

Article

Rhizosheath Research at the Root–Soil–Microbiome Interface: A Bibliometric and Thematic Analysis of Stress Adaptation and Crop Resilience

Elshafia Ali Hamid Mohammed ^{1,2} , Mahbubjon Rahmatov ³, Mohammed Elsafy ³ , Rodomiro Ortiz ^{3,*} , Nataliya Bilyera ⁴, Michaela A. Dippold ^{4,5}  and Tilal Abdelhalim ^{4,6,*}

- ¹ Department of Animal Husbandry, Institute of Animal Science, Biotechnology and Nature Conservation, Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, 4032 Debrecen, Hungary; elshafia@agr.unideb.hu
- ² Agricultural Research Corporation, Integrated Pest Management Research Center, Wad Madani 21111, Sudan
- ³ Department of Plant Breeding, Swedish University of Agricultural Sciences (SLU), P.O. Box 190, 234 22 Alnarp, Sweden; mahbubjon.rahmatov@slu.se (M.R.); mohammed.elsafy@slu.se (M.E.)
- ⁴ Geo-Biosphere Interactions, Department of Geosciences, University of Tuebingen, 72076 Tuebingen, Germany; nataliya.bilyera@uni-tuebingen.de (N.B.); michaela.dippold@uni-tuebingen.de (M.A.D.)
- ⁵ Cluster of Excellence (EXC 3121): TERRA—Terrestrial Geo-Biosphere Interactions in a Changing World, University of Tübingen, 72076 Tübingen, Germany
- ⁶ Biotechnology and Biosafety Research Center, Agricultural Research Corporation, Shambat, Khartoum North P.O. Box 30, Sudan
- * Correspondence: rododmiro.ortiz@slu.se (R.O.); tilalkosti@yahoo.com (T.A.); Tel.: +46-725-418-386 (R.O.)

Abstract

The rhizosheath is a dynamic plant–soil interface in which root traits, microbial activity, and soil physical properties jointly regulate plant adaptation to drought and nutrient limitation. Despite the growing interest in this field, it remains conceptually fragmented. This study mapped the development, structure, and emerging directions of rhizosheath research at the intersection of microbiome interactions, stress adaptation, and root-trait genetics. Bibliometric and science-mapping analyses were performed on 136 publications (2015–2026) retrieved from the Web of Science Core Collection. Using the Bibliometrix framework, we examined publication dynamics, collaboration networks, citation patterns, keyword co-occurrence, and thematic structures. The dataset comprised 136 publications, 6366 cited references, and 723 authors, with 54.41% international co-authorship. Logistic modeling described the accumulation of publications through 2025, identifying a growth inflection at 2022.54; a reliable saturation level could not be estimated because the 2026 data cover only a partial year. Document coupling resolved nine clusters dominated by soil–root interface processes ($n = 51$; 1358 citations) and plant–microbe interactions ($n = 18$; 895 citations). Thematic analysis positioned soil and rhizosheath as central domains and identified water stress as a key motor theme, whereas mucilage, hydraulic functioning, and microbiome assembly emerged as recent trends. Rhizosheath research is transitioning from descriptive characterization toward more integrated, mechanistic perspectives linking root traits, soil processes, and microbial dynamics. Progress will depend on resolving genotype $\times$ soil $\times$ microbiome interactions and advancing field-based cross-scale phenotyping to support climate-resilient cropping systems.



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Keywords: mucilage; soil aggregation; hydraulic conductivity; microbiome; genotype $\times$ environment interactions; bibliometric analysis

1. Introduction

The rhizosheath, a layer of soil that remains physically attached to roots through the combined action of root hairs, mucilage, root exudates, and microbial adhesives, is increasingly recognized as a functional component of the rhizosphere rather than a passive by-product of root growth [1–4]. It is important to distinguish the rhizosheath from a broader rhizosphere. The rhizosphere encompasses the entire soil volume influenced by root activity, including chemical gradients, microbial communities, and nutrient depletion zones. In contrast, the rhizosheath refers specifically to the physically bound layer of soil particles that remains attached to the roots upon excavation [4,5]. This distinction is critical because the rhizosheath mass, the most used metric, captures a defined structural trait, whereas rhizosphere processes extend across a broader, more diffuse spatial domain. More importantly, the rhizosheath mass represents the amount of adhering soil and should not be interpreted as a direct measure of the hydraulic, nutritional, or microbial functions operating at the root–soil interface.

Over the past decade, the rhizosheath has emerged as a measurable root-associated trait that links rhizosphere structure to plant–water relations and nutrient acquisition under environmental stress [1,6–8]. Studies on cereals, legumes, and drought-adapted species have shown that rhizosheath development enhances root–soil contact, modifies water retention and rewetting, and improves access to poorly mobile nutrients, particularly phosphorus, under drying or nutrient-limited conditions [9–12]. These functions position the rhizosheath as part of an extended root phenotype, in which plant traits actively modify soil physical and biological processes to improve resource acquisition and plant performance [3]. Therefore, the rhizosheath is better understood as an emergent plant–soil phenotype than as an isolated morphological property of the root [13].

Mechanistically, rhizosheath formation results from tightly integrated interactions between root structural traits, rhizodeposition chemistry, soil physical properties, and the rhizosphere microbiota. Root hairs provide a structural framework that anchors the soil particles. In contrast, mucilage and root exudates act as physicochemical agents that promote soil aggregation, regulate moisture retention, and influence nutrient diffusion at the root–soil interface [2,14,15]. Mucilage and other rhizodeposits can also modify soil wettability, viscosity, pore connectivity, and the dynamics of drying and rewetting around the roots [16–18]. However, the magnitude and direction of these effects depend on soil texture, water content, root development, and physicochemical properties of the released compounds.

These processes are further reinforced by rhizosheath-associated microbial communities, whose extracellular polymeric substances enhance soil adhesion, stabilize aggregates, and contribute to nutrient cycling [7,19,20]. Rhizosheath-associated bacteria and fungi may also transform nutrients, modify plant hormonal signaling, and interact with root hairs and exudates. Studies in crops such as rice, barley, sorghum, pearl millet, and switchgrass indicate that soil drying and plant genotype can restructure rhizosheath microbial communities, while selected bacterial taxa can enhance rhizosheath formation through auxin- or ethylene-related pathways. Accordingly, rhizosheath development results from dynamic plant–soil–microbe interactions shaped by plant genotype, soil texture, and moisture regime, rather than being a purely structural property of the root [20].

