

## Mapping Plant Biotechnology Research for Low Heavy Metal Accumulation and Crop Safety: A Bibliometric–SLR Study Highlighting CRISPR-Cas9

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| Article Information                                                                                                                                                 | ABSTRACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| <b>Article History</b><br><br><b>Received</b> : December 04, 2025<br><b>Revised</b> : December 25, 2025<br><b>Published</b> : January 10, 2026                      | <p>Heavy metal contamination in agriculture presents a growing risk to food security, underscoring the need for precise and scalable biotechnological solutions. This study maps the research landscape of plant biotechnology for reducing heavy metal accumulation using an integrated bibliometric analysis (Bibliometrix/Biblioshiny and VOSviewer) combined with a PRISMA-based SLR of 43 English-language empirical articles published between 1997 and 2025. The analysis identifies four major thematic clusters: tolerance mechanisms, field applications, multi-omics, and genome editing that indicating a shift from early physiological studies toward precision biotechnology. The focused SLR reveals that CRISPR-Cas9, although still limited in publication volume, has emerged as a strategically positioned research front, particularly in recent crop-focused genome-editing studies involving agriculturally relevant species. Geographical patterns show strong research productivity in Asia and high scientific influence in Western countries. Despite the modest dataset, this study provides a strategic roadmap for prioritizing CRISPR applications, strengthening interdisciplinary integration, and accelerating biotechnology-based solutions for food safety and sustainable agriculture.</p> |
| <b>Keywords:</b><br><br><i>Bibliometric–SLR;</i><br><i>CRISPR-Cas9;</i><br><i>Food security;</i><br><i>Heavy metal accumulation;</i><br><i>Plant biotechnology.</i> |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

## INTRODUCTION

Heavy metal contamination in agricultural systems poses a serious threat to global food security by reducing crop productivity, degrading food quality, and undermining agricultural sustainability (Genchi et al., 2020; Vasilachi et al., 2023). In plants, toxic metals disrupt essential metabolic pathways, causing stunted growth, chlorosis, root browning, and eventual plant death. Their accumulation in edible tissues also elevates human health risks, including arsenic-related carcinogenicity, cadmium-induced renal toxicity, and neurological impairment from lead and mercury exposure (Chouhan et al., 2016; Shao et al., 2025).

Existing remediation technologies remain limited. Chemical precipitation and membrane filtration are restricted by high costs, low selectivity, and waste generation (Ahmad et al., 2024; Jepsen et al., 2018), while microbial-based treatments are highly sensitive to environmental variability and metal toxicity (Mandal et al., 2025). These constraints have increased the appeal of plant biotechnology as a scalable and sustainable approach for managing heavy metal accumulation.

Recent advances support diverse biotechnological strategies, including manipulation of metal transporter genes, regulation of stress-response pathways, and multi-omics analyses of metal uptake, translocation, and detoxification. Although these developments have been reviewed, the

broader research landscape remains insufficiently mapped, particularly regarding precision genome-editing tools such as CRISPR-Cas9. Emerging studies highlight its potential to modify metal-binding proteins, regulate cadmium transporters, and alter cell wall remodeling in crops like rice and tobacco (Y. Wang et al., 2024; Zhao et al., 2022; X. Zheng et al., 2024). However, these contributions are dispersed across disciplines, obscuring overarching trends and strategic research priorities.

The rapid growth of publications has also produced a fragmented knowledge structure. Existing reviews, which are largely narrative in nature (Acharya et al., 2025; Mohamed et al., 2025), provide valuable mechanistic and physiological insights into heavy metal stress and phytoremediation, but remain limited in capturing large-scale patterns, collaboration networks, and emerging research fronts. Only a few studies have mapped the evolution of biotechnology related to heavy metal regulation, and even fewer have examined how CRISPR-Cas9 is positioned within this broader domain. Unlike prior narrative reviews that mainly synthesize mechanisms or individual case studies, this study adopts an integrated bibliometric and Systematic Literature Review (SLR) approach to quantitatively map the intellectual structure, thematic evolution, and emerging research fronts of plant biotechnology for heavy metal accumulation. Importantly, this approach positions CRISPR-Cas9 not merely as a standalone technique, but as a strategically emerging connector between mechanistic insights and applied crop-oriented solutions. The objectives of this study are to map the development and intellectual structure of the field and to identify emerging research fronts, with particular emphasis on the growing role of CRISPR-Cas9. Practically, the findings provide guidance for research prioritization, strengthen interdisciplinary collaboration, and support the advancement of precision biotechnological tools for reducing heavy metal accumulation and enhancing global food security.

