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Genetic Diversity of Annual Crops in Africa - A Structured Exploratory Synthesis and Evidence Map to Inform a Systematic Review

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Abstract

The genetic diversity of annual crops provides a resource for conserving and improving African agricultural systems. Its interpretation remains challenging because of differences among species, molecular markers and sampling strategies. To organize knowledge on genetic diversity, differentiation, domestication and the use of genetic resources, and to prepare a reproducible systematic review protocol. Targeted literature searches conducted on 30 October 2026 identified 19 original studies or reanalyses published between 2007 and 2026. References and key information were checked against bibliographic records and publisher sources; 12 full texts were also archived in XML format. A narrative synthesis, a partial map of countries of germplasm origin and an analysis of terms in article titles were conducted. The corpus covers eight crop groups. It comprises 11 publications on cereals, five on legumes, two on sesame and one on okra. Seven studies provide explicitly coded country-of-origin information covering 18 countries. The studies link domestication history, geographical structure and potential breeding applications. Diversity estimates cannot be directly pooled across species or platforms. Conservation should integrate ecological provenance, population history and seed management practices.

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Keywords

Genetic diversity; annual crops; Africa; genomics; plant genetic resources; population structure; conservation; crop improvement.

Introduction

Annual crops complete their life cycle primarily through seed reproduction. Their genetic diversity therefore connects the biological processes of reproduction with human decisions about seed conservation, exchange and selection.

In African farming systems, the same crops may contribute to human food, animal feed, income and the maintenance of seed resources. An assessment of their diversity cannot therefore be confined to counting alleles: it must specify the material examined, the environments represented and the traits associated with the observed variation.

The category of annual plants does not, in itself, constitute a genetically homogeneous group. It encompasses species that differ in mating system, ploidy, domestication history and population structure. Here, we consider seed-propagated plants managed as annual crops, while distinguishing the wild relatives included in comparative panels. This operational definition excludes perennial crops harvested early and species propagated

predominantly through vegetative means. The present synthesis does not assess all wild annual plants in Africa.

Research on fonio illustrates how questions and tools have evolved. Adoukonou-Sagbadja *et al.,* (2007) used AFLP markers to investigate differentiation between two species and among their geographical origins. Abrouk *et al.,* (2020) subsequently combined a reference genome with resequencing of a panel of cultivated and wild accessions.

Ibrahim Bio Yerima *et al.,* (2021) characterized a different regional panel using SNPs. These studies are not repeated measurements of the same population; they provide complementary levels of resolution.

In African rice, genomics has reshaped interpretations of domestication. The analyses by Wang *et al.,* (2014), Meyer *et al.,* (2016), Cubry *et al.,* (2018) and Veltman *et al.,* (2019) examine different panels and historical models.

They show why a review should present conflicting interpretations rather than regard a single geographical origin as definitively established. Agreement on the importance of a reduction in diversity can coexist with disagreement over the locations and stages of domestication.

Genetic structure is also linked to seed circulation. Westengen *et al.,* (2014) examined the relationship between genetic and ethnolinguistic distributions in sorghum. In cowpea, Huynh *et al.,* (2013) and subsequently Fiscus *et al.,* (2024) described a major geographical pattern in African germplasm using collections of different sizes. These findings suggest that seed networks should be considered in sampling and interpretation, without treating every cultural correlation as evidence of causality.

The central question of this review is therefore: what verifiable molecular evidence can describe and support the use of genetic diversity in African annual crops, and what limitations still prevent robust comparisons among studies?

The objectives are to characterize the documentary coverage, compare measurement approaches, synthesize findings by crop and propose a conservation and research strategy. The visualizations address these objectives; their number cannot substitute for corpus quality or the comparability of estimates.

Materials and Methods

Synthesis type and scope

This version is a structured exploratory synthesis intended to inform a systematic review. It was not prospectively registered and did not undergo independent duplicate screening. PRISMA 2020 and PRISMA-S provide transparency frameworks for identifying the information available and the elements that remain to be documented (Page *et al.,* 2021; Rethlefsen *et al.,* 2021). Using these frameworks does not certify compliance. Counts of identified, deduplicated or excluded records have not been artificially reconstructed.

