





Review

Global Trends in Biotic and Abiotic Stress Mitigation Strategies for Common Bean: A Bibliometric Study

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Abstract

Common bean (*Phaseolus vulgaris* L.) is a cornerstone of global food security, yet its production is persistently challenged by biotic and abiotic stresses. This study conducted a bibliometric analysis following PRISMA guidelines on 549 documents published between 1971 and mid-2025, using Biblioshiny, VOSviewer, and CiteSpace. Results reveal a scientific output concentrated in leading institutions such as Michigan State University (MSU, USA) and the International Center for Tropical Agriculture (CIAT, Colombia). Collaboration networks are dominated by influential authors including Beebe, S. and Kelly, J.D., with Euphytica and Crop Science emerging as primary publication outlets. Research trends highlight salinity tolerance, oxidative stress, and chromosomal mapping, where advanced technologies such as SNP chips have supplanted RAPD markers. Critical challenges remain, including limited phenotyping capacity and the complexity of polygenic resistance, with urgent implications for developing countries where beans are vital for food security but face barriers to technology adoption and restricted participation in global research networks. Concurrently, mitigation strategies have shifted toward sustainable approaches, incorporating beneficial microorganisms for biotic stress and bio-stimulants or plant extracts for abiotic stress. Since 2020, the field has increasingly embraced multifunctional strategies leveraging natural mechanisms to enhance crop resilience. This analysis offers a comprehensive knowledge base to guide future research agendas.

Keywords: bibliometric analysis; crop resilience; food security; global research networks; molecular breeding; *Phaseolus vulgaris*



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1. Introduction

The common bean (*Phaseolus vulgaris* L.) is a staple food worldwide, valued for its high protein content, mineral composition, and bioactive compounds [1,2]. For centuries, it has played a fundamental role in food security and human well-being [3]. Its protein levels, ranging from 16% to 33% depending on the genotype [4], surpass those of other legumes such as faba bean (*Vicia faba* L.), cowpea (*Vigna unguiculata*) [5], lentil (*Lens culinaris* Medik), and chickpeas (*Cicer arietinum* L.) [6]. In addition, its integration into cropping systems reduces dependence on synthetic nitrogen fertilizers, thereby promoting soil health and

fertility while enhancing productivity [6,7], since this legume forms symbiotic associations with nitrogen-fixing bacteria [4].

Despite its nutritional and agronomic value, common bean productivity is constrained by multiple challenges, primarily biotic, and abiotic stresses [5,8–10]. Among biotic constraints, foliar diseases such as anthracnose (*Colletotrichum lindemuthianum*), angular leaf spot (*Pseudocercospora griseola*), rust (*Uromyces appendiculatus*), common bacterial blight (*Xanthomonas axonopodis* pv. *phaseoli*), common bean mosaic virus (BCMV), bean golden yellow mosaic virus (BGYMV) and scab (*Elsinoë phaseoli*) [11,12] are particularly destructive. Of these, anthracnose and BCMV are the most devastating, with potential yield losses of up to 100% and 70%, respectively, under favorable conditions [13,14].

These threats necessitate the development of more efficient and precise approaches for identifying genes associated with resistance to biotic stress [14,15]. Although progress has been made in discovering novel genetic sources and mapping genes and quantitative trait loci (QTLs), the durability of resistance is often undermined by the emergence of new pathogen races [14]. Sustainable alternatives include the development of varieties with durable resistance, either through the incorporation of quantitative resistance traits or pyramiding of multiple genes [14,16,17]. Breeding programs aimed at strengthening host resistance remain critical tools for disease management, particularly in developing countries [18,19]. However, reliance on single resistance genes has proven inadequate under field conditions, underscoring the need for strategies that integrate multiple genes to broaden both the spectrum and durability of resistance [12,20].

Abiotic stresses—including drought, salinity, and extreme temperatures—pose equally severe constraints on common bean production [21–23]. These stressors are exacerbated by global climate change and unsustainable agricultural practices, such as excessive fertilizer use [24], which contribute to the annual loss of 1–2% of arable land worldwide [25]. Drought, second only to diseases in its impact, affects approximately 60% of rainfed bean production and can reduce yields by up to 80% [26–28]. Its severity is amplified by the fact that water stress can occur at any developmental stage but is particularly detrimental during reproduction, when flowering and pod filling take place [29,30]. Enhancing drought tolerance has therefore become a central goal of bean breeding programs, requiring the identification of molecular markers to accelerate selection [31,32]. Progress, however, is hindered by the difficulty of testing genotypes across sufficiently diverse environments, since experimental water-stress trials rarely replicate the variability and complexity of field conditions [33,34]. Understanding how drought influences bean growth and yield is thus essential for advancing adaptive breeding [35,36]. The magnitude of stress-induced physiological impacts is shaped by both environmental factors—such as climate, soil characteristics, and CO₂ levels—and the genetic background of individual cultivars [33,37].

From a global perspective, numerous research groups across institutions worldwide have contributed to understanding biotic and abiotic stresses in common bean through diverse approaches. Their findings, disseminated through scientific journals and academic databases, have ensured broad accessibility and usability of the generated knowledge [38,39]. Against this backdrop, the present bibliometric review seeks to systematize and critically analyze the body of scientific literature on common bean stress responses, with a particular focus on biotic stresses (e.g., pests and diseases) and abiotic stresses (e.g., drought, salinity, and extreme temperatures). The objective is to provide an integrative perspective of the most developed research lines, highlight existing knowledge gaps, and identify potential synergies across disciplines. The insights gained will contribute to advancing the scientific agenda on this crop and its alignment with the production and environmental challenges faced in regions where common bean remains a vital food security resource [40,41]. Accordingly, this study sets out three specific objectives: (i) to

conduct a bibliometric analysis of scientific publications addressing biotic and abiotic stresses in common bean from 1971 to mid-2025; (ii) to identify the main thematic research trends in this field; (iii) to analyze the evolution of stress-mitigation strategies applied to common bean.

2. Materials and Methods

2.1. Database Selection

The most widely used databases for bibliometric studies are Web of Science, Scopus, and Dimensions [42]. For this study, Scopus was selected as the primary source due to its broad multidisciplinary coverage of peer-reviewed scientific literature [43], encompassing journals, conference proceedings, books, and other academic outputs. Notably, an estimated 99.11% of journals indexed in Web of Science are also covered by Scopus [42], ensuring comprehensive representation of scientific knowledge. Scopus further offers advanced search tools and citation-tracking capabilities that facilitate the retrieval of relevant records and the analysis of research trends, collaborations, and scientific impacts related to biotic and abiotic stress in common bean cultivation [44]. It should also be noted that Web of Science does not provide abstracts or keywords for articles published between 1965 and 1990 [45]; limiting its coverage of the study period.

2.2. Inclusion and Exclusion Criteria

Eligible documents included research articles, reviews, book chapters, and conference proceedings published in English, Spanish, Portuguese, Turkish, Chinese, Persian, or German. This linguistic scope was adopted to capture scientific advances generated across diverse regions, acknowledging the global relevance of biotic and abiotic stress in common bean production. Exclusion criteria applied to keywords referring to legume species outside the scope of this review, such as *Vicia faba* (broad bean), *Vigna radiata* (mung bean), *Glycine max* (soybean), *Cicer arietinum* (chickpea), *Lens culinaris* (lentil), *Pisum sativum* (pea), *Lupinus* spp. (lupin), *Arachis hypogaea* (peanut), and *Vigna unguiculata* (cowpea). The review was therefore restricted to *Phaseolus vulgaris* and other *Phaseolus* species. The time window was defined from 1971 to 2025, and the search was restricted to the subject area of Agricultural and Biological Sciences.

2.3. Search and Data Extraction Strategy

The study followed the PRISMA framework, a set of evidence-based guidelines that ensure transparency, methodological rigor, and reliability in systematic reviews [46]. An advanced search was performed in Scopus using Boolean operators (AND, OR, NOT). Core search terms included *Phaseolus vulgaris*, "common bean", "bean seeds"; *Phaseolus acutifolius*, and *Phaseolus coccineus*. These relatives of *P. vulgaris* were included as they are often used as reference species in genetic improvement and agronomic research due to their comparatively higher resilience to stress. These terms were combined with descriptors of biotic and abiotic stresses such as "salinity stress," "salt stress," "temperature stress," "heat stress," "cold stress," "drought stress," "water stress," "biotic stress," "disease resistance," "pathogen resistance," "pest resistance," "fungal infections," "bacterial infections," "viral infections," and "nematode resistance." Additionally, keywords related to management and mitigation strategies were included, such as "seed treatments," "priming," "coating," "biological methods," "chemical methods," "biostimulants," "growth enhancement," "resistance strategies," "tolerance strategies," "mitigation," "stress management," "microbial applications," "fertilization," "irrigation," "breeding," "genetic improvement," "biotechnology," "molecular approaches," and "physiological methods." Searches were restricted to the "TITLE-ABSTRACT-KEYWORDS" field.

The search was conducted on 19 June 2025, and results were exported in both comma-delimited (.csv) and plain text (.txt) formats. The initial search yielded 629 records. During the screening phase, 42 duplicates were removed using R software. Subsequently, three authors independently reviewed titles and excluded 38 records that were not directly related to stress factors in common bean, leaving 549 records for eligibility assessment. Abstracts of these records were then screened, and all were retained as they provided relevant information on biotic or abiotic stress in common bean. Ultimately, 549 documents were included in the bibliometric analysis (Figure 1).

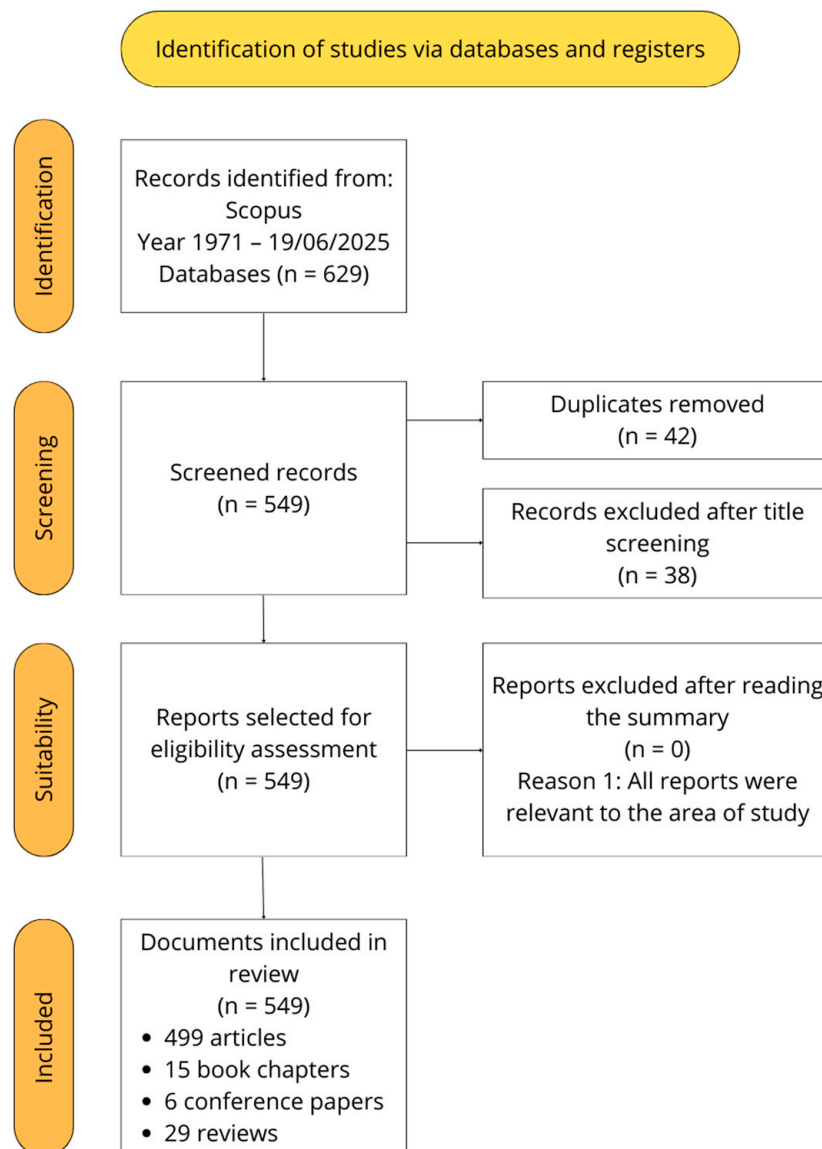


Figure 1. PRISMA flow diagram illustrating the study selection process for the bibliometric review of biotic and abiotic stresses in common bean (*Phaseolus vulgaris* L.).

2.4. Data Analysis

Quantitative analyses were conducted using Biblioshiny, the web-based interface of the Bibliometrix package in R version 4.4.1 [47]. Keyword mapping and co-occurrence networks were visualized with VOSviewer version 1.6.20, while author co-citation analysis was carried out using CiteSpace version 6.3.R1 [48]. For data management and statistical operations, including the calculation of percentages, regressions, and correlation analyses, datasets were exported from Biblioshiny in spreadsheet format (.xlsx) and subsequently processed in R.

3. Stress Factors in Common Bean

The production of common bean is severely constrained by a wide range of diseases and pests that occur throughout its phenological cycle, causing damage to different plant organs and ultimately reducing crop yield [49]. Table 1 summarizes the major biotic stresses affecting common bean (*Phaseolus vulgaris* L.) and the corresponding damage they inflict, based on evidence compiled from the 549 documents included in this review.

Table 1. Major biotic stress factors affecting common bean (*Phaseolus vulgaris* L.) and associated damage.