## RESEARCH METHODS

This study employed a sequential explanatory mixed-methods design integrating bibliometric analysis with a Systematic Literature Review (SLR). The workflow consisted of two phases. Phase 1 generated a quantitative overview of publication trends, thematic structures, and intellectual linkages in plant biotechnology for heavy metal accumulation. Phase 2 provided qualitative depth by reviewing emerging genome-editing applications identified from bibliometric mapping. This sequential structure ensured that the SLR focus was grounded in empirical trends, strengthening transparency and reproducibility (Donthu et al., 2021; Tlili et al., 2022).

### Data Collection and Screening Process

Data were retrieved from the Scopus database (<https://www.scopus.com>) on 15 October 2025 (publications indexed thereafter were not included), using a structured search query covering three conceptual domains: plant species, low metal accumulation traits, and biotechnological approaches. The full query was (TITLE-ABS-KEY("Oryza sativa" OR Arabidopsis OR crop OR "food plant")) AND (TITLE-ABS-KEY("low metal accumulation" OR "metal exclusion" OR "heavy metal avoidance" OR "reduced uptake")) AND (TITLE-ABS-KEY(biotechnology OR "molecular breeding" OR "genetic engineering" OR "genome editing" OR CRISPR OR "gene editing")). To ensure comparability and reproducibility, this study limited the dataset to Scopus-indexed journal articles. Scopus was selected because it provides standardized bibliographic metadata required for bibliometric network analysis while offering broad coverage in environmental science and plant biotechnology. The analysis focused exclusively on empirical studies to capture evidence-based research outputs, particularly genome-editing outcomes derived from primary experiments. Review articles were excluded due to their distinct citation patterns, which may distort thematic structures in bibliometric mapping.

The search yielded 98 documents (1992–2025). Screening followed PRISMA 2020 guidelines (Figure 1). Documents were first filtered by source type, excluding books, conference proceedings, book series, and trade journals, resulting in 75 items. Review articles were then removed to retain only empirical studies (n=46), followed by exclusion of non-English

publications, yielding 43 final articles (Published in 1997-2025). Potential biases should be acknowledged. Using a single database may introduce selection bias, and limiting inclusion to English-language publications may result in language bias. To mitigate these effects, the search query covered three conceptual domains—plant species, low-accumulation traits, and biotechnology approaches—combining general and precision-breeding terms (e.g., genome editing, CRISPR). Article screening was conducted following PRISMA guidelines, with inclusion and exclusion criteria applied consistently to all records.