The scope includes molecular studies of annual crops and African germplasm, including global panels that explicitly allow this material to be interpreted. Comparative genomic analyses are included when they inform diversity, structure or domestication. Secondary reviews, publications used to verify author affiliations and statistical references provide context or methodological support; they are not counted among the 19 studies.

Literature identification and verification

The searches conducted on 30 October 2026 combined Web searches concerning author identities, African annual crops and molecular diversity. Sources identified included PubMed, PubMed Central, journal websites and a university repository. Corpus records were searched by PubMed identifier, DOI or title in Europe PMC to check the metadata. Sixteen records were retrieved through this route; three were completed using publisher pages or the institutional repository. Twelve full-text XML files were archived. This verification of selected references should not be described as an exhaustive search of Europe PMC.

The thematic search blocks included “annual crops Africa genetic diversity”, “African rice genome domestication”, “sorghum Africa genomic diversity”, “cowpea gene pools”, “bambara groundnut genetic diversity”, “sesame Africa population structure” and “okra genetic diversity”. Searches were adapted to the species encountered.

Data extraction and counting units

Each row in the supplementary file represents a publication. The fields include title, year, authors, DOI, crop, main method, panel size when identifiable,

explicitly verified countries of origin and the level of document access. Reanalyses are retained as separate publications in bibliographic plots, but are not treated as independent biological samples. Sample sizes are never summed across articles because of possible overlaps and differences among accessions, individuals, lines and genomes.

The main method is assigned to one of five mutually exclusive categories: AFLP, SSR, ISSR and targeted sequences, SNP genotyping, and resequencing and assembly. This classification describes the dominant platform; it does not imply that a study used only one tool. SNPs derived from resequencing are therefore assigned to the final category. For the sorghum study by Faye *et al.,* (2021), the genotyped sample size of 756 is used rather than the 845 accessions initially assembled.

Mapping and term analysis

The map uses Natural Earth national boundaries at a scale of 1:110 million. A study–country association is coded only when the origin of the material is explicitly verified in the information examined. Seven studies contribute to this map. A grey country is uncoded in this subset: this indicates neither an absence of research nor an absence of genetic diversity. Researchers' affiliations and genotyping locations are not used as countries of germplasm origin.

The textual analysis is restricted to the 19 original titles. A dictionary of 12 terms and their English variants groups, for example, "genome", "genomic" and "genomics" under "genome". Frequency is the number of titles containing at least one occurrence. An edge connects two terms when they occur together in at least two titles; only the 16 most frequent associations are displayed. Manually paraphrased abstracts are excluded from this analysis. The network describes title vocabulary, rather than author-supplied keywords or the themes of the entire African literature.

Synthesis of genetic findings

Findings are compared by crop and biological question. Observed heterozygosity Ho, expected heterozygosity He, nucleotide diversity π, genetic differentiation FST, polymorphism information content and AMOVA partitions are distinguished. The foundations of FST and AMOVA follow Weir and Cockerham (1984) and Excoffier *et al.,* (1992), respectively. STRUCTURE and DAPC groupings are interpreted as model outputs that depend on the data and analytical settings (Pritchard *et al.,* 2000; Jombart *et al.,* 2010).

Results and Discussion

Corpus composition and distribution

The 19 publications span 2007–2026 and cover eight crop groups. African rice accounts for four publications; fonio, sorghum and cowpea each account for three; Bambara groundnut and sesame each account for two; and pearl millet and okra each account for one. These frequencies describe the working literature selection. They neither rank the agronomic importance of the species nor estimate their share of global research.

Documented African origins

The available geographical coding links seven studies to 18 African countries. Fonio and the West African sorghum panel contribute to the coverage of West Africa; the Bambara groundnut panel adds several southern African origins; the sesame studies document Ethiopia and Mozambique; and the okra study contributes a collection from Ghana. Continental studies and global panels that have not been fully recoded are not artificially apportioned among countries.

In the 2021 fonio panel, 128 accessions originated from Nigeria, 42 from Benin, 29 from Guinea, 28 from Mali, 28 from Niger and four from Burkina Faso (Ibrahim Bio Yerima *et al.,* 2021). Accession numbers are therefore highly uneven among countries. National comparisons must account for this collection design; the most extensively sampled country cannot automatically be declared the most genetically diverse.