Fungal Diseases	Damage	References
Anthracnose (<i>Colletotrichum lindemuthianum</i>)	Infects leaves, stems, pods, and seeds, producing sunken necrotic lesions that may lead to yield losses of up to 100%.	[50,51]
Angular leaf spot (<i>Pseudocercospora griseola</i>)	Causes angular, depressed lesions on leaves, stems, and pods, leading to defoliation, reduced grain quality, and yield losses of up to 80%.	[52–54]
Rust (<i>Uromyces appendiculatus</i>)	Produces reddish pustules with a yellow halo on leaves, stems, pods, and seeds, reducing photosynthesis, pod filling, and grain quality, with yield losses reaching 67%.	[55,56]
White mold (<i>Sclerotinia sclerotiorum</i>)	Infects aerial parts during vegetative and reproductive stages, forming small water-soaked lesions that develop into white mycelium and black sclerotia. Leads to irreversible wilting, tissue necrosis, and yield losses up to 100%.	[57,58]
Root rot (<i>Rhizoctonia solani</i>)	Affects roots, producing reddish-brown necrotic lesions that cause seedling wilting. In severe cases, delays growth and induces premature plant death, with yield losses up to 100%.	[59,60]
Vascular wilt (<i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i>)	Infects the vascular system, causing foliar chlorosis, leaf drop, progressive wilting, and internal vascular discoloration, particularly in basal leaves. Early infections reduce growth and produce stunted plants, with yield losses up to 100%.	[61,62]
Powdery mildew (<i>Erysiphe polygoni</i>)	Primarily infects leaves, producing white powdery patches that cause curling and chlorosis. Severe infections cover foliage with mycelium reducing photosynthesis and the assimilation of carbon dioxide, with yield losses up to 69%.	[63]
Bacterial diseases	Damage	References
Common bacterial blight (<i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i>)	Produces necrotic spots with yellow halos on leaves, stems, pods, and seeds, causing yield losses up to 36%.	[64,65]
Bacterial halo blight (<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i>)	Produces chlorotic halos around necrotic lesions on leaves, pods, and petioles, with yield losses up to 43%.	[66,67]
Viral diseases	Damage	References
Bean Common Mosaic Virus (BCMV), Bean Common Mosaic Necrosis Virus (BCMNV), Bean Golden Mosaic Virus (BGMV), Cowpea Mild Mottle Virus (CPMMV)	Infect leaves, stems, pods, and seeds, causing mosaic patterns, chlorosis, deformation, necrosis, and reduced seed quality, with yield losses up to 35%.	[68,69]

Table 1. *Cont.*

Fungal Diseases	Damage	References
Insect pests	Damage	References
Bean weevil (<i>Acanthoscelides obtectus</i>)	Infects stores seeds; larvae bore into seeds while adults perpetuate infestation through oviposition, causing 7–40% yield losses.	[70–73]
Bean fly (<i>Ophiomyia phaseoli</i>)	Larvae mine stems and petioles, while adults feed on leaves and lay eggs. Leads to reduced growth, defoliation, and plant death in severe cases, with yield losses of 10–100%.	[74]
Thrips (<i>Frankliniella occidentalis</i>)	Feeds on leaf parenchyma and pollen, reducing photosynthetic activity. Also acts as a viral vector, with potential yield losses up to 60%.	[75]

Common bean is also exposed to multiple abiotic stresses that reduce yield potential and influence the performance of different genotypes across diverse environments. These stresses are further exacerbated by the effects of climate change [9]. Table 2 summarizes the main abiotic stresses affecting common bean, providing their definitions and descriptions of plant responses.

Table 2. Major abiotic stresses affecting common bean (*Phaseolus vulgaris* L.) and their physiological effects.

Type of Stress	Definition/Plant Effects	References
Drought	Refers to prolonged water deficit that reduces soil water availability and limits root absorption. It affects cell turgor, vegetative growth, and leaf expansion. Plants respond by stomatal closure, which decreases transpiration but also photosynthesis. Additional physiological changes include reductions in relative water content and stomatal conductance, along with increased antioxidant defenses and osmoprotectant accumulation in sensitive genotypes. Collectively, these responses reduce biomass and compromise pod filling and yield potential.	[76–78]
Salinity	Involves the accumulation of soluble salts in the rhizosphere, which decreases soil osmotic potential and restricts water and nutrient uptake. This stress impairs plant development and growth. Salinity frequently co-occurs with drought, thereby intensifying the abiotic stress burden on the crop.	[79,80]
Heat	Results from exposure to high temperatures over extended periods, leading to physiological alterations that disrupt reproductive processes, pollen viability, seed filling, and photosynthetic efficiency, ultimately reducing yield.	[81]
Cold	Caused by exposure to low temperatures, either chilling (0–15 °C) or freezing (<0 °C), leading to tissue injury, foliar wilting, and impaired physiological processes such as photosynthesis, metabolism, and stomatal function. Cold stress also induces the accumulation of reactive oxygen species (ROS), generating oxidative stress that compromises growth and productivity.	[82]

4. Bibliometric Analysis and Discussion

4.1. Analysis of Global Scientific Production

To assess the growth of publications and the variation in annual average citations, a combined bar and line chart was generated in R using annual scientific output and citation data exported from Biblioshiny (Figure 2). The dataset comprised 549 documents related to biotic and abiotic stresses in *P. vulgaris* (hereafter referred to as the “field of study”).

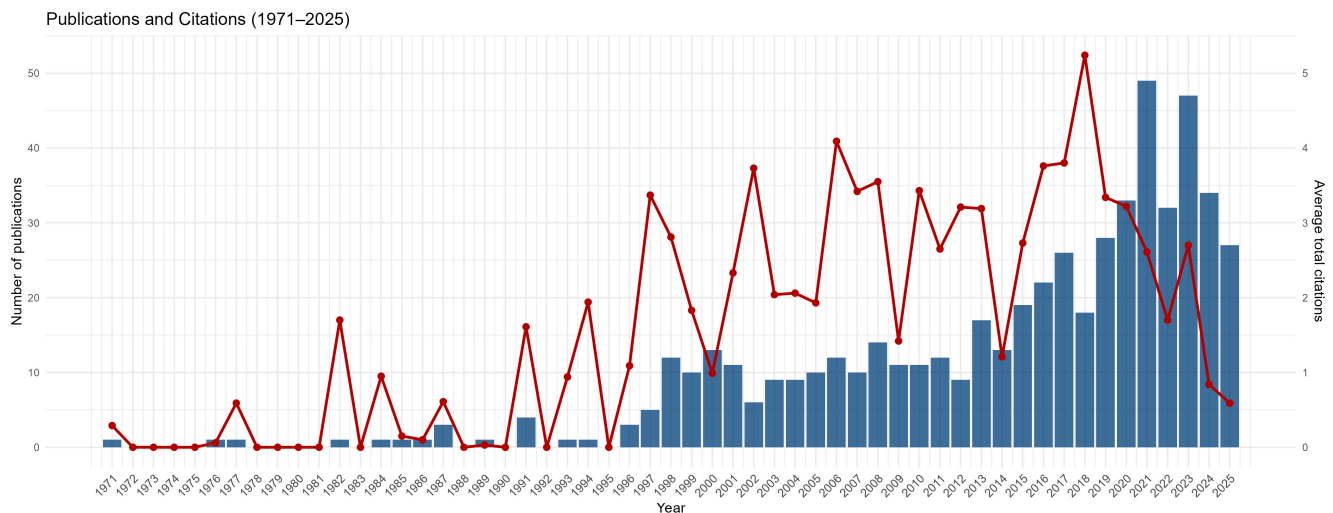


Figure 2. Annual trends in scientific output (blue bars, left axis) and average citations per article (red line, right axis) on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.) from 1971 to mid-2025.

The annual evolution of scientific production and citation rates was evaluated from 1971 to mid-2025. Scientific output displayed an annual growth rate of 6.29%, following a clear exponential trend with strong model fit ($R^2 = 0.867$). This pattern reflects the intensification of research interest in the field, likely driven by increasing recognition of common bean as a strategic crop for food security and climate change adaptation [83,84]. In contrast, the trend in average annual citations showed greater variability, with a second-degree polynomial model providing the best fit ($R^2 = 0.544$). This finding suggests that years of high publication output were not always associated with proportionally higher academic impact. Several factors may explain this discrepancy, including differences in journal visibility, the geographical scope of studies, or the applied and context-specific nature of many investigations, which, while highly relevant, often receive fewer immediate citations [85].

Furthermore, the relationship between the number of publications and the average number of citations per year was assessed using Spearman's rank correlation, as both variables deviated from normality (Shapiro–Wilk, $p < 0.001$). The analysis revealed a strong and highly significant positive correlation ($\rho = 0.78$; $p < 0.001$), confirming a general trend in which peaks of productivity were also associated with higher levels of academic impact. This pattern is likely linked to the accumulation of critical mass in specific research lines, such as drought tolerance or resistance to fungal diseases. At the level of individual contributions, the field is characterized by a markedly collaborative scientific community, with an average of 5.26 co-authors per article, only 21 single-authored papers among the 1,928 identified authors, and a mean document age of 10.7 years. This collaborative dynamic mirrors trends observed in other agricultural disciplines, where institutional partnerships are essential to address the multifactorial nature of biotic and abiotic stresses [86].

4.2. Countries, Affiliations, Authors, and Sources with the Highest Scientific Output

To identify the countries, institutions, authors, and journals with the highest productivity in this research field, we compiled a ranking of the top ten entities in each category based on the data processed in Biblioshiny (Table 3).

Table 3. Leading countries, institutions, authors, and journals in studies on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.).

Rank	Country	N	Affiliation	N	Author	N	Source (Q)	N
1	United States	97	Michigan State University	47	Beebe, S.	30	Euphytica (Q2)	36
2	Brazil	86	International Center for Tropical Agriculture	46	Kelly, J.D.	29	Crop Science (Q2)	33
3	Colombia	27	University of KwaZulu-Natal	43	Miklas, P.N.	25	Canadian Journal of Plant Science (Q3)	19
4	Spain	24	Universidade Estadual de Maringá	34	Singh, S.P.	19	Agronomy (Q1)	18
5	Turkey	24	Instituto Agronômico	28	Rao, I.M.	16	Frontiers in Plant Science (Q1)	16
6	India	20	North Dakota State University	27	Chiorato, A.F.	15	Theoretical and Applied Genetics (Q1)	15
7	Canada	19	Islamic Azad University	22	Carbonell, S.	14	Plants (Q1)	14
8	Mexico	19	Instituto Agronômico de Campinas	21	Porch, T.G.	14	Crop Breeding and Applied Biotechnology (Q3)	1
9	Iran	17	University of California	21	Pastor-Corrales, M.A.	13	Field Crops Research (Q1)	11
10	Egypt	15	University of Nebraska	20	Beaver, J.S.	11	Journal of the American Society for Horticultural Science (Q2)	11

Note: N: number of publications; Q: quartile.

Geographically, the United States and Brazil dominate scientific production, jointly accounting for 33.4% of the publications, with 97 and 86 documents, respectively. This concentration underscores the hegemony of countries with strong institutions and advanced technological capacities in crop breeding and physiology. Similar trends have been reported in other bibliometric studies, where the scientific dominance of high-income economies, particularly the United States, reinforces global asymmetries in knowledge generation [87]. In contrast, regions highly dependent on common bean as a food security crop, such as Sub-Saharan Africa (e.g., Cameroon, Ghana, Nigeria, Uganda, Zimbabwe) and parts of Latin America (e.g., Peru, Ecuador), remain underrepresented in the literature. This imbalance highlights the need to strengthen scientific and technological capacity in these regions to ensure a more equitable distribution of knowledge and the development of locally adapted solutions.

Among the most productive institutions, Michigan State University (MSU) and the International Center for Tropical Agriculture (CIAT) lead with 47 and 46 publications, respectively. MSU's leadership is supported by robust programs such as the Dry Bean Breeding and Genetics Program, which focuses on developing cultivars resistant to major diseases including rust, anthracnose (ANT), common bean mosaic virus (BCMV), white mold (WM), root rots, and common bacterial blight (CBB), while also targeting tolerance to drought and improved technological quality [88]. Furthermore, MSU coordinates the Feed

the Future Legume Systems Research Innovation Lab, funded by the United States Agency for International Development (USAID) with a budget of USD 13.6 million, which aims to strengthen legume production systems in Africa and Latin America through collaborative research, and is active until 2028 [89,90]. Similarly, CIAT played a pivotal role in the Tropical Legumes Project (2007–2019), an initiative supported by CGIAR and the Bill & Melinda Gates Foundation. This program released 266 improved varieties and nearly 500,000 tons of certified seed, benefiting more than 25 million smallholder farmers across Sub-Saharan Africa and South Asia [91]. In addition, CIAT has implemented recurrent selection programs to generate breeding lines with superior performance under drought and phosphorus-deficient soils [92].

With respect to individual productivity, Beebe, S. (CIAT) ranks as the most prolific author, followed by Kelly, J.D. (MSU), and Miklas, P.N. and Singh, S.P., both affiliated with U.S.-based institutions. The concentration of highly productive researchers within MSU and CIAT not only reinforces the leadership of these institutions but also constitutes a key factor underpinning the United States’ position as the leading country in scientific output in this field.

The 549 reviewed documents were published across 191 scientific journals, with *Euphytica* emerging as the most prolific outlet, concentrating the highest number of publications in the field.

The three-field plot generated in Biblioshiny (Figure 3) illustrates the relationships among authors (AU), their countries of affiliation (AU_CO), and publication sources (SO). Each rectangle represents a node, with its size proportional to its relevance within the network, while connecting lines indicate co-publications; thicker lines denote higher publication volumes. Beebe, S. emerges as the most internationally collaborative researcher, bridging multiple countries and journals, underscoring his strategic role in knowledge articulation and the promotion of international cooperation. Such “bridge researchers” have been identified as key actors in agricultural innovation, as they facilitate knowledge flows and technological adaptation across diverse agroecological contexts [93].

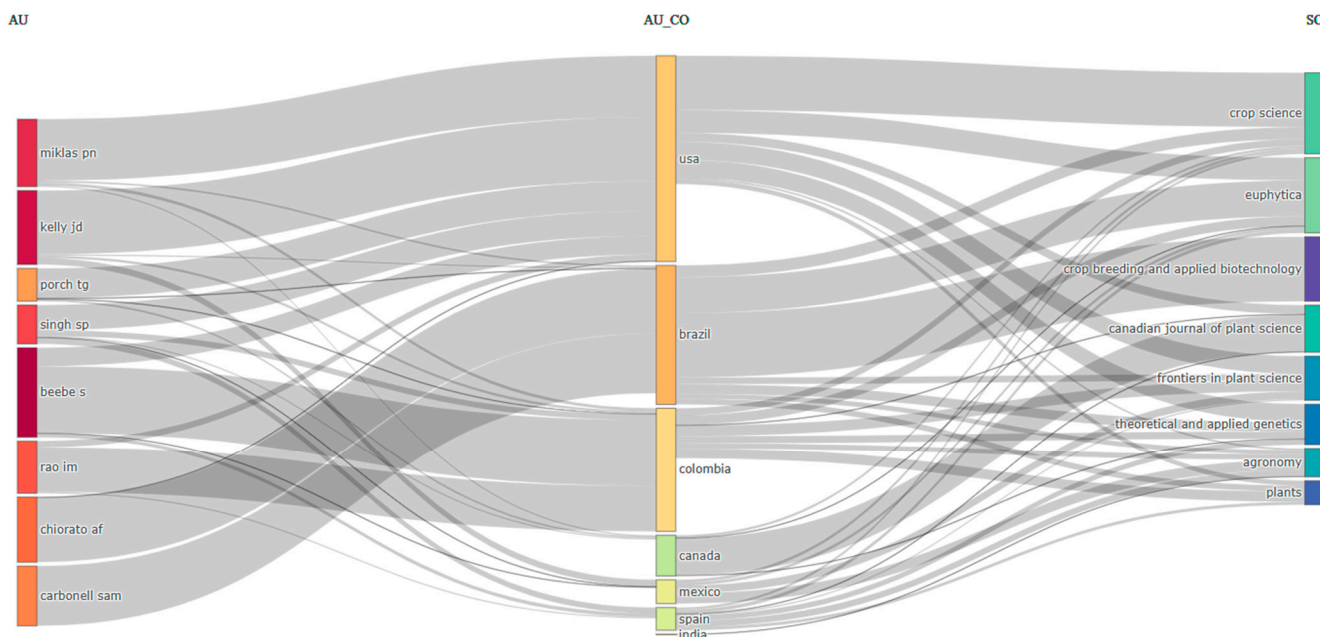


Figure 3. Three-field graph linking authors (AU), authors’ countries of affiliation (AU_CO), and publication sources (SO). Rectangle size represents each node’s relative weight in the network, while line thickness reflects the number of co-authored documents.