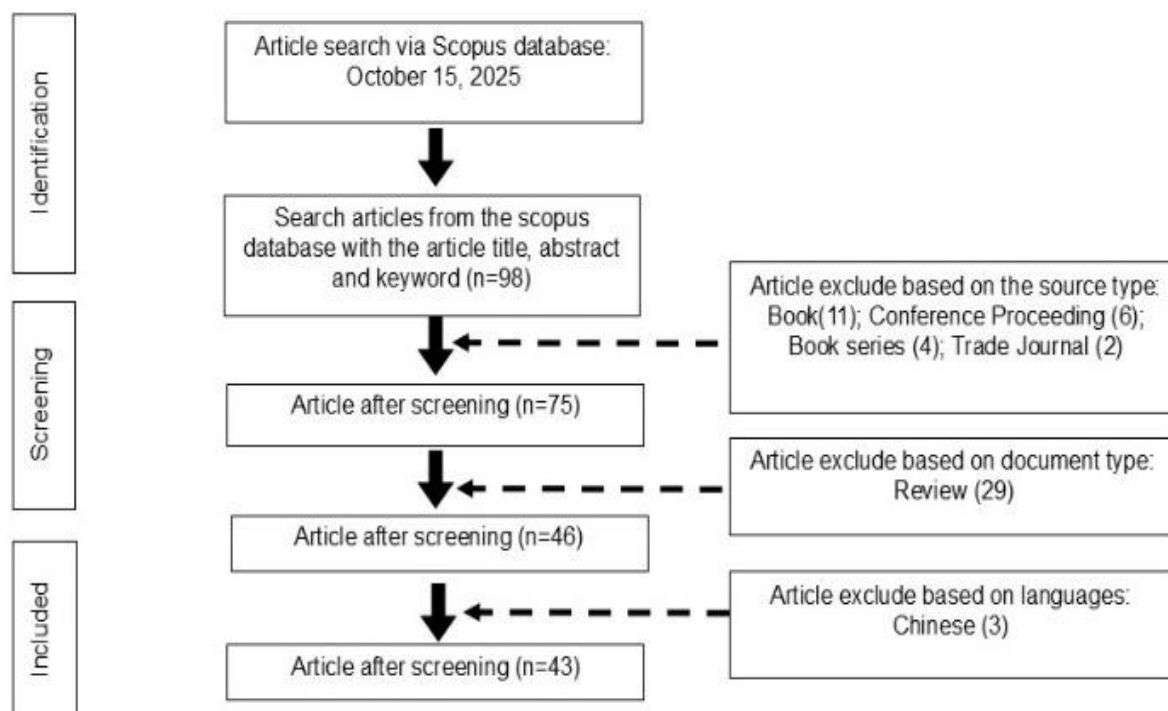


Figure 1. PRISMA Flow

### Bibliometric Analysis Methods

Bibliometric analysis was conducted using Biblioshiny (Bibliometrix R, version 4.2.2) and VOSviewer (version 1.6.20). Data cleaning included removal of duplicates, harmonization of spelling variants, and standardization of synonymous keywords for example Cd” and “cadmium”. Analytical procedures consisted of bibliographic coupling to identify intellectual groupings and keyword co-occurrence analysis to construct conceptual maps. Association strength was used as the normalization method, and cluster detection followed the default VOS algorithm.

A dual-threshold strategy was used to capture both mature and emerging themes. Higher thresholds (minimum occurrence = 2; link strength = 15) reliably identify well-developed topics, but applying them uniformly would exclude recent terms such as CRISPR-Cas9, which appear infrequently due to their novelty. Therefore, a lower threshold (minimum occurrence = 1) was applied for genome-editing keywords to ensure that early-stage but strategically important research fronts remained visible in the conceptual map.

### Systematic Literature Review (SLR) Method

The SLR comprised the second phase of analysis. Articles relevant to CRISPR-Cas9 and genome editing were identified based on bibliometric cluster outputs and keyword networks. Full-text screening applied thematic coding to extract information on targeted genes, edited pathways, phenotypic outcomes, and methodological constraints. Cross-comparison was conducted to identify repeated strategies, divergences between crops, and remaining research gaps. This

integrative design allowed the SLR to contextualize emerging genome-editing advances within the broader biotechnology landscape.

The methodological implementation in both phases was guided by two overarching research questions:

- (1) What are the major trends, themes, and research trajectories in plant biotechnology for low heavy metal accumulation?
- (2) What is the intellectual structure of this field, and how are emerging CRISPR-Cas9 applications positioned within it?

## RESULTS AND DISCUSSION

### *Bibliometric Mapping and Research Trends*

Table 1 summarizes the main bibliometric indicators of the dataset. A total of 43 documents published between 1997 and 2025 were retrieved from 34 journals. The annual growth rate of 2,51% indicates a stable rather than explosive expansion of the field. The documents have an average age of 11 years and receive on average 60,33 citations per article, reflecting the long-term influence of foundational publications and the sustained relevance of the topic. An international co-authorship rate of 25,58% suggests that there is still ample room to strengthen global research collaboration.

**Table 1.** Main information

| Description                    | Results   |
|--------------------------------|-----------|
| Timeframe                      | 1997:2025 |
| Sources Documents              | 34        |
| Annual Growth Rate %           | 2,51      |
| Document Average Age           | 11        |
| Average citations per doc      | 60,33     |
| International co-authorships % | 25,58     |

Publication and citation dynamics indicate that research on plant biotechnology for low heavy metal accumulation has evolved through several distinct phases and is now entering a stage of scientific maturity. Annual scientific production (Figure 2A) can be divided into four periods. The first phase (1997–2015) was characterized by low but steadily increasing productivity, representing an exploratory period when the topic began to attract attention. The second phase (2016–2017) shows an initial surge, coinciding with growing concern over environmental pollution and advances in molecular tools. The third phase (2018–2021) represents a period of accelerated growth, with the most consistent output and peak productivity. The most recent phase (2022–2024) is marked by relatively stable publication numbers, suggesting a transition from broad exploration to more focused application of specific technologies.

