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Global Scientific Overview of Somaclonal Variation in Strawberry Plant: Evolution, Networks and Research Frontiers

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Abstract

The strawberry plant (*Fragaria x ananassa*) has great economic and social importance, being widely propagated vegetatively by stolons. However, this method can favor the spread of diseases, making tissue culture an efficient alternative for the production of seedlings of high phytosanitary quality. Micropropagation, although widely used, can induce somaclonal variation, characterized by genetic and phenotypic alterations in plants regenerated *in vitro*. This variation can compromise the commercial uniformity of seedlings, but also represent as a source of genetic variability for breeding programs. Despite the growing scientific interest on the subject, there are still few studies that systematically synthesize and analyze the evolution of scientific production in this area. The objective of this study was to perform a scientometric analysis of the global scientific production on somaclonal variation in *Fragaria x ananassa*. The analysis was carried out using the scopus and web of science databases, with the help of the RStudio software for the mapping of scientific production for the entire period between 1970 (first article found) and 2025. Publications on somaclonal variation in strawberry grew 4.08 per year, with growth from 2018 onwards. Asia concentrated the largest number of studies, with emphasis on China. Regarding international collaborations, it was observed that 4.32% of the articles were published in co-authorship between researchers from different countries. The analysis of the key terms indicated three main research axes: (i) studies based on classical concepts of genetic variability, represented by the terms *evolution*, *selection* and *genetic diversity*; (ii) research focused on the relationship between micropropagation and somaclonal variation, highlighting the terms *micropropagation* and *somaclonal variation*; and (iii) investigations directed to genetic variability in strawberry, associated with the terms *Fragaria × ananassa*, *strawberry* and *genetic variation*. Thus, the present study provides a structured overview of the scientific evolution on somaclonal variation in *Fragaria x ananassa*, identifying knowledge gaps and pointing out strategic directions for future research, contributing to advances in micropropagation techniques and genetic improvement of strawberry.

Introduction

The strawberry plant (*Fragaria x ananassa*) is a fruit tree of great economic importance in several regions of the world, appreciated for its flavor, aroma and nutritional value (Banerjee et al., 2023; Mondal & Valliath, 2023; Mukherjee & Gantait, 2024). Its traditional propagation occurs mainly through stolons, lateral stems that develop from the parent plant and form new plants (Sharma et al., 2025; Toyoda et al., 1991). However, this method has limitations, such as the low multiplication rate and the risk of spreading diseases, especially viruses, which can reduce productivity and fruit quality over successive production cycles (Banerjee et al., 2023; Mondal & Valliath, 2023). In this context, plant biotechnology, in particular micropropagation, acts as a promising tool for the propagation and improvement of strawberry plants. This technique allows for the rapid and large-scale multiplication of vigorous and disease-free plants from small tissue parts or cells grown under aseptic and controlled conditions (Banerjee et al., 2023; Neri et al., 2022).

Despite the advantages of micropropagation, during the *in vitro* culture process a phenomenon known as somaclonal variation can occur (Krishna et al., 2016; Kumar Maurya & Bahadur, 2022). Somaclonal variation refers to genetic and, consequently, phenotypic changes that arise in cells of plants grown *in vitro*, resulting in differences between the regenerated plants and the mother plant(Kumar Maurya & Bahadur, 2022; Niemirowicz-Szczytt, 1990). These changes can be induced by several factors associated with the cultivation conditions, including the presence of growth regulators, the physiological stress resulting from the *in vitro* environment, and the number of subcultures performed (Krishna et al., 2016; Rodríguez-Enríquez et al., 2011).

Somaclonal variation can manifest in different ways, affecting morphological characteristics, such as plant height, leaf morphology, and plant architecture, as well as agronomic characteristics, such as yield and fruit quality (Paul & Singh, 2021; Yoo et al., 2022). The genetic underpinnings of these changes are complex and can involve gene mutations, changes in the number and structure of chromosomes, somatic recombination, and epigenetic changes such as DNA methylation(Krishna et al., 2016; Kumar Maurya & Bahadur, 2022; Rodríguez-Enríquez et al., 2011).

The occurrence of these modifications can compromise the uniformity of the micropropagated plants, which is undesirable for commercial production, which seeks homogeneous genetic materials (Naing et al., 2019). On the other hand, this variability can also be exploited as a source of genetic diversity for strawberry breeding, allowing the selection of plants with new desirable agronomic characteristics, greater resistance to diseases, tolerance to water or saline stresses, or improvement in fruit quality(Biswas et al., 2009; Yoo et al., 2022).

Despite the relevance of somaclonal variation to producing strawberry seedlings, scientific knowledge about this phenomenon in *Fragaria x ananassa* is still fragmented in the literature, with studies distributed among different methodological approaches, scales of analysis and experimental approaches. Thus, there is still a lack of quantitative synthesis capable of integrating this information and allowing the understanding of the temporal evolution of research, the geographical distribution of scientific production, as well as the main authors, journals, collaboration networks and thematic trends associated with this field of study.

Therefore, we aim with this work to perform a scientometric analysis of the global scientific production on somaclonal variation in *Fragaria x ananassa* to identify temporal, geographic and collaborative patterns, map the conceptual structure of the area and highlight gaps and emerging trends in the research. By providing a systematized view of the scientific development of this theme, the study aims to contribute to the direction of future investigations and to the strengthening of research in biotechnology applied to horticulture.