In terms of country-level networks, the United States, Brazil, and Colombia hold the majority of connections, reaffirming their leadership in scientific output. The predominance of publications in specialized journals such as *Euphytica* and *Crop Science* reflects both the community's preference for high-visibility outlets and the central role of these journals in validating and consolidating technical knowledge in plant genetics, breeding, and physiology. These journals serve as quality filters through rigorous peer review, ensuring the credibility of disseminated findings [94]. They also host many highly cited papers, making them strategic hubs within the scientific communication network and increasing the probability of broader academic impact [95]. Beyond academia, these journals function as intermediary platforms that indirectly channel innovations to agricultural development stakeholders, including extension services and participatory breeding programs [96].

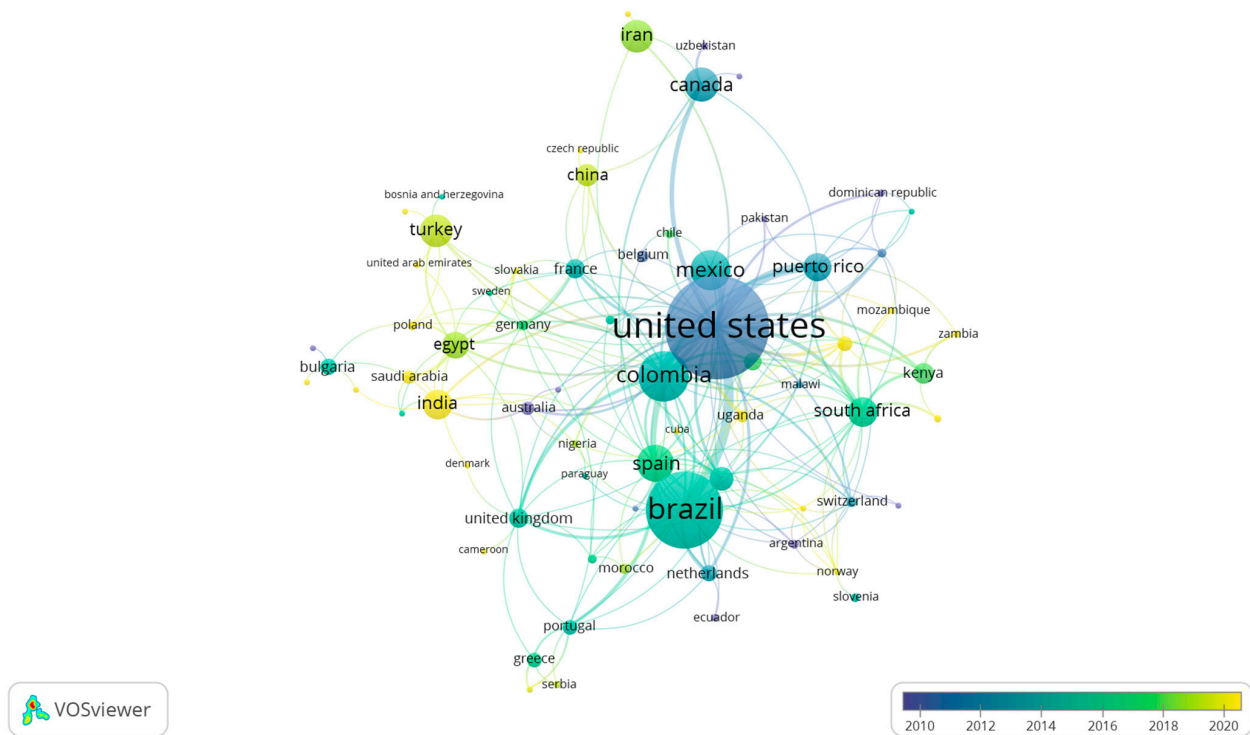
4.3. Local and International Collaboration

International collaboration in the field reached 33.64%, reflecting substantial participation of researchers from multiple countries in the production of scientific knowledge. To evaluate the extent and temporal evolution of cooperation, co-authorship networks were analyzed in VOSviewer, allowing identification of the most frequent connections and visualization of regional interaction dynamics over time. The results revealed a prominent international collaboration network, with strong partnerships between the United States and Brazil (21 joint publications) and between the United States and Colombia (10 publications). These countries occupy central positions in the co-authorship map due to their extensive linkages with both neighboring and distant partners. Temporally, the United States emerged as one of the earliest participants in collaborative research, while countries such as Iran, Turkey, China, and Egypt have strengthened their presence in more recent years. Newcomers such as India, Saudi Arabia, and Uganda, represented in yellow tones in the visualization, highlight the growing inclusion of traditionally underrepresented regions. (Figure 4A). This diversification is largely attributed to technological advances, reduced travel costs, and, critically, the initiative of scientists themselves to collaborate internationally, thereby enhancing research quality. Against the backdrop of global challenges such as climate change and food security, international scientific cooperation is indispensable [97]. A notable example is the development of black bean genotypes by USDA-ARS, the University of Nebraska, and the University of Puerto Rico, registered as germplasm with tolerance to multiple stresses. These genotypes exhibited superior yields under heat stress and comparable performance to controls selected for drought and heat tolerance [98]. Nonetheless, countries with low connectivity may face increasing isolation as central nodes continue to consolidate their collaborations [99].

Figure 4B presents the 20 most productive countries in the field. Single-country publications (SCP) represent documents authored within one nation, while multiple-country publications (MCP) indicate those produced through international collaboration. The MCP ratio was calculated as the proportion of internationally co-authored publications relative to a country's total output. Among the leading countries, the United States not only ranked first in publication volume but also in international collaboration, with an MCP ratio of 0.402. Portugal and Chile are particularly notable cases, as all their publications were produced in collaboration with foreign partners, yielding an MCP ratio of 1, indicative of full integration into international networks. By contrast, Iran registered an MCP ratio of 0, meaning that all of its publications were developed without external participation. Among these was a study highlighting the genotype KS21486 for its superior water-use efficiency (WUE) [100]. Such contrasts may be linked to institutional capacities, open science policies, or barriers related to language and logistics [101]. Overall, these findings reinforce that international collaboration not only broadens the reach of science but also enhances the

quality and visibility of academic production in research on biotic and abiotic stresses in common bean.

A



B

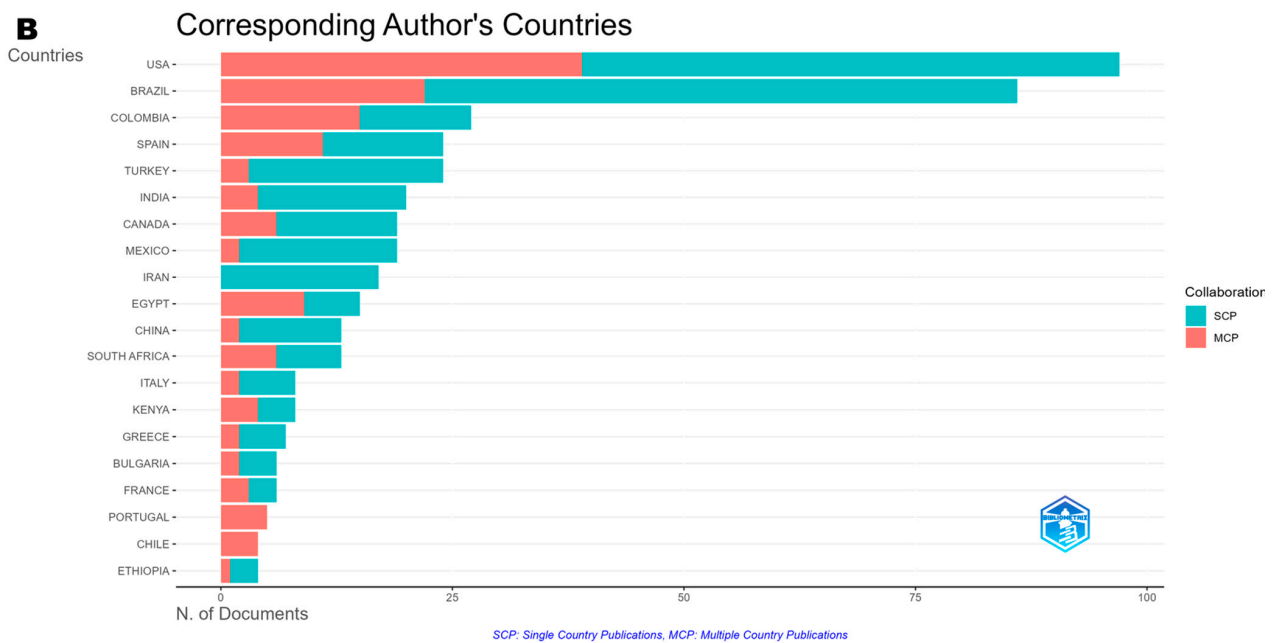


Figure 4. Networks and distribution of publications on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.). (A) International collaboration map generated with VOSviewer. Node size represents the number of publications per country, and line thickness indicates collaboration intensity. Colors reflect the temporal evolution of country participation, highlighting the progressive incorporation of new nations. (B) Distribution of documents according to the country of the corresponding author, distinguishing between single-country publications (SCP) and multinational publications (MCP).

4.4. Citation Analysis

To identify the countries, authors, and journals with the highest scientific impact, a ranking of the top ten in each category was generated based on citation data processed in Biblioshiny (Table 4). The ranking includes the total number of citations, h-index, g-index, m-index, and year of first publication for authors and journals.

The citation analysis revealed a strong concentration of scientific impact within a small number of countries, authors, and journals. The ten most-cited countries accounted for 80.1% of all citations in the field, with a total of 13,247 citations. Among these, the United States stood out with 4896 citations, representing 46.1% of the group total, thereby consolidating its position as the most influential country. This pattern aligns with previous findings showing that countries with high investments in research and development tend to dominate citation-based measures of scientific influence [102].

At the author level, the ten most-cited researchers accounted for 15.8% of the 75,519 citations accumulated across all authors. Within this group, Kelly, J.D. was the most prominent, with 2470 citations (20.7% of the top ten total) and the highest h-index (21). Among journals, *Euphytica* (Q2) emerged not only as the most productive outlet but also as the most cited (1919 citations; h-index = 19), underscoring its historical role in disseminating knowledge in this field. However, *Crop Science* (Q2), with 1879 citations and a higher h-index (22 vs. 19), reflected greater consistency in the average quality of its publications. Among Q1 journals, *Frontiers in Plant Science* showed rapid growth (m-index = 1.1 since 2016), while *Theoretical and Applied Genetics* maintained a strong contribution (h-index = 13). These findings corroborate observations by [103,104] that the evaluation of scientific influence requires considering both productivity and quality through composite indicators (h-, g-, and m-indices), as publication volume alone does not guarantee proportional recognition. Furthermore, the concentration of citations among a small group of authors supports prior bibliometric evidence [105,106] that a minority of researchers attain disproportionate visibility through consolidated collaboration networks and publication in high-impact journals, thereby amplifying citation rates.

To further assess research impact, a ranking of the ten most-cited documents in the field was compiled, including publication source, year, total citations, and average citations per year (Table 5). These ten publications accounted for 17.2% of all citations (16,154). The most-cited work was a review on breeding for biotic and abiotic stress resistance in common bean (431 citations) [107], followed by an analysis of drought impacts on yield (342 citations) [108] and a study evaluating the role of rhizosphere bacteria in resistance to *Fusarium oxysporum* (322 citations) [109]. Other highly cited works included a review on quantitative disease resistance (QDR) and its applications (274 citations) [110], an article on the origin and genetic diversity of common bean (264 citations) [111], and research characterizing the drought tolerance of six cultivars (249 citations) [112]. Additional influential studies focused on bean physiology under water stress (229 citations) [113], genetic mapping and QTL identification for resistance traits (229 citations) [114], the genetic manipulation of *Rhizobium etli* for drought tolerance (224 citations) [115], and a CIAT breeding program that developed drought-resistant lines (222 citations) [92].

Table 4. Leading countries, authors, and journals with the highest scientific impact in studies on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.).

Rank	Country	TC	Author	h-index	g-index	m-index	TC	PY_start	Source	h-index	g-index	m-index	TC	PY_start
1	United States	4896	Kelly, J.D.	21	29	0.538	2470	1987	Euphytica	19	35	0.345	1919	1971
2	Brazil	1478	Beebe, S.	20	30	0.833	2258	2002	Crop Science	22	33	0.733	1879	1996
3	Colombia	1294	Miklas, P.N.	18	25	0.563	1595	1994	Field Crops Research	10	11	0.286	784	1991
4	Mexico	709	Blair, M.W.	10	11	0.5	1174	2006	Theoretical and Applied Genetics	13	15	0.406	724	1994
5	Spain	511	Rao, I.M.	11	16	0.611	1166	2008	Frontiers in Plant Science	11	16	1.1	507	2016
6	Egypt	432	Singh, S.P.	14	19	0.318	1001	1982	Sciencia Horticulturae	8	8	0.381	444	2005
7	France	361	Gepts, P.	8	10	0.276	620	1997	Journal of the American Society for Horticultural Science	9	11	0.321	435	1998
8	South Africa	332	Acosta-Gallegos, J.A.	6	9	0.171	563	1991	Isme Journal	2	2	0.25	416	2018
9	Canada	315	Ramírez-Vallejo, J.P.	2	2	0.069	561	1997	Molecular Breeding	5	5	0.179	384	1998
10	Chile	282	Porch, T.G.	9	14	0.45	545	2006	Agricultural Water Management	7	8	0.538	376	2013

Note: PY: Publication Year Start.

Table 5. Most cited publications on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.).

Rank	Title	Source	Year	TC	TC per Year
1	Common bean breeding for resistance against biotic and abiotic stresses: From classical to MAS breeding [107]	Euphytica	2006	431	21.5
2	Traits related to drought resistance in common bean [108]	Euphytica	1998	342	12.2
3	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function [109]	The ISME Journal	2018	322	40.3
4	Quantitative disease resistance and quantitative resistance loci in breeding [110]	Annual Review of Phytopathology	2010	274	17.1
5	Broadening the genetic base of common bean cultivars [111]	Crop Science	2001	264	10.6
6	Effect of drought stress on the osmotic adjustment, cell wall elasticity and cell volume of six cultivars of common beans (<i>Phaseolus vulgaris</i> L.) [112]	European Journal of Agronomy	2007	249	13.1
7	The effect of drought stress on yield, leaf gaseous exchange, and chlorophyll fluorescence of dry beans (<i>Phaseolus vulgaris</i> L.) [113]	Agricultural Water Management	2017	229	25.4
8	Tagging and mapping of genes and QTL and molecular marker-assisted selection for traits of economic importance in bean and cowpea [114]	Field Crops Research	2003	229	10
9	Improvement of drought tolerance and grain yield in common bean by overexpressing trehalose-6-phosphate synthase in rhizobia [115]	Molecular Plant-Microbe Interactions	2008	224	12.4
10	Selection for drought resistance in common bean also improves yield in phosphorus-limited and favorable environments [92]	Crop Science	2008	222	12.3

Note: TC per Year: Total Citations per Year.

