JOURNAL OF AGRICULTURE AND APPLIED BIOLOGY
2026, Vol. 7, No. 1, 62 - 85
http://dx.doi.org/10.11594/jaab.07.01.05
E-ISSN: 2723-5106

Research Article

Coffee Genetic Diversity and Genomics: A Bibliometric Tropical Perspective

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Article history:

Received 22 March 2026
Revised 27 June 2026
Accepted 23 July 2026
Published 31 August 2026

Keywords:

Coffea
Coffee genetics
Genomics
Tropical agriculture
VOSviewer

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Abstract

Coffee genetic resources play a fundamental role in supporting sustainable production, crop improvement, and climate resilience. Over the past decades, rapid advances in molecular genetics and genomics have transformed coffee research; however, a comprehensive understanding of the intellectual development, thematic evolution, and future research directions of this field remains limited. This study aimed to systematically map the global landscape of coffee genetics and genomics research through a bibliometric analysis of 867 English-language journal articles indexed in the Scopus database and published between 1974 and 2024. Bibliometric analyses were conducted using Microsoft Excel, Harzing's Publish or Perish, and VOSviewer to evaluate publication trends, leading journals, countries, authors, citation networks, co-authorship, co-citation, and thematic evolution based on co-occurrence and overlay visualizations. The results demonstrate a substantial increase in scientific output over the past five decades, with France and Brazil emerging as the leading contributors to publication productivity and international collaboration. Co-citation analysis identified Philippe Lashermes and Bertrand B. as central figures shaping the intellectual structure of the field, while thematic analyses revealed a clear transition from studies emphasizing genetic diversity and phylogenetic characterization toward integrative genomics, functional genomics, molecular breeding, bioinformatics, and high-throughput sequencing. The overlay visualization further indicates an increasing emphasis on computational biology and genomics-driven approaches in recent years. Overall, this study provides a comprehensive bibliometric perspective on the evolution of coffee genetics and genomics research and identifies future research priorities, including multi-omics integration, artificial intelligence-assisted genomic prediction, genome editing, and expanded genomic characterization of wild *Coffea* species to support biodiversity conservation and the development of climate-resilient coffee cultivars in tropical production systems.

How to cite:
Permatasari, N., Fauziah, L. K., Sari, R. P. K., Hardani, M., Aliyah, S. H., & Priyambodo (2026). Coffee Genetic Diversity and Genomics: A Bibliometric Tropical Perspective. *Journal of Agriculture and Applied Biology, 7*(1): 62 - 85. doi: 10.11594/jaab.07.01.05

1. Introduction

Coffee, one of the world's most traded agricultural commodities, plays a pivotal role in global economies, cultural traditions, and ecological systems, particularly across tropical and subtropical regions where its cultivation predominates (Abrhám et al., 2021). With over 2.25 billion cups consumed daily, coffee supports millions of smallholder farmers while contributing significantly to biodiversity conservation, ecosystem services, and rural livelihoods (Vegro & de Almeida, 2020). As climate change, emerging pests and diseases, and evolving production demands increasingly threaten coffee cultivation, the conservation and effective utilization of coffee genetic resources have become fundamental to ensuring the long-term sustainability of the global coffee sector (Davis et al., 2019). Among the 120 recognized *Coffea species*, *Coffea arabica* and *Coffea canephora* dominate global production due to their superior beverage quality and commercial value (Campuzano-Duque et al., 2021). However, the narrow genetic base of *C. arabica* heightens its susceptibility to biotic and abiotic stresses, including pest outbreaks, emerging diseases, and climate change, posing substantial challenges for sustaining coffee cultivation in tropical regions that serve not only as major production areas but also as important reservoirs of *Coffea* genetic diversity (Nasiro, 2024; Krishnan, 2022). In contrast, wild *Coffea* species, such as *C. racemosa*, offer broader genetic diversity and represent untapped reservoirs of adaptive traits that are critical for enhancing resilience, breeding innovation, and long-term sustainability (Pedrazzani et al., 2023). Conserving and harnessing these tropical genetic resources are therefore essential not only for biodiversity conservation but also for advancing genomic research, accelerating the development of climate-resilient coffee cultivars, and supporting sustainable coffee production under future environmental change.

Driven by the growing importance of coffee genetic resources for sustainable production and climate resilience, coffee genetics and genomics research have undergone transformative advancements, mirroring broader developments in molecular biology, bioinformatics, and plant genomics. Early investigations primarily relied on morphological traits, cytogenetics, and low-resolution molecular markers such as RAPD, AFLP, and SSR to characterize cultivar diversity, population structure, and evolutionary relationships (Ferrão et al., 2013; Anthony et al., 2002; Kage et al., 2016). These foundational studies were particularly relevant for mapping genetic diversity within tropical biodiversity hotspots where wild *Coffea* species flourish under diverse ecological pressures (Magos Brehm et al., 2022). However, the last two decades have marked a paradigm shift, driven by next-generation sequencing (NGS), single nucleotide polymorphism (SNP) markers, transcriptomics, and genome-wide association studies (GWAS), enabling unprecedented resolution in understanding trait architectures and evolutionary histories (Spinoso-Castillo et al., 2021). These technological breakthroughs have accelerated the development of elite F1 hybrids, improved cultivars, and advanced conservation strategies, ultimately supporting climate adaptability and disease resistance within tropical coffee agroecosystems (Alemayehu et al., 2023). At the same time, these advances have generated an increasingly large, multidisciplinary, and rapidly evolving body of literature, making it more challenging to comprehensively identify research trends, intellectual structures, collaborative networks, and emerging priorities through conventional narrative reviews alone (Chawla & Goyal, 2022).

Despite these advances, the ecological and socioeconomic stakes surrounding coffee production in tropical regions demand more integrative genetic and genomic strategies (Ngure & Watanabe, 2024). Southeast Asia, including Indonesia and Vietnam, represents one of the world's largest coffee-producing regions and a global hotspot of tropical biodiversity (Suryana et al., 2024). Yet, compared to other production centers, the genetic diversity of local coffee populations remains significantly underexplored (Cahyono et al., 2024). Although research in coffee genetics and genomics has expanded considerably over the past five decades, the resulting body of knowledge has become increasingly diverse, multidisciplinary, and fragmented, making it difficult to comprehensively understand its intellectual development, collaboration patterns, and emerging research priorities. Existing bibliometric studies have primarily focused on topics such as coffee quality, chemical composition, production systems, or precision agriculture (Santana et al., 2021; Guadalupe et al., 2024; Góngora Orjuela, 2010; Kumar et al., 2024), but they have not specifically synthesized the evolution of research on coffee genetic diversity and genomics. Moreover, these studies have not examined how advances in coffee genetics relate to the broader context of tropical biodiversity conservation, sustainable breeding, and the resilience of coffee production systems, despite tropical regions representing both the primary centers of coffee cultivation and the richest reservoirs of *Coffea* genetic resources. This gap highlights the need for a comprehensive bibliometric assessment capable of integrating publication dynamics, intellectual structures, thematic evolution, and collaborative networks to provide an evidence-based understanding of the development and future direction of coffee genetics and genomics research from a tropical perspective.

To address these knowledge gaps, bibliometric analysis provides a robust framework for systematically mapping the intellectual structure, publication patterns, thematic evolution, and collaborative networks that have shaped coffee genetics and genomics research (Abdelwahab et al., 2024). Beyond quantifying publication trends, bibliometric approaches enable the identification of influential research themes, emerging knowledge frontiers, and evolving scientific priorities that are often difficult to capture through conventional narrative reviews alone (Kumar, 2025). Within the context of tropical agriculture, bibliometric analysis also facilitates the interpretation of scientific development in relation to tropical biodiversity, the conservation of genetic resources, sustainable breeding strategies, and the resilience of coffee production systems. Accordingly, this study presents a comprehensive longitudinal bibliometric assessment of coffee genetic diversity and genomics research spanning 1974–2024, combining quantitative bibliometric techniques with qualitative content analysis to provide a more comprehensive understanding of the evolution of research themes and their biological significance. Rather than examining publication patterns in isolation, this study interprets bibliometric findings through a tropical perspective to identify knowledge gaps, research hotspots, collaboration patterns, and future research priorities that can support biodiversity conservation, genomic innovation, and the sustainable development of coffee production.

Accordingly, this study aims to comprehensively map the evolution, intellectual structure, collaboration patterns, thematic development, and emerging research priorities in coffee genetic diversity and genomics research over the period 1974–2024 through an integrated bibliometric and content-based approach. By combining quantitative bibliometric techniques with qualitative content analysis, this study extends beyond conventional publication mapping to provide biological interpretation of research trends and their implications for tropical coffee production, genetic-resource conservation, and sustainable breeding. By integrating bibliometric mapping with qualitative content analysis, this study provides new insights into the evolution of coffee genetics and genomics research and its implications for tropical biodiversity conservation and sustainable breeding. This integrated perspective contributes to a more comprehensive understanding of how scientific knowledge in coffee genetics has evolved and identifies priority areas for future research in response to emerging challenges associated with climate change, biodiversity conservation, and genomic innovation. The findings have significant implications for multiple stakeholders. For researchers, this study consolidates fragmented literature, highlights influential studies, and identifies knowledge gaps that guide future scientific inquiry. For policymakers and funding agencies, it provides an evidence-based foundation to prioritize genomic innovations, conservation of tropical biodiversity, and sustainable farming initiatives. For industry stakeholders, it identifies emerging genetic tools and strategies essential for breeding climate-resilient coffee cultivars and ensuring sustainable production systems. Overall, this study provides an evidence-based framework for aligning future research agendas with biodiversity conservation, genomic innovation, and the long-term sustainability of coffee production in tropical regions.