Material and methods

Data collection and selection

The search for publications was carried out on the Web of Science (WoS) and Scopus databases. Records were retrieved when they included topic-related terms in the title or abstract fields using the following search string: ("*strawberry*" OR "*Fragaria x ananassa*" OR "*Fragaria*") AND ("*somaclonal variation*" OR "*somaclonal variability*" OR "*genetic instability*" OR "*genetic variation*" OR "*epigenetic variation*" OR "*clonal instability*"). The search covered the entire period of publication and indexing of databases, covering the years 1945 to December 2025 for Web of Science and from 1988 to December 2025 for Scopus. The screening and selection of studies were conducted according to the guidelines of the PRISMA method (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) (Page et al., 2021). Review articles, letters, corrected versions of previously published studies, as well as articles that did not fall within the scope of this study were excluded. For inclusion criteria, only articles that addressed somaclonal variation in *Fragaria x ananassa* were considered.

Scientometric analysis

After the selection stage, the article records were processed in the statistical software R version 4.5.2 (R Core Team, 2025), where the files from the different databases were merged and the duplicates removed. The identification of the duplicates was initially carried out by the DOI and, in its absence, by the title of the publications. The compiled data were later analyzed in RStudio, using the Bibliometrix package, with the objective of carrying out the scientific mapping of the area (Aria & Cuccurullo, 2017). Bibliometric indicators were analyzed, such as number of publications per year, collaboration between countries, number of articles per author, most productive authors, and the temporal evolution of the scientific production of the main authors. The productivity of the researchers was evaluated using the h-index (Hirsch & Cardona, 2007) and the number of citations per article. The descriptive metrics were calculated considering the 10 most productive authors in the area.

A three-field graph, based on the Sankey diagram, was generated to visualize the relationships between the top 10 authors, 10 keywords, and 10 journals, also using Bibliometrix (Aria & Cuccurullo, 2017). To analyze the conceptual structure of the research on somaclonal variation in *Fragaria x ananassa*, the temporal trends of the main keywords were evaluated and the analysis of the conceptual structure of the scientific production was performed.

Results

Selection of studies and characterization of the base

The search in the Web of Science (WoS) and Scopus databases resulted in the retrieval of 136 and 174 papers, respectively. After the application of the filtering protocol (PRISMA), 109 papers from WoS and 137 from Scopus were selected. Subsequently, duplicates were removed, resulting in 139 papers that were reliable for the scope of the study (Fig. 1).

The first identified article was published in 1970. Thus, the period analyzed comprised the years 1970 to 2025. The 139 selected articles were published in 94 scientific journals. The average annual growth in the publication of scientific articles was 4.08 articles per year, with an average citation rate per document of 21.73. In total, 555 authors were identified as involved in publications on the subject, and 4.3% of the papers presented collaboration between authors from different countries (Table 1).

Table 1
Main metrics analyzed from the studies screened on the somaclonal variation in *Fragaria x ananassa*.

Metrics	**Value**
Timespan	1970:2025
Sources (Journals, Books, etc)	94
Documents	139
Annual Growth Rate %	4.08
Document Average Age	11.4
Average citations per doc	21.73
References	4208
Keywords Plus (ID)	628
Author's Keywords (DE)	430
Authors	555
Co-Authors by Doc	4.9
International co-authorships %	4.317

Geographical distribution and scientific collaboration

The geographical distribution of the publications showed a strong performance of research groups in the Asian continent, with 68 records, which represents the largest portion of the studies analyzed (Fig. 2). This result is mainly driven by China (28 publications) which leads the global ranking, followed by South Korea (14), Indonesia (11) and India (7). Together, these countries correspond to approximately 49% of the available publications. Europe represents another important center of scientific production in this area, with 18 publications, distributed mainly between Norway (6), Finland (4) and the United Kingdom (4), in addition to contributions in France, Germany and Italy. In North America, 13 publications were identified, mostly concentrated in the United States (12). Meanwhile, in South America, the highlight is Chile (6), responsible for all the publications of the continent in the set analyzed. The African continent

and Oceania had a reduced participation, with 3 publications each, represented by Morocco and Australia, respectively. Brazil does not have any publications on the subject studied.

The research groups from China and the USA led the number of publications and the international collaboration network confirms this leadership, revealing that they not only produce more, but also establish the main axis of scientific cooperation, with the most robust link in the graph. The European research groups act as important intermediaries in these connections, establishing links with Asian and North American countries as well as with South America, evidencing the globalized character of research on somaclonal variation in *Fragaria x ananassa*.

Temporal evolution of scientific production

Scientific production on somaclonal variation in plants of the genus *Fragaria* began in 1970 and fluctuated over the decades, with a more significant increase from the 2010s onwards. The year 2020 concentrated the highest number of publications (13 articles), followed by 2023 (10), 2021 (9), and 2022 (9), indicating recent and growing interest in the topic (Fig. 3).

Authorship and contribution standards

Despite the increase in scientific production on the somaclonal variation in *Fragaria* over the years, it remains relatively fragmented, with low recurrence of authorship. Considering the 139 articles analyzed, 555 authors were identified, with an average of 0.25 articles per author, indicating that most researchers contributed with only one publication. This pattern suggests that studies on somaclonal variation in *Fragaria* are conducted, in large part, by different research groups, with occasional participation of the authors over time.