These integrated processes are directly relevant to drought tolerance and nutrient acquisition, particularly under water-limited and low-soil-fertility conditions. Maintaining hydraulic continuity at the root–soil interface reduces air gaps and sustains water flow to the roots, thereby buffering plants against transient drought stress [1,12,21]. The chemically active microenvironment within the rhizosphere also promotes phosphorus mobilization through rhizodeposition and microbial activity, which is critical in soils with

limited nutrients [11,19,22]. Moreover, evidence of genetic variation in rhizosheath traits across crops, such as wheat, barley, sorghum, and legumes, highlights their potential as targets for phenotyping and breeding aimed at improving resource-use efficiency under climate stress [20,23–25]. However, the functional and agronomic relevance of rhizosheath variation remains uncertain because rhizosheath mass is influenced by plant development, soil conditions, sampling procedures, and genotype $\times$ environment interactions. Consequently, a larger rhizosheath does not necessarily improve water or nutrient acquisition, stress tolerance, or productivity. Therefore, distinguishing structural expression from physiological function and breeding value is essential before rhizosheath traits can be reliably incorporated into phenotyping and climate-resilient crop improvement. Despite these advances, the conceptual understanding of rhizosheath biology remains fragmented across disciplines such as plant physiology, soil physics, and microbial ecology. In addition, commonly used metrics, such as rhizosheath mass, do not fully capture the structural and functional complexity of rhizosphere processes, particularly under heterogeneous soil conditions or when measured in disturbed systems [9]. This fragmentation limits the integration of rhizosheath traits into predictive frameworks and breeding strategies. This situation raises a question that a narrative review alone cannot readily answer: how has rhizosheath research actually developed and organized itself across these disciplines, and is the field consolidating toward an integrated, function-oriented understanding or remaining anchored to structural description?

Bibliometric analysis provides a systematic approach to address this limitation by quantitatively mapping the development, structure, and thematic evolution of research fields. By combining performance indicators (e.g., publication output, citation impact, and collaboration networks) with science-mapping techniques (e.g., co-citation, bibliographic coupling, and keyword co-occurrence), these approaches reveal how knowledge domains are organized and how research priorities have evolved [26,27]. This is especially valuable for a young, fast-growing, and terminologically heterogeneous field such as rhizosheath research, whose relevant literature is dispersed across plant physiology, soil physics, microbial ecology, and crop breeding; in such a field the overall intellectual structure, the dominant versus neglected themes, and the balance between structural and functional research are difficult to discern from any single disciplinary vantage point, and hence from a conventional review. Such analyses enhance conventional reviews by pinpointing dominant research clusters, emerging topics, and underexplored areas that narrative syntheses alone may not easily detect. However, bibliometric networks alone cannot explain the biological significance of the relationships they reveal. Combining bibliometric mapping with thematic synthesis addresses this limitation by identifying influential publications, research communities, and emerging topics while clarifying their underlying mechanisms, applications, and knowledge gaps through a critical examination of the literature.

In this context, the present study conducted a bibliometric and thematic synthesis of rhizosheath research published between 2015 and 2026. We hypothesized that rhizosheath research remains predominantly anchored to structural description, centered on rhizosheath mass, and organizationally fragmented across disciplines, with integrative, function-oriented work emerging only in the most recent period. Bibliometric performance analysis, science mapping, and thematic evolution provide a direct test of this expectation by revealing whether the field's dominant themes, cluster structure, and cross-disciplinary linkages reflect structural anchoring or genuine functional integration.

To our knowledge, this is the first bibliometric and thematic synthesis focused specifically on rhizosheath research at the root–soil–microbiome and stress-adaptation intersection. Prior quantitative mapping has been confined to a single subtopic: a recent bibliometric review of rhizosheath carboxylates [28], whereas broader science-mapping efforts have tar-

geted rhizosphere microorganisms rather than the rhizosheath specifically [29]. The present study therefore provides the first field-level bibliometric and thematic map of rhizosheath research at the root–soil–microbiome and stress-adaptation intersection. It examined the development of the field through publication output, citation influence, source distribution, author contributions, and international collaboration. This study further mapped the intellectual and conceptual structure by identifying influential publications, dominant research clusters, and the evolution of themes related to root traits, soil physical processes, microbiome interactions, drought responses, nutrient acquisition, genetics, and breeding. Particular attention was given to the conceptual and methodological gaps that limit the translation of rhizosheath formation into measurable physiological functions, field-relevant phenotypes, and agricultural applications. By integrating performance analysis, science mapping, and content-based interpretation, this study provides a reproducible overview of the field. This review outlines the research priorities for incorporating rhizosheath-related traits into climate-resilient crop phenotyping and breeding.

2. Materials and Methods

2.1. Research Questions

This bibliometric study examined the development and structure of rhizosheath research, with an emphasis on rhizosheath–microbiome interactions and plant stress adaptation. A combined bibliometric and thematic synthesis design was employed. Performance analysis characterized research productivity and influence; science-mapping techniques examined the social, intellectual, and conceptual organization of the literature; and qualitative examination of titles, abstracts, and keywords interpreted the biological meaning of the resulting clusters.

Four questions guided this analysis:

- (a) How did publication output, citation influence, source distribution, geographical contributions, and international collaboration evolve during the study period?
- (b) Which authors, publications, journals, and collaboration networks shaped the intellectual and social structure of rhizosheath research?
- (c) Which thematic clusters and conceptual structures characterized the field, and how did themes related to root traits, soil physical processes, microbial interactions, plant stress responses, nutrient acquisition, genetics, and breeding evolve?
- (d) Which conceptual and methodological gaps constrain the translation of rhizosheath formation into functional phenotyping, field application, and climate-resilient crop improvement?

2.2. Data Source, Search Strategy, and Eligibility Criteria

The analysis was based on the Web of Science Core Collection (WoSCC; <https://www.webofscience.com/>). The search was conducted on 10 March 2026, using the following query: TS = (rhizosheath) AND TS = (microbiome OR microbiota OR bacteria OR fungi OR drought OR breeding OR genetics OR “root hair”). In WoSCC, the TS field searches the title, abstract, author keywords, and Keywords Plus fields. The search period extended from 1 January 2015 to 10 March 2026; consequently, the publication output for 2026 represented only a partial year and was interpreted accordingly. Citation counts were also recorded as they appeared in WoSCC on 10 March 2026, because citation indicators are dynamic and may change after the search date.

This strategy combined the core concept of rhizosheath with key biological, ecological, and stress-related terms to capture studies on root–soil–microbiome interactions and plant adaptive processes. The Boolean structure intentionally restricted the dataset to publications that contained “rhizosheath” together with at least one of the selected microbiological,

stress-related, genetic, or root-trait terms. Therefore, it represents a focused subset of the broader rhizosphere literature rather than an exhaustive inventory of every publication mentioning rhizosphere. For reference, a broader query using TS = (rhizosphere) alone, restricted to the same period and document types, retrieved 219 records in the Web of Science Core Collection. The 136 publications analyzed here therefore correspond to approximately 63% of the WoS-indexed rhizosphere literature for this period, confirming that the Boolean filter defined a deliberately focused subset centered on microbiome, stress, genetic, and root-trait themes rather than an exhaustive census of the field.