2. Materials and Methods

2.1 Bibliometric analysis

Bibliometric analysis has become an essential methodological framework for systematically mapping the evolution of scientific knowledge and understanding the intellectual structure of research fields (Gutiérrez-Salcedo et al., 2018). By applying quantitative techniques, it enables researchers to evaluate patterns of scholarly influence, identify emerging research frontiers, and trace the flow of ideas across disciplines. In the present study, bibliometric analysis was integrated with qualitative content analysis to examine the evolution, intellectual structure, thematic development, and collaborative patterns of coffee genetic diversity and genomics research. This combined approach enabled quantitative mapping of the scientific literature while providing biological interpretation of major research themes from a tropical perspective.

In this study, bibliometric techniques were integrated with qualitative content analysis to capture both structural patterns and intellectual trajectories in coffee genetics and genomics research over the past five decades. This integrated approach enabled the identification of publication trends, intellectual structures, thematic evolution, collaboration networks, and emerging research priorities while providing biological interpretation of the major research themes identified through bibliometric mapping. A distinctive feature of this assessment lies in adopting a tropical perspective, recognizing that coffee production is concentrated in biodiversity-rich tropical regions where environmental pressures, genetic variability, and agricultural practices are deeply interlinked. Situating bibliometric findings within these ecological and socio-economic contexts enables a deeper understanding of how collaborative networks, research priorities, and technological innovations have shaped scientific progress. Accordingly, the tropical perspective served as an interpretative framework for relating bibliometric evidence to biodiversity conservation, sustainable breeding strategies, and climate-resilient coffee production, rather than merely describing publication patterns. This perspective also highlights implications for biodiversity conservation, sustainable coffee cultivation, and climate resilience across tropical agroecosystems.

Data were retrieved from the Scopus database on May 11, 2025, which was selected because of its broad coverage of high-quality peer-reviewed literature and its widespread use in bibliometric studies. The literature search was performed in the Title, Abstract, and Keywords (TITLE-ABS-KEY) fields using the following Boolean search strategy: TITLE-ABS-KEY(("coffee" OR "robusta coffee" OR "arabica coffee" OR "liberica coffee" OR "*Coffea canephora*" OR "*Coffea arabica*" OR "*Coffea liberica*") AND ("genetic" OR "coffee genetic" OR "coffee evolution" OR "coffee genetic evolution")) AND PUBYEAR > 1973 AND PUBYEAR < 2025 AND LIMIT-TO(SUBJAREA,"BIOC") AND LIMIT-TO(SRCTYPE,"j") AND LIMIT-TO(LANGUAGE,"English") AND LIMIT-TO(DOCTYPE,"ar"). The Boolean search strategy was developed to maximize the retrieval of publications related to coffee genetics and genomics while minimizing the inclusion of studies outside the scope of the present bibliometric analysis. The search was limited to English-language journal articles published between 1974 and 2024 within the subject area of Biochemistry, Genetics and Molecular Biology, as specified in the search strategy. An overview of the literature retrieval, screening, and selection process is presented in Figure 1.

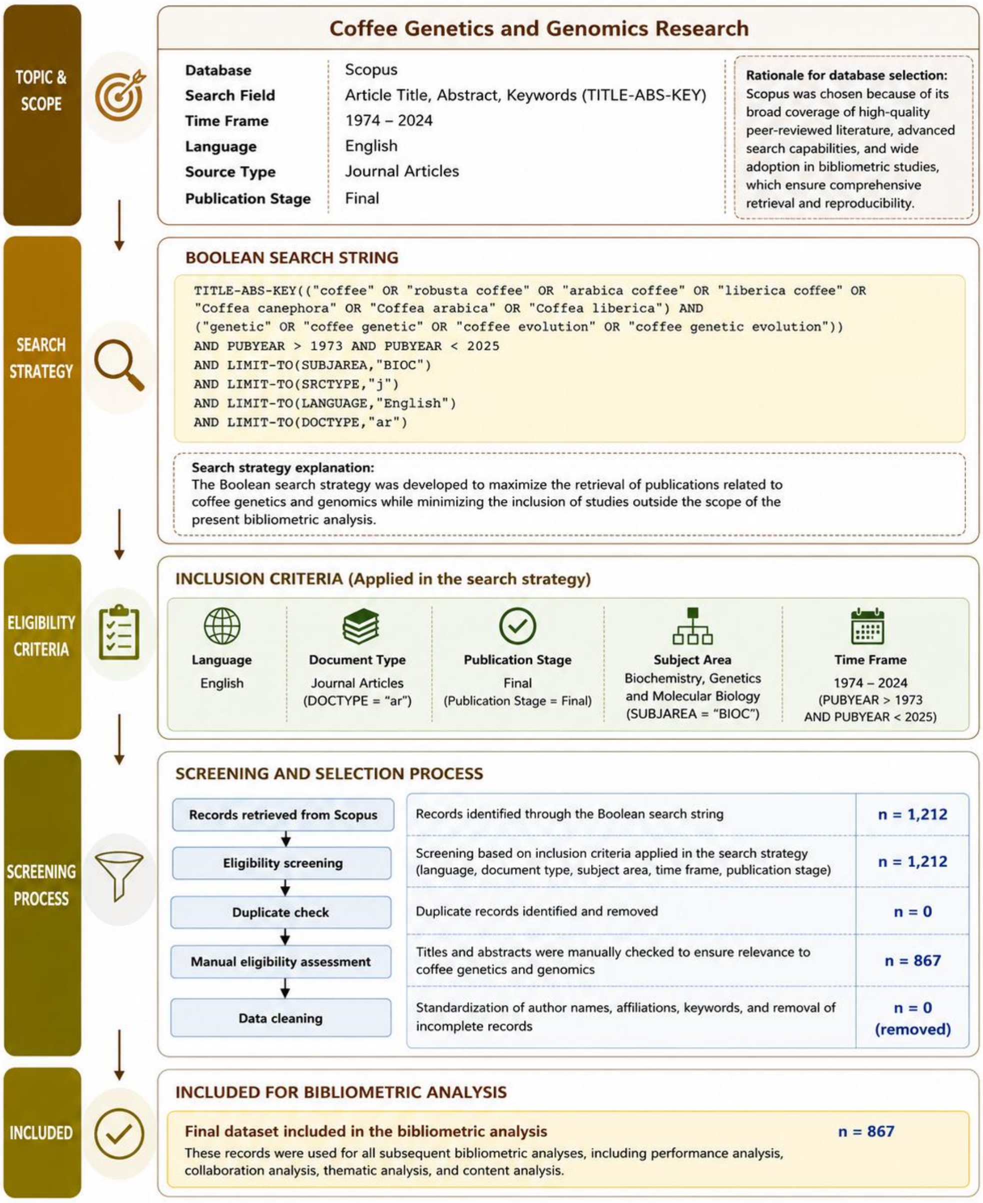

Figure 1. Workflow of the literature retrieval, screening, eligibility assessment, data cleaning, and final study selection employed in this bibliometric analysis of coffee genetics and genomics research. The diagram illustrates the complete search framework, including database selection, search scope, Boolean search strategy, predefined inclusion criteria, record screening, and preparation of the final dataset for bibliometric analysis. The workflow was adapted from the PRISMA framework and modified for bibliometric research

2.2 Data analysis

This study retrieved a total of 867 bibliographic records from the Scopus database, encompassing metadata such as authorship information, article titles, abstracts, author-supplied keywords, publication years, and cited references, all of which were exported in plain-text format for subsequent analysis. Prior to analysis, the dataset was examined to verify duplicate records and the completeness and consistency of bibliographic metadata. No duplicate records were identified, and the retrieved records were subsequently prepared for bibliometric analysis. The dataset was then subjected to descriptive statistical analysis, bibliometric mapping, network analysis, and qualitative content analysis to examine publication trends, intellectual structure, collaboration patterns, thematic evolution, and emerging research directions in coffee genetics and genomics.

Descriptive statistics were applied to summarize the bibliographic characteristics of the retrieved publications, including annual publication trends, distribution across leading journals, contributions from the most productive countries, and the identification of the most influential authors within the research field. Citation performance and publication impact were subsequently evaluated using Harzing's Publish or Perish software to calculate citation-based performance indicators and identify the most influential publications within the dataset. The overall analytical framework employed in this study is illustrated in Figure 2.

