and singular and plural variants were not merged, so terms such as "goat" and "goats" appear as separate nodes. In the overlay map, each keyword is coloured by the average publication year of the articles in which it occurs. Journal h-index, SCImago Journal Rank (SJR), and quartile values were taken from SCImago for the 2025 reference year (SJR 2025), using each journal's best quartile across its subject categories.

RESULTS AND DISCUSSION

1. Publication Trends and Growth (2015–2025)

The corpus comprises 1,312 articles in 308 journals, with a compound annual growth rate of 12.49% (Table 2; formula in the Data Analysis section), which exceeds long-term estimates of the growth of science as a whole (Bornmann & Mutz, 2015). Output rose gradually until 2018 (fewer than 75 articles per year), accelerated to almost 170 articles in 2022, dipped slightly in 2023, and peaked at nearly 190 articles in 2025 (Figure 1). The acceleration after 2018 coincides with cheaper NGS and better sheep

reference genomes (Archibald et al., 2010; Davenport et al., 2022). Only 8 articles had a single author, reflecting the resource-intensive and multidisciplinary nature of livestock molecular genetics (Eggen, 2012), and the average document age of 4.79 years shows that the field is still young.

Table 2. Main information on the analysed dataset

Description	Result	Description	Result
Timespan	2015–2025	Annual growth rate	12.49%
Journals	308	Document average age (years)	4.79
Documents	1,312	Average citations per document	11.96
Authors	4,570	References	157,040
Single-authored documents	8	Author's keywords	2,726

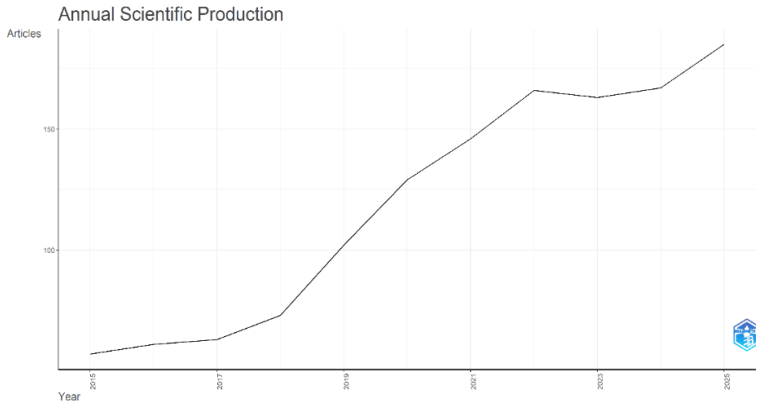


Figure 1. Annual scientific production, 2015–2025 (number of articles per publication year in the Scopus corpus, n = 1,312; generated with Biblioshiny)

2. Citation Impact of Published Articles

Table 3 ranks the ten most cited articles. Cui et al. (2018) led with 117 citations for an InDel in *KDM6A* associated with litter size in goats. After normalisation, Ruiz-González et al. (2015) had the highest impact (NTC = 5.07), reflecting lasting interest in pregnancy recognition in ewes, in which uterine exosomes, endogenous retroviruses, and toll-like receptors interact at a stage critical for embryo survival.

Table 3. Ten most cited articles on reproductive traits and molecular genetics in small ruminants

Reference	Article title	Journal	TC	NTC
Cui et al. (2018)	Insertion/Deletion Within the KDM6A Gene Is Significantly Associated With Litter Size in Goat	Frontiers in Genetics	117	4.79
Ruiz-González et al. (2015)	Exosomes, endogenous retroviruses and toll-like receptors: pregnancy recognition in ewes	Reproduction	111	5.07
Xu et al. (2018)	Genome-Wide Association Analyses Highlight the Potential for Different Genetic Mechanisms for Litter Size Among Sheep Breeds	Frontiers in Genetics	107	4.38
Feng et al. (2018)	Genome-wide differential expression profiling of mRNAs and lncRNAs associated with prolificacy in Hu sheep	Bioscience Reports	89	3.64
Wang et al. (2019)	Two strongly linked single nucleotide polymorphisms (Q320P and V397I) in GDF9 gene are associated with litter size in cashmere goats	Theriogenology	89	4.31
Miao et al. (2016)	Ovarian transcriptomic study reveals the differential regulation of miRNAs and lncRNAs related to fecundity in different sheep	Scientific Reports	79	3.49
Guo et al. (2016)	Possible mechanisms of host resistance to Haemonchus contortus infection in sheep breeds native to the Canary Islands	Scientific Reports	78	3.45
Bérénos et al. (2016)	Genomic analysis reveals depression due to both individual and maternal inbreeding in a free-living mammal population	Molecular Ecology	76	3.36
H. Y. Chen et al. (2015)	Differential Gene Expression in Ovaries of Qira Black Sheep and Hetian Sheep Using RNA-Seq Technique	PLOS ONE	72	3.29
Yang et al. (2021)	Melatonin promotes male reproductive performance and increases testosterone synthesis in mammalian Leydig cells	Biology of Reproduction	71	4.64