Average citations per year (Figure 2B) show a declining trend in recent years. This pattern does not indicate a loss of relevance but reflects a typical citation life cycle. Early landmark publications tend to receive high citations because they serve as conceptual and methodological foundations. Newer studies are often more specialized and distributed across niche topics, requiring time to accumulate comparable citation counts. Overall, the contrast between stable productivity and declining average citations suggests a shift from general exploratory work toward more application-oriented and diversified research.

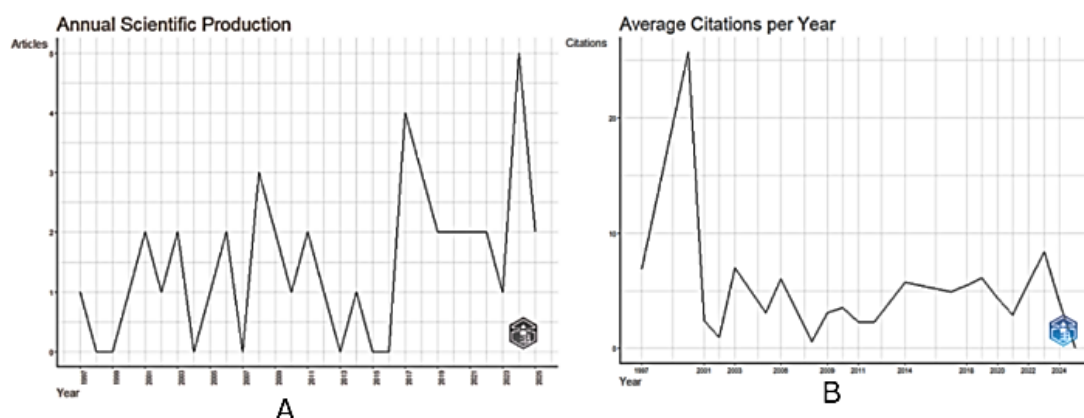


**Figure 2.** Productivity trends and impact shifts. (A) Annual scientific production and (B) average citations per year

### Conceptual and Intellectual Structure

Keyword co-occurrence analysis (Figure 3) clarifies the conceptual structure of the field. Each node represents a keyword, with node size indicating frequency of occurrence, line thickness representing co-occurrence strength, and color denoting cluster membership. Four major thematic clusters emerge. The blue cluster groups physiological mechanisms and model species such as *Arabidopsis thaliana*, phytochelatins, and metallothioneins, representing the mechanistic foundation of metal detoxification. The green cluster contains applied and field-oriented terms, including bioremediation, lead, chromium, and water contamination, linking basic mechanisms to practical environmental applications. The red cluster brings together advanced biotechnology and omics concepts such as genetic engineering, proteomics, metabolomics, and ionomics, reflecting the integration of molecular innovations into system-level analyses. The yellow cluster is dominated by CRISPR-Cas9, genome editing, rice, and tobacco, signaling the emergence of precision biotechnology as a new research front.

These clusters are interconnected by central themes of phytoremediation and heavy metals, illustrating an evolution from ecophysiological studies to increasingly sophisticated biotechnological approaches. Nonetheless, the link between mechanistic research (blue) and large-scale field applications (green) remains relatively weak, and the use of advanced tools such as CRISPR-Cas9 in non-model hyperaccumulator plants is still limited. Temporal co-occurrence patterns (Figure 4) and topic trends (Supplementary Figure 2) show how research priorities have shifted over time. Early topics such as chromium, *Brassica juncea*, and phytochelatins (blue) correspond to the phase of metal identification and basic tolerance mechanisms. Intermediate topics such as cadmium, heavy metals, and bioremediation (green) bridge exploratory studies and applied remediation strategies. Recent topics, visualized in yellow, are dominated by gene editing, genome engineering, and CRISPR-related terms, reflecting the transition toward molecular precision tools for enhancing plant-based remediation and low-accumulation traits. Supplementary Figure 2 also shows that generic topics such as “heavy metals” and “phytoremediation” have long discussion spans, whereas cadmium remains a consistently active and high-frequency subject.