Among the most productive authors are Whitaker VM (n = 8), Shaw DV (n = 6), and Ashman TL (n = 5), respectively linked to the University of Florida, Florida (USA), University of California, Davis (USA), and University of Pittsburgh (USA) (Fig. 4). When considering the h-index metric, the same authors also stand out within the set of publications analyzed: Whitaker VM (h = 7), Shaw DV (h = 5), and Ashman TL (h = 4). There is also a predominance of researchers linked to North American institutions among the most engaged authors. In terms of national distribution of publications, 28 articles were conducted by research groups from China, 14 from South Korea, and 12 from the United States, evidencing the international relevance of the theme. It is also noteworthy the absence of Brazilian publications related to the theme in the set analyzed. Among the most productive authors, Shaw DV stands out as one of the pioneers in the area, with publications between 1996 and 2009, followed by Ashman TL with publications between 1999 and 2015, and Whitaker VM with more recent publications from 2012 to 2024.

The papers with the greatest impact, considering the total number of citations, are mainly concentrated between the end of the 1990s and the beginning of the 2000s, a period in which studies were published that became references for the understanding of the somaclonal variation in *Fragaria x ananassa*. The

work of Bhat & Subbarao (1999)(287) stands out, with the highest absolute number of citations, followed by classic studies of and Wilson et al. (1999) (100)and Ashman (2003) (97), which exerted a lasting influence on the area. In contrast, more recent publications, but with a lower total number of citations, exhibit high annual citation rates, indicating increasing scientific impact. In this context, the study reached the Zhang et al. (2020) highest average number of citations per year (11.84), evidencing the current relevance of contemporary approaches and recent methodologies for the advancement of knowledge about somaclonal variation in strawberry plants.

Thematic structure and conceptual evolution

The thematic structure of the scientific production on the somaclonal variation in strawberry was analyzed based on the relationship between authors, indexing terms and scientific journals (Fig. 5). A concentration of terms associated with the name of the species studied, both scientific and popular (*strawberry, Fragaria and Fagaria x ananassa*) was observed. These terms are predominantly connected to keywords related to genetic variability and plant biotechnology, such as somaclonal variation, genetic variation, genetic diversity, and micropropagation. This pattern indicates that the topic is mostly investigated in the context of tissue culture and applied genetics. In the publication channels, the studies are distributed in consolidated journals in the large area of agricultural sciences, such as the Journal of the American Society for Horticultural Science, a journal whose terms are included in greater quantity, followed by horticulture research and Horticulture Research Frontiers in Plant Science.

The conceptual structure of the research field was examined through the analysis of the conceptual structure based on the dimensional reduction of the keywords (Fig. 6). The dimensional reduction resulted in two main dimensions that, together, explain the significant variability of 89.16% of the data (Dimension 1: 65.99% and Dimension 2: 23.17%), indicating high representativeness of the model. The cluster analysis revealed the formation of three distinct thematic groups. The first group, located in the upper left quadrant (in blue), associates terms such as "*evolution*", "*selection*", "*heritability*" and "*genetic diversity*", reflecting studies focused on population genetics, classical breeding and evolutionary aspects of the crop. The second group, positioned in the lower central region (in red), concentrates the taxonomic object of study ("*strawberry*", "*Fragaria*", "*Fragaria x ananassa*") associated with "*genetic variation*", serving as the nucleus that connects the crop to its variations. Finally, the third group, isolated in the upper right quadrant (in green), connects "*micropropagation*" and "*somaclonal variation*", highlighting a small or little explored niche of specific research where biotechnology and tissue culture are the primary tools, clearly differentiating itself from conventional breeding approaches.

The temporal evolution of the main keywords showed the progressive consolidation of approaches related to genetic variability in studies with *Fragaria* (Fig. 7). The use of the term '*Fragaria x ananassa'* appears more consistently from 2003 onwards, following the taxonomic standardization of the crop in scientific literature. The term *'somaclonal variation'* has been incorporated into studies since 2009, reflecting the increased interest in biotechnological approaches associated with tissue culture. Other terms such as *'genetic diversity'*, *'evolution'* and *'selection'* have had greater recurrence in more recent

periods, indicating the gradual integration between genetics, breeding and biotechnology studies in the investigation of genetic variability of strawberry plants.

The scientometric analysis of the scientific production on somaclonal variation in *Fragaria x ananassa* shows recent growth, although the area presents thematic fragmentation, low recurrence of authorship and geographic concentration of scientific production. Classical studies have established important bases for the understanding of the genetic mechanisms associated with somaclonal variation, it is observed, for example, that contemporary approaches remain concentrated in specific research niches, especially linked to micropropagation and tissue culture.

The conceptual structure of the field reveals a partial dissociation between conventional genetic improvement studies and biotechnological-based research, indicating opportunities for greater methodological and interdisciplinary integration. In this context, the expansion of international collaborations, the strengthening of continuous lines of research, and the incorporation of molecular and epigenetic tools emerge as promising paths for the advancement of knowledge and for a more consistent application of somaclonal variation in the breeding and sustainable production of strawberry.

Discussion

The scientometric analysis of the scientific production on somaclonal variation in *Fragaria x ananassa* revealed a recent growth in scientific interest in the subject, although the field still presents thematic fragmentation, low recurrence of authorship and geographical concentration of scientific production. These results indicate that, despite the relevance of somaclonal variation for strawberry micropropagation and breeding, the area remains relatively restricted to certain research groups and regions of the world. In recent years, several studies have contributed to evaluating the impacts of this anomaly and the functioning of tissue culture techniques, resulting in the establishment of different protocols aimed at understanding the causes and consequences of genetic and epigenetic alterations associated with *in vitro* culture. Even so, research on this topic remains relatively little disseminated in scientific literature.