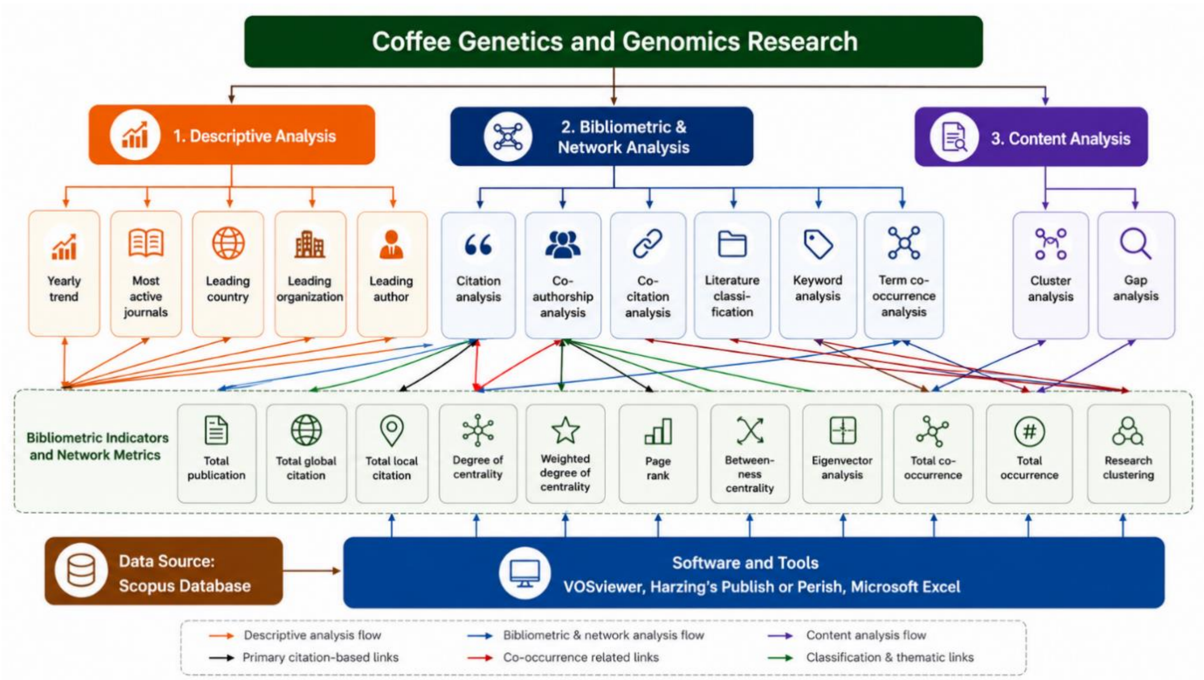

Figure 2. Analytical framework employed in this study, illustrating the integration of descriptive analysis, bibliometric and network analysis, and qualitative content analysis. The workflow summarizes the analytical components, bibliometric indicators, network metrics, and software packages used to evaluate publication performance, intellectual structure, collaboration patterns, thematic evolution, and emerging research directions in coffee genetics and genomics research (modified from Mohamad et al., 2023)

Bibliometric mapping and network visualization were performed using VOSviewer version 1.6.20, while Microsoft Excel was used for descriptive data organization and graphical presentation. The bibliometric analyses included citation analysis, co-authorship analysis, co-citation analysis, keyword co-occurrence analysis, term co-occurrence analysis, and literature classification to characterize the intellectual structure, collaboration patterns, thematic evolution, and conceptual relationships within the research field. Minimum occurrence thresholds were determined according to the characteristics of each bibliometric network to enhance visualization clarity while preserving representative relationships among items and minimizing network complexity. Finally, qualitative content analysis was conducted to interpret the biological significance of the dominant research themes, identify knowledge gaps, and formulate future research directions based on the quantitative bibliometric findings.

3. Result and Discussion

3.1 Publication Year

The annual publication trend demonstrates a substantial and sustained increase in scientific output on coffee genetics and genomics research between 1974 and 2024 (Figure 3). During the first two decades (1974–1995), publication activity remained very limited, generally comprising fewer than five articles annually. This period represents the formative stage of coffee genetics research, during which investigations primarily focused on conventional breeding, cytogenetics, and the application of early molecular markers. A gradual increase became evident from the late 1990s, followed by a marked acceleration after the early 2000s, when annual publication counts consistently exceeded 20 articles. The highest publication outputs were recorded during the most recent years of the study period, with more than 50 articles published annually, indicating that coffee genetics and genomics has evolved into a rapidly expanding research field.

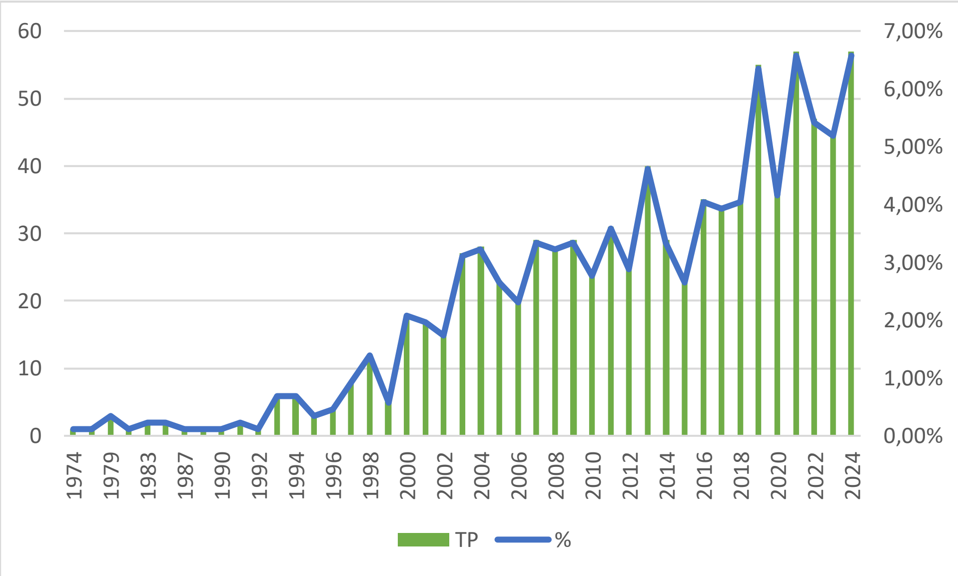

Figure 3. Annual publication trend of coffee genetics and genomics research (1974–2024). Green bars indicate the total number of publications (TP), whereas the blue line represents the percentage of publications relative to the complete dataset (n = 867)

The observed growth closely parallels major technological advances in molecular biology and plant genomics. Early studies relied predominantly on low-resolution molecular markers, including RAPD, AFLP, SSR, and RFLP, to investigate genetic diversity, cultivar identification, and phylogenetic relationships among Coffea species. The rapid expansion after the early 2000s coincides with the increasing accessibility of high-throughput sequencing technologies, single nucleotide polymorphism (SNP) markers, transcriptomics, and genome-wide analytical approaches, which substantially improved the resolution of genetic analyses and enabled more comprehensive investigations of gene function, domestication history, and adaptive evolution. These technological developments broadened research opportunities from basic genetic characterization toward functional genomics, comparative genomics, and molecular breeding (Singh et al., 2020; Singh et al., 2021).

Another important factor contributing to the increasing publication trend is the growing global concern regarding climate change, emerging pests and diseases, and the long-term sustainability of coffee production (Bilen et al., 2022). As coffee cultivation is concentrated primarily in tropical regions that are highly vulnerable to increasing temperatures and changing precipitation patterns, genetic improvement has become a major research priority (Krishnan et al., 2021). Consequently, scientific attention has shifted toward identifying genes associated with drought tolerance, disease resistance, beverage quality, and environmental adaptation. This transition reflects the increasing integration of genomics into breeding programs designed to develop climate-resilient coffee cultivars capable of sustaining productivity under future environmental conditions.

From a broader tropical perspective, the continuous increase in publication output also demonstrates the strategic importance of conserving coffee genetic resources within biodiversity-rich tropical regions. Although molecular technologies have substantially advanced the understanding of coffee genetics, the accelerating publication trend suggests that numerous research opportunities remain, particularly regarding the exploration of wild *Coffea* germplasm, population genomics, genome-assisted breeding, and multi-omics integration. Collectively, these findings indicate that coffee genetics and genomics research have progressed from descriptive genetic characterization toward integrative genomic research that supports biodiversity conservation, sustainable breeding, and climate-resilient coffee production in tropical agroecosystems.

3.2 Most Productive Country

The bibliometric dataset revealed contributions from 93 countries, demonstrating the broad global distribution of coffee genetics and genomics research. The ten most productive countries, summarized in Table 1, accounted for a substantial proportion of the total scientific output, indicating that research activity is concentrated within a relatively small number of countries. Overall, the results highlight the important contributions of both major coffee-producing nations and research-intensive countries in shaping the development of coffee genetics and genomics research.

