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Bridging genomics and traditional knowledge in sweetpotato: a scientometric pathway for participatory breeding

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Sweetpotato (*Ipomoea batatas* (L.) Lam.) is a globally important root crop cultivated in more than one hundred countries. To map how genetics research has evolved and where actionable gaps remain, we conducted a scientometric analysis of 590 records from Web of Science (WoS) covering 1960 to 2022, of which 213 full-text papers were retained after relevance filtering. Output increased sharply over the last two decades, with the United States, China, and Brazil among the most prolific contributors. Within the corpus, plant breeding accounts for 43 percent of studies, followed by conservation genetics and plant biology. Although molecular tools are increasingly available, only 17.8 percent of the analyzed papers applied omics approaches such as transcriptomics, genomics, proteomics, or metabolomics, which underscores persistent barriers to adoption in key producing regions. Beyond counts, we assessed how the literature supports an operational bridge between omics and Traditional Knowledge (TK) by scoring study level evidence tied to farmer maintained materials, on farm evaluation, and quantitative outcomes. The analysis shows that field relevant measures such as yield with units, adoption in percent, and diversity indices are more common companions to omics than explicit documentation of TK or the use of Participatory plant breeding (PPB) and participatory varietal selection (PVS). Taken together, these results identify where evidence is strong, where it is missing, and how targeted additions, notably explicit documentation of TK and on farm participatory selection, can align genetic signals with community priorities and improve the relevance and adoption of sweetpotato genetics research.

KEYWORDS

community seed banks, diversity indices, landrace diversity, molecular marker applications, on farm evaluation, yield performance

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1 Introduction

The sweetpotato (*Ipomoea batatas* (L.) Lam), a prominent member of the Convolvulaceae family, is one of the world's most important root vegetables due to its high yield, adaptability, and nutritional value (Sapakhova et al., 2023; Gurmu et al., 2014; Alam, 2021; Qin et al., 2022). It contributes significantly to global food security, with over 93 million tons produced worldwide in 2023 (FAO, 2024). Beyond its role as food for humans and animals, the crop also serves as a raw material for starch, alcohol, and pigments (Padmaja, 2009; Katayama et al., 2017). Historically, it has been a staple for Indigenous populations across multiple continents, including Central and South America, the Ryukyu Islands, Africa, the Caribbean, the Māori, Hawaiians, and Papua New Guineans (Bovell-Benjamin, 2007).

Despite its global importance, clonal propagation through stem cuttings and roots increases vulnerability to pest and disease spread (Abrham et al., 2021), with virus complexes reducing yield and root quality (Villalba et al., 2024). Meristem culture and *in vitro* propagation are essential to ensure phytosanitary integrity and large-scale production of clean planting material (Wondimu et al., 2012).

Sweetpotato also exhibits remarkable genetic variability, mainly due to its sporophytic incompatibility and hexaploid genome, which promote cross-pollination and high heterozygosity (Devarajan et al., 2013; Fraher et al., 2024). This complexity makes genetic inheritance less understood than in diploid crops like maize or soybeans, although recent studies have advanced both genetic conservation and improvement (Simion, 2018; Xiao et al., 2022).

Scientometric analysis provides a strategic approach to map and guide research trends, enabling identification of priorities in breeding, conservation, and theoretical studies (Hood and Wilson, 2001; Mingers and Leydesdorff, 2015; Aria and Cuccurullo, 2017). However, few studies apply this method to plant genetics, limiting coordinated progress and evidence-based policy development. Notable exceptions include analyses in sugarcane, coffee, and Caryocaraceae, which demonstrate the method's potential to broaden understanding of plant research landscapes (Oliveira et al., 2019; Pabon et al., 2020; Nunes et al., 2020).

Beyond scientometrics, integrating TK into genetic research is crucial. TK held by Indigenous Peoples and smallholder communities organizes landrace names, uses, and performance traits, offering context for interpreting genetic signals. Community seed banks and farmer associations serve as natural entry points for connecting farmer-maintained materials with molecular data and breeding goals (Vernooy et al., 2015). Applying ethical data governance, such as the CARE Principles, ensures that research aligns with community priorities and equitable benefit sharing (Carroll et al., 2020).

This study uses scientometric analysis to characterize global research on sweetpotato genetics and assess how omics approaches are connected, or disconnected, from TK. The objective is to make farmer- and Indigenous-held knowledge explicit and usable for breeding, aligning molecular targets with community-defined priorities, supporting on-farm adoption, and conserving useful diversity. By mapping publication patterns and methodological gaps, the study aims to inform both the scientific community and policymakers seeking to enhance sweetpotato cultivation worldwide.

2 Materials and methods

2.1 Data collection and filtering

An automated search was conducted in the Web of Science database (WoS) (available at: http://apps.webofknowledge.com) covering the period from 1960 to 2022, using the keywords *Ipomoea batatas* and *genetics* combined with the Boolean operator "AND" which resulted in 590 retrieved documents. Recent studies (2023-2024) were included for contextual discussion only. The results were filtered according to the following criteria: (1) English as the written language and (2) Genetics as the research focus. Other media formats (e.g., books, conference papers, reviews), duplicates, studies in other languages, and records unrelated to the subject were excluded. After this refinement, the dataset was evaluated based on titles and abstracts to identify relevant studies on sweetpotato genetic research. This led to a final selection of 213 papers, which were thoroughly evaluated and from which key parameters were extracted. Articles with insufficient information in abstracts, titles, or keywords were downloaded and further examined for relevance.

2.2 Variable extraction

From the dataset, general information was gathered, including (i) article ID, (ii) year of publication, (iii) journal, (iv) title, (v) authors, (vi) corresponding author, and (vii) countries involved in the research, in order to assess publication trends related to sweetpotato genetic research. A scheme of the analysis framework is presented in Figure 1.

A qualitative classification was created based on five major areas, conservation, phytopathology, plant biology, plant breeding, and pre-breeding, each with its respective sub-areas. Whenever a paper presented data spanning more than one area, it was analyzed and assigned accordingly. For broader analytical purposes, two grouped classifications were also defined: breeding/plant biology and plant biology/conservation. This scheme allowed the inclusion of multiple related fields within coherent themes, enabling both qualitative and quantitative assessments of publication trends over the study period. We also obtained information about the methodological techniques employed in the extracted records. When an omics technology approach was identified in the study, it was classified into: genomics, transcriptomics, proteomics, or metabolomics. Additionally, genetic tools and techniques were identified and categorized based on their application. Polymerase chain reaction (PCR), single nucleotide polymorphisms (SNPs), amplified fragment length polymorphism (AFLP), RNA sequencing (RNA-seq), quantitative real-time polymerase chain reaction (qRT-PCR), and Southern blotting (Southern blot) were primarily used for genetic mapping, marker development, and gene expression

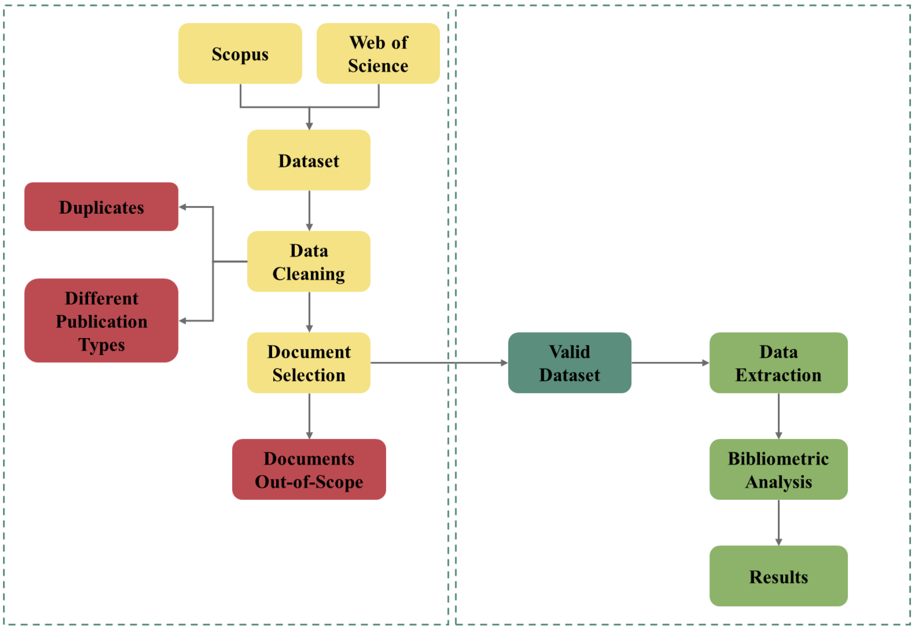


FIGURE 1
Analysis framework applied for the scientometric analysis of sweetpotato (*Ipomoea batatas*) genetics articles.

analysis. Identifying these tools allowed us to highlight key technological trends in sweetpotato genetics, reflecting the growing integration of molecular biology and genetic engineering approaches in the field.