We acknowledge that this keyword-based approach may have excluded relevant studies using alternative terminology such as mucilage, soil aggregation, root hydraulics, rhizodeposition, root–soil contact, water retention, or phosphorus dynamics. Conversely, records in which a search term appeared only in Keywords Plus could have been retrieved despite limited relevance to the study objectives. These limitations were addressed through title and abstract relevance screening and were considered when interpreting the resulting networks and research trends. We also queried a single database, the Web of Science Core Collection, rather than combining sources. This was deliberate: bibliographic coupling and co-citation analyses depend on consistently formatted cited-reference fields, and merging records across databases (e.g., WoS and Scopus) introduces duplicate entries and heterogeneous reference formatting that can distort coupling and co-citation networks unless extensively reconciled. For a focused corpus of this size, we therefore prioritized the internal consistency and curated cited-reference metadata of the WoS Core Collection over broader but less uniform multi-database coverage. We nonetheless acknowledge that Scopus and other databases index additional rhizosphere records, and that absolute counts and the network periphery would differ under a multi-database strategy; the patterns reported here should be read as specific to the WoS Core Collection.

The search was limited to English-language publications from 2015 to 2026 and included original articles, reviews, and conference proceedings; other document types were excluded to ensure consistency. Document type was applied as a pre-specified inclusion criterion during database refinement: original research articles, review articles, and conference proceedings were retained a priori, whereas all other types (e.g., editorials, corrections, book chapters, and meeting abstracts) were excluded. One proceedings paper met every eligibility criterion and was therefore retained; as a single record (<1% of the corpus), it does not materially affect the performance or network analyses, and excluding an otherwise eligible study solely because of its document type would have introduced an arbitrary exclusion.

Records were eligible if their title, abstract, or keywords addressed at least one aspect of rhizosphere formation, function, measurement, microbial association, environmental response, genetic variation, or agricultural application. No records met these exclusion conditions, so all retrieved publications were retained.

The query retrieved 136 documents: 118 research articles, 17 review articles, and one conference proceeding. Records were exported in the BibTeX format with full metadata (authors, titles, abstracts, keywords, affiliations, cited references, publication year, source titles, and document types) in accordance with established bibliometric guidelines [30].

2.3. Data Processing and Bibliometric Analysis

Analyses were performed in RStudio (version 2026.01.1-403; RStudio Team, Posit, PBC, Boston, MA, USA) using the Bibliometrix R package (version 4.3.0), a widely adopted open-source framework for bibliometric and scientometric analyses [31]. The BibTeX file was imported and converted into a structured data frame using the `convert2df()` function [32]. Preprocessing included verification of metadata completeness, harmonization

of author names and keywords, and confirmation that no duplicate or incomplete records were present. Outputs were tabulated and visualized using Microsoft Excel (Microsoft Corporation, Redmond, WA, USA).

Two complementary approaches were applied. Performance analysis summarized annual publication output, leading journals, authors, and country contributions, whereas science mapping explored the intellectual and conceptual structure through citation, co-authorship, and keyword co-occurrence networks [26,27]. Networks were constructed from co-occurrence and co-citation matrices. The two network types were thresholded differently because they operate on different units. Keyword co-occurrence and thematic mapping are computed over terms, a large proportion of which occur only once; retaining terms with a minimum occurrence of two (the Bibliometrix default) removes these singletons, which would otherwise fragment the map and add noise without contributing stable structure. Document coupling, by contrast, operates over documents rather than terms, and its edges are weighted by the number of shared cited references; applying a term-frequency threshold here would arbitrarily exclude eligible publications, so all 136 documents were retained and weighted by coupling strength. Association-strength normalization and Walktrap community detection were then applied following standard Bibliometrix procedures to identify the major thematic and intellectual structures. Community detection used the Walktrap algorithm with the default random-walk length of four steps, as implemented in Bibliometrix/igraph. The number of communities was not fixed a priori; in each network it was determined algorithmically by modularity optimization, yielding nine clusters for document coupling, three for keyword co-occurrence, and seven for the thematic map. No manual merging, splitting, or fixing of cluster counts was performed, so the reported cluster numbers are fully reproducible from the deposited BibTeX dataset and the stated parameters.

The resulting cluster-size imbalance, a large, densely coupled core of soil–root interface studies alongside several small satellite clusters, is characteristic of a young, coalescing field rather than an artifact of thresholding; because coupling applied no frequency cut-off, this structure does not depend on the keyword threshold. Small clusters ($n = 2\text{--}3$) are reported for completeness but interpreted with caution, as they may represent emerging or loosely connected subtopics rather than established research fronts. No additional generic-term (stop-word) removal was applied beyond the keyword harmonization described above; broadly used descriptors such as growth and responses were therefore retained, and their effect on betweenness centrality is addressed in the interpretation (Section 3.6).

2.4. Screening and Data Extraction

The Web of Science Core Collection query returned 136 publications for the period 2015 to the first quarter of 2026: 118 research articles, 17 reviews, and one conference proceeding. Because a single database was queried, no cross-database duplicates were present, and no additional records were removed: all 136 publications met the eligibility criteria and were carried forward in full. Title and abstract screening served to confirm topical relevance rather than to exclude records.

Retrieved records were screened against predefined inclusion criteria (publication year, language, and document type) following established guidelines for bibliometric analysis [26,27]. Metadata completeness was verified for all records, and none required removal for missing or duplicate information. Key metadata, authorship, publication year, source, author keywords, institutional affiliations, document type, and citation counts, were extracted to compute descriptive indicators and construct science-mapping networks [33]. The original BibTeX dataset and analysis outputs were retained throughout to ensure transparency and reproducibility [31].

3. Results

3.1. Dataset Overview and Growth Dynamics

The bibliometric dataset comprised 136 publications on rhizosheath research published between 2015 and 2026 across 60 sources, with 6366 cited references and 723 authors (Table 1). The annual publication growth rate during the study period was -3.62% , the mean document age was 4.29 years, and the average citation impact was 31.71 citations per document. Content analysis identified 501 Keywords Plus and 470 author keywords. Multi-author collaborations dominated, with only one document being single-authored, an average of 8.25 co-authors per document, and 54.41% of the international co-authorship.

Table 1. Presents the main bibliographic characteristics of rhizosheath publications (2015–2026).