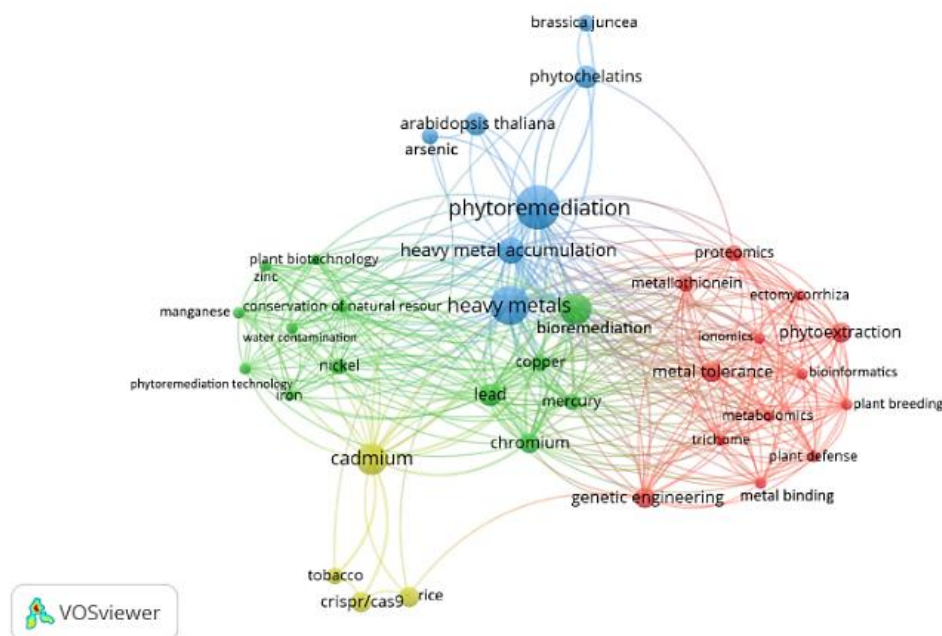


**Figure 3.** Visualization of the co-occurrence network (keyword association map)

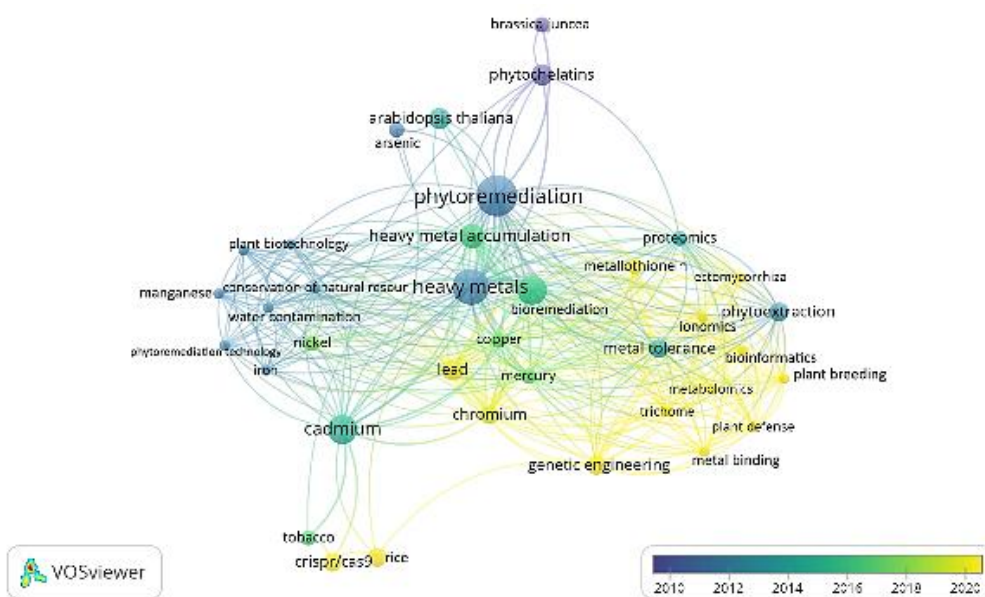


**Figure 4.** Co-occurrence visualization (map of relationships between keywords based on period of appearance)

Analysis of the most relevant sources (Supplementary Table 1) indicates that research in this area is concentrated in reputable journals, notably *Environmental Pollution* (four articles), *International Journal of Phytoremediation* (three articles), and *Applied and Environmental Microbiology* (two articles). This concentration suggests that studies on heavy metal tolerance and phytoremediation are primarily disseminated through environmental science and biotechnology outlets, providing clear reference points for future publication strategies.