2.3 Vosviewer analysis

The interaction analyses were conducted in VOSviewer (Van Eck and Waltman, 2010), utilizing WoS records exported as "Full Record and Cited References" in plain-text format. A custom thesaurus file was applied to merge synonymous terms, standardize terminology, and exclude generic entries that might distort the analysis.

To ensure the selection of the most relevant terms, the term co-occurrence analysis used a minimum threshold of 10 occurrences. This threshold was selected to reflect terms with a relevance indicator above 0.5%, meaning that only terms appearing frequently enough in the literature on sweetpotato genetics were included. Twenty-eight terms met this threshold. By applying this minimum occurrence, we ensured that only terms with substantial representation in the sweetpotato genetics literature were considered, highlighting the most relevant keywords for the research and preventing the inclusion of terms with minimal relevance.

In addition to selecting the most relevant terms, the custom thesaurus file was employed to exclude generic and irrelevant terms that could skew the analysis. Terms such as "region", "plant", "identification", "species", "yield", "data", "sample", and "isolate" were excluded from the co-occurrence network because they are broadly used across many scientific fields and do not provide specific, focused information for an analysis centered on sweetpotato genetics and breeding.

For author co-authorship analysis, the examination was conducted at the author level using the full counting method, which accounts for all contributions by each author without reducing their contribution based on co-authorship frequency. Publications with more than 25 authors were excluded, as these are typically associated with large collaborative efforts that do not reflect individual contributions adequately. Although this threshold removes some consortium-led studies, it prevents artificial inflation of collaboration metrics and ensures comparability with similar scientometric works. A threshold of five publications per author was applied, which is the default setting in VOSviewer. This criterion resulted in the inclusion of 38 authors who met the threshold. However, the analysis software identified nine authors as the most relevant based on their connections, and these authors were highlighted in the results.

Total link strength (TLS) is a measure used to represent the strength of connection between the nodes in the co-authorship or co-occurrence network. This value is calculated based on the number of links between two nodes (e.g., two authors or two terms) in the network. The higher the TLS, the stronger the connection between the nodes, indicating greater collaboration or co-occurrence between the analyzed elements. In the context of this study, TLS helps visualize the countries, institutions, or authors that are most interconnected, highlighting their relevance and collaborative strength within the field of sweetpotato research.

The size of the nodes corresponds to the number of documents associated with that node, while the thickness of the lines indicates the strength of the connection (TLS). To ensure consistency, the labels were standardized using the thesaurus, unifying different naming conventions without altering the underlying counts.

Additional maps were generated to represent the networks of institutions and countries. For the institutional analysis, the default setting of VOSviewer was applied, which included 906 institutions with a minimum of five documents. A total of 38 institutions met this threshold, but only 31 were linked in the network. For the country-level network, only nations with a minimum of eight documents were considered. This resulted in the inclusion of 26 countries, ensuring that the network met the required minimum TLS of three. In all cases, association-strength normalization, full counting, the VOS layout, and modularity-based clustering were applied to optimize the network visualization and identify patterns within the data.

2.4 Operationalizing the omics and TK bridge

We assembled a full-text corpus of 213 peer-reviewed publications on sweetpotato genetics (plant biology, conservation genetics, breeding) and manually evaluated every article, extracting parameter signals that characterize how each study relates to the omics and TK perspective. The screening used 12 concept families, each with a predefined weight: TK explicit, participatory plant breeding (PPB) and participatory varietal selection (PVS) [weight 3]; farmer priorities, on-farm/seed systems, landraces, ethics and data governance, co-production/co-creation [weight 2]; ethnobotany/ethnography/folk taxonomy, omics to Breeding (e.g., (e.g., *SNP*, *quantitative trait loci (QTLs)*, *genome-wide association studies (GWAS)*, *genotyping-by-sequencing (GBS)*, *genomic selection (GS)*, and *marker-assisted selection (MAS)*, policy instruments (e.g., seed law, International Union for the Protection of New Varieties of Plants - UPOV), quantitative outcomes (e.g., yield with units, adoption in percent, diversity indices), and farmer organizations [weight 1]. For each parameter k, we assigned a signal s_k ∈ {0,1,2} (0 = absent; 1 = single mention; 2 = multiple independent mentions). Each parameter k was also assigned a predefined weight w_k. The weighted score was calculated as:

$$\text{Score}_{\text{weighted}} = (\Sigma\_\{k = 1\}\ n\ s\_k\ w\_k)/(\Sigma\_\{k = 1\}\ n2w\_k)$$

We report Adherence as: Adherence_% = $100 \times \Sigma(w_i \cdot s_i)/\Sigma(w_i \cdot 2)$, where s_i is the signal assigned to parameter i (0 = absent; 1 = single mention; 2 = multiple independent mentions), w_i is the predefined weight of parameter i, and i indexes the set of evaluated parameters. This corpus-level index underlies all descriptive statistics (mean, median, quartiles), co-occurrence counts, and conditional proportions. From the ranked corpus we interpreted a focused Top-10 subset to illustrate study-level bridging. For these ten studies, we summarized the six core bridge elements, TK, on-farm/seed systems, PPB/PVS, omics to Breeding, adoption/quantitative outcomes, and governance, using binary presence (Yes/No). To provide a simple intensity index for this subset, we also computed the bridge Average (0–100) over the same six elements, reusing the 0/1/2 signals and applying an equal-weight normalization: Average = (Σ scores/12) × 100. Because the index is bounded between 0–100 and derived from categorical signals, it should be interpreted comparatively, not as an absolute measure.

Importantly, this adherence index is not intended as a normalized measure of national or institutional research capacity. We did not apply country-level covariates (e.g., research funding, infrastructure, or number of researchers) to adjust scores; therefore, geographic comparisons should be interpreted as differences in reporting and study design within the published literature, not as a level-ground assessment of capacity.

Finally, we distilled a seven-step pipeline that operationalizes the minimum additions needed to complete the bridge in practice, reflecting patterns frequent among higher-adherence studies and the gaps observed in the corpus. In brief: (A) community set-up and consent; (B) elicitation of TK and farmer preferences; (C) on-farm phenotyping and acceptance; (D) linking omics evidence to selection decisions; (E) PVS with farmers; (F) tracking quantitative outcomes (adoption, yield gain, optional diversity metrics); and (G) feedback, local seed access, and reporting.

All steps are reproducible from the corpus plus the parameter list and weights described above. A Supplementary Materials package provides the corpus-level matrix (12 parameters, signals, counts, Adherence_%), a study-level matrix for the top subset (element-level presence and the bridge Average), and the full pipeline specification, along with an ID-to-reference dataset map (author–year–title–DOI) to ensure traceability.

2.5 Statistical analysis

Descriptive statistics (i.e., summarization and frequencies) were applied to analyze the dataset, coupled with visualization techniques to characterize the state of the art in publications of sweetpotato genetic research. All analyses were implemented in R Core Team (2024), using the tidyverse package (Wickham, 2019).

Temporal trends in research collaboration, indicated by the number of co-authors per paper, were analyzed with a linear regression fitted with the lm function implemented in the stats package in R Core Team (2024).

3 Results

3.1 Publication trends

The temporal evolution of sweetpotato genetics research demonstrates a marked acceleration in the last three decades. Between 1992 and 2007, annual output remained very low, usually fewer than five publications per year, with only minor fluctuations. From 2007 onward, a clear upward trend emerged, and after 2012 the growth rate became steeper, culminating in a peak of approximately 25 publications in 2021 (Figure 2).

3.2 Keywords and research themes

The VOSviewer term co-occurrence map (Figure 3) reveals three main thematic clusters that define the structure of research in sweetpotato genetics. Each node represents a keyword, with node size proportional to its frequency of occurrence and line thickness indicating the strength of co-occurrence between terms.