France emerged as the most productive country, contributing 175 publications (20.18%), closely followed by Brazil (174; 20.07%) and the United States (166; 19.15%). Collectively, these three countries accounted for 59.4% of the total publications, highlighting their dominant role in advancing coffee genetics and genomics research. Beyond these leading contributors, the distribution of scientific output reflects a combination of research-intensive countries, including the United Kingdom, Germany, and Sweden, and major coffee-producing nations, such as Brazil, India, and Colombia. China also ranked among the top contributors, indicating the growing involvement of Asian countries in coffee genetics and genomics research.

Table 1. Top ten countries that contributed to the publications

Number	Country	Total Publications	% (n=867)
1	France	175	20.18
2	Brazil	174	20.07
3	United States	166	19.15
4	China	85	9.80
5	United Kingdom	56	6.46
6	Germany	51	5.88
7	India	51	5.88
8	Italy	36	4.15
9	Colombia	34	3.92
10	Sweden	30	3.46

Although global coffee production is concentrated in tropical countries such as Brazil, Vietnam, Colombia, Indonesia, and Ethiopia, scientific productivity in coffee genetics and genomics is not solely determined by production capacity (Torok et al., 2018). The prominence of France and the United States alongside Brazil suggests that internationally recognized research institutions, long-term investment in plant genomics, and extensive international collaborations play a decisive role in shaping scientific output. This pattern is further reflected in the dominance of French-affiliated researchers among the most prolific authors identified in the present study (Madrid-Casaca et al. 2021). From a tropical perspective, these findings highlight the importance of strengthening collaborative research networks between biodiversity-rich coffee-producing countries and research-intensive institutions to accelerate genomic innovation, conserve coffee genetic resources, and support the development of climate-resilient coffee cultivars for sustainable tropical agroecosystems. Ultimately, bridging the gap between biodiversity-rich tropical regions and research-intensive institutions will be fundamental for transforming coffee genetic resources into innovations that enhance global coffee sustainability.

3.3 Publishing Activity by Journal

A total of 867 publications on coffee genetics and genomics research were distributed across 32 scientific journals, demonstrating the multidisciplinary nature of this research field (Table 2). However, publication activity was concentrated within a relatively small number of journals, indicating the existence of several core publication outlets that have played a central role in disseminating advances in coffee genetics and genomics. This concentration reflects the tendency of researchers to publish in journals with strong scopes in plant genetics, crop improvement, molecular biology, and plant biotechnology.

Table 2. Most active source title

Journal	Total Publications	% (n=867)	Publisher
Euphytica	47	5.42	Springer
Genetics and Molecular Research	29	3.34	Fundacao de Pesquisas Cientificas dRP
Tree Genetics and Genomes	20	2.31	Springer
Genetic Resources and Crop Evolution	19	2.19	Springer Nature
Crop Breeding and Applied Biotechnology	18	2.08	Brazilian Society of Plant Breeding
Theoretical and Applied Genetics	18	2.08	Springer Verlag
Plant Pathology	16	1.85	John Wiley and Sons Inc
Genome	12	1.38	National Research Council of Canada
International Journal of Molecular Sciences	12	1.38	MDPI
Nucleic Acids Research	12	1.38	Oxford University Press

Among the indexed journals, Euphytica was the most productive source, publishing 47 articles (5.42%), followed by Genetics and Molecular Research (29 articles) and Tree Genetics and Genomes (20 articles). Other important publication outlets included Genetic Resources and Crop Evolution, Crop Breeding and Applied Biotechnology, Theoretical and Applied Genetics, Plant Pathology, Genome, International Journal of Molecular Sciences, and Nucleic Acids Research. The predominance of these journals demonstrates that coffee genetics and genomics research is strongly embedded within the broader disciplines of plant genetics, molecular biology, crop breeding, and genetic resource conservation rather than being confined to commodity-specific agricultural research.

The predominance of these journals is closely related to their editorial scope, which emphasizes plant genetics, molecular breeding, genome analysis, and crop improvement, making them the primary publication outlets for coffee genetics and genomics research (Cortés & Du, 2023).

The dominance of internationally recognized journals specializing in genetics and molecular biology reflects the scientific evolution of coffee research from conventional genetic characterization toward genomics-driven approaches. The increasing publication of coffee-related studies in journals emphasizing genomics, molecular breeding, and genetic resources coincides with the widespread adoption of next-generation sequencing, transcriptomics, comparative genomics, and other high-throughput molecular technologies during the past two decades. From a tropical perspective, this publication pattern indicates that coffee genetics has become increasingly integrated into global plant science, emphasizing the growing importance of genomic innovation for conserving tropical coffee genetic resources, accelerating the development of climate-resilient cultivars, and supporting sustainable coffee production under changing environmental conditions. Collectively, these findings demonstrate that publication activity not only reflects the maturation of coffee genetics and genomics as a scientific discipline but also serves as an indicator of the increasing global commitment to developing evidence-based strategies for coffee improvement, biodiversity conservation, and long-term agricultural sustainability.

3.4 Publishing Activity by Author

The bibliometric dataset revealed a broad international research community contributing to coffee genetics and genomics over the past five decades. Nevertheless, scientific productivity was concentrated among a relatively small group of researchers, indicating the presence of several influential authors who have played central roles in shaping the intellectual development of this research field (Table 3). Their sustained scientific contributions have significantly advanced knowledge on coffee genetic diversity, molecular breeding, genome evolution, and the conservation of coffee genetic resources.

Table 3. Top ten of the author(s)

Author Name	Total Publications	% (n=867)	Affiliation	Country
Lashermes, P.	37	4.27	University of Montpellier	France
Combes, M.C.	31	3.58	IRD, University of Montpellier	France
Bertrand, B.	27	3.11	IICA/PROMECAFE, Coronado	Costa Rica
Leroy, T.	26	3.00	CIRAD-CP, Montpellier	France
Charrier, A.	22	2.54	ENSAM/ORSTOM, Montpellier	France
Hamon, S.	20	2.31	IRD, UMR DIAPC, Montpellier	France
Caixeta, E.T.	18	2.08	Universidade Federal de Viçosa	Brazil
Montagnon, C.	15	1.73	RD2 Vision, Valflaunes	France
Poncet, V.	15	1.73	UMR, Montpellier	France
Etienne, H.	14	1.61	CIRAD-CP, Montpellier	France

Among the most productive researchers, Lashermes P. ranked first with 37 publications (4.27%), followed by Combes M.C. (31 publications), Bertrand B. (27 publications), Leroy T. (26 publications), and Charrier A. (22 publications). A notable finding is that most of the leading authors are affiliated with French research institutions, particularly the University of Montpellier, IRD, and CIRAD, while Caixeta E.T. from the Universidade Federal de Viçosa represents Brazil among the most productive contributors. This distribution closely mirrors the country-level analysis, where France emerged as the leading contributor to global coffee genetics and genomics research.

The strong representation of French researchers reflects the long-term commitment of French research institutions to coffee genetic resources, molecular breeding, and evolutionary studies (Etienne et al., 2018; Bergheaud et al., 2025). Organizations such as CIRAD, IRD, and the University of Montpellier have maintained long-term collaborative programs involving germplasm exploration, molecular breeding, and genomics research across Africa, Latin America, and Asia, thereby providing sustained scientific productivity over several decades. The presence of Brazilian researchers among the leading contributors further highlights Brazil's dual role as both the world's largest coffee producer and an important center for coffee genetics research. From a tropical perspective, these findings emphasize that future progress in coffee genetics and genomics will increasingly depend on strengthening collaborative partnerships between biodiversity-rich coffee-producing countries and internationally recognized research institutions. Such collaboration is essential for accelerating genomic innovation, conserving coffee genetic resources, and developing climate-resilient coffee cultivars capable of supporting sustainable coffee production under changing environmental conditions.

3.5 Citation Network Analysis

Citation network analysis was performed to identify the publications that have exerted the greatest scientific influence on the development of coffee genetics and genomics research. Unlike publication counts, citation-based indicators provide insight into the intellectual foundations of a research field by highlighting studies that have substantially shaped subsequent scientific advances. Using the bibliometric dataset of 867 publications, citation analysis was conducted to evaluate research impact, identify landmark publications, and characterize the evolution of knowledge within coffee genetics and genomics.

The citation metrics of the retrieved publications are summarized in Table 4.

Table 4. Citations metrics

Citation metrics	Data
Papers	867
Citations	37,151
Annual Citations	728.45
Citations per paper	42.85
Citations per author	9.166
h-index	85
g-index	160

Collectively, the dataset accumulated 37,151 citations, corresponding to an average of 728.45 citations per year and 42.85 citations per publication. The dataset also achieved an h-index of 85 and a g-index of 160, indicating a mature and highly influential body of literature. These metrics demonstrate that coffee genetics and genomics has developed into an internationally recognized research field characterized by sustained scientific impact and continuous knowledge accumulation over the past five decades.

The most highly cited publications identified in the dataset are presented in Table 5. The most influential publication was T-Coffee: A Novel Method for Fast and Accurate Multiple Sequence Alignment by Notredame et al. (2000), which accumulated 5,869 citations, followed by TranslatorX by Abascal et al. (2010) with 1,138 citations, and the genome sequence study by Abad et al. (2008) with 984 citations. Other highly cited publications include The EMBL-EBI Bioinformatics Web and Programmatic Tools Framework and Kalign, both of which have become widely adopted computational resources for sequence analysis and comparative genomics.