The intellectual evolution of plant biotechnology for heavy metal accumulation and tolerance is further clarified by local and global citation patterns. Locally cited references highlight foundational works within the dataset, whereas globally cited documents indicate broader international influence. Seminal local references include Baker & Brooks (1989), Cobbett (2000), Clemens (2001), which established the concepts of hyperaccumulator plants, molecular tolerance

mechanisms, and phytochelatin-mediated detoxification, respectively. Methodological classics such as Bradford (1976) and the floral dip transformation method of Clough & Bent (1998) demonstrate how biochemical assays and genetic transformation technologies supported later advances.

Globally cited documents such as Pence et al., (2000), Salt et al. (1997), and Roth et al. (2006) have shaped the broader trajectory of the field by linking physiological observations to molecular and omics-based approaches. Together, these references trace a coherent pathway from hyperaccumulation and tolerance physiology to system-scale biology and precision biotechnology, providing the intellectual foundation for CRISPR-based interventions.

The role of journals as communication channels, evaluated through local H-index and Bradford's Law (Supplementary Figure 5 and Supplementary Table 1), shows that Environmental Pollution and International Journal of Phytoremediation occupy core positions, combining relatively high publication counts, strong citation impact, and core-zone status. Other journals, including Applied and Environmental Microbiology and Ecotoxicology and Environmental Safety, play complementary roles as interdisciplinary bridges that connect microbial biotechnology, environmental toxicology, and plant science. Contributor analysis at the author, institutional, and country levels reveals a globally distributed yet interconnected research landscape. At the individual level, local H-index values (Supplementary Figure 6) show a relatively even distribution of influence, with researchers such as Clemens S., Kumar V., Bones AM., Peltier G., and Nehnevajova E. each having a local H-index of 2. The absence of a single dominant figure suggests that progress is driven by cumulative contributions from multiple laboratories, consistent with the interdisciplinary nature of phytoremediation biotechnology.

Institutional analysis (Supplementary Figure 7) indicates that Nanjing Agricultural University leads in productivity with ten publications, followed by the University of Bucharest and the Zhengzhou Tobacco Research Institute of CNTC with eight articles each. The Institute of Floriculture, the Kuwait Institute for Scientific Research, and Shanxi University form a second tier with six to seven publications. Temporal analysis of institutional output (Supplementary Figure 8) shows that Nanjing Agricultural University has maintained steady productivity since around 2011, whereas the other institutions experienced more recent surges between 2016 and 2024, reflecting a shift from basic research to commodity-oriented and agroecologically specific applications. At the country level, scientific production and citation impact display a notable divergence (Table 2). China leads in publication volume with 72 articles, followed by India (31) and Pakistan (21). In contrast, the United States records the highest total citations (866) and the greatest average citations per article (433), followed by France, Germany, and Korea. These patterns indicate that Asian countries dominate empirical output, whereas North American and European countries exert greater conceptual and methodological influence. Countries such as South Korea and Sweden, which have relatively few publications but high citation averages, demonstrate high citation efficiency and strong research quality.

Overall, the global contributor map depicts a multi-centered ecosystem in which Asia serves as the primary source of empirical data, while America and Europe act as hubs for theoretical development and methodological innovation. This division of roles underscores the importance of international collaboration as a driver of progress in heavy metal accumulation biotechnology and suggests that future advances should be assessed not only by publication volume but also by the strategic interplay among productivity, impact, and cross-regional cooperation.

### ***Emerging Research Fronts and Focused SLR***

Integrating the results of RQ1 and RQ2 highlights three major, actively evolving research fronts. CRISPR-Cas9 genome editing has emerged as the most prominent frontier. It is concentrated in the yellow cluster of the co-occurrence network (Figure 3), primarily associated with rice and tobacco, and appears as one of the most recent topics in the temporal map (Figure 4) during the 2022–2024 period. Conceptually, CRISPR-Cas9 connects mechanistic tolerance

studies in model systems with applied biotechnology in crops, underscoring its strategic role as a bridge between basic and applied research.