The red cluster, dominated by *Ipomoea batatas* and genetic diversity, centers on breeding, molecular characterization, and population structure. It includes terms such as markers, microsatellite markers, germplasm, landraces, AFLP, and wild relatives, reflecting the emphasis on genetic variability and the use of molecular tools in diversity studies. The green cluster represents

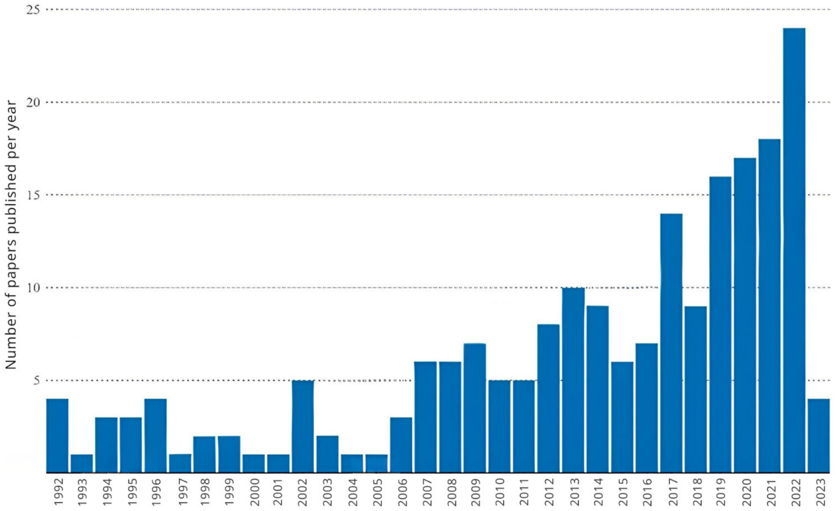


FIGURE 2
Scientific production in sweetpotato (*Ipomoea batatas)* genetics, in number of published documents extracted from WoS from 1960 to 2022.

applied studies on resistance and pest–host interactions, highlighting terms like resistance, homoptera populations, whiteflies, *Bemisia tabaci*, and tomato. These links point to the interface between sweetpotato and related crops affected by viral and vector-borne diseases, emphasizing integrated pest management and cross-crop comparative genetics. The blue cluster is associated with viral diseases and molecular diagnostics, including chlorotic stunt virus, potyvirus, feathery mottle virus, and molecular characterization. The presence of evolution and genome in this region of the network indicates that virology and phylogenetic approaches remain central to understanding pathogen dynamics and their impact on crop performance. Together, these clusters show that sweetpotato serves as a hub linking molecular breeding, pest–disease resistance, and viral genetics, reflecting a balanced focus on crop improvement, pathogen management, and genetic resource conservation.

3.3 Main scientific journals and impact factor

The distribution of sweetpotato genetics research across multiple journals reveals that key journals play a significant role in disseminating knowledge on the subject (Figure 4). Crop evolution, plant pathology, and horticulture journals dominate the publication landscape, suggesting the relevance of genetic diversity, disease resistance, and crop breeding in the field of sweetpotato genetics.

PLOS ONE stands out as the leading journal, with ten published papers (IF = 2.6, 2023). Genetic Resources and Crop Evolution

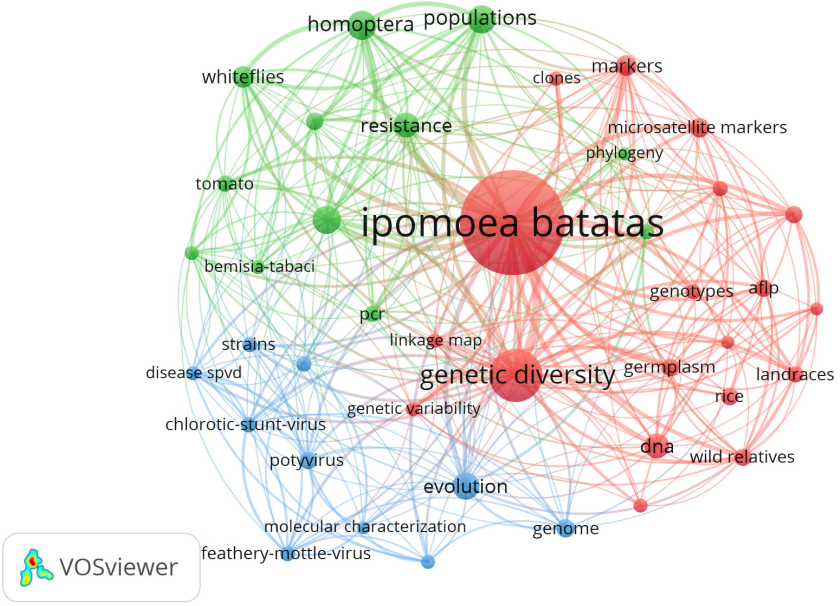


FIGURE 3
VOSviewer term co-occurrence network for sweetpotato research. The term "*Ipomoea batatas*" anchors the map and bridges the other themes.

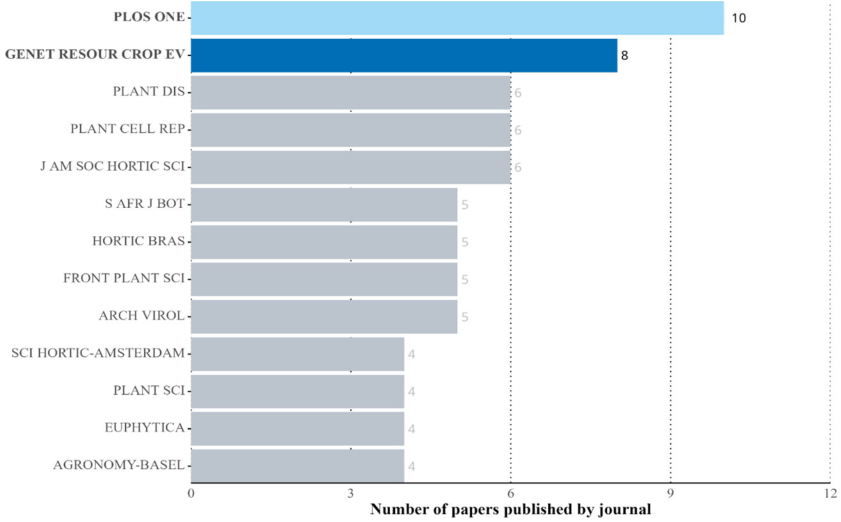


FIGURE 4
Scientific journals with the highest number of published articles on sweetpotato (*Ipomoea batatas*) genetics, based on data extracted from the WoS (1960-2022).

(GENET RESOUR CROP EV) follows with eight papers (IF = 1.6, 2023). Additionally, Plant Disease (PLANT DIS), Plant Cell Reports (PLANT CELL REP), and Journal of the American Society for Horticultural Science (J AM SOC HORTIC SCI) each contributed with six papers, with IF values of 4.5, 3.7, and 1.2, respectively (2023). Other relevant outlets include South African Journal of Botany (S AFR J BOT), Horticultura Brasileira (HORTIC BRAS), Frontiers in Plant Science (FRONT PLANT SCI), and Archives of Virology (ARCH VIROL), each publishing five papers, with IF values of 2.5, 0.7, 4.8, and 2.6, respectively (2023). The presence of these journals, which span plant biology, pathology, horticulture, and virology, demonstrates the global and multidisciplinary character of sweetpotato genetics research.

3.4 Prominent authors and co-authorship network

Author productivity and collaboration were assessed using a two-panel figure (Figure 5). Figure 5A ranks the most prolific authors and summarizes productivity across the full dataset, while Figure 5B maps co-authorship ties among prolific authors.