Table 5. Top ten cited publications

Cites	Authors	Title	Year	Cites Per Year	Cites Per Author	Author Count
5869	C. Notredame, D.G. Higgins, J. Heringa	T-coffee: A novel method for fast …	2000	234.76	1956	3
1138	F. Abascal, R. Zardoya, M.J. Telford	TranslatorX: Multiple alignment of …	2010	75.87	379	3
984	P. Abad, J. Gouzy, …, P. Wincker	Genome sequence of the metazoan …	2008	57.88	98	54
815	W. Li, A. Cowley, …, R. Lopez	The EMBL-EBI bioinformatics web …	2015	81.5	91	9
570	C.H. Pernar, …, L.A. Mucci	The epidemiology of prostate cancer	2018	81.43	143	4
564	T. Lassmann, E.L.L. Sonnhammer	Kalign - An accurate and fast multiple …	2005	28.2	282	2
382	A. Nehlig	Interindividual differences in caffeine …	2018	54.57	382	1
285	M.A. Van Sluys, …, J.P. Kitajima	Comparative analyses of the …	2003	12.95	29	58
254	A.S. Hamid, …, Y. Zhang, Z.G. Zhang	Aflatoxin B1-induced hepatocellular …	2013	21.17	64	4
247	L. Dal Maso, C. Bosetti, …, S. Franceschi	Risk factors for thyroid cancer: An …	2009	15.44	62	4
240	F. Anthony, …, P. Lashermes	The origin of cultivated Coffea arabica L. …	2002	10.43	40	6

The citation network (Figure 4) further illustrates that these highly cited publications occupy central positions within the knowledge structure of the field, indicating their broad influence on subsequent research and their role as foundational references for later genetic and genomic studies.

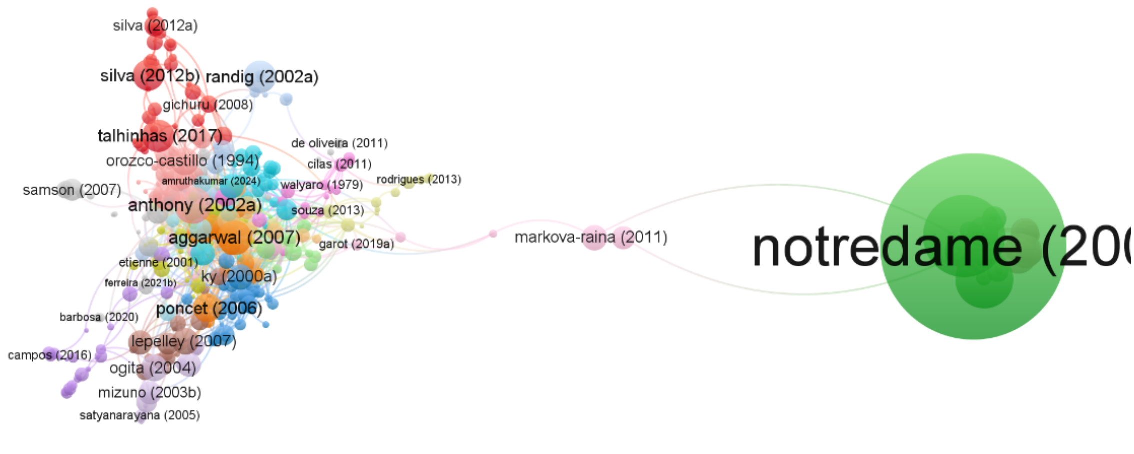

Figure 4. Citation network of influential publications highlighting the central role of highly cited documents in shaping the development of coffee genetics and genomics research

An important finding emerging from the citation analysis is that the most influential publications are dominated by methodological and bioinformatics studies rather than coffee-specific biological investigations. Sequence alignment algorithms, genome annotation platforms, and computational analysis tools form the intellectual foundation upon which coffee genetics and genomics research has evolved (Sabonsolin & Lao, 2026). This pattern indicates that advances in coffee genomics have been driven not only by biological discoveries but also by continuous innovations in computational biology, molecular data analysis, and genome informatics. The increasing accessibility of these analytical tools has substantially accelerated studies on genetic diversity, comparative genomics, transcriptomics, and molecular breeding in *Coffea* species (Ariyoshi et al., 2022).

From a tropical perspective, these findings emphasize that future advances in coffee genetics and genomics will increasingly depend on integrating biodiversity research with high-throughput genomic technologies and advanced bioinformatics approaches. Tropical countries possess extensive coffee genetic resources, yet maximizing their scientific and breeding potential requires continued investment in computational infrastructure, genomic databases, and international research collaboration (Cudjoe et al., 2023). Consequently, the intellectual evolution of coffee genetics and genomics is expected to move beyond descriptive molecular characterization toward integrative multi-omics, functional genomics, and genome-assisted breeding strategies that support biodiversity conservation and climate-resilient coffee production.

3.6 Citation Network by Country

Citation network analysis was conducted to evaluate the intellectual connections among countries contributing to coffee genetics and genomics research (Sallin et al., 2024). Unlike publication counts, which measure scientific productivity, citation network analysis illustrates the influence of countries within the global knowledge network by considering both publication output and citation linkages. The country-level citation network generated using VOSviewer is presented in Figure 5, applying a minimum threshold of one publication and one citation per country.

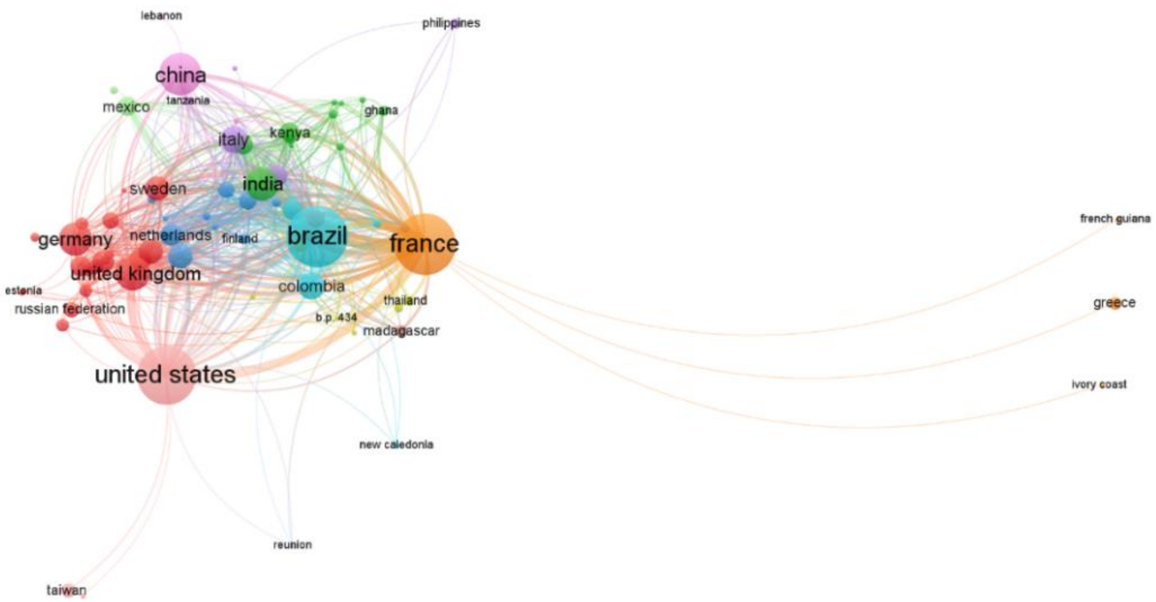

Figure 5. Country-level citation network depicting citation linkages among countries and highlighting the leading contributors shaping the global development of coffee genetics and genomics research

Of the 99 countries represented in the dataset, 98 satisfied the inclusion criteria, while 76 countries formed interconnected citation networks that were organized into 12 clusters. These clusters indicate extensive international interactions and reveal that coffee genetics and genomics research has developed through broad global collaboration rather than isolated national efforts. France occupied the most central position within the citation network with 176 publications and 63 citation links, followed by the United States (165 publications; 53 links) and Brazil (174 publications; 48 links). The prominent positions of these countries indicate their substantial influence on the intellectual development of coffee genetics and genomics research.

The citation network further demonstrates that scientific influence is determined not only by publication productivity but also by the strength of international knowledge exchange (Isfandyari-Moghaddam et al., 2023). France's central position is consistent with the previous analyses showing its dominance in publication output and the presence of several highly productive authors affiliated with internationally recognized institutions such as CIRAD, IRD, and the University of Montpellier. Likewise, Brazil combines high scientific influence with its status as the world's largest coffee producer, reflecting the successful integration of extensive coffee genetic resources with sustained investment in molecular breeding and genomics research. From a tropical perspective, the strong citation linkages among research-intensive countries and biodiversity-rich coffee-producing nations highlight the importance of international collaboration in advancing coffee genomics, conserving tropical genetic resources, and accelerating the development of climate-resilient coffee cultivars for sustainable coffee production.