The analysis highlights a strong concentration of impact within a limited set of contributions. The review by Miklas, P.N.—one of the field’s most influential researchers—stands out as the most cited paper, reinforcing the link between sustained productivity and academic influence. The recurring presence of authors such as Singh, S.P., Kelly, J.D. and Beebe, S., previously identified as leaders in the field, illustrates how scientific elites concentrate both output and visibility. Notably, the most-cited articles often involve large author teams, frequently within the framework of international collaborations, and are published in high-impact specialized journals [116]. This trend is reflected in the prominence of *Euphytica* and *Crop Science*, which host several of the top-cited documents and confirm their historic role as leading platforms for bean research dissemination. At the same time, prestigious interdisciplinary journals such as *Annual Review of Phytopathology* and *ISME Journal* signal the growing importance of frontier approaches that attract attention from broader scientific communities [103,117]. Together, these findings underscore that leadership in the field is structured around a relatively small set of highly cited contributions, strategic journals, and consolidated scientific networks.

4.5. Co-Citation Analysis

The co-citation network quantifies the frequency with which two documents are cited together, allowing the thematic structure of the field and its temporal evolution to be mapped [118]. The quantitative analysis and generation of the author co-citation map were conducted using *CiteSpace*, considering publications from 1995 to 2024. The resulting network comprised 145 authors grouped into 11 well-defined thematic clusters. The network structure displayed high modularity ($Q = 0.8177$) and a high average silhouette value ($S = 0.9478$), indicating clear and coherent segmentation among the identified co-citation groups (Figure 5). The silhouette coefficient, developed by [119], evaluates clustering quality by comparing internal cohesion and external separation; values close to +1 denote well-defined clusters, whereas lower values indicate potential thematic overlaps.

Cluster #0, labeled Whole-genome sequencing, included 14 authors with a silhouette value of 0.93. The most cited contributor was Schwartz, H.F. (45 citations). Cluster #1, Heat-stress tolerance, also comprised 14 authors, with a silhouette value of 0.96; the most cited was Ramírez-Vallejo, P. (45 citations). Cluster #2, Superior performance, consisted of 12 authors and achieved a maximum silhouette value of 1.00, with Beebe, S.E. (86 citations) as the most cited.

Cluster #3, Angular leaf spot, comprised 11 authors (silhouette = 0.96), with Miklas, P.N. (110 citations) as the most cited. Cluster #4, Molecular tagging, included 11 authors and achieved a perfect silhouette value of 1.00, with Porch, T.G. (40 citations) as the most cited. Cluster #5, Morpho-physiological resistance to drought, was formed by 10 authors (silhouette = 0.89), with Assefa, T. (36 citations) as the most cited.

Cluster #6, QTLs for drought tolerance, grouped 10 authors (silhouette = 0.97), with Singh, S.P. (152 citations) as the most cited. Cluster #7, Genetic dissection, included 10 authors (silhouette = 1.00), with Mukeshimana, G. (19 citations) as the most cited. Cluster #8, Root architecture under drought, comprised 9 authors (silhouette = 0.84), with Broughton, W.J. (55 citations) as the most relevant.

Cluster #9, Resistance to multiple pathogens, included 9 authors (silhouette = 0.88), with Lander, E.S. (16 citations) as the most cited. Finally, Cluster #10, Common bean breeding, contained 9 authors (silhouette = 0.96), with Gepts, P. (47 citations) as the most cited.

Within Cluster #0, the most cited study was [120], which generated a linkage map with markers distributed across all 11 *P. vulgaris* chromosomes and identified gene clusters associated with anthracnose resistance. This genomic framework provided key insights into host–pathogen interactions and supported breeding programs. In Clusters #1, #2, and #3,

the most cited paper was [121], a genome-wide association study (GWAS) of 256 *P. vulgaris* genotypes that evaluated yield components and photosynthetic traits under drought. The study identified candidate genes and chromosomal regions linked to water-stress tolerance and photosynthetic efficiency. Its presence across multiple clusters reflects its relevance to abiotic stress tolerance, superior agronomic performance, and interactions with foliar disease signaling pathways (e.g., abscisic acid and ubiquitination).

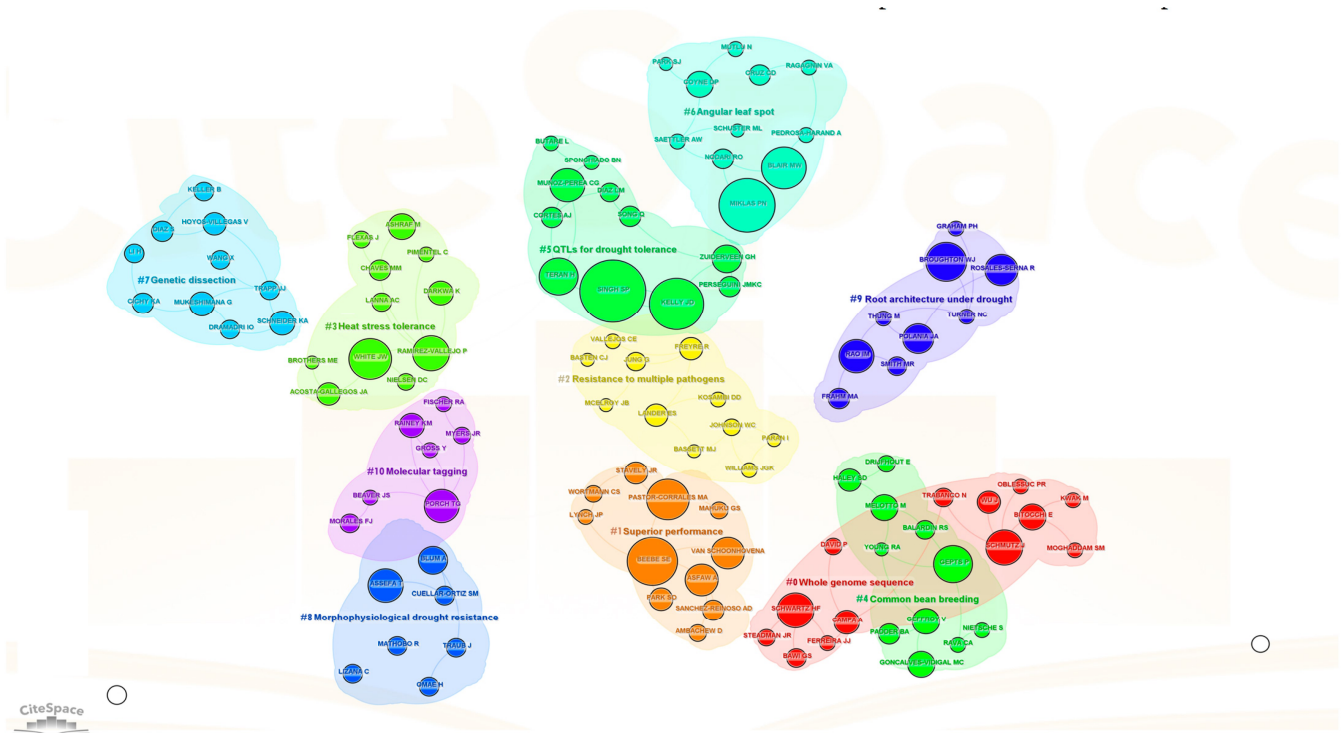


Figure 5. Author co-citation network generated using CiteSpace. Node size corresponds to the co-citation frequency of an author. Link thickness represents the strength of the co-citation relationship between authors. Colors represent distinct thematic clusters. The high modularity ($Q = 0.82$) and silhouette ($S = 0.95$) scores indicate a robust and well-defined cluster structure.

Similarly, ref. [122], cited in Clusters #4 and #7, focused on genomic regions controlling seed weight and yield under irrigated and drought conditions. Using multiple GWAS approaches, it reported numerous QTLs and candidate genes, advancing marker-assisted selection. Its inclusion in Cluster #4 reflects the importance of molecular markers for adaptive trait tracking, while in Cluster #7 it highlights the genetic dissection of drought tolerance and yield potential.

In Cluster #5, ref. [123] demonstrated that shoot and root traits—such as deep root systems and efficient mobilization of photoassimilates into pods and seeds—are critical for maintaining yield under drought, validating their role as breeding targets. In Cluster #6, ref. [124] identified QTLs for water-stress tolerance in Andean genotypes, underscoring the utility of QTL-based tools for marker-assisted selection. In Cluster #8, ref. [125] emphasized root architecture as a drought-avoidance mechanism, reporting QTLs associated with greater root depth and volume in the DOR364 \times BAT477 population. In Cluster #9, ref. [126] documented loci conferring resistance to bacterial, fungal, and viral diseases, providing essential genetic resources for enhancing crop resilience.

Finally, the most cited study in Cluster #10 was ref. [107], a comprehensive review on *P. vulgaris* breeding that summarized advances in disease resistance and agronomic adaptation. The review also noted limited progress in pest control, emphasizing the need for more integrative breeding strategies targeting both biotic and abiotic stresses simultaneously.

stresses interact in complex and synergistic ways. Such gaps constrain the development of genotypes with holistic resilience and underscore the need for multidisciplinary approaches that integrate plant physiology, genomics, and pathology to effectively tackle current challenges posed by climate change.

4.7. Thematic Map

The thematic map provides a strategic visualization of research topics, positioning them in a two-dimensional space according to their centrality (relevance within the field) and density (degree of internal development) [127]. This analysis enables the identification of thematic areas by clustering keywords based on their co-occurrence patterns [128].

Basic themes represent well-established areas that, while relevant to the field, still lack advanced specialization or depth. In this study, such themes include plant genetic improvement, drought, and yield components. Motor themes, in contrast, exhibit both high centrality and high density, indicating mature, robust, and high-impact research fronts. These include epistasis, marker-assisted selection (MAS), and salt stress, which reflect consolidated lines of inquiry central to advancing knowledge in common bean research.

Niche themes are characterized by high density but low centrality, suggesting that although they are highly developed, they remain specialized and less connected to the core of the field. Examples include studies on *Pseudomonas* spp., begomoviruses, and leaf area index. Finally, emerging or declining themes refer to topics that are either in early stages of development or losing relevance. These include biostimulants, *Sclerotinia sclerotiorum*, and the bean weevil *Acanthoscelides obtectus*.

Using Biblioshiny, a total of 21 research themes were identified and distributed across the four quadrants of the thematic map (Figure 7).

Table 6 complements the thematic map presented in Figure 7 by detailing the frequency, centrality, and density values associated with the 21 research themes identified. To facilitate interpretation, these parameters were classified into four categories (very low, low, high, and very high) based on the minimum and maximum values obtained. The ranges established were as follows: frequency (3–340), categorized as very low (3–87), low (88–172), high (173–256), and very high (257–340); centrality (0–1.65), categorized as very low (0.00–0.41), low (0.42–0.82), high (0.83–1.23), and very high (1.24–1.65); and density (30.00–77.78), categorized as very low (30.00–41.95), low (41.96–53.90), high (53.91–65.85), and very high (65.86–77.78). This classification enabled a clearer interpretation of the degree of relevance, internal development, and frequency of each theme, while also allowing precise comparisons across clusters in the subsequent subsections.

Table 6. Thematic description of the 21 clusters generated from the thematic map on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.).

N	Cluster Label	Terms	Cluster Frequency	Callon Centrality	Callon Density
1	Drought	Pod harvest index, yield, irrigation, crop adaptation, cultivar description, diallel, black bean, <i>Phaseolus acutifolius</i> , landrace, abiotic stress, drought tolerance, water deficit, vegetative growth, canopy temperature, photosynthesis, proline, abscisic acid (ABA), common bean rust, iron, proteomics, vegetation indices, genetic improvement, genetic resources, genome-wide association study (GWAS)	340	1.65	36.23

Table 6. Cont.

N	Cluster Label	Terms	Cluster Frequency	Callon Centrality	Callon Density
2	Anthraxnose (<i>Colletotrichum lindemuthianum</i>)	Molecular marker, common bacterial blight, genome-wide association study (GWAS), <i>Uromyces appendiculatus</i> , <i>Pseudocercospora griseola</i> , angular leaf spot, gene pyramiding, Bean Common Mosaic Virus (BCMV), molecular breeding, quantitative trait loci (QTL), disease resistance genes, gene clusters	105	0.76	38.07
3	Plant breeding	Biotic stress, climate change, genetic diversity, food security, <i>Phaseolus acutifolius</i> , crop improvement, high temperature, nitrogen fixation, sustainable agriculture, biofortification, domestication, soil salinity, abscission, biodiversity, EMS mutagenesis	82	0.92	42.21
4	Salt stress	Osmolytes, stomatal conductance, deficit irrigation, salicylic acid, water productivity, antioxidant system, crop yield, drip irrigation, foliar application	54	0.43	52.79
5	Yield components	Combining ability, gene pools, <i>Fusarium</i> wilt, heat tolerance, heritability, ideotype	32	0.34	32.46
6	Grain yield	Heat stress, chlorophyll fluorescence, biomass, energy use	25	0.29	41.11
7	Epistasis	Linkage, pathogens, indirect selection, gene cluster	17	0.52	71.25
8	Antioxidant enzymes	Arbuscular mycorrhizal fungi, pod quality, biofertilizers, cyanobacteria	16	0.17	49.67
9	<i>Pseudomonas</i> spp.	Indole-3-butyric acid (IBA), 2,6-dichloroisonicotinic acid (INA), Beta-aminobutyric acid (BABA), cell wall, epigenetics	15	0.08	77.78
10	<i>Sclerotinia sclerotiorum</i>	Genetic resistance, partial resistance, association mapping	15	0.06	37.85
11	<i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i>	Area Under the Disease Progress Curve (AUDPC), disease-resistance inheritance, disease severity	14	0.02	45.31
12	Gene expression	Root-knot nematode, aquaporins, gene	13	0.056	47.222
13	Seed priming	Antioxidant activity, biostimulant, chitosan, dry matter	11	0.25	66.67
14	Marker-Assisted Selection (MAS)	Marker-assisted selection (MAS), <i>Xanthomonas campestris</i> pv. <i>phaseoli</i> , common bacterial blight resistance	8	0.33	53.70
15	Random Amplified Polymorphic DNA (RAPD)	<i>Phaeoisariopsis griseola</i>	8	0.43	30.00
16	Leaf area index	Chlorophyll, chlorophyll content	7	0.00	55.56
17	Bacterial blight	Bean cultivars, breeding methods	6	0.00	66.67
18	Germination	Quantitative Reverse Transcription Polymerase Chain Reaction (qRT-PCR)	6	0.11	38.89
19	Biostimulants	Temperature stress	6	0.00	38.89
20	Begomovirus	Genomic prediction	4	0.00	62.50
21	<i>Acanthoscelides obtectus</i>	Bean weevil	3	0.00	33.33

N: number of clusters.