Note: TC: total citations; NTC: normalized total citations (TC divided by the mean TC of corpus articles published in the same year); citation counts as recorded in Scopus on 1 June 2026

Most other highly cited studies address the genomic basis of prolificacy. Xu et al. (2018) showed by GWAS that litter size is controlled by different mechanisms in different sheep breeds, and Wang et al. (2019) associated two linked *GDF9* SNPs with litter size in cashmere goats. Ovarian RNA sequencing studies (H. Y. Chen et al., 2015; Feng et al., 2018; Miao et al., 2016) identified long non-coding RNAs (lncRNAs) and microRNAs (miRNAs) involved in folliculogenesis, signalling a move from static DNA markers toward gene regulation, while Yang et al. (2021) (NTC = 4.64) extended attention to male reproduction through the effect of melatonin on testosterone synthesis. Studies on parasite resistance (Guo et al., 2016) and inbreeding depression (Bérénos et al., 2016) show that reproduction is often examined together with health and population genetics.

3. Most Productive Journals

Animals (MDPI; 102 articles) and *Theriogenology* (Elsevier; 83) were the most productive journals, while the other eight published 31–44 articles each (Table 4). The lead of *Animals* is consistent with its open-access model and fast editorial process; MDPI titles process manuscripts considerably faster than other large publishers yet remain embedded in international citation networks (Márquez-Bustos et al., 2026). *Theriogenology* (h-index 160) and *Animal Reproduction Science* (Q1) form the specialised core of reproductive science, whereas genomics journals such as *BMC Genomics*, *Frontiers in Genetics*, and the *International Journal of Molecular Sciences* (highest SJR, 1.316) reflect the shift toward marker-based selection (Eggen, 2012).

Table 4. Ten most productive journals on reproductive traits and molecular genetics in small ruminants

Journal	Publisher	h-index	SJR (Quartile)	Articles
Animals	MDPI	114	0.722 (Q1)	102
Theriogenology	Elsevier	160	0.780 (Q1)	83
Animal Biotechnology	Taylor & Francis	44	0.500 (Q2)	44
Animal Reproduction Science	Elsevier	129	0.697 (Q1)	39
BMC Genomics	Springer Nature (BMC)	218	0.985 (Q1)	38
Genes	MDPI	119	0.823 (Q2)	38
Reproduction in Domestic Animals	Wiley-Blackwell	89	0.471 (Q2)	37
Frontiers in Genetics	Frontiers Media	147	0.833 (Q2)	35
Frontiers in Veterinary Science	Frontiers Media	101	0.753 (Q1)	35
International Journal of Molecular Sciences	MDPI	365	1.316 (Q1)	31

Note: h-index, SJR, and quartile values were obtained from SCImago for the 2025 reference year (SJR 2025); quartiles are each journal's best quartile across its subject categories

4. Country-Level Contribution and Productivity

China dominated with 631 articles (48.09%) and 7,973 citations, far ahead of India (72 articles) and Iran (65) (Table 5). This concentration is consistent with China's position as the largest producer and consumer of sheep and goat meat, where breeding goals have shifted from wool to meat and hence toward reproductive efficiency (Wang et al., 2024). However, bibliometric data alone cannot show that these production priorities drive research output, and other factors, such as national research funding and the size of the research community, may also contribute. Iraq, Turkey, and Egypt were also active, which is consistent with the importance of small ruminants in hot and marginal environments (Joy et al., 2020). Although less productive, the United Kingdom (21.50

citations per article) and the USA (17.70) had the highest citation efficiency. This is a descriptive result: citations per article are sensitive to a few highly cited papers when output is small (14 articles for the United Kingdom), and the indicator alone does not explain research performance. One possible but untested explanation is their central role in sheep genome resources: the Roslin Institute led the initial reference genome strategy of the International Sheep Genomics Consortium (Archibald et al., 2010) and later worked with US institutions on an improved assembly (Davenport et al., 2022). Indonesia produced 15 articles with 3.27 citations per article, which may reflect a reliance on partial DNA sequence markers, as in phylogenetic studies of local goats (Lestari et al., 2018), rather than on GWAS or whole-genome resequencing.