The panorama of world production shows a strong contribution from countries such as China, South Korea and the USA, which together represent approximately 49% of the publications identified in this study These countries also stand out for their world leadership in research related to plant tissue culture as described by Negi et al. (2024) andPérez-Molina et al. (2025). The Asian continent leads in number of publications, due to the high production of this crop on this continent, totaling 5 million tons (48.7%) in 2024 (FAO/ONU, 2025). In addition, the presence of consolidated scientific infrastructure and continuous investments in plant biotechnology favors the development of research in this area. The U.S. leads the Americas in the number of publications, as well as the most productive researchers. The collaboration network analysis showed that China and the US form the main axis of international cooperation, while European groups act as important intermediaries, establishing connections between different regions. The prevalence of these countries within this thematic axis corroborates the concern about geographic

inequality within science, where the technological epicenter, investments and infrastructure of the entities and universities that apply and develop research with somaclonal variation are only in these countries, implying the exclusion of sub-regions.

The temporal analysis of scientific production provides a comprehensive view of studies published over the time frame between 1970 and 2025. The evolution of the number of publications, although increasing, was not uniform with years such as 1971 to 1986 without any publications. The cumulative frequency of publications revealed that more than 57% of studies on somaclonal variation in strawberry were published in the last decade, reflecting the recent increase in this area. This growth may be associated with advances and refinement in tissue culture techniques and, especially, with the development of molecular tools and genotyping technologies capable of detecting genetic anomalies with greater precision. This growth trend coincides with the technological transition observed in literature, while the initial decades relied on dominant and less reproducible markers, such as the RAPD (Porebski & Catling, 1998). In contrast, the recent increase in the volume of publications goes hand in hand with the adoption of codominant markers, such as microsatellites (SSR), which allow for more robust assessments of the genetic stability of micropropagated plants (Park et al., 2010). The use of these tools enabled greater reliability in the genetic validation of regenerated plants, as demonstrated by Thakur et al. (2023), who combined different methodologies to assess genetic homogeneity *in vitro* propagated materials.

The authorship analysis of these studies demonstrated that few researchers are engaged in research on this topic. Considering the 139 articles analyzed, the average was only 0.25 articles per author, and approximately 85% of the researchers contributed with only one publication. This pattern indicates that many studies are conducted in a punctual or exploratory manner, without continuity by the same research groups. This behavior may reflect both the thematic fragmentation identified in this study and the interdisciplinary nature of the theme, which often involves researchers in the areas of genetics, biotechnology, plant physiology and plant breeding.

The conceptual structure of the research field was grouped into three main sets, which correspond to the grouping of words that occur and interconnect. The first, composed of the term's *evolution, selection e genetic diversity*, which represents the classical theoretical basis associated with genetic diversity and the evolutionary processes involved in the domestication and improvement of the strawberry plant. Fan & Whitaker (2024) demonstrated that the process of recombination and artificial selection involves recurrent introgressions between wild and cultivated populations of *Fragaria x ananassa*, in addition to clear signatures of divergent selection throughout domestication and adaptation to different productive environments. This breadth of diverse collections of species indicates that the genetic variability and current population structure is the result of a continuous interaction between natural evolutionary processes and anthropogenic selection (Muñoz et al., 2024). Studies conducted in different regions, such as Europe (Prohaska et al., 2024) and the United States (Zurn et al., 2022), also indicate structural patterns associated with the geographic origin and selection history of cultivars. The cluster formed by evolution, selection and genetic diversity, therefore, represents the epistemological core of the field, from

which more recent investigations on genetic stability, vegetative propagation and induced variation unfold.

The second conceptual grouping, structured by the terms *micropropagation and somaclonal variation*, shows an inflection in the field of strawberry research, in which genetic variability is no longer interpreted as a product of evolutionary processes and becomes a possible consequence of *in vitro* cultivation conditions. Somaclonal variation, defined as genetic or epigenetic alterations observed in plants regenerated via tissue culture, has been described as a result of the interaction between oxidative stresses, hormonal imbalances, successive subcultures, and the type of explant used (Majumder et al., 2025). This study was conducted by Bae et al. (2022) a laboratory with cryopreserved and propagated *in vitro* accessions demonstrated that procedures such as vitrification and exposure to concentrated solutions can represent sources of cellular stress with risk of inducing polymorphisms detectable by molecular markers. The influence of the micropropagation protocol on genetic stability has also been demonstrated in different strawberry cultivars regenerated from meristems grown under different concentrations of cytokinin (Naing et al., 2019). Thus, the consolidation of the term somaclonal variation in the literature, which was initially described only as off-types or clonal instability, shows a conceptual maturity of the field, allowing molecular and epigenetic approaches to be incorporated. Therefore, cluster micropropagation – somaclonal variation represents the recognition that intensive clonal production requires close monitoring of genetic stability.

As for the *Fragaria x ananassa, strawberry and genetic variation* grouping, which are different from the previous clusters, which emphasize distinct origins of variability, this axis presents itself as an integrating unit of these dynamics. *Fragaria x ananassa* has a complex genetic constitution, being an allo-octoploid species resulting from interspecific hybridization. This genomic architecture expands heterozygosity and favors high genetic plasticity, which has historically supported breeding and adaptation programs to different productive environments (Zurn et al., 2022). At the same time, this complexity also requires rigor in maintaining genetic stability during vegetative propagation, especially in commercial micropropagation systems (Fan & Whitaker, 2024). The term genetic variation assumes an ambivalent character. On the one hand, variation is a strategic resource for breeding, allowing the selection of superior genotypes. On the other hand, unplanned variations, resulting from *in vitro* processes, can compromise phenotypic uniformity and agronomic performance (Bae et al., 2022; Naing et al., 2019). The intermediate position of this cluster in the structural map indicates a conceptual transition in the field, which explains the growth of studies aimed at the molecular evaluation of genetic stability, whether for the purposes of breeding, germplasm conservation or seedling certification. This axis gives coherence to the conceptual structure identified in this study, indicating a field that evolves the understanding of diversity towards the refined control of genetic stability.