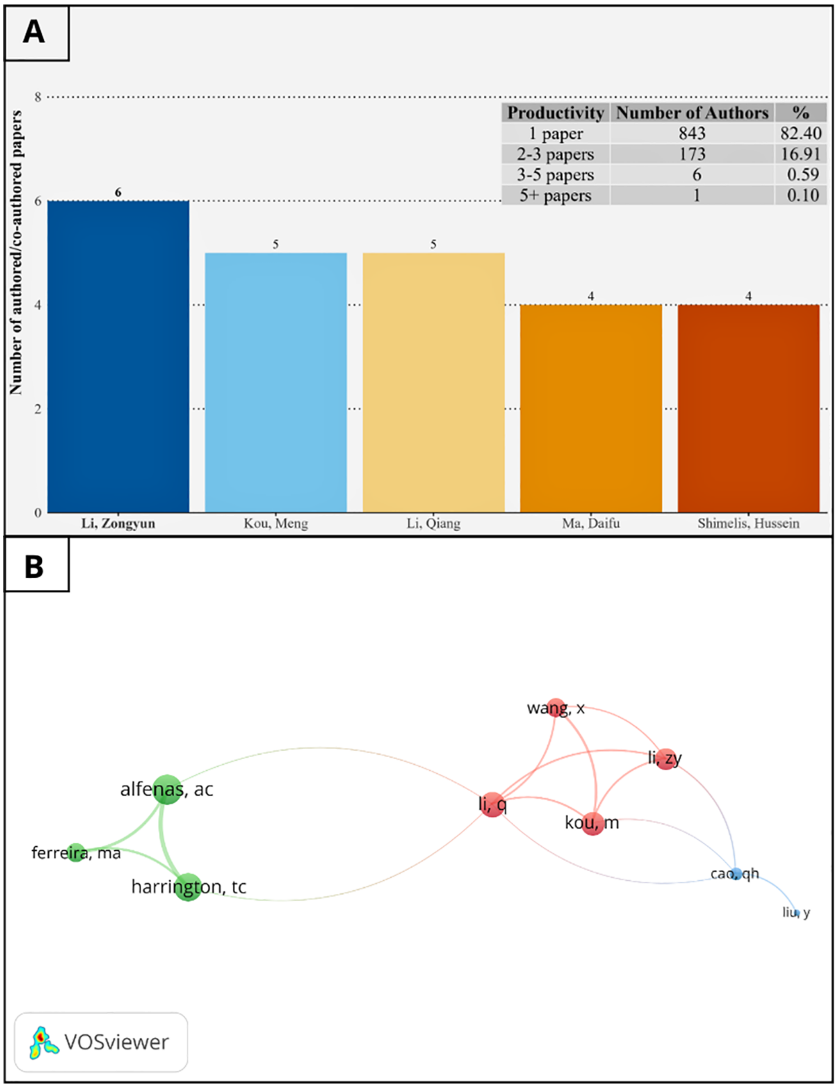
The scientific production in sweetpotato genetics is led by Zongyun Li (six publications), followed by Meng Kou and Qiang Li (five publications each), with Daifu Ma and Hussein Shimelis (four publications each). The distribution is heavily skewed: among 2,567 authors, 82.4% published only one paper, 16.91% produced two to three papers, and 0.59% reached three to five papers, indicating that the field is driven by a small core of prolific contributors (Figure 5A). Figure 5B further explores the co-authorship network of these leading authors, examining whether their collaborations form cohesive ties within the research community.

Using the threshold of five publications, 36 prolific authors were identified, but only nine authors were connected in the co-authorship network. The node size reflects the number of documents, and the thickness of the lines indicates the strength of the co-authorship connection, measured by TLS. The network is fragmented: Maria A. Ferreira (Universidade Federal de Lavras), Thomas C. Harrington (Iowa State University), and Acelino C. Alfenas (Universidade Federal de Viçosa) are strongly connected, forming a central collaboration core, with tight ties between them. This group led by Alfenas, AC, has a more cohesive network, reflecting consolidated and frequent collaboration. In contrast, Li, Zongyun, Li, Qiang, and Kou, Meng, all from Jiangsu Normal University, Xuzhou, China, are in the same co-authorship core, but their connections are more dispersed and not as strongly interlinked as the group of Brazilian and American researchers. This suggests that, although these prolific authors share some collaborations, the co-authorship network still offers opportunities to strengthen relationships between groups and expand interactions between different areas of research.

Higher thresholds (e.g., six or seven publications) were tested, which reduced the network to only four or two authors, respectively, and significantly decreased the overall connectivity. Although these higher thresholds provide a cleaner visualization of the central collaborative relationships, they exclude a significant portion of productive authors. Therefore, the five publication threshold (software default) was retained to ensure a more comprehensive analysis, highlighting the fragmentation of the network and the opportunities to strengthen collaboration across various research groups.

3.5 International collaboration (countries)

Country-level authorship and co-authorship were analyzed using WoS records from 1960 to 2022. In total, 87 countries contributed with at least one paper. To establish the network analysis, a minimum threshold of ≥8 publications per country was applied. In result, 26 countries met this criterion and were included in the co-authorship map. Figures 6 and 7 report, respectively, the geographic distribution of output and the international co-authorship structure.



Productivity	Number of Authors	%
1 paper	843	82.40
2-3 papers	173	16.91
3-5 papers	6	0.59
5+ papers	1	0.10

FIGURE 5
(A) Top authors of sweetpotato (*Ipomoea batatas*) genetics articles, based on publications extracted from WoS from 1960 to 2022. **(B)** VOSviewer co-authorship network for sweetpotato genetics (threshold ≥ 5 documents; n = 9). Node size reflects the number of documents per author and link thickness the co-authorship strength (TLS).

Figure 6 depicts the spatial distribution of publications by country using five classes (1; 2–5; 5–10; 10–20; ≥20 papers). The output is broadly distributed across the Americas, Europe, Africa, Asia, and Oceania, with several countries falling in the 10–20 and ≥20 classes. Large areas of Central Africa, Eastern Europe, and Central Asia show little or no indexed output over the period studied, indicating uneven coverage.

Figure 7 presents the VOSviewer international co-authorship network for the 26 countries above the threshold. Node size is proportional to the number of documents and link thickness represents TLS.

The red cluster, led by the United States, forms the primary global hub, linking with the United Kingdom, China, Brazil, Canada, Spain, and Pakistan. This cluster integrates collaborations across the Americas, Europe, and Asia, demonstrating the pivotal role of the United States in coordinating international research. The green cluster encompasses a strong Europe–Africa–Latin America network, with countries such as France, Germany, Italy, Norway, Kenya, Uganda, Tanzania, Peru, Colombia, and Finland. These links reflect long-standing agricultural and development partnerships focused on breeding, germplasm conservation, and participatory projects.

The blue cluster represents the Asia–Pacific alliance, connecting Australia, South Africa, India, Japan, South Korea, Indonesia, Taiwan, and Israel. This group highlights growing scientific exchange on genomics, stress-tolerance, and climate-adaptation studies. The yellow cluster is comparatively smaller and centers on China, which maintains strong connections with the United States, Japan, South Korea, and Australia, emphasizing China's expanding contribution to omics and high-throughput breeding research.

Overall, the network demonstrates that while the United States remains the key intercontinental connector, Europe–Africa linkages (e.g., United Kingdom–Kenya–Uganda–Tanzania) and South–South collaborations (e.g., Brazil–Peru–Colombia) are increasingly important. Despite this diversification, several regions, including parts of Central Asia and the Middle East, still appear peripheral,

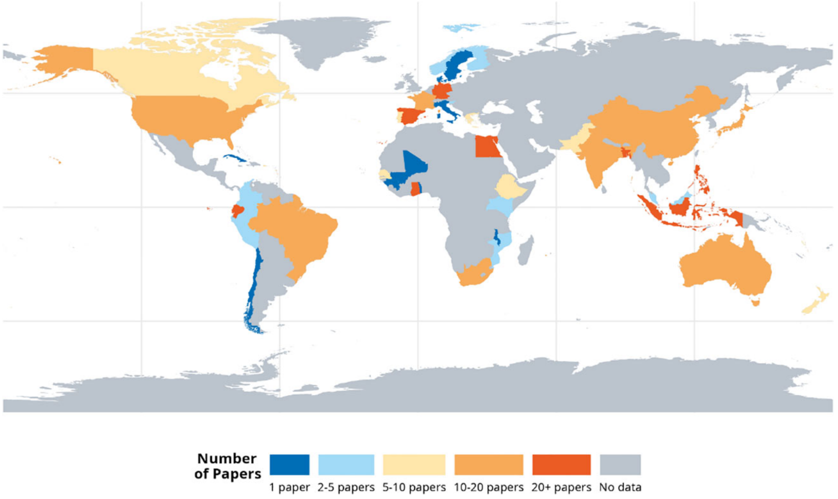


FIGURE 6
Geographic distribution of scientific publications on sweetpotato (*Ipomoea batatas*) genetics. The map highlights the top 36 countries with the highest number of publications in this field, based on data from WoS between 1960 and 2022.

indicating opportunities to strengthen global integration in sweetpotato genetics research.

3.6 Institutional contributions and collaborations

The institutional co-authorship network generated with VOSviewer (Figure 8) reveals 22 institutions organized into five main collaboration clusters, representing regional and transcontinental partnerships in sweetpotato genetics.

The red cluster centers on the International Potato Center (CIP), linking with the International Institute of Tropical Agriculture (IITA), North Carolina State University (NCSU), University of California Davis (UC Davis), USDA Agricultural Research Service (USDA ARS), Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), and University of Pretoria (UP). This group connects the Americas, Africa, and Europe through long-standing partnerships in breeding and disease resistance. The purple cluster associates the University of Helsinki (UH), University of Western Australia (UWA), and Makerere University (MAK), reflecting collaborations between Northern and Southern institutions, particularly on genetic diversity and participatory breeding.