Multi-omics approaches, including proteomics, metabolomics, ionomics, and transcriptomics, form an integrated methodological front within the red cluster. These approaches translate early detoxification concepts into system-level analyses that support precision breeding and gene prioritization. Their intermediate temporal position indicates that they function as a transition from foundational molecular studies to recent genome-editing applications.

Precision genetic engineering represents the conceptual evolution from classical transgenic strategies toward more targeted, trait-specific interventions. This front extends the original hyperaccumulator paradigm of Baker & Brooks (1989) into deliberate engineering of low-accumulation traits and refined metal partitioning, consistent with the field's maturation from broad physiological observations to focused technological applications. Taken together, these fronts justify the selection of CRISPR-Cas9 as the primary focus of the SLR phase.

The SLR synthesis shows that heavy metals such as cadmium (Cd), lead (Pb), mercury (Hg), and arsenic (As) induce complex metabolic, signaling, and gene-regulatory disruptions in plants (Mohamed et al., 2025). Transporter families including HMA, NRAMP, ZIP, ABC, and CAX regulate metal entry into roots and translocation to stems, leaves, and seeds (Acharya et al., 2025). Studies in perennial ryegrass (*Lolium perenne* L.) demonstrate that high-accumulating genotypes store metals predominantly in vacuoles and soluble fractions, whereas low-accumulating genotypes immobilize metals in the cell wall, thereby restricting mobility and toxicity (Cao et al., 2025).

**Tabel 2.** Country scientific production and most cited countries

| No | Country        | Most Cited Countries |                           | Country Scientific Production |
|----|----------------|----------------------|---------------------------|-------------------------------|
|    |                | Total Citation       | Average Article Citations | Frequency                     |
| 1  | USA            | 866                  | 433                       | 18                            |
| 2  | France         | 271                  | 90,3                      | 18                            |
| 3  | India          | 266                  | 38                        | 31                            |
| 4  | Germany        | 251                  | 83,7                      | 6                             |
| 5  | Korea          | 177                  | 177                       | 3                             |
| 6  | China          | 173                  | 17,3                      | 72                            |
| 7  | Poland         | 102                  | 102                       | 7                             |
| 8  | Sweden         | 97                   | 97                        | 3                             |
| 9  | Canada         | 86                   | 28,7                      | 12                            |
| 10 | Switzerland    | 65                   | 65                        | 9                             |
| 11 | United Kingdom | 56                   | 56                        | 4                             |
| 12 | Kuwait         | 41                   | 41                        | 8                             |
| 13 | Romania        | 30                   | 15                        | 9                             |
| 14 | Japan          | 28                   | 28                        | 4                             |
| 15 | Pakistan       | 26                   | 13                        | 21                            |
| 16 | Greece         | 23                   | 23                        | 4                             |
| 17 | Italy          | 21                   | 21                        | 6                             |
| 18 | Iran           | 0                    | 0                         | 4                             |
| 19 | Norway         | 0                    | 0                         | 4                             |
| 20 | Saudi Arabia   | 0                    | 0                         | 2                             |
| 21 | Thailand       | 0                    | 0                         | 1                             |
| 22 | Tunisia        | 0                    | 0                         | 1                             |

Transporter-mediated distribution is tightly linked to oxidative stress. In rice exposed to Cd, metal accumulation in roots and shoots elevates reactive oxygen species, increases proline, reduces chlorophyll content, disrupts water homeostasis, and impairs growth (Zheng et al., 2025; Haque et al., 2021). CRISPR-Cas9-based genome editing now offers precise tools to modulate these pathways (Kumar et al., 2023). Knockout of *NrNRAMP6c* in tobacco significantly reduces Cd uptake, improves root and shoot biomass, and increases chlorophyll content, indicating its role as a plasma membrane Cd transporter (Zheng et al., 2024). Edits targeting *OsHIPP56* in rice reveal its key function in Cd detoxification, with knockout lines displaying altered metal sensitivity and tolerance (Zhao et al., 2022). In contrast, site-directed mutations in *OsPME31*, *OsPME34*, and *OsPME79* in rice promote pectin methylation, loosen cell-wall structures, enhance biomass porosity, increase enzymatic saccharification, and elevate Cd accumulation, particularly for phytoremediation applications (Wang et al., 2024).