The temporal evolution of the keywords evidences the recent inclusion of the term somaclonal variation, even with the description of the term being consolidated previously, other words were used to explain and name the changes, as well as effects because of the successive rebounds of the crops. In general, the results of this scientometric analysis demonstrate that research on somaclonal variation in

strawberry has evolved from approaches focused on the characterization of genetic variability to more integrated investigations involving tissue culture, molecular genetics and plant breeding. However, important gaps persist related to the geographical distribution of scientific production, the continuity of research lines, and the integration between different methodological approaches. The expansion of international collaborations, combined with the incorporation of emerging genomic and epigenetic tools, can contribute to the advancement of knowledge and the development of more efficient strategies for clonal propagation and strawberry breeding.

Conclusion

Over the last 55 years, studies on somaclonal variation and genetic instabilities in fragaria x ananassa have consolidated as an important biotechnological tool within tissue culture, with wide application in several species, but the effects and uses of this technique are still scarce when analyzing the scientific publications in these databases. Even with the constant increase in the number of publications over the years, many gaps still corroborate the non-diffusion of this technique. The scientometric analysis carried out in this work shows that China, the USA and South Korea play a strong leadership in research on this topic, together representing more than 50% of the publications, as well as leading, together with Europe, the construction of international partnerships that connect the research communities. The results of this study allow us to understand the structure and evolution of scientific production on somaclonal variation in Fragaria x ananassa, identifying influential authors, prominent journals and the main research topics. In addition, the mapping of trends and gaps in the field provides relevant subsidies to guide future research, especially those aimed at understanding the morphophysiological mechanisms associated with genetic instability and the potential use of this variability in micropropagation, adaptation and breeding programs of strawberry in global horticulture.

Declarations

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Author contributions

JLPA, AKML, LAD, ARN, FBS, PSAF and FGS conceived the research; JLPA and AKML performed data collection and analysis; JLPA, AKML, LAD, ARN, FBS, PSAF, and FGS wrote the paper. All authors have read and approved the final version of the manuscript.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

We declare that we have no financial and personal relationships with other people or organizations that can inappropriately influence our work, and there is no professional or other personal interest of any nature or kind in any product, service and/or company that could be construed as influencing the content of this paper.

"The authors do not have any relevant financial or non-financial interests to declare."

"The authors declare that there are no conflicts of interest relevant to the content of this article."

"All authors declare that they have no connection or involvement with any organization or entity that has a financial or non-financial interest in the subject matter or materials discussed in this manuscript."