Category	Indicator	Value
Data coverage	Timespan	2015–2026
	Sources (journals, books, proceedings)	60
	Documents	136
	References cited	6366
Publication dynamics	Annual growth rate (%)	-3.62
	Average document age (years)	4.29
	Average citations per document	31.71
Content	Keywords-plus	501
	Author keywords	470
Collaboration	Authors	723
	Single-authored documents	1
	Co-authors per document	8.25
	International co-authorship (%)	54.41
Document types	Articles	118
	Reviews	17
	Proceedings paper	1

The temporal distribution of rhizosheath publications followed a logistic growth pattern (Figure 1a), with an inflection point at 2022.54 and a life-cycle duration (Δt) of 9.15 years; the estimated peak annual output (~ 19 documents) occurred around 2022–2023. Cumulative output rose from 3 documents in 2015 to 136 by 2026 (Figure 1b; $R^2 = 0.587$, RMSE = 4.86). Although the model returned a fitted carrying-capacity parameter ($K = 159.64$), we do not interpret this as a reliable saturation estimate. Because the search closed on 10 March 2026, the final year covers only a partial period, which lowers the last cumulative point and suppresses the tail of the curve; a logistic model fitted to such data tends to underestimate the true ceiling and can misread the incomplete final year as early saturation. The apparent decline from 24 publications in 2022 to about 10 per year in 2023–2025, and the negative first-to-last-year growth rate (-3.62%), are consistent with this coverage artifact together with the expected post-inflection slowing of a logistic trajectory, rather than with a confirmed plateau. Figure 1b is therefore presented as a description of the observed accumulation of publications through 2025 rather than as a forecast of a saturation level.

Annual production began with one article in 2015, stabilized at eight publications per year between 2017 and 2019, increased to 14–15 in 2020–2021, peaked at 24 in 2022, and subsequently declined to 10 per year in 2023–2025 (Figure 1c).

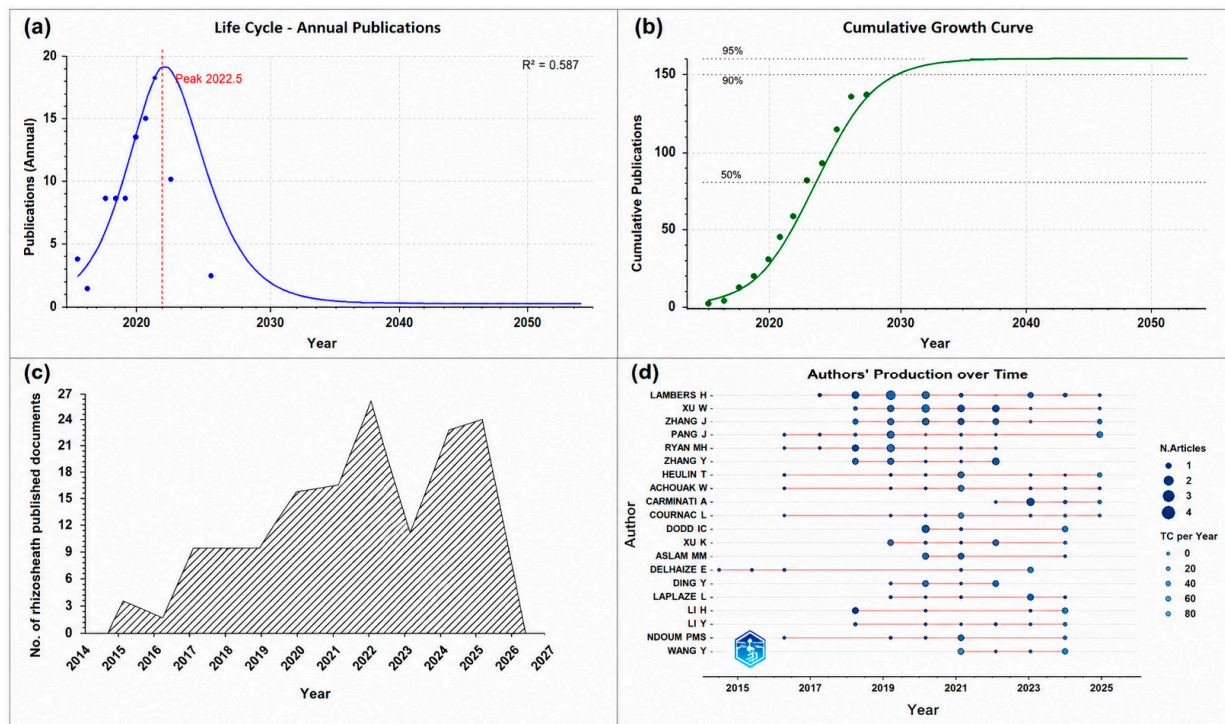


Figure 1. Publication dynamics of rhizosheath research (2015–2026). (a) Life-cycle curve: observed annual publications (points) with fitted logistic curve (line) and inflection point (dashed line); model parameters $K = 159.64$, $t_m = 2022.54$, $\Delta t = 9.15$. (b) Cumulative growth curve with observed values (points) and fitted logistic model (line); dotted lines indicate 50%, 90%, and 99% of the fitted logistic curve (shown to describe the observed growth trajectory, not as a saturation forecast). (c) Annual scientific production from WoSCC. (d) Top 20 authors' publication output over time; bubble size = number of articles per year, intensity = total citations per year (TCpY).

Among the most productive authors, W. Xu and J. Zhang sustained continuous activity from 2019 to 2025, while J. Pang and M.H. Ryan published consistently from 2017 onward (Figure 1d). More recent contributors included A. Carminati (2023–2026) and I.C. Dodd (2021–2025), reflecting the field's continued expansion.

3.2. Core Knowledge Sources and Leading Authors

Plant and Soil was the most frequent source, accounting for 27 articles ($\approx 20\%$ of the dataset), followed by New Phytologist (7) and Journal of Experimental Botany (6). The second tier, Annals of Botany, Frontiers in Plant Science, Plant, Cell & Environment, Rhizosphere, and Scientific Reports, each contributed five articles (Figure 2a). Bradford's Law analysis identified Plant and Soil, New Phytologist, Journal of Experimental Botany, and Annals of Botany as the core zone (Zone 1), beyond which the number of articles per journal progressively decreased (Figure 2b). This concentration should be interpreted with some caution. Plant and Soil is a high-output, broad-scope soil–plant journal whose thematic range overlaps extensively with rhizosheath terminology, so its leading position partly reflects journal size and scope rather than intellectual centrality alone. Accordingly, the Bradford core zone (Figure 2b) should be read as identifying the principal publication outlets for rhizosheath research, where the literature is concentrated and most accessible, rather than as a direct ranking of conceptual influence, which is better captured by the document-coupling and citation analyses (Section 3.4). The prominence of Plant and Soil is therefore consistent with both mechanisms, and the two are not mutually exclusive.