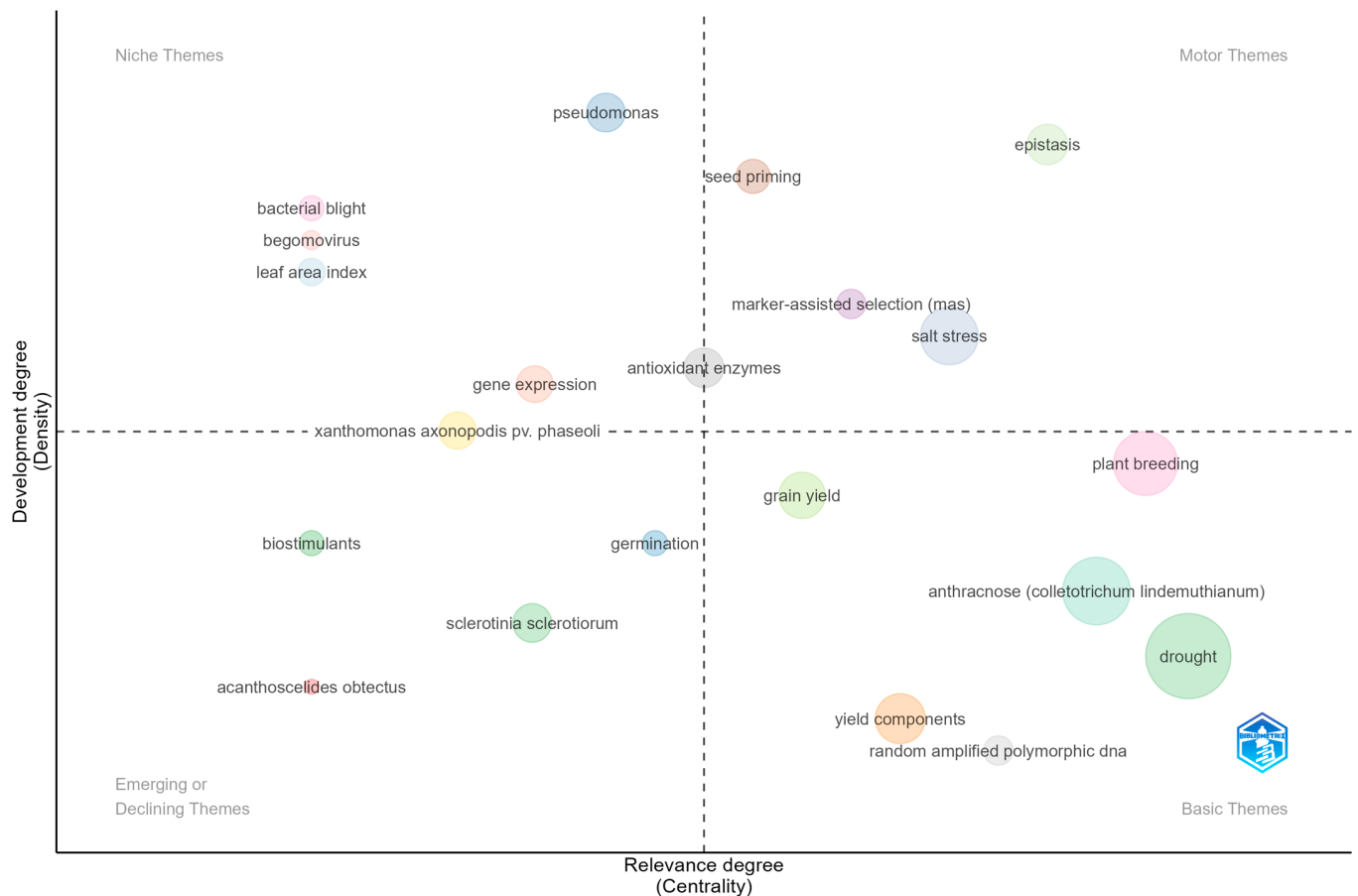


Figure 7. Thematic map of research on biotic and abiotic stress in *Phaseolus vulgaris* L., generated from 150 author keywords (minimum occurrence: 5 per 1000 documents). Bubble size represents the frequency of each keyword cluster. The x-axis (Centrality) indicates the theme's relevance to the overall field, while the y-axis (Density) reflects its internal development. The four quadrants classify themes as follows: (I) Motor (high centrality, high density), (II) Basic (high centrality, low density), (III) Emerging/Declining (low centrality, low density), and (IV) Niche (low centrality, high density).

4.7.1. Basic Topics

Drought

The cluster labeled “drought” presents a very high frequency (340), very high centrality (1.65), and very low density (36.23) (Figure 7; Table 6). This pattern indicates that drought has been extensively investigated and is highly connected with other research areas, but still lacks deep internal development compared with its strategic relevance. The cluster integrates a broad set of aspects related to drought tolerance, highlighting both its interdisciplinary nature and the existing opportunities to consolidate its scientific depth.

Root architecture emerges as a pivotal axis for drought adaptation. Traits such as basal root number, adventitious root abundance, and primary root length have been positively correlated with yield [129,130]. Deeper root systems and efficient redistribution of photoassimilates enhance biomass accumulation during pod filling under water stress [123,131]. Two contrasting adaptive strategies have been described: “consumer” genotypes with deep roots and high shoot biomass, which perform well under intermittent drought; and “saver” genotypes with shallow roots and reduced growth, better adapted to terminal drought [132]. Agronomic indicators such as pod harvest index and root-pulling resistance further support the selection of tolerant genotypes [131,133,134]. However, in tropical environments, low soil fertility, aluminum toxicity, and compaction often limit root development and water access, underscoring the need to integrate genetic resistance with

soil management practices [135]. For example, crop residue retention promotes deeper rooting by enhancing water conservation, whereas residue incorporation favors shallow root development due to increased water availability in the upper soil layers [136].

Vegetative growth habit is also linked to drought response. Determinate genotypes often outperform indeterminate ones under severe drought [137], although indeterminate types can adapt under deficit irrigation [138]. At the biochemical level, proline accumulation serves as a reliable marker of tolerance [139], facilitating osmotic adjustment, intermediate stomatal closure, and enhanced assimilate partitioning to pods and seeds during reproductive stages [140]. Physiologically, *P. vulgaris* maintains leaf turgor under stress through greater cell wall elasticity and efficient osmotic regulation [112]. In the Pinto Villa genotype, sucrose mobilization to developing pods demonstrated effective carbon allocation under drought [141]. Aquaporin gene regulation has also been implicated, with differential repression and recovery of *PvPIP2;7* and *PvTIP1;1* observed in contrasting genotypes [142].

Yield is primarily shaped by environmental conditions, followed by genotype–environment interaction and, to a lesser extent, genotype alone [143]. Elevated levels of starch, soluble sugars, and amino acids have been associated with higher yields under drought [144]. Several genotypes—including EN-70, ZABRA16575–86F22, SEN-56, SCN-2 Viva, NW 63, UI 239, and Common Red Mexican—have demonstrated strong yield potential, nutritional quality, and short growth cycles [145–149]. Other notable drought-tolerant genotypes include PER1003544 [150], BAT 477, Lechinta, Zecak, Maksa, Medijana, and Sataja 425 [151,152]. Additional lines such as Awash-1, Gofta, Othello, Common Red Mexican, and NW 63 exhibit higher water-use efficiency and proline accumulation [153,154], while SB-DT2 and SB-DT3 combine drought tolerance with rust resistance [155]. *Phaseolus acutifolius* (tepary bean) has shown superior root efficiency compared with *P. vulgaris* [156], and mutant lines such as CMT 38, CMT 109, and CMT 187 have demonstrated high climatic resilience [157].

Modeling approaches have been employed to assess the impacts of irrigation regimes and climate change on yield [158–162], while tools for real-time monitoring of plant water status [163–165] and predictive analyses of future climate scenarios [166–168] are increasingly applied. High-throughput phenotyping has accelerated trait discovery, with UAVs, multispectral imaging, NDVI, and physiological modeling enabling robust screening for drought tolerance [169–172]. Genetic studies, including stable QTL identification [125,173,174], molecular characterization of stress-response pathways [175–177], and GWAS analyses [122,178–181], have expanded our understanding of tolerance mechanisms. Although QTL × environment interactions remain a challenge—with only 22% of loci consistent across environments [180]—introgression from wild relatives such as *P. acutifolius* [182,183], genomic selection, and gene editing offer promising strategies to broaden the genetic base. Transcriptomic and proteomic analyses have further identified key genes (e.g., *LEA3*, dehydrins, *PvMLP19*), regulatory networks involving lncRNAs and circRNAs, and stress-protective proteins such as HSP70 and antioxidant enzymes [78,175,184]. Nevertheless, their practical application is limited by tissue-specific expression and a lack of standardized field protocols.

Overall, the “drought” cluster reflects a mature but still expanding research area with strong interdisciplinary connections and clear translational potential. Progress will require harmonizing methodologies across research platforms, strengthening collaborative data-sharing initiatives, and integrating multi-omics approaches to dissect tolerance mechanisms. Functional validation of candidate genes through genome editing, coupled with high-throughput field phenotyping, is critical to bridge the gap between discovery and application. Addressing these challenges will accelerate the development of drought-

resilient bean genotypes, a necessity for ensuring food security in the face of climate change, especially in vulnerable agricultural systems.

Anthracnose

The cluster labeled “anthracnose” presents a low frequency (105), low centrality (0.76), and very low density (38.07) (Figure 7; Table 6). This distribution suggests that anthracnose research remains underrepresented compared with other thematic areas, with relatively weak connections across the field. At the same time, the very low density underscores the substantial opportunities for methodological expansion and interdisciplinary integration to enhance its scientific development and translational impact.

This cluster also encompasses other major diseases such as angular leaf spot (ALS), common bacterial blight (CBB), rust, and bean common mosaic virus (BCMV). The occurrence of terms such as molecular markers, GWAS, molecular breeding, gene pyramiding, quantitative trait loci (QTLs), gene clusters, and resistance genes highlights a strong research orientation toward unraveling the genetic basis of disease resistance in *P. vulgaris* and applying molecular tools in breeding pipelines (Table 6).

Anthracnose (ANT) is characterized by high race variability, which adds considerable complexity to resistance breeding [185–187]. Multiple resistance loci (Co) have been identified across different chromosomes, with genotypes displaying differential responses to specific virulent races. Resistant materials such as Andecha, A252, and Beija Flor have been reported, while cultivars like Othello and Maverick exhibit high susceptibility to the most aggressive ANT races [120,188–194]. These findings confirm the necessity of broad-spectrum resistance sources and multilocus strategies to sustain durable protection.

Substantial progress has also been achieved in ALS resistance, particularly through fine mapping of QTLs on Pv04, development of tightly linked molecular markers, generation of resistant lines, and optimization of field-based evaluation methodologies [185,195–199]. Such advances illustrate the potential of integrating conventional and molecular approaches to accelerate resistance breeding.

Table 7 summarizes the resistance and susceptibility profiles of common bean genotypes from different countries against key diseases affecting this crop. This comparative evidence reinforces the importance of germplasm diversity as a foundation for resistance breeding.

Table 7. Disease resistance and susceptibility in common bean (*Phaseolus vulgaris* L.) genotypes.

Genotype	Country	Disease Response	Reference
Island	Canada	R: <i>Sclerotinia sclerotiorum</i> S: <i>Colletotrichum lindemuthianum</i>	[200]
BRS Esplendor	Brazil	R: <i>Colletotrichum lindemuthianum</i> , <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> , <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i>	[201]
BRSMG Uai	Brazil	R: <i>Colletotrichum lindemuthianum</i> , Bean Common Mosaic Virus, <i>Fusarium</i> <i>oxysporum</i> f. sp. <i>Phaseoli</i> S: <i>Pseudocercospora griseola</i>	[202]
Longyundou 19	China	R: <i>Colletotrichum lindemuthianum</i> , <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> , Bean Common Mosaic Virus	[203]
NUA 48/NUA 64	Tanzania	R: <i>Colletotrichum lindemuthianum</i>	[204]

Table 7. Cont.

Genotype	Country	Disease Response	Reference
Coyne	United States	R: <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> , <i>Uromyces appendiculatus</i> , Bean Common Mosaic Virus	[205]
Panhandle Pride	United States	R: <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> , Bean Common Mosaic Virus	[206]
AAC Black Diamond 2, OAC Rex	Canada	R: <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i>	[207,208]
TARS-LFR1	Puerto Rico, United States	R: <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> , Bean Common Mosaic Virus	[209]
0221-14 y 0452-03	Spain	R: <i>Colletotrichum lindemuthianum</i> , <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> , <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> , Bean Common Mosaic Virus	[210]
BRS FC402	Brazil	R: <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> , <i>Colletotrichum lindemuthianum</i>	[211]
Kikatiti	Tanzania	R: Bean Common Mosaic Virus, Bean Common Mosaic Necrosis Virus, <i>Uromyces appendiculatus</i> , <i>Xanthomonas</i> <i>axonopodis</i> pv. <i>phaseoli</i> ; S: <i>Pseudocercospora griseola</i>	[212]
Tepehuán-RS	Mexico	R: Bean Common Mosaic Virus, <i>Colletotrichum lindemuthianum</i>	[213]
ND Polar	United States	R: Bean Common Mosaic Necrosis Virus, <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i>	[214]
Aporé, Ouro Negro, Macarrão Atibaia, Alabama #1	Brazil	R: <i>Meloidogyne javanica</i> , <i>Meloidogyne</i> <i>incognita</i>	[215,216]
Carioca, Enxofre, Mulatinho Comun, Rio Doce	Iran, Colombia	S: <i>Meloidogyne javanica</i> , <i>Meloidogyne</i> <i>incognita</i>	[216]

Note: R denotes resistance and S denotes susceptibility.

Overall, while anthracnose and associated diseases represent a cluster of relatively low structural maturity within the bibliometric landscape, they remain of high strategic importance for bean improvement. Expanding collaborative, genomics-enabled breeding programs that combine GWAS, molecular markers, and gene pyramiding with robust phenotyping platforms will be essential to achieve durable resistance. Addressing this gap not only strengthens plant health management but also ensures yield stability in regions where beans are a dietary and economic cornerstone.

4.7.2. Motor Themes

Epistasis

The cluster “epistasis” presents a very low frequency (17), low centrality (0.52), and very high density (71.25) (Figure 7; Table 6). This indicates that although the topic has been relatively underexplored and remains weakly connected to other areas, the studies that do exist exhibit a solid and methodologically robust foundation. This maturity underscores the strategic value of epistasis research for advancing genetic improvement in common bean.