Table 5. Fifteen most productive countries

Country	Art.	%	TC	CPA	Country	Art.	%	TC	CPA
China	631	48.09	7,973	12.64	Egypt	26	1.98	228	8.77
India	72	5.49	659	9.15	France	22	1.68	344	15.64
Iran	65	4.95	632	9.72	Brazil	21	1.60	177	8.43
USA	47	3.58	832	17.70	Poland	18	1.37	154	8.56
Italy	39	2.97	421	10.79	Indonesia	15	1.14	49	3.27
Iraq	36	2.74	253	7.03	Australia	14	1.07	201	14.36
Turkey	34	2.59	193	5.68	United Kingdom	14	1.07	301	21.50
Spain	33	2.52	478	14.48					

Note: Art.: number of articles; %: share of the 1,312 articles; TC: total citations; CPA: average citations per article. Each article was assigned to the country of its corresponding author; citation counts as recorded in Scopus on 1 June 2026

5. Most Influential Authors

Mingxing Chu leads on almost every local indicator (h-index 21; 1,221 citations; 103 articles), followed by Xiaoyun He and Chuanying Pan (h-index 18) and Xianyong Lan (17) (Table 6). All ten authors are based in China and mostly belong to two overlapping groups: the Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (IAS-CAAS; Chu, He, Di, Liu, and Xiangyu Wang) and Northwest A&F University (Lan and Pan). Chu is the senior author of a series of IAS-CAAS studies on fecundity genes, for example in Small Tail Han ewes with different *FecB* genotypes (Tang et al., 2018). Pan and Lan have higher g-indices (31 and 30) than Chu (27), indicating a few exceptionally well-cited papers, in line with their low-cost InDel markers such as that in *KDM6A* (Cui et al., 2018). Because the h-index only grows with time, the m-index divides it by the years since the first publication (Hirsch, 2005); He and Pan (2.000) and Lan (1.889) exceed Chu (1.750), showing faster accumulation of impact. As

most of these findings come from Chinese breeds, extrapolation to African, Middle Eastern, or Southeast Asian breeds requires caution.

Table 6. Ten most influential authors (local impact within the corpus)

Author	Scopus ID	h-index	g-index	m-index	TC	NP
Mingxing Chu	23134453200	21	27	1.750	1,221	103
Xiaoyun He	57360795300	18	24	2.000	846	66
Chuanying Pan	21734653000	18	31	2.000	1,048	48
Xianyong Lan	57205314944	17	30	1.889	1,040	51
Ran Di	26023095700	16	23	1.333	714	53
Lei Qu	36775943100	15	27	1.667	789	27
Xiangyu Wang	56645044800	15	23	1.667	642	46
Qiuyue Liu	37099954300	14	20	1.167	475	30
Feng Wang	57211808828	14	27	1.273	775	41
Jinlong Zhang	55657190400	14	21	1.273	460	25

Note: TC: total citations; NP: number of publications in the corpus. The h-, g-, and m-indices are local indices computed from each author's articles in the corpus (see Data Analysis); citation counts as recorded in Scopus on 1 June 2026