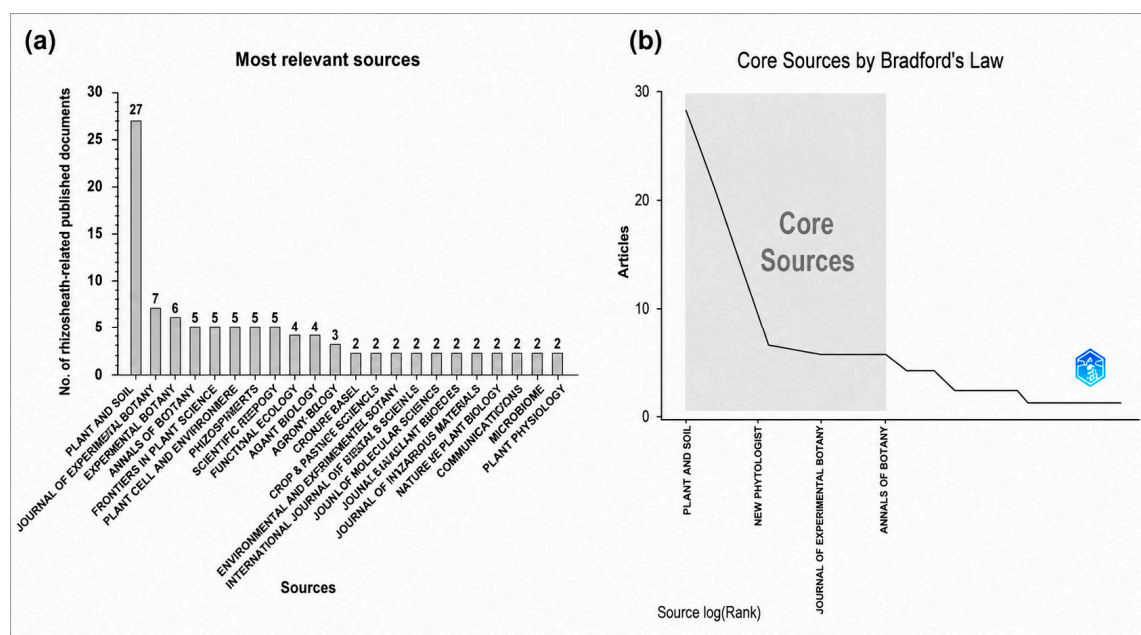


Figure 2. Core scientific sources. (a) Distribution of rhizosphere-related publications across leading journals (2015–2026; N = 136). (b) Core journals identified by Bradford's Law. H. Lambers and W. Xu were the most productive authors, each contributing 15 publications (fractionalized 1.74 and 1.77, respectively), followed by J. Zhang (14; 1.34), J. Pang (12; 1.36), and M.H. Ryan (10; 1.28) (Table 2). I.C. Dodd showed the highest fractional contribution among mid-productivity authors (1.33 from 7 publications), indicating leading authorship roles.

Table 2. Key contributors to rhizosphere research: top authors by productivity and top countries by citation impact (2015–2026).

Top Authors	Articles	Fractionalized	Top Countries	Articles (n)	TC	Average Citations/Article
Lambers H	15	1.74	China	48	1235	25.7
Xu W	15	1.77	Australia	23	849	36.9
Zhang J	14	1.34	United Kingdom	11	631	57.4
Pang J	12	1.36	Pakistan	3	331	110.3
Ryan MH	10	1.28	Saudi Arabia	4	291	72.8
Zhang Y	9	1.01	Germany	10	243	24.3
Heulin T	8	0.85	Iran	6	179	29.8
Achouak W	7	0.77	France	7	130	18.6
Carminati A	7	0.74	Brazil	2	90	45.0
Dodd IC	7	1.33	Senegal	3	88	29.3

3.3. Global Scientific Production and Collaboration

China led the field with 48 corresponding-author articles (35.29%; 30 SCP and 18 MCP), followed by Australia (23; 14 SCP and 9 MCP), the United Kingdom (11; 5 SCP and 6 MCP), and Germany (10; all MCP) (Figure 3a; Table 2). African and Latin American contributions were present but limited, with Ghana, Senegal, Brazil, and Nigeria each producing 1–3 articles, predominantly via international collaborations.

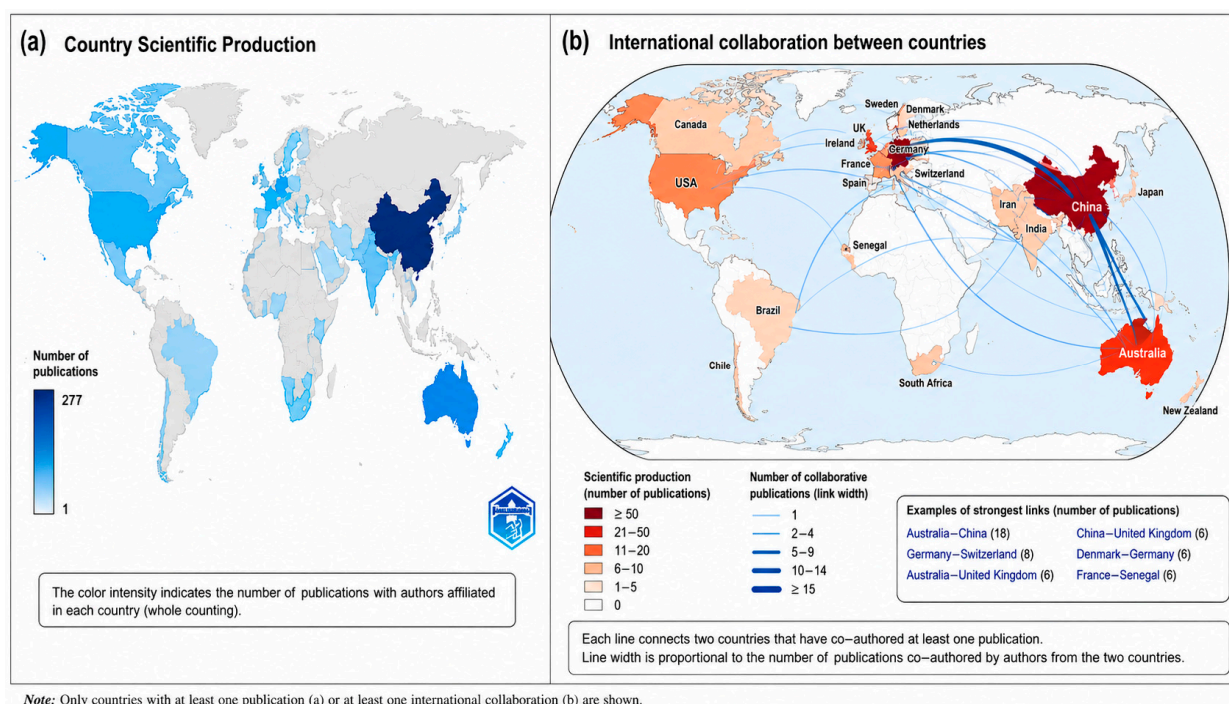


Figure 3. Geographic structure of rhizosheath research. (a) Distribution of corresponding authors' countries, showing single-country (SCP) and multi-country (MCP) publications. (b) Global collaboration network of corresponding-author countries. Node size is proportional to a country's number of multi-country publications, and edge width and color intensity are proportional to the number of co-authored publications linking each country pair.