The green cluster brings together the University of Florida (UF), USDA ARS, and the Consejo Superior de Investigaciones Científicas (CSIC), emphasizing joint research on molecular characterization and germplasm management between the Americas and Europe. The blue and yellow clusters, corresponding to Asian institutions, are dominated by the China Agricultural University (CAU), which acts as a central hub linked to the Chinese Academy

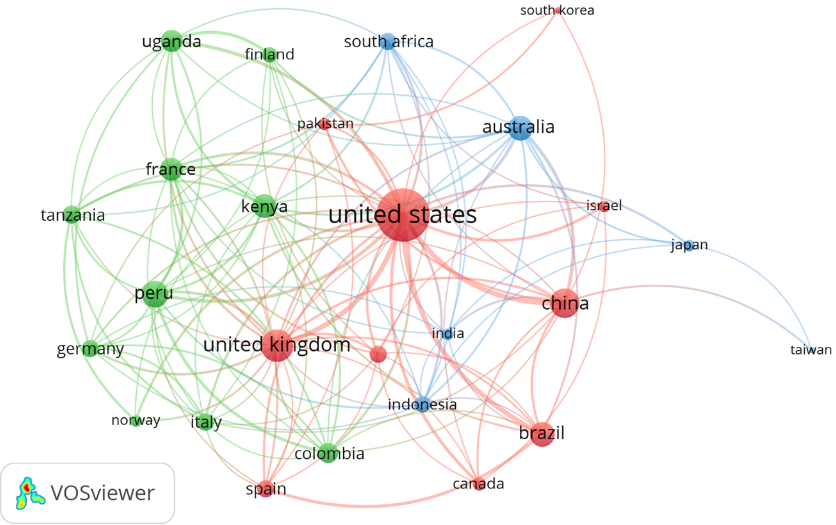


FIGURE 7
International co-authorship network on sweetpotato research, showing countries grouped into six collaboration clusters. Node size reflects the number of documents per country, and link thickness represents the strength of co-authorship ties.

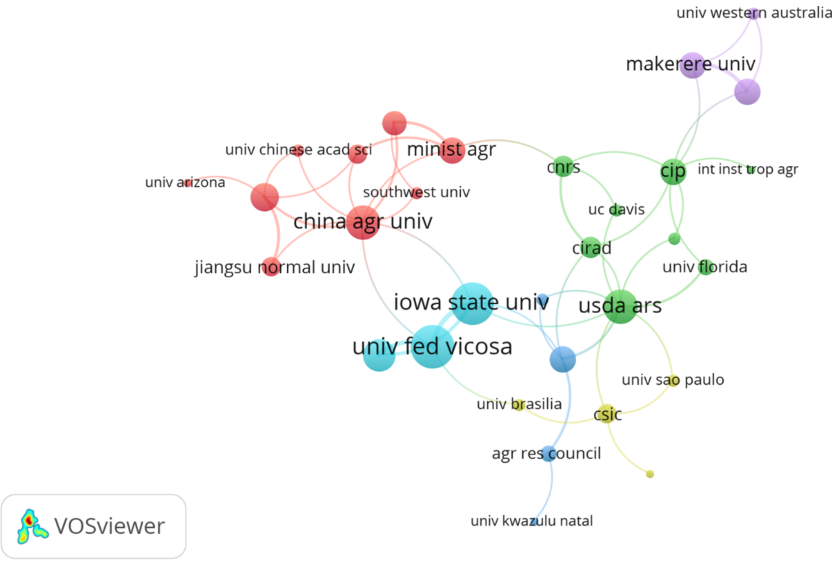


FIGURE 8
Institutional co-authorship network on sweetpotato research, showing organizations grouped into eight collaboration clusters.

of Agricultural Sciences (CAAS), Chinese Academy of Sciences (CAS), Zhejiang University (ZJU), Ministry of Agriculture of China (MoA), Henan Academy of Agricultural Sciences (HAAS), and University of Arizona (UA). These connections demonstrate China's pivotal role in integrating omics and genomic selection approaches into breeding networks.

The cyan cluster highlights Brazil–United States collaborations, centered on the Universidade Federal de Viçosa (UFV), Universidade Federal de Lavras (UFLA), and Iowa State University (ISU), underscoring South American participation in sweetpotato genetic improvement. Collectively, the network shows a combination of strong regional clusters with relatively few cross-cluster bridges. The USDA ARS and CIP serve as major transcontinental connectors, linking Africa, the Americas, and Asia. Despite these key nodes, inter-cluster connectivity remains limited, indicating that global integration in sweetpotato genetics research is still emerging.

3.7 Cited articles

The most impactful research articles in this field, ranked by the number of citations they have received, are shown in Table 1. The citations indicate the influence and relevance of these studies within the scientific community. The most cited article is authored by Ling et al. (2010), titled "Field evaluation of yield effects on the USA heirloom sweetpotato cultivars infected by Sweetpotato leaf curl virus", with 106 citations. This suggests a strong focus on virus infections, which are critical to sweetpotato cultivation and yield. The high number of citations reflects the importance of viral resistance in improving crop productivity. Okada et al. (2019) ranks second, with 95 citations for a publication on Genome-Wide Association Studies (GWAS) for Yield and Weevil Resistance in sweetpotato. GWAS is a powerful tool for identifying genetic markers linked to important agronomic traits such as yield and Weevil resistance, emphasizing the practical application of genomics in crop improvement.

Several studies focus on genome sequencing, molecular markers, and transcriptomics, such as Hirakawa et al. (2015), with 94 citations for a survey of genome sequences in the wild sweetpotato, *Ipomoea trifida*, and Wang et al. (2022), with 90 citations for transcriptome analysis related to potassium deficiency. These articles highlight the significant role that molecular biology plays in understanding the genetic basis of important traits in sweetpotatoes. The article on salt tolerance, written by Luo et al. (2017), which received 90 citations, indicates that abiotic stress resistance is another major area of focus in sweetpotato research. Given the global challenges posed by climate change and soil degradation, studies that address how crops like sweetpotato can adapt to stressful environments are highly relevant.

3.8 Research focus and methodological trends

The qualitative analysis shows that most studies (43%) concentrate on plant breeding, followed by conservation genetics (32%) and plant biology (25%). Figure 9 provides further detail, indicating that within breeding research, the main subareas are molecular approaches (65 papers), plant disease resistance (53), population genetics (44), pre-breeding (22), and classical breeding (8).

The analysis of tools used in genetic research revealed distinct patterns in their frequency of application (Figures 10A, B). Most tools (81.03%) were employed only once, 12.93% had moderate use, and 5.17% were highly used. A small fraction (0.86%) fell into an unspecified category.

Morpho-Agronomic Traits (MAT) was the most prominent used tool, appearing in 28 studies (Figure 10B). While the tools RT-PCR and RNA-seq were used in 13 and 12 studies, respectively. SSR appeared in 11 studies, followed by PCR in seven, and qRT-PCR in

TABLE 1 Top five cited articles on sweetpotato (*Ipomoea batatas*) genetics studies extracted from WoS.

First author	DOI	Title	Citation	Year
Ling et al.	10.1016/j.cropro.2010.03.007	Field evaluation of yield effects on the USA heirloom sweetpotato cultivars infected by Sweetpotato leaf curl virus	106	2010
Okada et al.	10.1007/s00299-019-02445-7	Genome-Wide Association Studies (GWAS) for Yield and Weevil Resistance in sweetpotato (*Ipomoea batatas* (L.) Lam)	95	2019
Hirakawa et al.	10.1093/dnares/dsv002	Survey of genome sequences in a wild sweetpotato, *Ipomoea trifida* (H. B. K.) G. Don	94	2015
Wang, F.	10.1186/s12864-022-08870-5	Transcriptome analysis of sweetpotato responses to potassium deficiency	90	2022
Luo et al.	10.1038/s41598-017-09241-x	Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild relative of sweetpotato	90	2017

six. Other tools, including RAPD, AFLP, morphological characterization, and combined RT-PCR with RNA-seq, appeared in fewer than six studies each.

Across the 213 papers analyzed, omics approaches were employed in 38 studies (17.8 percent), while the remaining 175 (82.2 percent) did not adopt these methodologies. Among the omics based studies, transcriptomics was the most frequent (21; 55.3 percent), followed by genomics (12; 31.6 percent). Two studies combined proteomics and metabolomics, two combined transcriptomics and genomics, and one focused exclusively on proteomics. For this review, omics refers to transcriptomics, genomics, proteomics, and metabolomics. These corpus level counts provide the backdrop for Table 2, which examines how the highest adherence studies operationalize the link between omics and TK at the study level.