6. Dominant Research Topics and Potential Research Gaps

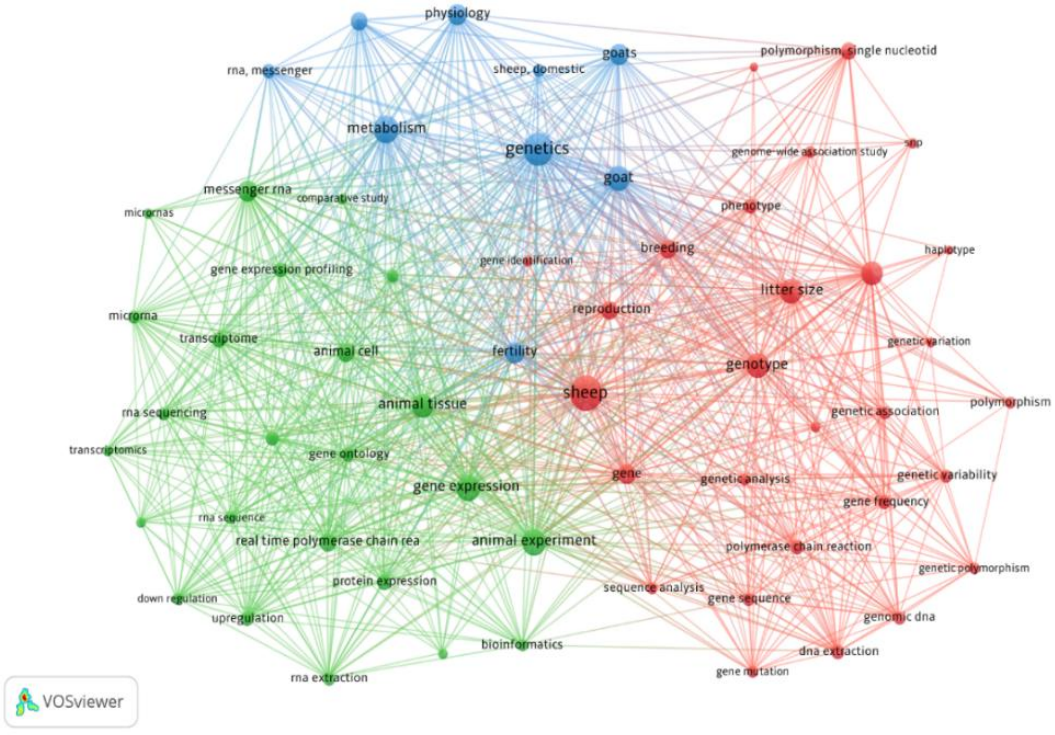


Figure 2. Keyword co-occurrence network (VOSviewer 1.6.20; settings in the Data Analysis section). Node size is proportional to the number of occurrences, line thickness to the strength of co-occurrence, and colour indicates cluster membership (blue: classical genetics and physiology; green: transcriptomic and gene-expression methods; red: litter size genomics)

With the settings described in the Data Analysis section, keyword co-occurrence produced three clusters (Figure 2): a blue cluster of classical genetics and physiology ("genetics", "physiology", "metabolism"), a green cluster of methods ("gene expression", "transcriptome", "microRNA", "RNA sequencing"), and a red cluster centred on "sheep", "litter size", and "genotype". "Sheep" is the largest and most central node, and "litter size" and "genotype" are among the largest nodes of the red cluster and are linked to terms in the other two clusters; this structure suggests that candidate gene studies and GWAS on litter size form the core of the field. Beyond the TGF-β genes, new candidates such as *NTRK2*, which is involved in follicle formation and oocyte survival, continue to emerge from GWAS (Esmaeili-Fard et al., 2021).

The overlay map (Figure 3) shows that physiology, genetics, and metabolism are established topics (around 2019.5), whereas RNA sequencing, transcriptomics, cell proliferation, and DNA extraction intensified later (2020.5–2021.0). This pattern is consistent with growing interest in non-coding RNAs as regulators of fecundity; for example, ovarian miRNA sequencing of high- and low-fecundity sheep revealed 51 differentially expressed miRNAs (Yousuf et al., 2025). The field therefore appears to be moving from single SNPs toward regulatory networks, which is consistent with the many links between the green and red clusters.

Read together with the cited literature, the keyword structure suggests three potential research gaps. Because a low keyword frequency indicates relative under-representation in this Scopus corpus rather than an absence of research, these gaps should be regarded as indicative rather than definitive. First, the effects of the classical major genes vary across populations; a meta-analysis prompted by conflicting reports found that the *GDF9* G4 polymorphism, but not G1, was associated with litter size in sheep (Budiyanto et al., 2023), while the most productive authors in this corpus work mainly with Chinese breeds (Table 6), so standardised validation is needed in tropical breeds, including Indonesian ones. Second, non-coding RNA terms remain peripheral in the network, and studies that integrate GWAS data with transcriptomic and epigenetic layers in tropical sheep and goats are scarce. Third, none of the labelled keywords in the map refers specifically to male reproduction (e.g., semen, sperm, or testis), suggesting that male fertility receives comparatively little attention, although semen proteomics of Duolang rams with different *FecB* genotypes showed that major prolificacy genes also

affect sperm biology (Zhang et al., 2025). These gaps match recent calls for affordable low-density genomic panels for smallholders, the inclusion of microbiome and epigenome information in breeding evaluations, and CRISPR-based validation of candidate genes (Cao, 2026).