Molecular tools and panel sizes

Eight publications rely primarily on resequencing or genome assembly; seven on SNP genotyping; two on SSRs; one on AFLPs; and one on ISSRs combined with targeted sequences. The crop–method matrix highlights the tools represented in the corpus. Zero-valued cells indicate only a combination not represented in the assembled selection.

Panels with an explicit principal sample size range from 28 okra accessions to 2,021 cowpea accessions. Figure 8 preserves the descriptive nature of these counts. The 206 genomes reanalysed by Veltman *et al.,* (2019) do not represent a new collection and are not added to earlier

datasets. The cowpea reference assembly and the sorghum study combining a continental panel with a local investigation are left without a single sample size in this plot.

Findings by crop

Fonio. The corpus combines an AFLP study of 122 accessions, a genomic study of 183 cultivated and wild accessions, and a SNP panel of 259 individuals (Adoukonou-Sagbadja *et al.,* 2007; Abrouk *et al.,* 2020; Ibrahim Bio Yerima *et al.,* 2021). The three publications address different questions: interspecific and geographical differentiation; genomic resources and domestication; and regional structure and linkage disequilibrium. Differences in the inferred numbers of groups do not demonstrate a temporal change in diversity.

African rice. Wang *et al.,* (2014) analysed 20 Oryza glaberrima accessions and 94 O. barthii accessions in their domestication study. Meyer *et al.,* (2016) examined 93 landraces and linked loci to salt-tolerance traits. Cubry *et al.,* (2018) used 246 new genomes to propose a history linked to the Inner Niger Delta and environmental change. The reanalysis of 206 genomes by Veltman *et al.,* (2019) highlights a more complex geographical diversification. These interpretations should be discussed in relation to the data and historical hypotheses.

Sorghum. Mace *et al.,* (2013) documented genomic diversity in 44 lines from the principal panel. Westengen *et al.,* (2014) identified genetic structure associated with broad ethnolinguistic groupings and described the seed management practices of a local group. Faye *et al.,* (2021) genotyped 756 accessions from four national programmes, retaining 159,101 SNPs. Their work links genetic resources to flowering-time and plant-height traits. These findings support parental selection that combines genetic distance with agronomic relevance rather than relying solely on differences between countries.

Pearl millet. The study by Varshney *et al.,* (2017) combines a reference sequence with resequencing of 994 lines in a global panel. It creates opportunities to define heterotic groups and predict hybrid performance. The inclusion of African material makes the study relevant to this synthesis, but the sample size of 994 should not be presented as an exclusively African collection.

Cowpea. Huynh *et al.,* (2013) studied 422 cultivated landraces, together with comparative wild material, and described two major African groups. Lonardi *et al.,* (2019) developed a reference genome and identified a large structural variant. Fiscus *et al.,* (2024) analysed 2,021 accessions from a global collection conserved at IITA and confirmed a major geographical pattern. The number of loci, genome architecture and phenotypic traits provide distinct information; a single overall measure of diversity cannot capture all of these dimensions.

Bambara groundnut. Uba *et al.,* (2021) characterized 270 accessions using SNPs and attributed 89% of variance to within populations, 8% to among regions and 3% to an among-population level in their partition. Minnaar-Ontong *et al.,* (2021), using 78 accessions and 19 SSRs, reported 92% of variance within the groups examined and 8% among groups. The predominance of the within-group component is informative, but grouping levels and markers differ: the percentages are not directly interchangeable replicates.

Sesame. Gelashe *et al.,* (2026) examined 188 Ethiopian accessions and retained 5,163 SNPs; the published mean values were He = 0.201 and Ho = 0.193. Muteti *et al.,* (2026) studied 109 accessions from Mozambique using 11,502 SNPs, with both He and Ho reported as 0.30 at the overall level. The latter study discusses an excess of heterozygotes within subpopulations and the possible presence of paralogous loci. The difference between collections therefore does not, by itself, demonstrate greater diversity at the national level.