A representative example is the identification of QTLs such as *SU91* and *BC420*, whose recessive epistatic interaction requires the simultaneous presence of both resistant alleles to confer effective protection against common bacterial blight (CBB). Moreover, *SU91* in its recessive form suppresses the effect of *BC420*, highlighting the functional importance of epistatic interactions in genetic resistance. Such findings reinforce the need to incorporate complex gene–gene interactions into breeding strategies to achieve durable resistance [217].

Seed Priming

The cluster “seed priming” is characterized by very low frequency (11), very low centrality (0.25), and very high density (66.67) (Figure 7; Table 6). This suggests that while relatively few studies exist and connections to other research themes remain weak, the field has achieved notable methodological and experimental progress. The high density is explained by the wide diversity of strategies explored, including treatments with bioactive compounds such as melatonin [218,219], chitosan [220], vitamin B12 [221], INA [222], and essential oils [223], as well as the use of beneficial microorganisms such as *Bacillus subtilis* y *Rhizobium* spp. [224,225].

These studies have demonstrated significant improvements in germination, vigor, yield, and resilience to abiotic stresses such as drought and salinity, as well as to pathogens. Epigenetic potential has been reported for INA priming [222], while chitosan treatment has enhanced drought tolerance and modulated protein expression profiles [220]. Similarly, halopriming and essential oils have increased tolerance to salinity [223,226].

Despite these advances, the very low centrality suggests that seed priming remains weakly integrated into systemic breeding frameworks. This gap offers an opportunity to link priming approaches with higher-centrality clusters such as epistasis or abiotic stress tolerance. Integration with genomic selection, epigenomic tools, and gene editing could amplify the practical impact of seed priming in future breeding programs.

Marker-Assisted Selection

The cluster “Marker-Assisted Selection” (MAS) displays very low frequency (8), very low centrality (0.33), and low density (53.70) (Figure 7; Table 6). This indicates that MAS has been applied in relatively few studies, with limited connectivity across the field, yet with moderate methodological development and clear technical applications in existing research. While MAS is widely recognized as a strategic tool in genetic improvement, its use in common bean remains incipient and underexploited at scale.

Representative applications include the simultaneous introgression of resistance genes against ANT, ALS, and rust into the cultivar Diamante Negro through marker-assisted backcrossing with SCAR and SNP markers, using Rudá-R as the donor parent. Genes such as *Co-4*, *Co-6*, *Co-10*, *Phg-1*, and *Ur-ON* were successfully pyramided [227–229]. Similarly, advanced genotypes from the IAC breeding program (Brazil) were found to carry *Co-6*, *Co-4²*, *Co-3³*, and *Co-5*, conferring combined resistance to multiple ANT races [230].

Rust resistance has been another major focus, with pyramiding of genes *Ur-4*, *Ur-11*, *Ur-5*, and *Ur-14* in snap bean and carioca genotypes, achieving effective resistance to diverse pathogen races [231–233]. In a more integrative approach, MAS facilitated the incorporation of rust and virus resistance genes (*Ur-4*, *Ur-5*, *Ur-11*, *bc-3*, and *bgm-1*) in genotypes such as PR0806-80 and PR0806-81, conferring combined protection against BCMV and BGMV [234]. Additional studies have compared recurrent selection and gamete selection strategies, revealing specific advantages in recombination frequency and efficiency for gene accumulation through MAS [235].

The low frequency and centrality values suggest that MAS remains underutilized in common bean breeding. Greater integration with multidisciplinary research programs

and validation across diverse environments is required to fully realize its potential as a cornerstone of modern breeding.

Salt Stress

The cluster “salt stress” presents a low frequency (54), low centrality (0.43), and low density (52.79) (Figure 7; Table 6). Although explored in a moderate number of studies, salt stress research remains weakly consolidated and underconnected to the broader field.

Mitigation strategies have focused on biostimulant applications, including natural regulators such as salicylic acid, spermidine, glycine betaine, melatonin, brassinosteroids, and proline; plant extracts from *Moringa oleifera*, *Lippia alba*, *Sacchorhiza polyschides*, and *Ulva intestinalis*; protein derivatives such as pumpkin seed hydrolysates; algal extracts such as *Spirulina platensis*; and compound formulations such as humic acid + cytokinin + arginine and zinc + manganese + vitamin B12. Microbial applications have included *Aneurinibacillus aneurinilyticus*, *Paenibacillus* sp., *B. subtilis*, *Rhizobium tropici* combined with trehalose, and *Glomus irradicans*. Mineral supplementation with silicon and phosphorus, nanoparticle-based amendments (hydrated copper–potassium sulfate), and halopriming techniques have also been investigated [24,218,219,221,223–226,236–254].

Together, these studies demonstrate promising avenues for enhancing salt tolerance, but the limited centrality highlights the need for broader integration with genetic and physiological approaches to generate durable, field-relevant solutions.

4.7.3. Niche Themes

The cluster “bacterial blight” shows very low frequency (15), very low centrality (0.00), and very high density (66.70) (Figure 7; Table 6). Although the number of studies is limited and poorly connected to broader themes, this cluster concentrates specialized and robust knowledge. Associated terms such as *bean cultivars* and *breeding methods* (Table 6) suggest that research has mainly focused on disease management and genetic improvement of resistant varieties, yielding notable methodological progress despite its narrow scope and low interconnection with other themes.

Similarly, the cluster “*Pseudomonas* spp.” presents very low frequency (15), very low centrality (0.08), and very high density (77.78). While explored in only a few studies, this cluster compiles detailed information on abiotic stress mitigation strategies. Associated terms such as INA, BABA, cell wall, and epigenetics highlight the role of *Pseudomonas* spp. in inducing resistance mechanisms, triggering epigenetic changes, and reinforcing cell structures, positioning them as a biotechnological tool for enhancing stress tolerance in common bean.

Both clusters reveal a critical gap between specialized knowledge and its integration into comprehensive breeding programs. Their very low centrality indicates that, although they are methodologically robust, their isolation limits applicability in multidisciplinary frameworks. Future research should prioritize field validation of these advances and their articulation with genomic tools and agronomic practices to maximize practical impact.

4.7.4. Emerging Themes

Acanthoscelides obtectus

The cluster labeled “*Acanthoscelides obtectus*” presents very low frequency (3), very low centrality (0.00), and very low density (33.30) (Figure 7; Table 6). This indicates that the topic has been scarcely studied, with minimal connection to other research areas and limited internal development. Existing studies have mostly examined the resistance of *Phaseolus acutifolius* (tepary bean) to this pest [72,255], yet these efforts remain relatively isolated and weakly integrated into broader agricultural research. Since *A. obtectus* directly

compromises the quality and viability of stored grains, the current focus on resistance in specific cultivars overlooks the development of comprehensive management strategies.

The marginalization of this topic in the literature reflects an underestimation of its socioeconomic impact, particularly in regions where post-harvest losses severely affect food security. The very low density further suggests that even the limited studies available lack methodological depth. Future work should integrate *A. obtectus* management into broader research agendas by linking it with climate adaptation, post-harvest technologies, and genetic improvement. Incorporating this pest into multidisciplinary frameworks—such as integrated pest management and genomics-guided resistance breeding—could help mitigate its impact on the common bean value chain.

Bioestimulants

The cluster “bioestimulants” is characterized by very low frequency (6), very low centrality (0.00), and very low density (38.39) (Figure 7; Table 6). These metrics indicate that research on this theme remains highly incipient, fragmented, and poorly connected to the wider field. Preliminary studies have explored a diverse range of compounds, including natural extracts [252,256], algal derivatives [257,258], protein hydrolysates [250,259], hormonal analogs [260–264], and commercial formulations [265,266]. However, these investigations remain largely exploratory, with limited methodological integration and little validation at applied or field scale.

The low density and centrality highlight the lack of connection with advances in plant physiology, genomics, and systems-based stress management. Current studies tend to evaluate isolated effects rather than synergistic interactions with agronomic practices or genetic improvement. Moving forward, research should prioritize standardized protocols, multi-environment validation, and the integration of bioestimulants into multidisciplinary frameworks. Such approaches would enhance their adoption in breeding and crop management, transforming bioestimulants from a fragmented niche into a strategic component of sustainable stress mitigation in common bean.

4.8. Thematic Evolution

Thematic evolution in the field (Figure 8) reveals a clear transition in research priorities from 1971 to mid-2025.

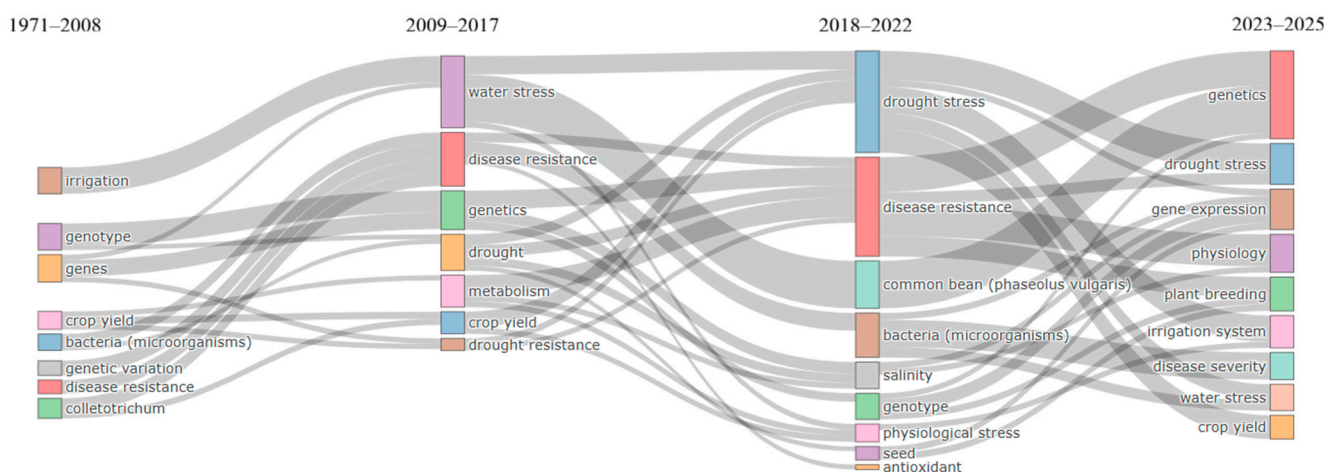


Figure 8. Sankey diagram illustrating the thematic evolution of research on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.). The diagram is divided into four time periods (1971–2008, 2009–2017, 2018–2022, and 2023 to mid-2025). Each rectangle represents a research topic, with its size

indicating the relative relevance or frequency of that theme during the corresponding period. The connecting lines depict the continuity, transformation, or emergence of topics over time, with line thickness proportional to the strength of thematic relationships between consecutive periods.

During the exploratory stage (1971–2008), research focused on broad topics such as irrigation, crop yield, genotypes, and genes, alongside early studies on disease resistance, reflecting an initial effort to establish the foundations of bean stress research.

Between 2009 and 2017, attention shifted toward water stress, drought, genetics, and metabolism, marking the emergence of more targeted investigations into physiological mechanisms underlying abiotic stress responses. This consolidation signaled a transition from exploratory studies to more mechanistic and hypothesis-driven research.

From 2018 to 2022, the research agenda expanded to include drought stress, disease resistance, and *Phaseolus vulgaris* as core themes, complemented by a growing emphasis on microorganisms, salinity, and physiological stress. This stage reflects the increasing recognition of the interplay between biotic and abiotic stress factors and the integration of microbial and physiological approaches.

Finally, in the most recent period (2023–mid-2025), key themes include genetics, drought stress, gene expression, and plant breeding, alongside concepts such as disease severity, irrigation systems, and crop physiology. This trajectory suggests a progressive shift toward the development of resilient cultivars using genomic tools, advanced phenotyping, and integrated management strategies capable of addressing multiple stresses simultaneously. The thematic evolution thus reflects a gradual sophistication of knowledge, from descriptive approaches toward applied and sustainable solutions for common bean cultivation in the context of climate change.

4.9. Trending Topics in Common Bean Research

The analysis of trending topics provides critical insights into the temporal dynamics of scientific priorities, allowing the identification of emerging areas, the persistence of established themes, and the decline of outdated approaches [47]. Figure 9 presents a trend topic map generated with Biblioshiny, where horizontal lines represent the lifespan of each theme in the literature, while the size of the circles reflects their relative frequency of occurrence.

The theme plant breeding emerges as the most consistent and enduring focus, maintaining uninterrupted relevance from 2001 to 2021 with a frequency of 74. Its persistence underscores the centrality of breeding efforts in addressing both biotic and abiotic stress in *Phaseolus vulgaris*. In contrast, *Random Amplified Polymorphic DNA (RAPD)* represents one of the least influential and now obsolete topics, with its presence in the literature ceasing by 2000 despite achieving a frequency of 16.

In recent years, new topics have gained prominence, reflecting methodological innovation and shifting research priorities. Notably, *salt tolerance*, *oxidative stress*, *chromosomal mapping*, and *germination* emerged strongly after 2021, marking a transition toward integrative approaches aimed at improving stress resilience and physiological performance. This shift illustrates the progressive replacement of earlier molecular tools with advanced genomic and physiological frameworks that align with the urgent need for climate-adaptive and high-yielding common bean genotypes.

Overall, the temporal trajectory revealed by the trend analysis highlights a research field in transition—from exploratory molecular techniques toward multidisciplinary strategies that integrate genomics, physiology, and stress biology. This evolution parallels broader trends in crop science, emphasizing the development of resilient cultivars under the pressures of climate variability and global food security demands.