Citation impact did not track productivity. Among countries with at least five articles, the United Kingdom (57.4; $n = 11$), Australia (36.9; $n = 23$), and Iran (29.8; $n = 6$) recorded the highest average citations per article, ahead of China (25.7; $n = 48$) and Germany (24.3; $n = 10$). Substantially higher averages were recorded for Pakistan (110.3), Saudi Arabia (72.8), and Brazil (45.0), but these rest on only two to four articles each ($n = 3, 4$, and 2, respectively) and are therefore driven by one or a few highly cited papers rather than sustained national output; they reflect individual-study effects rather than country-level citation performance (Table 2). This pattern indicates that, for several smaller contributors, national citation averages are shaped by a few highly cited international collaborations rather than by broad national output, so these averages should not be read as indicators of country-level influence on the field. The intellectual core of the literature is better identified through document coupling and citation structure (Section 3.4) than through country-level citation averages.

The collaboration network was centered on Europe, with Germany acting as a principal hub (Figure 3b). Germany's most frequent bilateral links were with Switzerland (8 co-authored publications), the Netherlands (5), and the United Kingdom and USA (3 each). The United Kingdom anchored additional cross-regional links to India, Pakistan, Japan, Kenya, Tunisia, and Saudi Arabia, whereas collaborations involving Africa, the Middle East, and Latin America were sparser. Because these counts derive from corresponding-author country co-authorships, they should be read as indicative of the principal collaboration axes rather than exhaustive bilateral totals.

3.4. Intellectual Structure: Document Coupling

Document coupling resolved the literature into nine clusters (Table 3). Because bibliographic coupling groups documents by their shared cited references, these clusters represent communities of publications built on a common intellectual foundation rather

than thematically defined research topics; topical structure is examined separately through the keyword co-occurrence network and thematic map (Sections 3.5 and 3.6). The clusters are therefore described below in terms of the shared literature base that links them, and the smallest clusters ($n \leq 3$) are treated as tentative groupings rather than as established research topics or directions.

The largest, Cluster 8 ($n = 51$; 1358 citations), captured soil–root interface processes, aggregation dynamics, and ecosystem-level functioning, anchored by Pang, Ryan, Siddique and Simpson [5], Brown et al. [34], Marin et al. [35], and Delhaize et al. [36]. Cluster 5 ($n = 18$, 895 citations) grouped studies on plant–microbe interactions and the functional rhizosphere [37,38].

Mechanistic dimensions of rhizosheath formation were distributed across three clusters: Cluster 1 ($n = 6$; 652 citations) focused on root trait regulation and rhizosheath formation (Wen et al. 2019, 2020; Pang et al. 2018); Cluster 4 ($n = 8$; 200 citations) addressed rhizosphere processes and root–soil interactions; and Cluster 2 ($n = 2$; 108 citations) covered rhizosphere microbiome interactions. The remaining clusters captured emerging or applied domains, including crop physiology and yield (Cluster 6), functional genomics (Cluster 7), soil management (Cluster 3), and agronomic applications (Cluster 9). Of the 136 publications, 36 (26.5%) shared too few references with the rest of the corpus to form coupling links and were therefore not assigned to any cluster. This high proportion of weakly coupled documents is itself informative: it indicates a young, still-fragmenting field in which many studies draw on separate, discipline-specific studies, plant physiology, soil physics, microbial ecology, and breeding, rather than a shared canon, consistent with the cross-disciplinary dispersion noted in the Introduction.

Table 3. Document coupling clusters, citation strength, thematic domains, and key references in rhizosheath research (WoSCC, 2015–2026).

Cluster	Docs (n)	Total Citations	Research Domain	Key References
1	6	652	Root trait regulation and rhizosheath formation	[39], (348); [5], (184); [40], (59)
2	2	108	Rhizosphere microbiome interactions	[10], (92); [41], (16)
3	3	21	Soil management and tillage effects	[38] (15); [42]; (6)
4	8	200	Rhizosphere processes and root–soil interactions	[39] (57); [40] (47); [41] (29)
5	18	895	Plant–microbe interactions and functional rhizosphere	[38] (271); [37] (136); [43] (83)
6	4	69	Crop physiology and yield-related responses	[44] (55); [45] (11)
7	3	55	Functional genomics and molecular regulation	[46] (29); [47] (15)
8	51	1358	Soil–root interface, aggregation, and ecosystem function	[5] (124); [34] (110); [35] (100); [36] (80)
9	5	57	Agronomic applications and sustainable systems	[48] (17); [49] (17)

3.5. Conceptual Structure: Keyword Co-Occurrence Network

High-frequency terms in rhizosheath research clustered around three conceptual domains (Figure 4a). Core terms, rhizosheath (60), soil (52), rhizosphere (49), and growth (46), dominated the dataset and occupied the largest treemap blocks. The second tier reflected crop and trait dimensions (wheat 22; tolerance 20; plant, root hairs, and traits each 19; phosphorus acquisition 18), while stress, nutrient, and microbial terms (water stress 16;

hydraulic-related processes as focal points of recent publication activity. Niche themes with high density but low centrality included root (density = 116.00), drought tolerance (100.92), and strategies (96.70), reflecting specialized but well-developed subdomains. Traits (centrality = 10.44; density = 90.94) occupied an intermediate position between the basic and motor themes. At the keyword level, the highest betweenness values were recorded for growth (1353.90), responses (1190.84), rhizosheath (1187.44), rhizosphere (1121.36), and soil (980.72). Two of these growth and response terms—broad, generic descriptors that co-occur with many terms and therefore accumulate high betweenness as connective elements rather than conceptual cores- should be interpreted with caution. The domain-specific hubs rhizosheath, rhizosphere, and soil are more informative, and their central positions confirm the rhizosheath–rhizosphere–soil interface as the structural backbone of the keyword network.

Table 4. Thematic clusters and temporal trends in rhizosheath research.