3.7 Keywords Co-occurrence Analysis

Keyword co-occurrence analysis was performed to identify the conceptual structure and major research themes in coffee genetics and genomics. Using VOSviewer, a network visualization was generated based on terms extracted from the titles and abstracts of the retrieved publications. A binary counting approach with a minimum occurrence threshold of five was applied, resulting in 1,144 eligible terms, of which 686 terms were automatically selected by VOSviewer for visualization according to their relevance scores. The resulting co-occurrence network is presented in Figure 6.

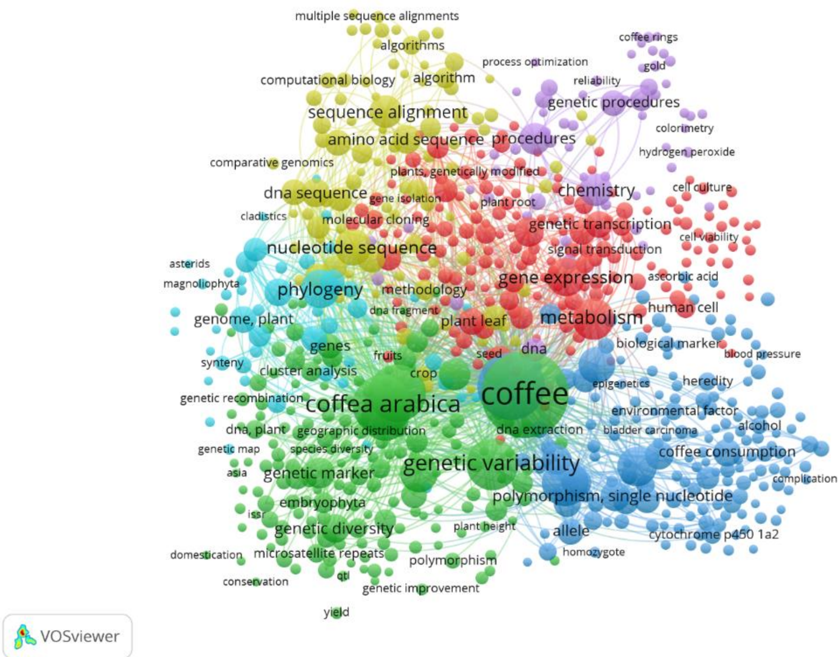

Figure 6. Network visualization of keyword co-occurrence depicting the conceptual organization and thematic landscape of coffee genetics and genomics research

The co-occurrence network revealed five major thematic clusters representing the principal research directions within coffee genetics and genomics. **The green cluster** is centered on *coffee*, *Coffea arabica*, *genetic variability*, *genetic diversity*, *genetic marker*, and *polymorphism*, reflecting studies focusing on genetic resource characterization, population genetics, and molecular breeding. The prominence of this cluster underscores the continued importance of genetic diversity as the foundation for coffee improvement programs. Comprehensive characterization of genetic resources not only supports the conservation of tropical coffee biodiversity but also provides essential genetic variation for developing cultivars with enhanced productivity, quality, and resilience to environmental stresses (Tapaça et al., 2023).

The red cluster is dominated by *gene expression*, *genetic transcription*, and *metabolism*, representing functional genomics and molecular regulatory mechanisms. The increasing prominence of this cluster indicates a shift toward understanding the molecular mechanisms underlying complex agronomic traits rather than merely describing genetic variation (Kakoulidou et al., 2021). Such knowledge is expected to accelerate the identification of candidate genes associated with stress tolerance, bean quality, and other economically important characteristics (Dwivedi et al., 2023).

The yellow cluster, characterized by *sequence alignment*, *DNA sequence*, *nucleotide sequence*, and *computational biology*, highlights the fundamental role of bioinformatics and sequence analysis in genomic research. The emergence of computational biology as a central research component reflects the rapid expansion of genomic datasets generated by high-throughput sequencing technologies (Liu & Zhang, 2024). Consequently, bioinformatics has become indispensable for genome assembly, comparative genomics, functional annotation, and large-scale molecular data integration.

The cyan cluster emphasizes *phylogeny* and *genome*, indicating research related to evolutionary relationships and comparative genomics. Research within this cluster provides the evolutionary framework necessary for understanding species diversification, domestication processes, and the utilization of wild *Coffea* species as valuable genetic resources for future breeding programs, whereas **the purple cluster**, represented by *genetic procedures* and *chemistry*, reflects methodological and analytical developments supporting molecular research. Although relatively smaller than the other clusters, methodological innovations represented in this cluster provide the analytical foundation that enables increasingly accurate, reproducible, and high-resolution genomic investigations across diverse coffee species.

The close interconnection among these clusters demonstrates that coffee genetics and genomics has evolved into a highly interdisciplinary research field integrating molecular genetics, evolutionary biology, bioinformatics, functional genomics, and plant breeding. The central position of *coffee*, *genetic variability*, and *Coffea arabica* indicates that genetic diversity remains the core research theme linking almost all major scientific domains. At the same time, the strong association between sequence analysis, computational biology, and functional genomics reflects the increasing importance of high-throughput sequencing technologies and bioinformatics in advancing coffee genomic research.

The overlay visualization (Figure 7) illustrates the temporal evolution of research topics in coffee genetics and genomics. Earlier studies (blue–cyan colors) were primarily associated with phylogeny, DNA sequence analysis, and genome characterization, reflecting the initial emphasis on species identification and genetic diversity assessment. More recent studies (green–yellow colors) increasingly focus on gene expression, metabolism, computational biology, sequence alignment, genetic procedures, and single nucleotide polymorphism, indicating a transition toward functional genomics, advanced bioinformatics, and genome-assisted breeding. This temporal shift demonstrates the progressive movement of coffee genetics research from descriptive molecular characterization toward integrative genomic approaches supported by high-throughput sequencing and computational analyses.

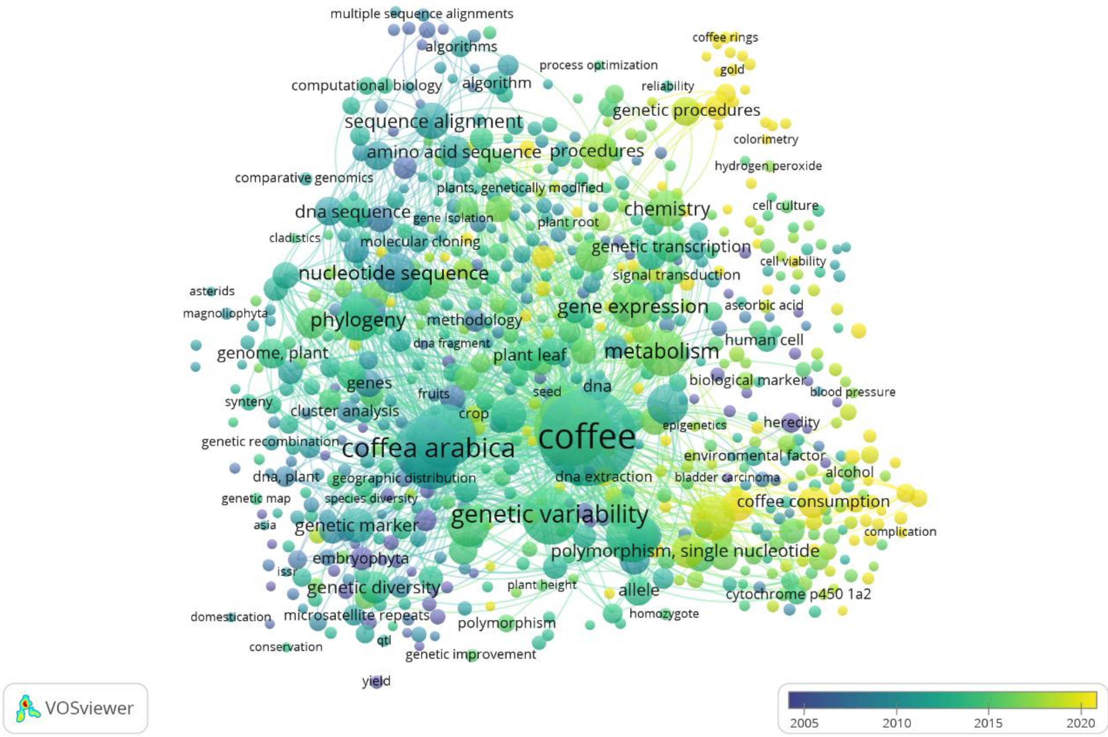

Figure 7. Overlay visualisation map of term co-occurrence of title and abstract field

From a tropical perspective, the observed thematic evolution reflects the growing recognition that conserving coffee genetic resources alone is insufficient to address emerging challenges associated with climate change, pests, diseases, and sustainable production. Future research is expected to increasingly integrate population genomics, functional genomics, bioinformatics, and genome-assisted breeding to support the development of climate-resilient coffee cultivars while strengthening the conservation and utilization of tropical coffee biodiversity.