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Figures

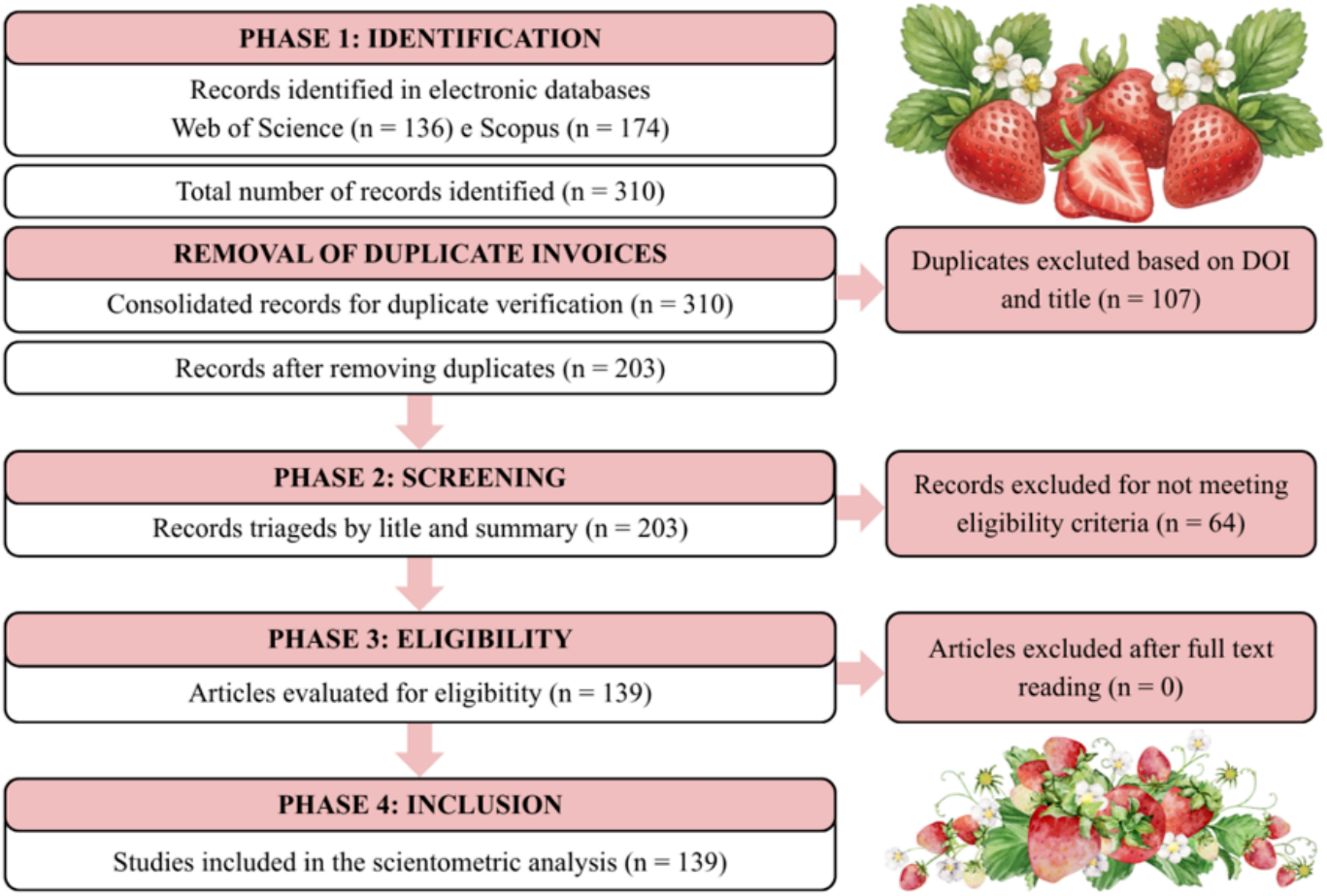


Figure 1

PRISMA Flowchart – Selection of studies included in the scientometric analysis.



Figure 2

World map of scientific collaboration in somaclonal variation *Fragaria x ananassa* (1970-2025). (Colors in stronger shades of blue indicate a higher volume of publications, while gray colors indicate a lack of publications on the subject).

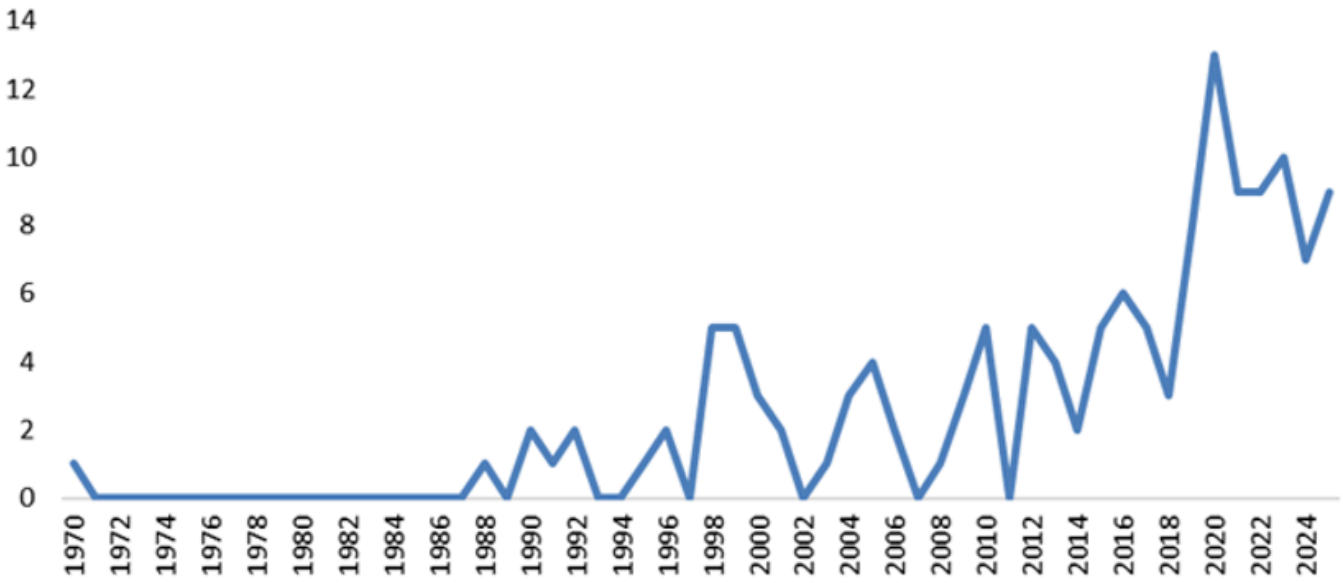


Figure 3

Scientific production on the somaclonal variation in *Fragaria x ananassa* in the last 55 years (1970-2025).