To move from corpus totals to study level evidence, Table 2 selects the ten highest adherence papers. Average (0 to 100) is the normalized mean of those six elements, with each element scored 0 when absent, 1 when present, and 2 when strong; Average: the sum of the six element scores divided by 12, multiplied by 100. In the column headers, TK: Traditional Knowledge; PPB: participatory plant breeding; PVS: participatory varietal selection. On farm and Seed systems refers to on farm trials, community seed banks, seed system or *in situ* evidence. omics to Breeding means that molecular or omics findings are tied to selection or breeding decisions. All ten studies report at least one quantitative outcome (for example yield with units, adoption in percent, or diversity indices). Diversity and Structure metrics lists only the metric families reported in the paper, for example AMOVA, Shannon, Nei, He, Ho, Fst.

Table 2 shows that omics evidence in sweetpotato is most often tied to landraces and farmer preferences and more frequently reports quantitative outcomes than it formalizes TK elicitation or PPB workflows. For completeness, the full study level matrix for all papers is provided as Supplementary Material (Supplementary Table 2). Across the full dataset (n = 213), adherence averaged 8.18 percent (median 4.76; interquartile range 0.00 to 14.29), indicating that most papers document only part of the omics and TK bridge. Among studies flagged with an omics to Breeding signal (n = 50), quantitative outcomes were the most frequent companion element: 40.0 percent reported yield with units, adoption in percent, or diversity indices, compared with 22.7 percent among non-omics papers. In contrast, TK protocols co occurred with omics in 6.0 percent of cases, PPB or PVS in 6.0 percent, and on farm or seed system evidence in 12.0 percent. Governance-related policy signals were rare overall (2.8 percent), and no explicit mention of

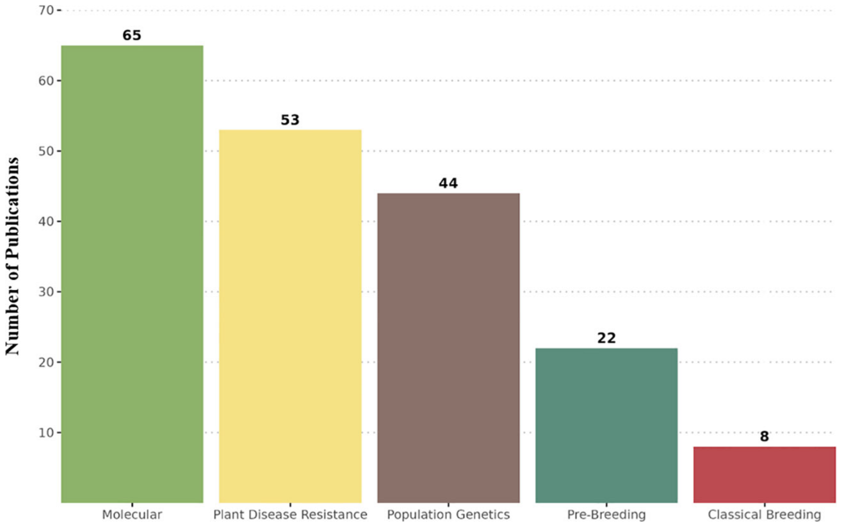


FIGURE 9
Distribution of articles on genetic studies in sweetpotato (*Ipomoea batatas*) in the different breeding subareas.

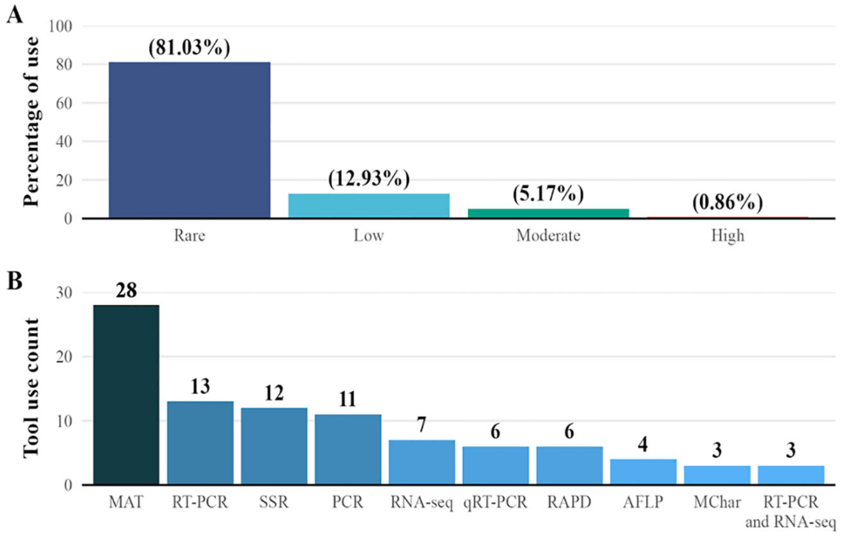


FIGURE 10
Frequency and distribution of methodological tools used in sweetpotato (*Ipomoea batatas*) genetic studies. **(A)** Percentage distribution showing how often tools were used across studies (single-use, moderate-use, and high-use categories). **(B)** The ten most frequently employed tools, ranked by number of studies in which they appeared. The size of each tool name represents its relative frequency of use.

recognized ethical frameworks such as FPIC, ABS, or DSI was identified in the dataset. This absence reinforces that, although some studies refer broadly to policy or benefit-sharing, formal documentation of data governance and ethical compliance remains virtually absent from sweetpotato genetics research.

To assess how adherence varies geographically, we linked each paper's ID from the full-text matrix to its WoS record (UT) and extracted the author address field. Countries were detected from the address string and mapped to world regions (Africa, Americas, Asia, Europe, Oceania). Because many papers involve authors from multiple countries, we used fractional counting: each paper contributed equally across its countries (and across regions), so that a single paper did not inflate totals for any one place. We then computed weighted mean adherence (weights = 1/number of countries per paper) and the median adherence per region and per country.

At the regional scale, Europe (≈12.9) and the Americas (≈11.9) show the highest weighted mean adherence, followed by Africa (≈10.6), Oceania (≈8.1) and Asia (≈6.7). Medians are consistent with these trends (Europe/Americas ≈9.52; Africa/Oceania ≈7.14; Asia ≈4.76). At the country scale, hubs with higher adherence tend to be those where omics outputs are more often accompanied by on-farm/seed-system evidence and quantitative outcomes. In contrast, several high-output countries in Asia exhibit lower adherence on average, reflecting designs that emphasize molecular characterization but less frequently formalize TK elicitation, PVS, or on-farm evaluation within the article text.

Taken together, these patterns indicate that the most direct way to complete the bridge in otherwise high adherence designs is to add two minimal modules: explicit TK elicitation and on farm PVS. We note, however, that uneven output and adherence patterns across countries likely reflect structural differences that are not captured by publication data alone. These include disparities in agricultural research and development (R&D) investment, laboratory and bioinformatics infrastructure, the number of trained scientists, and the stability of research funding and institutions. As a result, low indexed output in major producing regions should not be interpreted as low agronomic relevance of sweetpotato, but rather as constrained capacity to generate and publish genetics research in the indexed literature.

To operationalize the bridge empirically, the seven-step pipeline (Table 3) structures the minimal methodological components observed among high-adherence studies.

The pipeline presented in Table 3 summarizes how scientific data from omics technologies can be effectively linked to community-based breeding practices. It begins with community engagement and respect for local knowledge (TK and FPIC), ensuring that farmers and Indigenous groups are part of the decision-making process from the start. The following steps focus on participatory experimentation (PPB and PVS), where varieties are evaluated directly in farmers' fields under real growing conditions. Molecular tools such as GS and MAS are then applied to identify and select the best genotypes based on both laboratory data and farmer preferences. Community seed banks (CSB) serve as the foundation for maintaining and distributing improved materials, while governance mechanisms such as ABS and DSI regulate how genetic information is shared and how benefits return to the communities. Together, these sequential steps translate scientific advances into social impact, creating a transparent and reproducible model that respects ethical principles and enhances local adoption of new varieties.