Cluster	Centrality	Density	Frequency	Trend Keyword	Freq.	Q1	Median	Q3
Soil	30.08	71.73	381	Rhizosheath	60	2020	2022	2024
Rhizosheath	20.68	75.54	332	Soil	52	2019	2022	2024
Water stress	21.98	89.85	250	Rhizosphere	49	2020	2022	2024
Traits	10.44	90.94	138	Tolerance	20	2019	2021	2024
Root	9.83	116.00	111	Root hairs	19	2017	2021	2024
Drought tolerance	5.41	100.92	35	Responses	15	2021	2023	2024
Strategies	1.28	96.70	21	Drought	13	2022	2023	2023
				Water	11	2022	2024	2024
				Mucilage	9	2019	2023	2024
				Stress	9	2022	2024	2025

Centrality = degree of interaction with other themes; density = internal cohesion of the theme; frequency = total keyword occurrences within each cluster. Q1, Median, and Q3 indicate the quartile years of keyword occurrence; Freq. = total occurrences in the dataset.

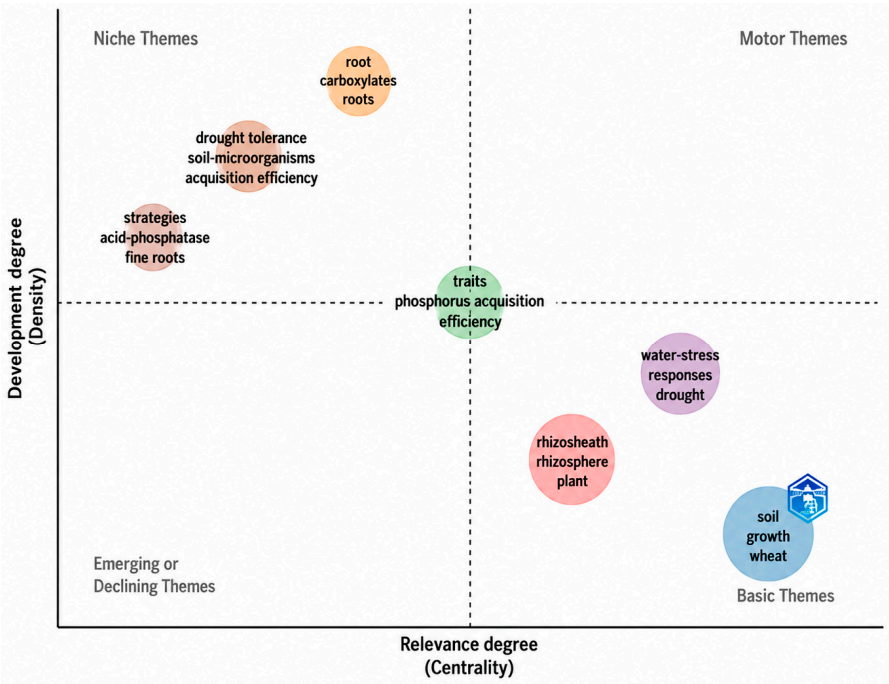


Figure 5. Thematic map of rhizosheath research based on keyword co-occurrence (2015–2026), showing basic, motor, niche, and emerging themes. The bubble size reflects the cluster keyword frequency, and the position indicates Callon centrality (x-axis) and density (y-axis).

These trend and thematic patterns describe how research attention has been distributed over time; they should not be read as measures of the biological or mechanistic importance of the underlying processes. Rising keyword frequency reflects growing publication activity on a topic, which may be driven by methodological accessibility, funding, or community interest as much as by mechanistic significance; therefore, establishing the functional importance of these processes requires experimental evidence from primary literature rather than bibliometric frequency alone.

4. Thematic Architecture and Way Ahead: A Synthesis of Rhizosheath Research

4.1. Conceptual Backbone: A Connected Rhizosheath–Soil–Rhizosphere System

The bibliometric synthesis of 136 publications and 6366 cited references (Table 1) revealed a highly interconnected research field anchored by a clear conceptual backbone. The dominance of rhizosheath, soil, rhizosphere, and growth in the treemap (Figure 4a) and their central positions in the keyword co-occurrence network (Figure 4b; rhizosheath betweenness = 261.55; soil = 150.98; rhizosphere = 147.22) indicate that the field is now organized around a tightly coupled rhizosheath–soil–rhizosphere continuum rather than treating these elements as separate entities.

This interpretation was supported by document coupling: the two largest clusters, soil–root interface processes (Cluster 8; $n = 51$; 1358 citations) and plant–microbe interactions (Cluster 5; $n = 18$; 895 citations), together represented more than half of the analyzed publications. Their prominence indicates that soil physical processes and biological interactions constitute the principal knowledge domains linking the literature.

Foundational contributions identified by these clusters [5,20,34] reframed the rhizosheath as a root-driven soil-engineering system rather than a passive adherent layer. Subsequent work confirmed that this interface emerges from the coordinated action of root hairs, mucilage, exudates, soil texture, moisture regime, and microbial communities [4,14,44,50]. However, recent evidence cautions that rhizosheath mass alone does not always capture broader rhizosphere structure or function across intact and disturbed soils [9]. Therefore, the conceptual backbone identified here should be interpreted as dynamic and environmentally contingent.

4.2. Functional Modules: Stress Adaptation, Resource Acquisition, and Microbial Interfaces

Building on this conceptual backbone, three interrelated functional modules emerged from bibliometric and thematic analyses.

First, stress adaptation was represented by the motor-theme position of the water stress cluster and the recent occurrence of responses, drought, water, and stress (centrality = 21.98; density = 89.85; Figure 5; Table 4), and was reinforced by the temporal rise in responses (median 2023), drought (2023), water (2024), and stress (2024) in trend topics (Table 4). The studies grouped in this module report that, across cereals and legumes, water deficit promotes rhizosheath development through coordinated ABA–auxin regulation of root hair growth, mucilage production, and exudation [1,40,43,51], positioning the rhizosheath as a dynamic adaptive interface rather than a static structural response [50].

Second, root traits and resource acquisition formed a second module anchored in document coupling Cluster 1 (root trait regulation and rhizosheath formation; 652 citations; Table 3) and represented in the keyword network by phosphorus acquisition (PageRank = 0.067), root hairs, and efficiency (Figure 4b). In these studies, root hair architecture and carboxylate exudation have been shown to jointly drive rhizosheath development and phosphorus mobilization, often enhanced by microbial activity [5,36,52,53].

The persistence of carboxylates as a trending topic from 2018 to 2023 (Table 4) reflects the durability of this research line.

Third, biochemical and microbial interfaces constitute a third module, captured by document coupling Cluster 2 (rhizosphere microbiome interactions; Table 3) and the recent emergence of mucilage (median 2023) as a trending topic. According to the studies in this cluster, polysaccharide-rich mucilage and exudates both structure the rhizosheath and selectively recruit microbial communities, including AMF and rhizobacteria, whose extracellular polymeric substances further stabilize aggregates and mobilize nutrients [10,22,44,54]. These reciprocal interactions identify the rhizosheath as a biologically active interface, rather than demonstrating that every rhizosheath necessarily functions as an equivalent microbial hotspot.