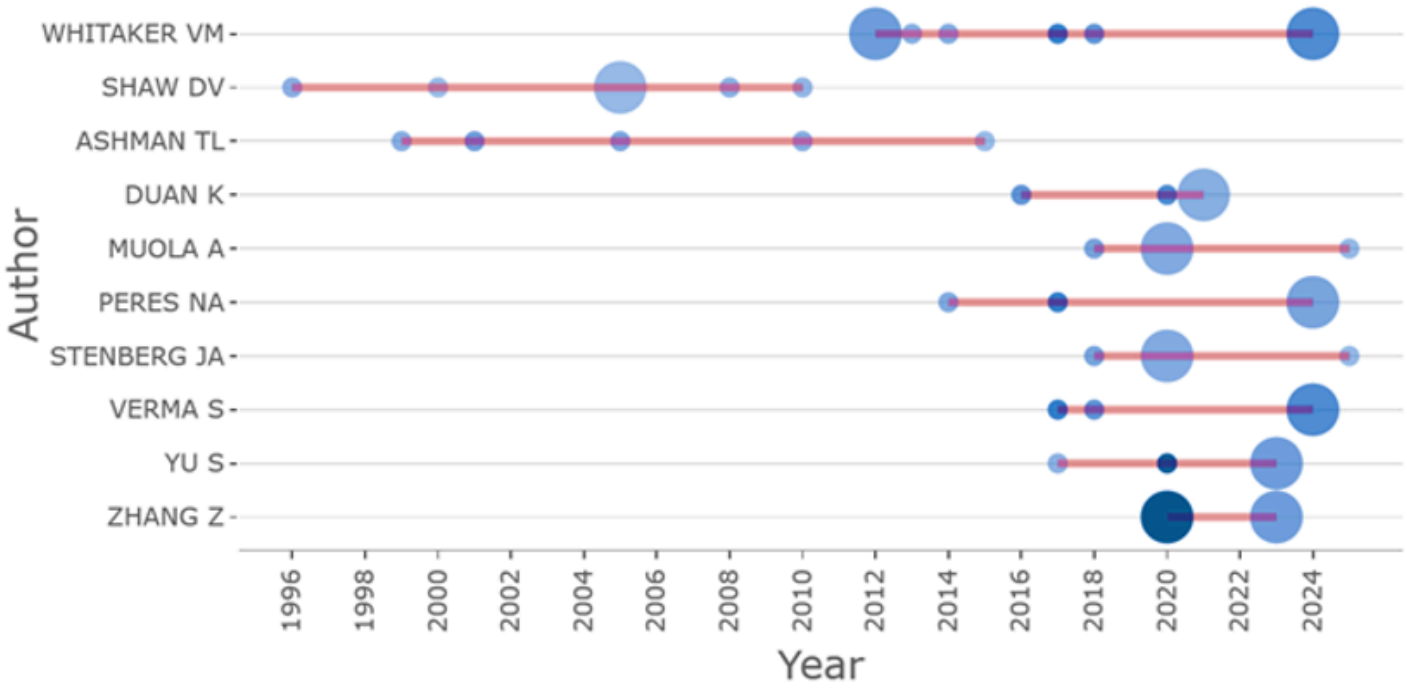


Figure 4

Temporal distribution of publications by the most productive authors in studies on somaclonal variation in *Fragaria x ananassa* (1996-2024). (The circles indicate the volume of publications of the author, the larger the circle, the greater the number of publications)

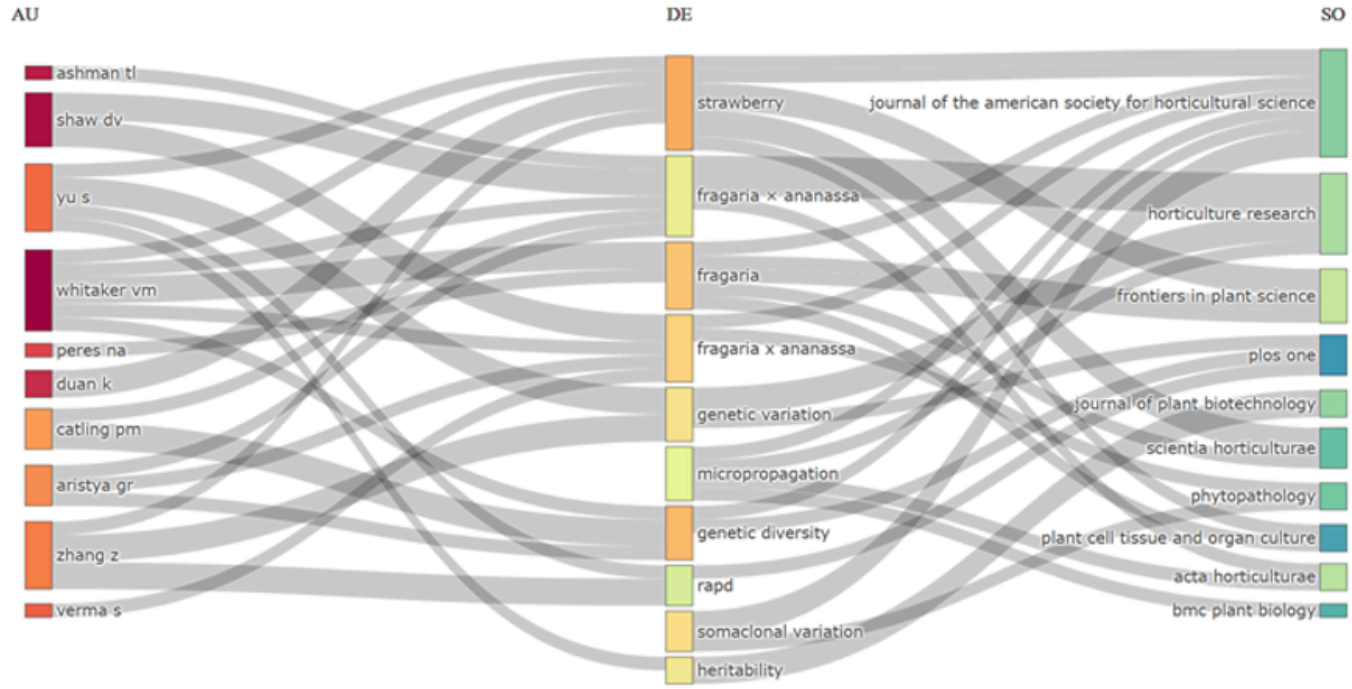


Figure 5

A three-field graph represents associations between authors, keywords and journals in the scientific production related to publications of somaclonal variation in *Fragaria x ananassa*.