3.8 Centrality analysis of the co-authorship network

Co-authorship network analysis was performed to examine collaborative relationships among researchers contributing to coffee genetics and genomics research. Scientific collaboration plays a fundamental role in advancing genomics research by facilitating knowledge exchange, integrating multidisciplinary expertise, and promoting the development of innovative approaches to coffee genetic improvement. Using VOSviewer with fractional counting, a minimum threshold of two publications and two citations per author was applied. Of the 4,171 authors identified in the dataset, 480 authors met the inclusion criteria, while 23 authors formed interconnected collaboration networks organized into five distinct clusters (Figure 8).

The co-authorship network reveals a well-defined collaborative structure consisting of several interconnected research communities. Lashermes, Philippe occupies the most central position within the network, acting as the principal bridge linking multiple collaborative groups. His close collaboration with Bertrand, B., Combes, M.C., Etienne, H., Eskes, A.B., Hamon, S., and Leroy, T. forms the largest and most densely connected research community, reflecting long-term scientific partnerships that have substantially advanced coffee genetics, molecular breeding, and genomics research. The central position of Lashermes also supports the previous findings from the publication productivity and co-citation analyses, confirming his prominent scientific influence within this research field.

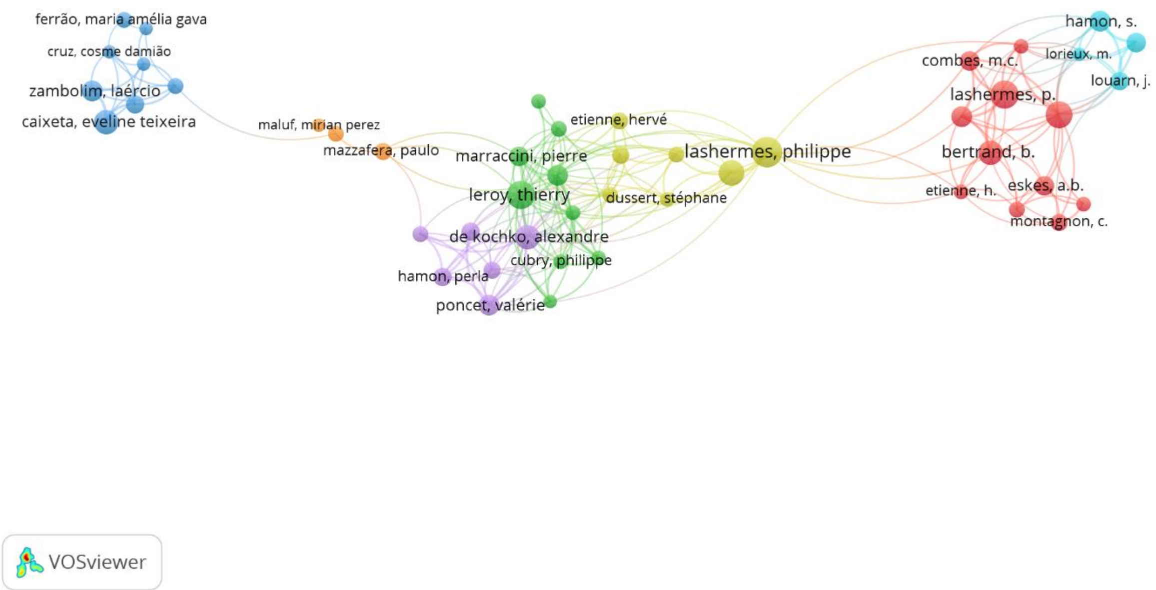

Figure 8. Network visualisation map of co-authorship by countries

Several additional collaborative communities are also evident within the network. One cluster is centered on Leroy, Thierry, Marraccini, Pierre, Cubry, Philippe, Dussert, Stéphane, and Etienne, Hervé, representing an active research group that maintains strong collaborative links with the Lashermes network. Another distinct cluster comprises Brazilian researchers, including Caixeta, Eveline Teixeira, Zambolim, Laércio, Cruz, Cosme Damião, and Ferrão, Maria Amélia Gava, illustrating Brazil's important contribution to coffee genetics and breeding research. Although geographically separated from the principal French collaboration network, this Brazilian cluster remains connected through intermediate collaborators, highlighting the international nature of research partnerships within the field.

Overall, the co-authorship network demonstrates that scientific progress in coffee genetics and genomics has been driven by several highly interconnected research communities rather than isolated individual researchers. The presence of bridging authors connecting different collaborative clusters indicates effective international knowledge exchange between research-intensive institutions and coffee-producing countries. From a tropical perspective, strengthening these collaborative networks will remain essential for integrating genomic technologies, conserving coffee genetic resources, and accelerating the development of climate-resilient coffee cultivars capable of supporting sustainable coffee production under future environmental challenges.

3.9 Co-citation Analysis

Co-citation analysis was performed to explore the intellectual structure of coffee genetics and genomics research by identifying authors who are frequently cited together in the scientific literature. Unlike publication or citation analyses, co-citation analysis reveals the conceptual relationships among influential researchers and identifies the principal knowledge communities that have shaped the development of the field. Using VOSviewer with fractional counting, a co-citation network was generated to visualize the relationships among cited authors, as presented in Figure 9.

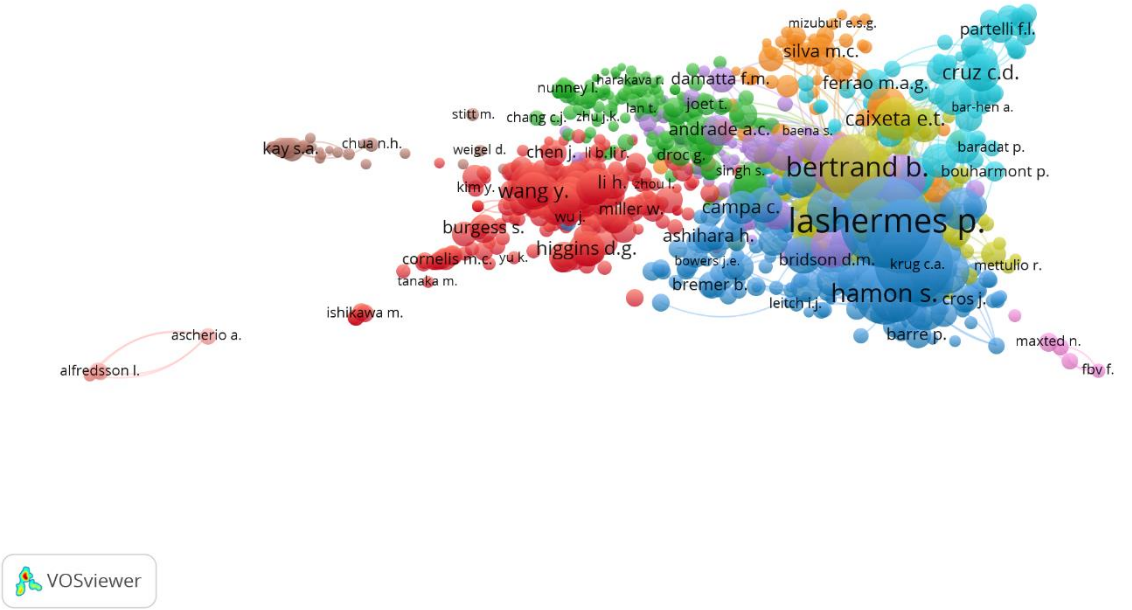

Figure 9. Network visualisation map of co-citation of cited authors

The resulting network reveals a densely connected intellectual structure composed of several interconnected clusters representing major research communities within coffee genetics and genomics. Lashermes P. occupies the most prominent and central position in the network, followed by other highly influential authors including Bertrand B., Hamon S., Caixeta E.T., Cruz C.D., and Partelli F.L. The large node sizes and extensive citation linkages among these authors indicate that their publications have served as fundamental references supporting subsequent research across multiple areas of coffee genetics, molecular breeding, genomics, and genetic resource conservation. The close connections among the dominant nodes further demonstrate that the intellectual development of this field has been driven by highly interconnected research communities rather than isolated scientific contributions.

A notable feature of the network is the presence of several well-defined co-citation communities linked through highly influential authors. The cluster centered on Lashermes P., Bertrand B., and Hamon S. forms the core of the network, reflecting their long-standing influence on the advancement of coffee genetics and genomics. Additional collaborative communities centered on researchers such as Caixeta E.T., Cruz C.D., and Partelli F.L. are closely connected to the main network, illustrating the complementary contributions of Brazilian and international research groups. The extensive interconnections among these communities indicate continuous knowledge exchange and the integration of diverse research approaches throughout the evolution of the field. The co-citation network also demonstrates strong consistency with the previous bibliometric analyses. Authors identified as the most productive contributors, particularly Lashermes P. and Bertrand B., also occupy the most influential positions within the co-citation network, indicating that high research productivity has been accompanied by substantial intellectual impact. This consistency strengthens the conclusion that a relatively small number of internationally recognized researchers have played pivotal roles in establishing the scientific foundation of coffee genetics and genomics.