4 Discussion

This study provides the first global, data-driven roadmap to integrate molecular signals with farmer-defined priorities, enabling

TABLE 2 **Bridge matrix of the top ten sweetpotato studies ranked by adherence to the omics and TK framework.**

Reference (Author, Year)	Title	Average (0–100)	TK	On farm/ Seed systems	PPB or PVS	Omics to Breeding	Adoption/ Quantitative outcomes	Diversity/ Structure metrics	Contribution to the Omics and TK bridge
Roullier et al., 2013	On the origin of sweet potato (*Ipomoea batatas* (L.) Lam.) genetic diversity in New Guinea, a secondary center of diversity	58.33	Yes	Yes	Yes	Yes	Yes	AMOVA; Fst	captures TK or Indigenous Knowledge; situates evaluation in on farm or community seed contexts; employs participatory breeding or varietal selection; links molecular markers to breeding decisions; reports quantitative outcomes tdat close tde field to lab loop.
Alves-Pereira et al., 2018	Patterns of nuclear and chloroplast genetic diversity and structure of manioc along major Brazilian Amazonian rivers	50	Yes	Yes	No	Yes	Yes	AMOVA; Shannon; Nei; Ho; Fst	captures TK or Indigenous Knowledge; situates evaluation in on farm or community seed contexts; links molecular markers to breeding decisions; reports quantitative outcomes that close the field to lab loop.
Aritua et al., 2009	Host Range, Purification, and Genetic Variability in Sweet potato chlorotic fleck virus	50	No	No	Yes	Yes	Yes	—	employs participatory breeding or varietal selection; links molecular markers to breeding decisions; reports quantitative outcomes that close the field to lab loop.
Moulin et al., 2012	Collection and morphological characterization of sweet potato landraces in north of Rio de Janeiro state	41.67	Yes	Yes	Yes	No	Yes	—	captures TK or Indigenous Knowledge; situates evaluation in on farm or community seed contexts; employs participatory breeding or varietal selection; reports quantitative outcomes that close the field to lab loop.
Veasey et al., 2007	Phenology and morphological diversity of sweet potato landraces of the Vale do Ribeira	41.67	No	Yes	No	Yes	Yes	AMOVA	situates evaluation in on farm or community seed contexts; links molecular markers to breeding decisions; reports quantitative outcomes that close the field to lab loop.
Amoanimaa-Dede et al., 2021	Development and characterization of Simple Sequence Repeat markers from the genomic sequence of sweet potato	41.67	Yes	No	No	Yes	Yes	Nei	captures TK or Indigenous Knowledge; links molecular markers to breeding decisions; reports quantitative outcomes that close the field to lab loop.
Veasey et al., 2008	Genetic diversity in Brazilian sweet potato landraces assessed with microsatellite markers	33.33	No	Yes	No	No	Yes	AMOVA	situates evaluation in on farm or community seed contexts; reports quantitative outcomes that close the field to lab loop.
Laurie et al., 2020	Assessment of the genetic diversity of sweetpotato germplasm collections for protein content	33.33	No	Yes	No	No	Yes	—	situates evaluation in on farm or community seed contexts; reports quantitative outcomes that close the field to lab loop.
Ramírez et al., 2023	Phenotyping of productivity and resilience in sweetpotato under water stress through UAV based multispectral and thermal imagery in Mozambique	25	No	Yes	No	No	Yes	—	situates evaluation in on farm or community seed contexts; reports quantitative outcomes that close the field to lab loop.
Roullier et al., 2013	Historical collections reveal patterns of diffusion of sweet potato in Oceania obscured by modern plant movements and recombination	25	Yes	No	No	No	Yes	—	captures TK or Indigenous Knowledge; reports quantitative outcomes that close the field to lab loop.

Average (0–100) is the normalized mean across six bridge elements that link omics and TK. Each element is scored per paper as 0 when absent, 1 when present, and 2 when strong, meaning two or more independent mentions or lines of evidence. Formula: Average = (sum of the six element scores divided by 12) × 100.

genetics research that is auditable, participatory, and socially anchored. The temporal evolution of publications on *Ipomoea batatas* genetics shows that research has undergone a substantial transformation over the last three decades. Until the early 2000s, the number of publications remained very low, reflecting the limited availability of molecular tools and a lower prioritization of sweetpotato in global agricultural agendas. The rapid acceleration after 2012 coincides with the increased accessibility of omics technologies (Dai and Shen, 2022; Kamali and Singh, 2023), which enabled more sophisticated analyses of genetic diversity and stress resilience. Similar surges have been reported in other crops, such as sugarcane (Oliveira et al., 2019) and date palm (Alhaider et al., 2014), indicating that progress in sweetpotato genetics has been primarily driven by technological readiness and the availability of shared genomic resources rather than by gradual scientific expansion alone.

The keyword analysis confirms that *genetic diversity* and *molecular markers* remain central to *sweetpotato* research, forming the conceptual backbone of studies that combine breeding and conservation. The strong clustering of terms related to *resistance*, *whiteflies*, and *Bemisia tabaci* underscores the prominence of phytopathology and host–vector interactions in safeguarding yield stability (Villalba et al., 2024). The dense connections among *microsatellite markers*, *AFLP*, *germplasm*, and *landraces* highlight sustained interest in characterizing farmer-maintained diversity and its potential use in pre-breeding. Conversely, the blue cluster, dominated by viral terms such as *potyvirus* and *feathery mottle virus*, points to continuing efforts to refine molecular diagnosis and epidemiological mapping. Although transcriptomics and RNA-seq terms are less prominent in the network, they are increasingly cited in recent years, indicating a gradual shift toward functional genomics aimed at linking stress-response mechanisms to breeding decisions (Luo et al., 2017; Wang et al., 2022). Meanwhile, aspects directly tied to genomic complexity, particularly polyploidy and interspecific hybridization, remain underrepresented, signaling opportunities for more integrative genetic mapping and introgression strategies (Mollinari et al., 2020).

The journal distribution reveals both internationalization and regional anchoring. Multidisciplinary journals such as PLOS ONE enhance visibility, while specialized outlets like Genetic Resources and Crop Evolution and Horticultura Brasileira focus on regionally relevant studies (Gichuki et al., 2003; Otoboni et al., 2020). High-impact platforms including Frontiers in Plant Science and Plant Cell Reports concentrate studies that apply advanced genomic tools (Okada et al., 2019; Zhang et al., 2022). This combination demonstrates a dual publication ecosystem that connects global visibility with local application priorities (Sapakhova et al., 2023).

Authorship and collaboration patterns reveal structural imbalances. Although prolific authors s Authorship and collaboration analyses reveal structural imbalances. A small number of prolific authors, including Zongyun Li, Meng Kou, and Qiang Li (Sun et al., 2019; Yu et al., 2022; Yan et al., 2022), dominate output, but co-authorship networks remain fragmented. The central collaboration cluster formed by Alfenas, Harrington, and Ferreira contrasts with isolated researchers such as Cao and Wang. This fragmentation restricts knowledge diffusion and centralizes capacity, especially in China, where large-scale projects dominate (Cheng et al., 2023). Global initiatives by institutions such as CIP have demonstrated how integrated networks can promote multi-country breeding and training efforts (Maquia et al., 2013; Mustamu et al., 2018). Expanding these collaborations through standardized data protocols and joint infrastructure would reduce redundancy and improve result reproducibility.

At the international level, the research network displays strong but uneven connectivity. The United States and China lead production and collaboration, followed by secondary hubs like the United Kingdom, France, and Brazil. Many African nations, although major producers of sweetpotato, remain peripheral in the scientific network, revealing a mismatch between production importance and research activity (Zawedde et al., 2015; Rahman et al., 2022; FAO, 2024).

In addition, cross-country comparisons based on indexed databases are affected by structural and visibility biases in scholarly communication. WoS coverage favors journals, languages, and publication outlets that are more accessible to well-resourced research systems, which can under-represent locally relevant work produced in major sweetpotato-growing regions. Therefore, low indexed output should be interpreted cautiously, as it may reflect both constrained research capacity and differential indexing and publication pathways, rather than an absence of knowledge generation on the crop.

Several drivers can explain this mismatch between production importance and indexed research output. In many low- and lower-middle-income settings, national budgets for agricultural R&D are limited, competitive grant access is constrained, and advanced facilities (e.g., genotyping platforms, sequencing, computational infrastructure, and supply chains for reagents) are scarce or discontinuous. These constraints reduce the ability to conduct omics-enabled studies and to sustain publication pipelines. Conversely, higher-output countries and hubs typically benefit from stable university-based research systems, graduate training programs, and institutional incentives that support continuous student-led projects and higher publication rates. This also helps explain why a small number of university-linked research groups and prolific senior authors can dominate parts of the publication landscape. A detailed, quantitative normalization of output by these structural covariates would be valuable, but it is beyond the scope of the present scientometric approach and available metadata.

Strengthening research capacity and collaboration in underrepresented regions is essential to balance scientific representation with agricultural significance. Institutional analysis reinforces these trends. USDA ARS and CIP act as transcontinental connectors linking the Americas, Africa, and Europe, while CAU, CAAS, and CAS lead the Asian network, reflecting China's growing role in molecular research. In Latin America, UFV and UFLA are key nodes connected to U.S. universities such as ISU and UF. European institutions including CIRAD and CSIC serve as secondary bridges. Despite these linkages, the global institutional network remains only moderately integrated. Increasing interregional cooperation, particularly between African and Latin American institutions, would enhance germplasm exchange, technology transfer, and participatory breeding innovation.