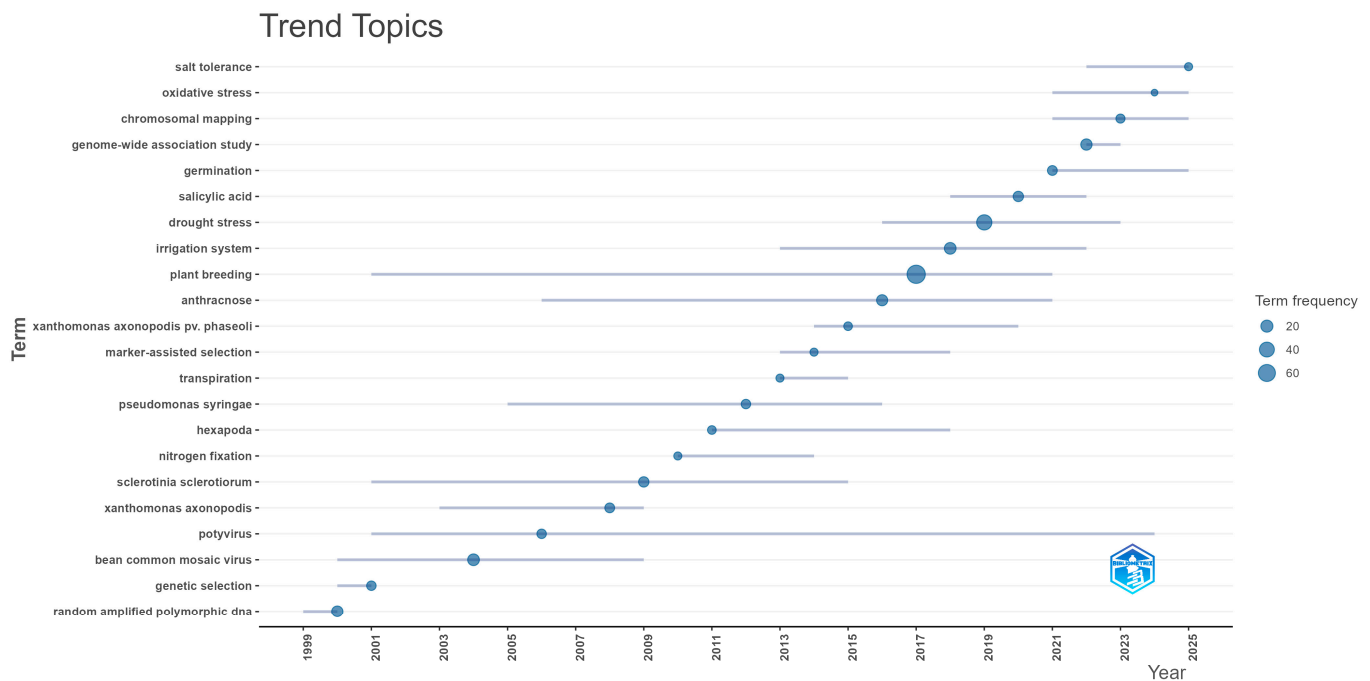


Figure 9. Trend topic map generated with Biblioshiny, illustrating the evolution of research topics on biotic and abiotic stress in common bean (*Phaseolus vulgaris* L.) between 1999 and mid-2025. Each horizontal line represents the duration of a topic's presence in the literature, while circle size is proportional to its frequency of occurrence. The most relevant and prominent term for each year is highlighted, revealing the emergence, persistence, or decline of research priorities over time.

4.9.1. Salinity Tolerance: An Emerging and Priority Challenge

Salinity tolerance has recently consolidated as a critical research frontier in common bean, reflecting both global agronomic priorities and advances in molecular biology. In 2023, six members of the *Diacylglycerol kinase* family (*PvDGK1*, *PvDGK2*, *PvDGK3*, *PvDGK5a*, *PvDGK5b*, and *PvDGK6*) were identified and characterized by conserved functional domains, with overexpression under saline conditions suggesting a regulatory role in adaptive responses [267]. More recently, a 2025 genome-wide study identified 43 *PvGT* transcription factors, several of which showed enhanced expression under salinity stress. Notably, *PvGT02* conferred improved tolerance in yeast, underscoring its potential as a candidate gene for marker-assisted breeding [268].

These findings are highly relevant given that soil salinization currently affects ~833 million hectares worldwide, equivalent to 8.7% of the Earth's terrestrial area [80], with projections indicating that more than 50% of arable land could be impacted by 2050 without effective mitigation [25]. The increasing prominence of salinity tolerance in common bean research thus reflects not only methodological innovation but also the urgent imperative to safeguard food security in arid and semi-arid regions.

4.9.2. Oxidative Stress: A Climate-Linked Axis of Research

Oxidative stress has emerged as a transversal theme in common bean research, tightly linked to climate change-driven stresses such as drought, heat, and salinity. These conditions exacerbate the accumulation of reactive oxygen species (ROS), impairing cellular integrity and reducing yield potential. Consequently, a wide array of biochemical and bio-stimulant strategies have been investigated, including honey, salicylic acid, folic acid, γ -aminobutyric acid, seaweed extracts, chitosan, glutathione, 24-epibrassinolide, selenium, nitric oxide, *Priestia aryabhattai*, and potassium supplements [220,256,257,260–266,269–283].

These interventions have been shown to enhance antioxidant enzyme activity, stabilize membranes, and mitigate oxidative damage.

The rising frequency of citations related to ROS management highlights oxidative stress as a unifying axis that connects plant physiology, stress biology, and applied agronomy. Its growing importance underscores a paradigm shift toward cost-effective and accessible mitigation strategies designed to buffer common bean production systems against the intensifying effects of climate variability.

4.9.3. Germination Under Abiotic Stress Conditions

Germination under stress has recently gained momentum as a trending topic, reflecting its direct implications for crop establishment under marginal or degraded soils. Strategies explored include inoculation with *Rhizobium* spp. strains under drought and heat stress [219,225,284], seed coating with polymers and beneficial rhizobacteria under water deficit [285], application of salicylic acid combined with *Moringa oleifera* extracts under salinity [237], and the use of rainbow trout (*Oncorhynchus mykiss*) hydrolysates to mitigate chilling stress [259].

The emphasis on germination is driven by both physiological and agronomic imperatives: securing reliable crop establishment is critical for production resilience under climate extremes. The growing body of literature on germination reflects an applied orientation toward low-cost, scalable biotechnologies that can be readily integrated into local agricultural systems.

4.9.4. Chromosomal Mapping and Precision Genomics

Chromosomal mapping has recently emerged as a trending research theme, closely linked to genome-wide association studies (GWAS) and single nucleotide polymorphism (SNP) analyses. Although these tools have been applied for over a decade, their integration with chromosomal mapping has substantially improved the resolution of gene localization, reinforcing their strategic importance in common bean breeding. This emphasis has remained consistent throughout the study period (Figure 9).

For anthracnose (ANT), integrative studies combining linkage mapping (Pv04) with GWAS (Pv04, Pv05, Pv10, Pv11) using the BARCBean6K_3 SNP chip identified loci associated with resistance to race 65. Despite the pathogen's virulence diversity, 25 genotypes were resistant to all isolates tested, making them valuable resources for durable resistance breeding [286]. Complementary studies incorporating phenotyping, biochemical assays, GWAS, and transcriptomics validated 24 marker–trait associations (MTAs), three of which on Pv07 were linked to resistance. This multi-layered approach enabled the identification of key differentially expressed genes, providing an integrated view of ANT resistance mechanisms [13].

Advances in pangenomics, including SNP chips, whole-genome sequencing (WGS), and k-mer analysis in the Andean Diversity Panel (ADP), have further enhanced mapping resolution for ANT and bean common mosaic virus (BCMV), enabling the discovery of novel resistance genes through individual assemblies [14]. In addition, 178 NBS-LRR genes have been identified, with corresponding NBS-SSR markers associated with ANT and common bacterial blight (CBB) [287]. Evaluation of 146 Portuguese genotypes against *Erysiphe diffusa* revealed variable resistance, with 11 genotypes exhibiting incomplete hypersensitive resistance and 80 showing partial resistance. GWAS analyses detected eight SNPs across Pv03, Pv09, and Pv10, leading to the proposal of seven candidate genes [63].

Significant progress has also been made in viral and nematode resistance. The *BLC7.1* locus on Pv07 was associated with resistance to lettuce curly top virus (BLCrV), explaining up to 16% of phenotypic variance and providing useful SNP markers for MAS [288]. For

BCMV, *RNase H-Like 1* was identified near the *bc-1* locus (Pv03), reducing viral spread in combination with *I* and *bc-u*, with SNP marker G03_4166082 enabling direct selection [289]. In BCMV, higher expression of *PvDGKs*, *PvGST*, *PvPAL*, *PvLOX*, *PvPOD*, *PvPR1*, *PvPR2*, and *PvPR3* was observed in tolerant genotypes, with *PvPR1* emerging as a key antiviral gene [290].

Nematode resistance has been mapped to multiple loci, with SNPs linked to egg mass number (Pv06, Pv07, Pv08, Pv11) and gall index (Pv01, Pv02, Pv05, Pv10) for *Meloidogyne incognita*, yielding 216 candidate genes, including 14 resistance analogs [291]. A study of 354 genotypes identified 11 QTLs conferring resistance to soybean cyst nematode (SCN) across Pv02, Pv03, Pv06, Pv09, Pv10, and Pv11, with 26 lines showing resistance and predictive accuracies of up to 75% when combining Mesoamerican and Andean populations. These findings also suggested a potential link between resistance loci and domestication processes [292].

Collectively, chromosomal mapping represents a cornerstone in precision breeding for common bean, enabling the dissection of resistance loci and agronomically relevant traits through advanced genomic platforms. However, its broad application is constrained by challenges including polygenic complexity, pathogen variability, and the limitations of reference genomes. Routine implementation remains difficult in low-infrastructure breeding contexts, underscoring the need for scalable, cost-effective applications that bridge cutting-edge genomics with practical breeding pipelines.

4.9.5. The Decline of Random Amplified Polymorphic DNA (RAPD): From Pioneer to Obsolescence

Although superseded by high-resolution genomic methodologies, Random Amplified Polymorphic DNA (RAPD) represented a significant milestone in common bean genetics during the 1990s and early 2000s. RAPD markers enabled the first associations between genomic regions and resistance genes, including *bc-3* [293], *Co-1²*, and *Co-1³* for anthracnose (ANT) [294], and *Ur-3* for rust [295]. They also facilitated the conversion of RAPDs into more specific SCAR markers, such as SBD51300 for *bc-1²* [296], and contributed to the identification of QTLs associated with resistance to *Fusarium oxysporum* (FOP) [297].

The decline in RAPD use illustrates a paradigmatic shift in bean genetics, moving from low-resolution tools toward scalable, high-precision genomic platforms. The near disappearance of RAPD-based studies after 2000 (Figure 9) reflects how the scientific community redirected its efforts toward methodologies with greater reproducibility, scalability, and direct applicability to precision breeding programs. This methodological transition underscores the dynamic nature of plant genomics, where pioneering tools provided the foundation for the adoption of more robust, genome-wide technologies that now underpin modern breeding pipelines.

4.10. Evolution of Mitigation Strategies for Biotic and Abiotic Stresses

To identify and visualize the mitigation strategies reported for biotic and abiotic stresses in common bean (*Phaseolus vulgaris* L.) between 1971 and mid-2025, timeline analyses were generated from strategies mentioned in the titles and abstracts of 549 Scopus-indexed articles.

The chronological analysis reveals a progressive transition in mitigation approaches, particularly for biotic stress management. During the 1970s, initial strategies relied on synthetic priming compounds such as isonicotinic acid (INA) [222,298,299] and β -aminobutyric acid (BABA) [300], which were applied primarily to control *Pseudomonas syringae* pv. *phaseolicola* (Psph).

From the 2010s onward, approaches diversified with the incorporation of beneficial microorganisms. Notable examples include inoculation with *Rhizobium etli* against Psph [301]

and the development of *Trichoderma harzianum* strains transformed via biolistics to overexpress the *Thaqp* gene, which displayed strong antagonism against FOP [302]. Concurrently, signaling molecules such as salicylic acid, spermidine, and riboflavin were tested for their ability to modulate endogenous defense responses against *Botrytis cinerea* [303,304].

In parallel, new-generation fungicides—including pyraclostrobin, azoxystrobin, fludioxonil, and metalaxyl-M—were evaluated as seed treatments and foliar sprays to manage ANT and angular leaf spot (ALS). Although effective under high disease pressure and potentially cost-efficient in intensive systems, their limited representation in the literature and the risk of inducing pathogen resistance constrain their indiscriminate adoption [305,306].

Overall, this evolution highlights a clear shift toward biotechnological and sustainable strategies that reduce dependence on agrochemicals while reinforcing natural resistance mechanisms (Figure 10). The trajectory mirrors broader trends in plant protection science, where integrated, environmentally conscious solutions are prioritized to balance productivity with ecological resilience.

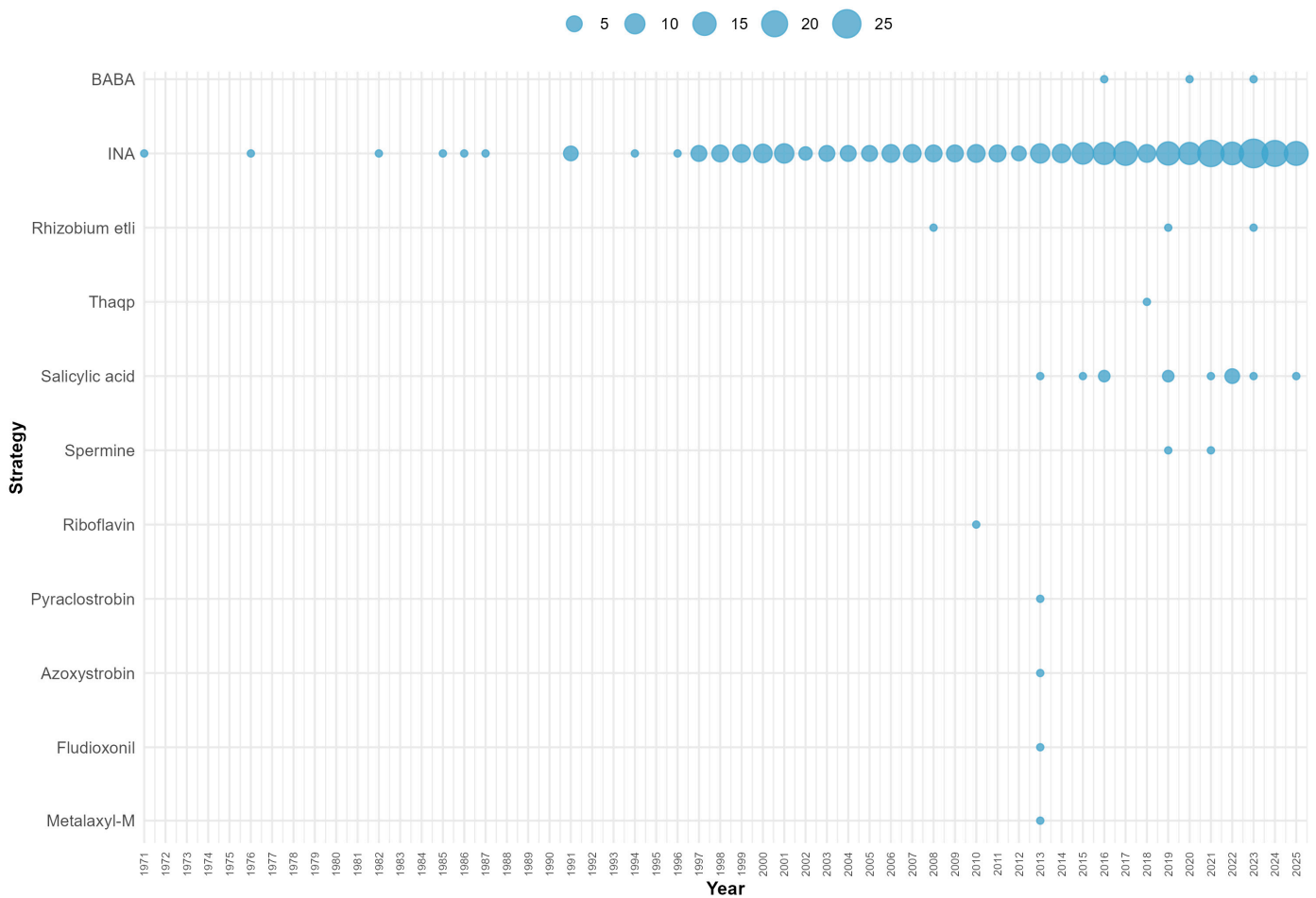


Figure 10. Evolution of strategies for mitigating biotic stresses in common bean (*Phaseolus vulgaris* L.) between 1971 and mid-2025. Each node corresponds to a scientific publication in which a strategy is mentioned, with sizes proportional to the number of studies per year. The X-axis indicates the year of publication, and the Y-axis shows the evaluated strategies.