4.3. Toward a System-Level Perspective

Although rhizosheath research has historically been partitioned across root genetics, microbiome ecology, and soil physics, the keyword co-occurrence network (Figure 4b) shows that terms from these domains frequently co-occur, linked through shared high-betweenness hubs such as rhizosheath (1187.44), rhizosphere (1121.36), and soil (980.72) (Section 3.6). Importantly, keyword co-occurrence captures only static lexical associations within the analyzed corpus and cannot, on its own, demonstrate genuine cross-disciplinary integration or convergence: the connectivity shows that these themes are discussed together in the literature, not that concepts, methods, or data are being integrated across the underlying disciplines. We therefore describe the field as showing growing thematic interconnection rather than demonstrated disciplinary integration. Testing whether cross-domain linkage is genuinely increasing would require comparing co-occurrence networks across successive periods, together with evidence from primary studies of methodological and conceptual cross-use; we identify this as an important direction for future work. Consistent with a picture of interconnection rather than integration, the thematic map (Figure 5) shows traits occupying an intermediate position between the basic (soil, rhizosheath) and motor (water stress) themes, which is compatible with crop-trait research spanning structural and stress-adaptation topics.

At the process level, primary studies report that root-derived compounds alter microbial assembly and soil aggregation, that microbial products further influence aggregate stability and nutrient turnover, and that resulting root–soil structure affects water and nutrient transport [12,19]. Imaging and modeling approaches are beginning to connect these microscale interactions with whole-root hydraulics and plant performance [55,56]. Nevertheless, robust system-level predictions will require the explicit separation of rhizosheath structure, physiological function, and agronomic value.

4.4. Way Forward: Four Strategic Directions

The intellectual and thematic structures of the dataset suggest four priorities. Each is motivated by a specific result of this analysis: the late-emerging trend topics and niche themes (Section 3.6) for the first, the high-betweenness keyword hubs (Section 3.6) for the second, the geographic concentration of output (Section 3.3) for the third, and the small, weakly coupled translational clusters (Section 3.4) for the fourth. Because bibliometric patterns describe the literature rather than biological mechanisms, these are offered as research priorities that the mapping highlights, not as conclusions it establishes.

4.4.1. From Structural Description to Mechanistic Understanding

This priority is motivated by the trend-topic and thematic-map results (Section 3.6): the late emergence of mucilage, water, and hydraulic terms and the high density of the root and drought-tolerance niche themes point to growing research attention to mechanisms.

Rhizosheath mass remains the most widely used descriptor, yet it does not distinguish among the contributions of root hairs, mucilage, rhizodeposition, microorganisms, and soil properties. Future research should quantify the relative and interactive contributions of root hair genetics, mucilage properties, exudate composition, microbial activity, and soil structure [15,57,58]. Realizing this will require greater standardization in how rhizosheath studies are conducted and reported. Because rhizosheath quantity is currently expressed in inconsistent units and measured under varied sampling and drying protocols, we suggest that studies adopt a minimum reporting standard, specifying genotype, root-hair and root-system metrics, soil texture and moisture regime, sampling and drying protocol, and the units used to express rhizosheath quantity, so that measurements become comparable across laboratories and the contributions identified above can be resolved.

4.4.2. From Isolated Traits to Integrated Root–Soil–Microbiome Systems

The frequent co-occurrence of the rhizosheath, rhizosphere, and soil hubs, which are among the highest-betweenness terms in the keyword network (Section 3.6), points to this direction; primary studies describe a framework in which structural and biological components act through coupled feedback [17,55]. Because keyword co-occurrence reflects lexical association rather than demonstrated integration (Section 4.3), realizing such a framework will require the approaches below. Cross-scale imaging, chemical characterization, microbial profiling, and mechanistic modeling are required to establish how local processes influence whole-root water and nutrient acquisition.

4.4.3. From Controlled Experiments to Field Validation

Geographical and collaboration analyses revealed that research activity was concentrated in a few countries and institutional networks; China alone contributed 48 of 136 articles (35%), with limited African and Latin American representation (Section 3.3). This concentration may restrict the range of soils, climates, crops, and management systems reported in the literature. Therefore, multi-location experiments and standardized field phenotyping are needed to quantify genotype $\times$ soil $\times$ microbiome interactions and test whether the responses observed under controlled conditions remain consistent in agricultural environments [21,59,60].

4.4.4. From Biological Understanding to Breeding and Agronomic Application

The small document-coupling clusters associated with functional genomics (Cluster 7, $n = 3$) and agronomic applications (Cluster 9, $n = 5$), alongside the modest crop-physiology cluster (Cluster 6), point to an emerging but not yet mature translational frontier. Genetic variation in rhizosheath mass, root hairs, and associated traits provides opportunities for breeding under drought and phosphorus limitations [13,25,57,61]. However, the rhizosheath mass should be treated as a structural proxy, and its relationship with water uptake, nutrient acquisition, and yield must be validated rather than assumed.

Combining rhizosheath measurements with root hair traits, physiological indicators, microbial profiles, and soil properties may improve selection accuracy. Multi-environment validation is essential because soil texture, moisture, and management can modify both trait expression and its relationship with crop performance [14,62]. Integrating genetic selection with microbiome and soil management interventions could ultimately support the development of crop ideotypes adapted to defined target environments [1,21].

5. Conclusions

This synthesis met its aim of mapping the structure and thematic evolution of rhizosheath research at the root–soil–microbiome and stress-adaptation intersection. The analysis identified the rhizosheath–rhizosphere–soil interface as the field’s conceptual

backbone, water stress as its principal motor theme, and mucilage, hydraulic functioning, and microbiome assembly as its most recent trends, together indicating a field maturing from descriptive characterization toward more integrated, mechanistic interpretation.

The central implication for rhizosheath biology is a persistent gap between structural measurement and functional interpretation: rhizosheath mass, the field's dominant descriptor, does not by itself quantify water uptake, nutrient acquisition, microbial activity, or crop performance, and should not be treated as a consistent proxy for them. As developed in the Discussion (Section 4.4), closing this gap will require two concrete steps. First, a minimum reporting standard for rhizosheath studies, specifying genotype, root-hair and root-system metrics, soil texture and moisture regime, sampling and drying protocol, and the units used to express rhizosheath quantity, so that measurements become comparable across laboratories. Second, standardized multi-environment trials that record rhizosheath structure alongside physiological, hydraulic, nutritional, microbial, and yield parameters across contrasting soils and water regimes using shared genotype panels, to establish where, and for which traits, rhizosheath size carries functional and breeding value. Because the present map characterizes a theme-focused subset of the literature rather than the entire rhizosheath field, these priorities are best pursued as targeted, hypothesis-driven extensions of the areas identified here.

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