TABLE 3 Pipeline that links omics and TK in sweetpotato (steps A to G).

Step	Objective	Minimal inputs	Methods	Expected outputs	Key indicators	Governance note
A	Set up community and ethics	Community leaders; CSB or farmer associations; consent templates	Meetings; FPIC; simple benefit sharing agreement; data management plan	Signed consent; advisory note; short data handling note	Consent coverage percent; number of partners; time to approval	Record FPIC and benefit sharing; state data sensitivity and reuse limits; ABS if applicable
B	Elicit TK and farmer preferences	Landrace list; farmer panels; short interview guide	Structured interviews; card sorting; matrix ranking by use and context	TK descriptors; farmer preference index by trait	Number of varieties described; number of priority traits; inter rater agreement	Label sensitive TK and consent scope for reuse
C	Phenotype and test on farm	Candidate materials; simple plot design; scoring sheets	Small multi location trials; field days; sensory evaluation when relevant	Yield with units; acceptance score; basic quality traits	t per ha or kg per ha; acceptance percent; number of sites and seasons	Operate via CSB or associations; share trial rules agreed with the community
D	Link omics to breeding	Tissue samples; minimal SNP or QTL panel; phenotypes from step C	Low density genotyping or targeted markers; association or prediction models; GS or MAS when feasible	Marker trait associations; candidate selections	Model accuracy; selection differential; number of candidates advanced	Check ABS and data sharing constraints, especially DSI and local regulations
E	Participatory selection cycle	Shortlist from step D; on farm results from step C	PVS walk-throughs; farmer scoring; joint decision meeting	Selected materials and clear rationale	Proportion selected; reasons mapped to TK and preferences	Make selection criteria transparent and co agreed with partners
F	Track quantitative outcomes	Adoption logs; yield records; diversity or structure metrics when applicable	Simple monitoring forms; follow up visits; compute Shannon, Nei, He, Ho, Fst, AMOVA when relevant	Adoption percent; yield gain; diversity or structure metrics	Adoption after one season; yield gain percent; change in diversity metrics	Publish metadata and data use limits; retain consent scope and acknowledgments
G	Feedback, seed access, and reporting	Selected materials; multiplication plan; plain language reports	Distribution via CSB or associations; short training; policy note if needed	Seed available locally; brief report; next cycle plan	Number of farmers accessing seed; time to availability; number of reports delivered	Record benefits delivered; archive joint decisions and credits

TK, Traditional Knowledge; PPB, participatory plant breeding; PVS, participatory varietal selection; GS, Genomic Selection; MAS, Marker Assisted Selection; CSB, Community Seed Bank; FPIC, Free Prior and Informed Consent; ABS, Access and Benefit Sharing; DSI, Digital Sequence Information.

These institutional patterns directly influence how omics and TK collaborations evolve across regions. The integration of omics and TK is not merely a methodological exercise but a requirement for socially equitable and contextually relevant crop improvement. Building a more connected global network would strengthen the omics–TK framework proposed in this study and enhance inclusivity in sweetpotato research.

The most cited studies emphasize virus resistance (Ling et al., 2010), genomic resource development (Hirakawa et al., 2015), and abiotic stress response (Luo et al., 2017; Wang et al., 2022). Okada et al. (2019) exemplify the use of GWAS to connect molecular markers with breeding traits, showing that the most impactful studies combine methodological innovation with agronomic application.

Thematic classification shows breeding as the dominant focus (43%), followed by conservation genetics (32%) and plant biology (25%). Within breeding, molecular approaches, disease resistance, and population genetics prevail, reflecting the complexity of the hexaploid genome and the challenges of parental selection (Mollinari et al., 2020; Sapakhova et al., 2023; Cheng et al., 2023). The integration between breeding and conservation remains partial, which limits the practical use of genetic diversity information in applied programs.

Methodological diversity shows a long-tail pattern, with many tools applied once and only a few in frequent use (MAT, RT-PCR, RNA-seq, SSR, PCR, qRT-PCR) (Xiao et al., 2022; Wang et al., 2022). Only 17.8% of studies employed omics approaches, highlighting persistent technical and financial barriers (Hirakawa et al., 2015; Okada et al., 2019). Expanding analytical infrastructure and bioinformatics training in developing regions would significantly broaden the reach of omics methodologies.

Conservation of genetic resources remains a strategic priority. Although crop-wide diversity has been documented (Gichuki et al., 2003; Monteros-Altamirano et al., 2021), integration of wild germplasm and traditional landraces into breeding programs remains limited. This gap increases the risk of genetic erosion and reduces long-term adaptability. Expanding germplasm banks, characterizing wild relatives, and developing pre-breeding programs are key measures, especially in regions where sweetpotato underpins food security.

Corpus-level evidence and high-adherence studies together demonstrate how molecular and community-based data can be combined effectively. The works of Roullier et al. (2013), Alves-Pereira et al. (2018), and Aritua et al. (2009) exemplify complementary aspects of this bridge: population structure, diffusion of diversity, and molecular characterization linked to field performance. Roullier et al. (2013) linked genetic evidence with ethnobotanical data to clarify patterns of diffusion. Alves-Pereira et al. (2018) demonstrated that population structure and community management can be jointly analyzed to reveal consistent units of diversity. Aritua et al. (2009) illustrated how molecular characterization of viruses complements farmer experience and varietal performance. Together, these studies show that molecular evidence becomes more actionable when interpreted through the lens of TK and on-farm validation.

Regional adherence patterns reinforce this idea. Europe and the Americas show higher integration of participatory and quantitative elements, while Asia, despite its omics productivity, documents fewer governance and TK components. Africa shows intermediate performance, increasingly combining molecular analysis with participatory frameworks. Programs aiming to enhance adherence should include explicit documentation of TK and participatory varietal selection, supported by clear governance frameworks such as FPIC, ABS, and DSI.

These insights indicate that molecular findings achieve greater impact when connected to field data, local varieties, and farmer collaboration. Adding TK and PVS modules enhances contextual relevance and adoption potential.

The study acknowledges three limitations: (1) the keyword-based parameter detection may overlook subtle forms of reporting; (2) adherence scores, although bounded to minimize bias, may not capture full engagement depth; (3) governance indicators detect only explicit mentions, possibly underestimating practical implementation. These factors highlight the need for transparent documentation and open data sharing through Supplementary Materials.

In summary, genetic structure, farmer-managed diversity, and molecular data should be analyzed jointly to maximize interpretability and impact. Supporting evidence from Veasey et al. (2007, 2008) strengthens this argument, combining agronomic descriptors with molecular information. For research teams, incorporating TK elicitation, on-farm validation, and targeted molecular modules can optimize both scientific rigor and social benefit. For policymakers, reinforcing seed networks, participatory structures, and ethical data management will facilitate broader adoption of genetic innovations.

Future research should validate the proposed pipeline empirically, employing before-and-after evaluations that report adoption rates, yield, and diversity metrics. Comparative analyses across sites can then identify which contextual variables influence success and guide refinement of the omics–TK framework for participatory crop improvement.

5 Conclusion

This study maps the contemporary landscape of sweetpotato genetics and demonstrates that molecular evidence is already interpreted alongside landraces, farmer participation, and field measurements, though less frequently with explicit protocols for documenting TK or participatory selection. The corpus-level adherence remains low to moderate, indicating that most studies capture only part of the link between laboratory research and livelihood outcomes. This analysis identifies where the evidence is strong, where it is absent, and how minimal methodological additions can make the bridge operational. By providing auditable metrics and a clear, stepwise framework that aligns molecular targets with community priorities, the study offers a practical roadmap for researchers and decision makers to enhance both the scientific relevance and on-farm adoption of sweetpotato genetics research.

Data availability statement

The original contributions presented in the study are publicly available. This data can be found here: https://figshare.com/s/0819c3111a819ba478e8.

Author contributions

GB: Formal analysis, Investigation, Methodology, Validation, Visualization, Writing – original draft, Writing – review & editing. EC: Formal analysis, Investigation, Methodology, Validation, Writing – original draft, Writing – review & editing. MES: Formal analysis, Investigation, Methodology, Writing – original draft, Writing – review & editing. LV: Investigation, Methodology, Writing – original draft, Writing – review & editing. RP: Formal analysis, Investigation, Writing – original draft, Writing – review & editing. MVS: Conceptualization, Formal analysis, Investigation, Methodology, Project administration, Writing – original draft, Writing – review & editing.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was not used in the creation of this manuscript.

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Supplementary material

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