Figure 11 illustrates the chronological trajectory of abiotic stress mitigation strategies in common bean (*Phaseolus vulgaris* L.) between 1971 and mid-2025, revealing a marked diversification after 2000 and a sharp increase in both frequency and variety of approaches since 2010, which accelerated notably after 2020.

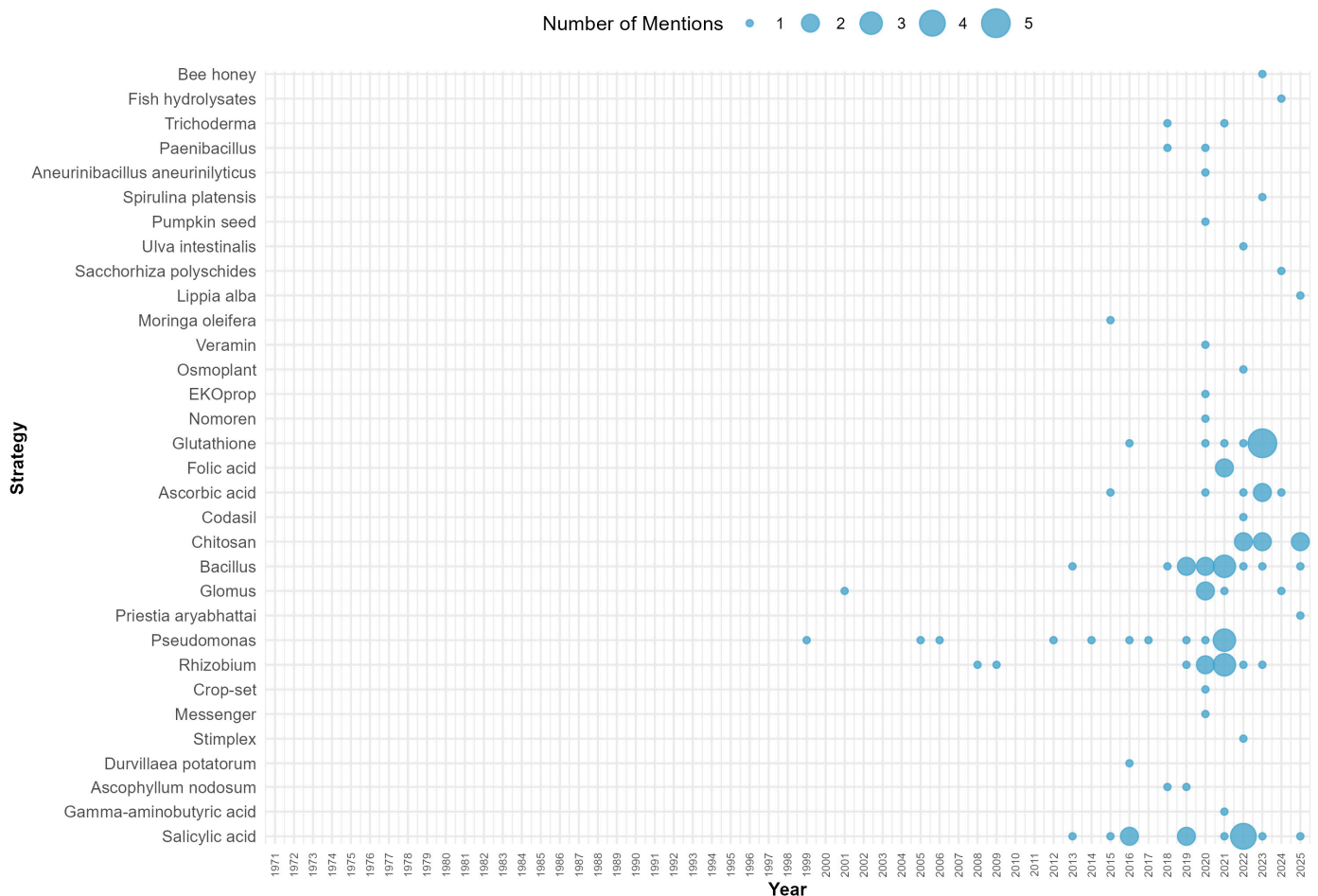


Figure 11. Evolution of strategies for mitigating abiotic stresses in common bean (*Phaseolus vulgaris* L.) between 1971 and mid-2025. Each node corresponds to a scientific publication in which a strategy is mentioned, with sizes proportional to the number of studies per year. The X-axis indicates the year of publication, and the Y-axis shows the evaluated strategies.

For drought stress, early interventions predominantly involved biological fertilization strategies such as seed inoculation with plant growth-promoting bacteria (PGPB). *Pseudomonas fluorescens* and *Rhizobium phaseoli* were among the first evaluated, enhancing nutrient uptake and drought tolerance [277]. Other *Rhizobium* species promoted the formation of larger, more efficient nodules, increasing yields under water-deficit conditions [284]. Subsequently, hormonal biostimulants such as salicylic acid gained prominence. Seed priming with salicylic acid improved root length, seedling biomass, and proteomic profiles under drought [262,307], while foliar applications reduced oxidative damage [238,263]. Comparative analyses showed that seed soaking was more effective than foliar spraying under drought [237], simultaneously improving germination and mitigating oxidative stress [248]. Another key compound, γ -aminobutyric acid (GABA), when applied foliarly, enhanced growth, membrane integrity, osmotic adjustment, antioxidant defense, and yield under drought [264].

Exogenous antioxidants such as ascorbic acid, folic acid, and glutathione have also been tested. Foliar applications of these compounds improved photosynthetic pigments, antioxidant activity, membrane stability, water content, osmolyte accumulation, and yield under water deficit [269,274,275]. Commercial formulations—including Nomoren and EKOprom, applied via irrigation—further enhanced yield under drought [308]. Natural biostimulants, such as bee honey applied foliarly, promoted growth, photosynthesis, and antioxidant defenses [256]. Similarly, commercial biostimulant formulations like Stimplex[®],

Messenger[®], and Crop-Set[®] improved water-use efficiency and stomatal conductance when applied foliarly [265,266], reflecting the gradual translation of scientific findings into agricultural practice.

Comparable strategies have been employed against salinity stress. Seed inoculation with *Rhizobium phaseoli* and *R. tropici* reduced oxidative stress, improved germination, and increased root density under saline conditions [219,225]. Salicylic acid was tested via both foliar application and seed priming, with the latter showing higher efficacy [237]. Foliar ascorbic acid improved growth, antioxidant capacity, and photosynthetic pigments under salinity stress [269]. Other approaches included plant extracts: *Moringa oleifera* applied foliarly improved nutrient uptake, growth, and photosynthesis in saline soils [237]; *Asco-phyllum nodosum* increased proline accumulation [257]; and pumpkin seed hydrolysates reduced salinity-induced oxidative damage when applied foliarly [250]. Emerging microbial inoculants, such as *Aneurinibacillus aneurinilyticus* and *Paenibacillus* spp., demonstrated positive effects on seed germination and antioxidant responses in saline environments [240].

Although less frequently studied, cold stress mitigation has also received attention. Notably, rainbow trout (*Oncorhynchus mykiss*) protein hydrolysates used as a seed pretreatment improved germination under low temperatures [259]. While comparatively underexplored, these studies signal an emerging diversification toward multi-stress strategies.

Taken together, the chronological evolution reveals a progressive diversification and sophistication of abiotic stress management strategies. After 2020, research showed accelerated incorporation of innovative approaches, including emerging microbial inoculants, unconventional plant extracts, and bioactive compound combinations. This trajectory highlights a paradigm shift toward sustainable and multifunctional agricultural practices that harness natural adaptation mechanisms. Such approaches are increasingly framed as essential responses to climate change, aiming to enhance crop resilience while minimizing environmental impact and maintaining productivity (Figure 11).

5. Study Limitations

A key limitation of this study lies in the exclusive use of a single bibliographic database for data retrieval, which may have restricted the coverage of relevant publications, particularly those appearing in journals not indexed within this source. This constraint could have led to a potential underestimation of the scientific output on biotic and abiotic stress in common bean. Future bibliometric assessments should therefore integrate multiple databases to provide a broader and more representative overview, especially considering that the topic under investigation addresses a global challenge.

Although analytical tools such as VOSviewer and Bibliometrix facilitated the bibliometric analysis without major methodological obstacles, their intrinsic limitations must be acknowledged. VOSviewer, despite its efficiency in processing large datasets, requires a steep learning curve and careful preprocessing of records to ensure accurate outputs [309]. Similarly, Bibliometrix, being R-based, demands advanced technical expertise and may encounter scalability challenges when handling very large datasets [47]. In both cases, the accuracy and interpretability of results remain highly dependent on appropriate parameter selection, underscoring the importance of methodological rigor in bibliometric mapping.

With regard to CiteSpace, one limitation was its inability to define a minimum threshold for publication years prior to 1995. Consequently, the co-citation analysis was restricted to the period 1995–2024, a decision justified by the sharp increase in scientific output after 1995, as shown in Figure 2. Additionally, the issue of self-citation, while common in academic practice, represents another limitation. Excessive reliance on self-citations can artificially inflate citation counts, potentially distorting the perceived influence of certain works and biasing the identification of key contributions within the field.

6. Conclusions

With respect to the first objective, the bibliometric analysis demonstrates a sustained increase in research activity, driven by the strategic importance of common bean for global food and nutritional security. Scientific production is highly concentrated in a limited number of countries, institutions, authors, and journals. Among the most influential researchers, Beebe, S. and Kelly, J.D. stand out for their leadership in both publication output and citation impact, playing a central role in consolidating international collaboration networks. The United States, Brazil, and Colombia emerge as the leading countries, supported by institutions such as Michigan State University (MSU) and the International Center for Tropical Agriculture (CIAT). This pattern underscores the advantage of nations with greater investment in agricultural research and advanced technological capacity. Similarly, journals such as *Euphytica* and *Crop Science* concentrate a significant share of publications and citations, including most of the top ten most-cited articles, confirming the critical role of high-impact outlets in scientific visibility and knowledge dissemination.

Regarding the second objective, the analysis reveals a clear methodological transition. While RAPD markers have become largely obsolete, they remain historically significant as early tools for the genetic characterization of *Phaseolus vulgaris*. In contrast, chromosomal mapping has emerged as a prominent theme in genetic improvement, integrating advanced tools such as genome-wide association studies (GWAS), transcriptomics, and pangenomics to more precisely identify loci linked to stress resistance. SNP-based genotyping platforms have enhanced the validation of functional genes and stress-responsive pathways. Nevertheless, challenges remain due to the polygenic architecture of resistance traits, pathogen virulence variability, and the underrepresentation of structural variants in current reference genomes, highlighting the need for individual genome assemblies and pangenomic datasets. The limited adoption of marker-assisted selection (MAS), particularly in developing countries, further illustrates the gap between genomic advances and their translation into practical, accessible, and locally adapted solutions. Emerging research trends—such as salinity tolerance, with validated candidate genes, and oxidative stress, with low-cost strategies including natural antioxidants—demonstrate the dual trajectory of high-resolution genomic research and applied agronomic solutions. Likewise, increasing emphasis on seed germination under abiotic stress through bio-inoculants, seed coatings, and plant extracts underscores the focus on ensuring reliable crop establishment under adverse conditions.

In relation to the third objective, the evolution of biotic stress mitigation strategies has progressed from synthetic priming agents (INA, BABA) and signaling molecules (salicylic acid, riboflavin) to beneficial microorganisms (e.g., *Rhizobium* spp., *Trichoderma* spp.) and next-generation fungicides (e.g., fludioxonil, metalaxyl-M). This trajectory reflects a shift toward sustainable methods with reduced environmental impact. Similarly, abiotic stress management strategies have undergone a marked diversification since the 2000s, with a sharp expansion after 2020. In drought management, early reliance on plant growth-promoting rhizobacteria (*Pseudomonas fluorescens*, *Rhizobium* spp.) has expanded to include hormonal priming agents (salicylic acid, γ -aminobutyric acid), exogenous antioxidants (ascorbic acid, glutathione), commercial biostimulants (*Nomoren*, *Stimplex*[®]), and natural products such as bee honey. In salinity tolerance, strategies have incorporated plant extracts (*Moringa oleifera*, *Ascophyllum nodosum*), seed hydrolysates (pumpkin seed), and emerging microorganisms (*Aneurinibacillus*, *Paenibacillus*), while for cold stress, the application of fish protein hydrolysates (rainbow trout) has shown promising results. Since 2020, the growth of research activity highlights a transition toward multifunctional and ecologically sustainable practices, increasingly grounded in natural adaptation mechanisms and aimed at enhancing crop resilience under climate change.

Overall, the findings indicate that research on common bean has advanced substantially in terms of scientific productivity, genomic tools, and stress mitigation strategies, yet critical challenges remain. These include the limited adoption of genomic technologies in breeding programs, the complexity of translating laboratory findings into field-ready practices, and the persistent disparities in research capacity between high- and low-investment countries. Addressing these gaps will require not only technical innovation but also targeted policies and international collaborations to ensure that advances in genomics and sustainable agronomy are effectively harnessed for improving the resilience and productivity of common bean worldwide.

Future Perspectives

Future research on biotic and abiotic stresses in common bean should prioritize the construction of pangenomes, the refinement of functional annotation of loci identified through GWAS and *k*-mer-based approaches, and the systematic inclusion of underrepresented genetic pools. Expanding the genetic sampling beyond elite germplasm toward landraces, wild relatives, and regionally adapted genotypes will be essential to capture the full extent of genetic diversity available for breeding.

Persistent limitations in phenotyping capacity and research infrastructure, particularly in low- and middle-income countries, highlight the urgency of strengthening international scientific cooperation and ensuring open access to genomic, phenotypic, and environmental datasets. Addressing these disparities is critical to avoid exacerbating the gap between regions with advanced technological resources and those most vulnerable to climate change.

Integrative frameworks that combine multi-omics approaches (genomics, transcriptomics, proteomics, metabolomics, and epigenomics) with high-throughput phenotyping platforms should be prioritized to accelerate the discovery of candidate genes and pathways. The ultimate objective is the development of robust molecular markers and predictive tools that can be seamlessly incorporated into breeding pipelines. Such tools must be designed with an emphasis on scalability, cost-effectiveness, and applicability across diverse production systems, thereby facilitating the generation of resilient bean cultivars adapted to multiple stressors.

Looking forward, the alignment of genomic innovation with sustainable agronomic practices will be pivotal. Research agendas should focus not only on enhancing productivity but also on improving climate resilience, nutrient-use efficiency, and resistance to emerging pathogens, ensuring that common bean continues to play a central role in global food security.

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