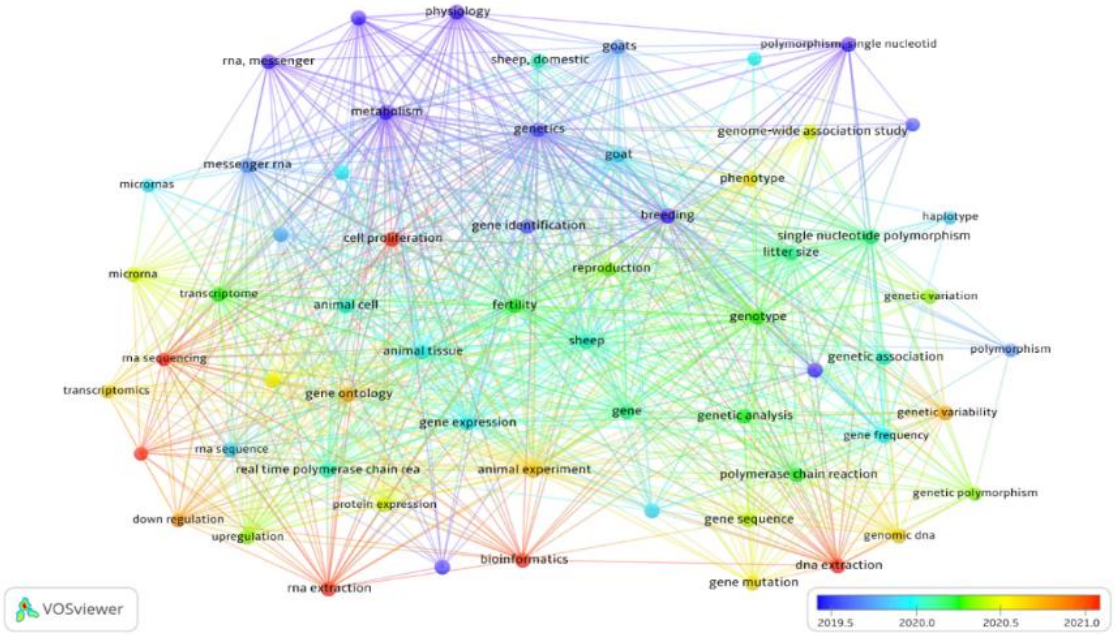


Figure 3. Overlay visualisation of keywords by average publication year (same network as Figure 2). Node colour shows the average publication year of the articles containing each keyword, from blue (2019.5 or earlier) to red (2021.0 or later)

CONCLUSION

Within the Scopus-indexed literature analysed here, research on reproductive traits and molecular genetics in small ruminants grew at a compound annual rate of 12.49% from 2015 to 2025. China dominates output through the IAS-CAAS and Northwest A&F University groups, whereas the United Kingdom and the United States achieve the highest citation efficiency, and *Animals* and *Theriogenology* are the main publication venues. The keyword overlay indicates a shift from single-marker discovery toward transcriptomic and regulatory studies. Based on the keyword structure and the cited literature, suggested priorities for future work are the validation of major fecundity genes in tropical breeds, multi-omics integration, and male reproductive genomics, ideally through international studies involving indigenous breeds from Southeast Asia, Africa, and the Middle East. Because Scopus was the only data source and only English-language articles were

included, publications indexed elsewhere, particularly in regional journals from developing countries, may be under-represented, so these patterns should not be read as a complete picture of global research. Future bibliometric studies could combine Web of Science, regional databases, and manual relevance screening to address these limitations.

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DATA AVAILABILITY STATEMENT

The bibliographic records analysed in this study were retrieved from Scopus on 1 June 2026 with the query given in Table 1, so the data set can be re-created by any Scopus subscriber, although citation counts will change with the retrieval date. Because Scopus data are subject to Elsevier's licensing terms, the exported records cannot be shared publicly; the list of Scopus EIDs and the Biblioshiny and VOSviewer settings and map files are available from the corresponding author on reasonable request.

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