From a tropical perspective, the co-citation structure highlights the importance of sustained international collaboration in advancing coffee genetic research. The central positions of authors from France and Brazil reflect the complementary roles of research-intensive institutions and major coffee-producing countries in generating influential scientific knowledge. These findings suggest that future progress in coffee genetics and genomics will continue to depend on strong international research networks integrating molecular genetics, genomics, bioinformatics, and breeding to conserve tropical coffee genetic resources and support the development of climate-resilient coffee cultivars.

3.10 Thematic Analysis and Future Research Directions

The bibliometric analyses conducted in this study reveal that coffee genetics and genomics research has undergone substantial conceptual transformation over the past five decades. The co-occurrence and overlay visualizations demonstrate that the field has evolved from conventional studies emphasizing genetic diversity and phylogenetic relationships toward increasingly sophisticated genomic, bioinformatics, and functional biology approaches. Rather than representing isolated research topics, the identified thematic clusters collectively illustrate the progressive integration of molecular genetics, computational biology, genome science, and plant breeding into a multidisciplinary framework supporting sustainable coffee improvement. This evolution reflects the growing recognition that conserving coffee genetic resources and improving cultivar performance require approaches that integrate biodiversity, genomics, and advanced analytical technologies.

The largest thematic cluster centers on coffee genetic diversity and germplasm conservation, represented by highly connected terms such as *coffee*, *Coffea arabica*, *genetic variability*, *genetic diversity*, *genetic marker*, and *polymorphism*. This cluster demonstrates that characterizing genetic resources has remained the intellectual foundation of coffee genetics research throughout the development of the discipline. Early investigations primarily employed molecular marker systems, including RAPD, AFLP, SSR, and TBP, to evaluate genetic relationships among cultivated and wild coffee populations. These studies established valuable baseline information for germplasm conservation and breeding while emphasizing the importance of preserving the extensive genetic diversity found within tropical coffee-producing regions, particularly Ethiopia, the primary center of origin of *Coffea arabica*. Despite significant advances in molecular characterization, future research should increasingly integrate population genomics, landscape genetics, and ecological genomics to better understand adaptive variation under changing environmental conditions and to strengthen the utilization of wild germplasm in climate-resilient breeding programs.

A second major research theme focuses on functional genomics and molecular regulation, characterized by closely associated terms including *gene expression*, *genetic transcription*, and *metabolism*. The prominence of these terms reflects a transition from descriptive genetic analyses toward mechanistic investigations exploring the molecular regulation of important agronomic traits. Studies within this cluster have increasingly employed transcriptomics and gene expression profiling to investigate pathways controlling caffeine biosynthesis, chlorogenic acid accumulation, sucrose metabolism, stress responses, and disease resistance. This transition demonstrates that coffee research is progressively moving beyond identifying genetic variation toward understanding how genes regulate economically important phenotypes. Nevertheless, many regulatory pathways governing adaptation to tropical environmental stresses remain insufficiently characterized, indicating substantial opportunities for integrating transcriptomics, metabolomics, and proteomics to reveal the complex biological networks underlying coffee productivity and quality.

The third thematic cluster emphasizes bioinformatics, sequencing technologies, and comparative genomics, represented by terms such as *DNA sequence*, *nucleotide sequence*, *sequence alignment*, *phylogeny*, *computational biology*, and *genome*. This cluster reflects the increasing dependence of coffee genetics research on computational methods for analyzing rapidly expanding genomic datasets. The citation analysis further supports this observation by identifying methodological publications describing sequence alignment algorithms and bioinformatics platforms among the most influential references within the field. These findings demonstrate that advances in coffee genomics have been driven not only by biological discoveries but also by continuous improvements in computational biology, genome assembly, sequence analysis, and comparative genomics. As sequencing technologies continue to become more accessible, future research is expected to increasingly employ pangenomics, structural variation analysis, and genome-wide comparative studies to accelerate the identification of genes controlling adaptation, yield, and beverage quality.

The overlay visualization further illustrates a clear temporal transition in research priorities. Earlier studies predominantly emphasized phylogenetic relationships, DNA sequencing, and genome characterization, whereas more recent publications increasingly focus on gene regulation, computational biology, sequencing technologies, and genomic analysis. This chronological shift reflects the rapid adoption of next-generation sequencing technologies and advanced computational approaches, enabling researchers to investigate increasingly complex biological questions. Importantly, the emergence of genomics-oriented topics demonstrates that coffee genetics has entered a new phase in which large-scale genomic resources, high-throughput sequencing, and bioinformatics have become indispensable components of scientific investigation.

Beyond the thematic evolution itself, the bibliometric evidence also reveals a highly collaborative international research ecosystem. Publication productivity, co-authorship, citation networks, and co-citation analyses consistently identify France and Brazil as the principal contributors to the intellectual development of coffee genetics and genomics. French research institutions have maintained long-standing leadership in molecular genetics, genomics, and breeding research, while Brazilian scientists have contributed substantially through extensive germplasm evaluation, quantitative genetics, and cultivar improvement. The close integration among these research communities illustrates that scientific advances have emerged through sustained international collaboration rather than isolated national efforts. Strengthening collaboration between research-intensive institutions and biodiversity-rich tropical countries will therefore remain essential for expanding genomic resources and accelerating scientific innovation.

Despite remarkable progress, several important knowledge gaps remain. Current research continues to be dominated by studies focusing on genetic characterization and gene discovery, whereas relatively fewer investigations integrate genomic variation with ecological adaptation, phenotypic plasticity, and long-term environmental responses. The limited availability of comprehensive genomic resources for many wild and underutilized *Coffea* species further restricts opportunities for exploiting valuable adaptive traits. Expanding reference genomes, pangenome resources, and functional annotation across diverse coffee species therefore represents an important priority for future research.

Future advances in coffee genetics and genomics will increasingly rely on multi-omics integration, combining genomics, transcriptomics, proteomics, metabolomics, and epigenomics to construct comprehensive models linking genotype to phenotype. Such approaches offer unprecedented opportunities to understand complex biological processes governing plant development, stress tolerance, secondary metabolite biosynthesis, and yield stability. At the same time, rapidly developing genome-editing technologies, particularly CRISPR-Cas systems, provide powerful tools for validating candidate genes and accelerating precision breeding. Although transformation efficiency remains challenging in *Coffea* species, continued methodological improvements are expected to expand the practical application of genome editing for coffee improvement.

Artificial intelligence and machine learning are also expected to become integral components of future coffee genomics research. The increasing availability of high-dimensional genomic and phenotypic datasets creates opportunities for predictive breeding, genomic selection, and data-driven decision support systems capable of identifying superior genotypes with greater efficiency than conventional breeding approaches. For tropical coffee production systems facing increasing pressures from climate change, emerging diseases, and fluctuating environmental conditions, AI-assisted genomic prediction represents a promising strategy for accelerating cultivar development while reducing breeding time and resource requirements.

From a tropical perspective, the thematic evolution identified in this study reflects a broader transition from descriptive molecular genetics toward integrative genomics capable of addressing the complex challenges facing global coffee production. Conserving tropical coffee biodiversity while simultaneously exploiting genomic innovation will become increasingly important for sustaining productivity under rapidly changing climatic conditions. Consequently, future research should prioritize interdisciplinary approaches integrating biodiversity conservation, functional genomics, computational biology, and genome-assisted breeding to support the development of climate-resilient coffee cultivars and ensure the long-term sustainability of tropical coffee agroecosystems.

4. Conclusion

This bibliometric study demonstrates the substantial evolution of coffee genetics and genomics research over the past five decades, progressing from conventional studies on genetic diversity and phylogenetic characterization toward integrative approaches combining functional genomics, bioinformatics, molecular breeding, and high-throughput sequencing. The findings reveal that scientific leadership is concentrated within a relatively small number of internationally recognized research communities, with France and Brazil playing pivotal roles in shaping the intellectual development of the field through strong publication productivity, collaboration, and citation impact. The thematic evolution identified in this study highlights the increasing importance of genomics-driven research for understanding coffee biology and supporting sustainable crop improvement. From a tropical perspective, the integration of biodiversity conservation with genomic innovation will be essential for developing climate-resilient coffee cultivars and ensuring the long-term sustainability of coffee production. Future research should therefore prioritize multi-omics integration, artificial intelligence-assisted genomic prediction, genome editing, and expanded genomic characterization of wild *Coffea* species to strengthen evidence-based breeding and conservation strategies.

Acknowledgement

The authors would like to express their sincere gratitude to the Directorate General of Research and Development, Ministry of Higher Education, Science, and Technology of the Republic of Indonesia, for the financial support provided through the Reputable Journal Publication Assistance Program 2025. This support has significantly contributed to the completion of this research and the publication of this article.

Author’s declaration

The authors declare that there are no competing interests, whether financial, professional, or personal, that could have influenced the work reported in this manuscript.

NP conceived the study and prepared the initial draft of the manuscript. SHA contributed to the development of the research methodology. LKF, RSKS, and MH critically reviewed and improved the manuscript. P contributed to data visualization and finalized the manuscript for submission. All authors have read and approved the final version of the manuscript.

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