These findings show that genome editing can be strategically directed either to suppress or to enhance metal uptake, depending on the intended use. CRISPR-based interventions reported in the literature can be grouped into two functional strategies. The first consists of phytoremediation-enhancing edits, which increase metal uptake or whole-plant accumulation to improve the efficiency of soil and water remediation, as exemplified by the *OsPME31/34/79* mutants. The second comprises food safety-oriented edits, which reduce metal uptake, root-to-shoot transport, or translocation to edible tissues, as seen in the manipulation of *NrNRAMP6c* in tobacco and *OsHIPP56* in rice. Together, these two strategies illustrate the dual role of CRISPR technology in enhancing plant-based remediation capacity on one hand and improving food safety through reduced accumulation on the other. Both contribute to sustainable agriculture by mitigating environmental contamination and reducing dietary exposure to toxic metals. The SLR thus confirms that CRISPR-Cas9-based genome editing has emerged as a versatile and strategically pivotal technology, providing a robust foundation for developing plants with either high-accumulation traits for phytoremediation or low-accumulation traits for food safety.

### **Research Gaps**

Despite substantial progress in plant biotechnology for heavy metal regulation, several critical research gaps remain. Bibliometric mapping reveals that major research clusters—physiological mechanisms, field applications, omics approaches, and precision biotechnology—have largely evolved in parallel, with limited integration between detailed mechanistic studies and complex field conditions. Advanced genome-editing tools, particularly CRISPR-Cas9, are still concentrated in a small number of model crops, while many non-model hyperaccumulator species and diverse food commodities remain underexplored. In addition, current studies often focus on single-metal scenarios under controlled environments, providing limited insight into multi-metal interactions and environmental variability. These gaps constrain the translation of molecular discoveries into scalable, field-relevant solutions for both food safety and environmental remediation.

### **Implications for Future CRISPR-Cas9 Applications**

Based on the gaps, several priority directions emerge for future CRISPR-Cas9 research:

1. Targeting metal translocation pathways for food safety. Genome-editing efforts should prioritize genes controlling root-to-shoot and grain translocation to minimize heavy metal accumulation in edible tissues.
2. Expanding CRISPR applications beyond model crops. Applying CRISPR-Cas9 to non-model hyperaccumulators and regionally important food crops is essential to improve ecological relevance and scalability.
3. Integrating CRISPR with multi-omics and environmental modeling. Combining genome editing with omics data and plant-soil modeling can enhance prediction of metal accumulation across diverse environments.

4. Aligning genome editing with dual-use objectives. Future studies should explicitly distinguish between CRISPR strategies aimed at reducing accumulation for crop safety and those enhancing uptake for phytoremediation, depending on the intended application.

Together, these implications position CRISPR-Cas9 as a pivotal tool for bridging fundamental knowledge and applied solutions, enabling more effective strategies to address heavy metal risks in agriculture.

## CONCLUSION

This study mapped the scientific landscape of plant biotechnology for heavy metal accumulation and identified CRISPR-Cas9 as a strategically emerging research frontier. Conceptually, this work clarifies the evolution of the field from physiological tolerance studies toward precision genome editing and highlights the dual role of biotechnology in food safety and phytoremediation. Methodologically, the integration of bibliometric analysis with a Systematic Literature Review represents a key contribution by providing a transparent, data-driven framework to connect historical foundations, thematic clusters, and emerging genome-editing applications. Practically, the findings offer a strategic roadmap to support research prioritization, guide crop-breeding strategies for low heavy metal accumulation, and inform international collaboration in sustainable agriculture and environmental risk management.

Future research should extend this framework by incorporating additional databases to improve coverage, applying full-text mining and semantic analysis to capture deeper methodological patterns, and conducting crop-specific analyses focused on major food staples such as rice, wheat, and maize. Empirical priorities include multi-metal genome-editing experiments, validation of edited lines across greenhouse and field conditions, and integration of CRISPR-based approaches with multi-omics and plant-microbe interactions. These directions will further strengthen the translation of precision biotechnology into scalable solutions for reducing dietary heavy-metal exposure and enhancing global food security.

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