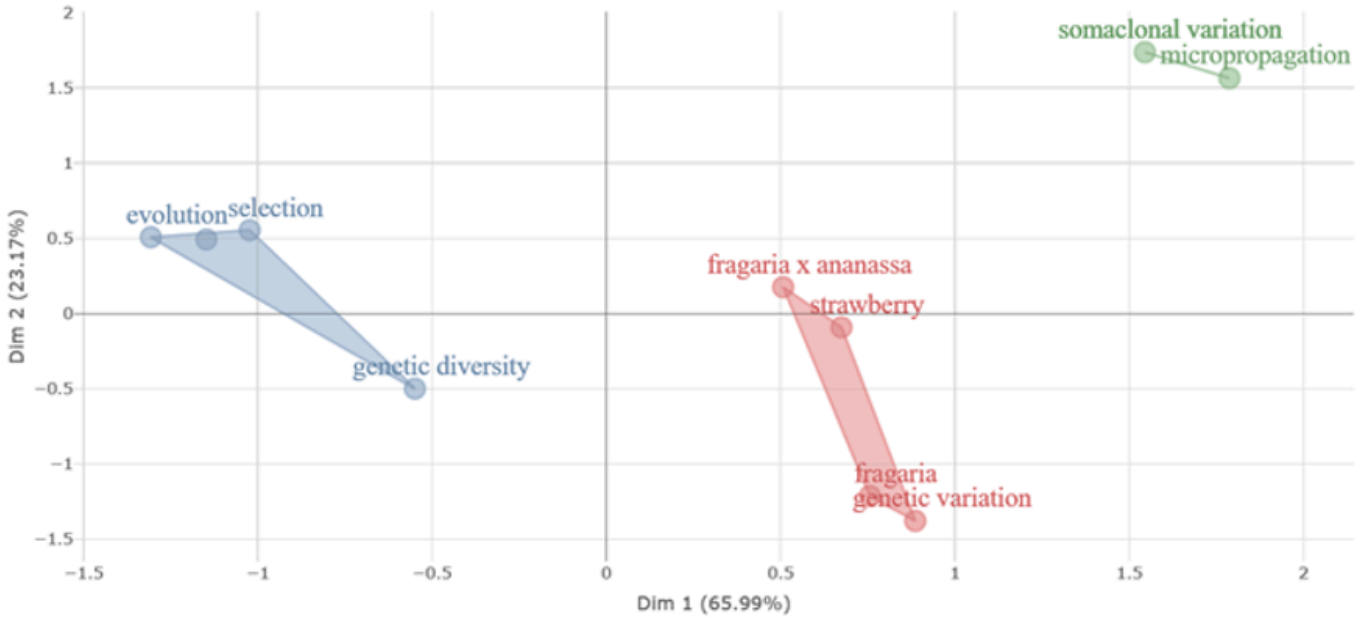


Figure 6

Conceptual structure of scientific production on somaclonal variation in *Fragaria x ananassa*.

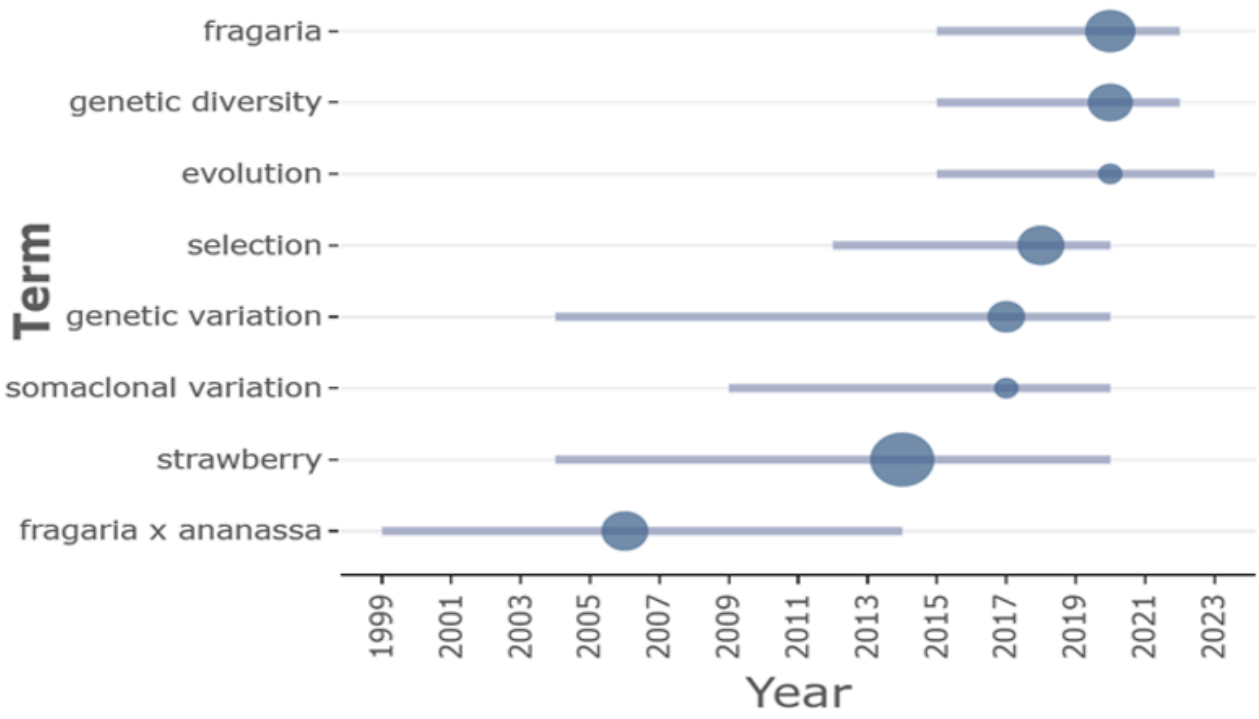


Figure 7

Graph of temporal trends of the Keywords referring to the publications on the somaclonal variation in *Fragaria x ananassa*.