Okra. Ahiakpa *et al.,* (2017) combined ten quantitative traits, six ISSR primers and three sequenced regions for 28 accessions collected in Ghana. Low variability in some markers does not imply an absence of valuable genetic resources; it may also reflect the resolving power of the regions examined. The value of additional characterization should be assessed in relation to the breeding question and molecular coverage.

Scientific vocabulary and term associations

In the titles, the “Africa” group and the selected national variants occur in 13 publications, “genome” in eight, “genetic diversity” in six, and both “population structure” and “SNP” in four. These frequencies are calculated using explicit variants retained in the

supplementary files. The analysis highlights how articles are framed in their titles; it does not establish that a theme absent from a title is absent from the full text.

Distinguishing biological diversity from measured diversity

The main finding of this synthesis is not a ranking of species, but the dependence of estimates on study design. A collection assembled to represent ecological zones, an association panel enriched for phenotypic variation and a set of parental breeding lines do not represent the same target population. Comparing them requires an explicit account of what can be inferred from the data. High diversity in a collection does not necessarily imply high diversity in a region's fields.

The mating system should inform interpretation, but it cannot explain every contrast. A highly self-pollinating crop may exhibit substantial variation among lines while retaining few heterozygous loci within individuals. Conversely, an apparent excess of heterozygotes may require checks of ploidy, marker specificity, read quality or the presence of paralogous sequences. Ho and He values should not be treated as evidence of adaptation without further examination.

Locus filtering also changes what is being measured. A minor allele frequency threshold removes some rare variants; a missing-data threshold changes genome coverage; and imputation introduces assumptions about relatedness and allele frequencies. A future quantitative synthesis should therefore extract the exact filters, sequencing depth, imputation method and biological unit. Comparing only final SNP counts could favour platforms with greater marker density without establishing the biological robustness of their findings.

Interpreting population structure and domestication histories

Genetic groups depend on the panel, method and permitted number of groups. STRUCTURE represents individuals as mixtures of hypothetical populations, whereas DAPC seeks multivariate separation among groups. Agreement between the methods may strengthen the description of a signal, but it does not automatically make a statistical group a relevant conservation unit (Pritchard *et al.,* 2000; Jombart *et al.,* 2010). An operational unit must also account for its stability, distribution, uses and value to farmers.

African rice illustrates that a reduction in diversity, geographical structure and a selection signature do not date or locate domestication in the same way. Studies may share a general historical signal while differing over the precise scenario.

In a review, the appropriate comparison therefore concerns the relationship among panel, model and conclusion. Competing hypotheses should be presented explicitly, particularly when reanalyses reuse data already represented in the corpus (Wang *et al.,* 2014; Meyer *et al.,* 2016; Cubry *et al.,* 2018; Veltman *et al.,* 2019).

Integrating seed conservation and crop improvement

Conservation should combine geographical coverage with descriptions of seed management practices and desired traits. Sampling based solely on administrative boundaries may overlook differentiated populations within a country. Conversely, selecting a single accession per molecular group could eliminate useful variation within that group. The Bambara groundnut panels illustrate the value of retaining this within-group component, while also showing that AMOVA partitions must be interpreted in relation to their grouping design (Uba *et al.,* 2021; Minnaar-Ontong *et al.,* 2021).

For crop improvement, genetic distance is a criterion for shortlisting parents, not a guarantee of complementarity. Highly divergent parents may differ in undesirable traits or be poorly adapted to the target area. Decisions should integrate measured performance, quality objectives and the feasibility of obtaining usable progeny. The value of a trait-associated locus remains conditional on validation in other genetic backgrounds and environments.

The association studies in the corpus provide leads rather than universal variety recommendations.

From an agro-sylvo-pastoral systems perspective, it would be useful to study cereal or legume grain and residues jointly, including food yield, straw and haulm quality, seasonal availability, land uses and trade-offs among objectives.

This proposal is a research direction derived from the synthesis, not an outcome measured across the 19 publications. It supports collaboration among plant genetics, agronomy, biometrics and animal sciences, without artificially including perennial forage species in a review of annual crops.

Figure.1 Documentary workflow for this version. The diagram shows the corpus actually assembled and the limitations of the counts; it does not replace a completed PRISMA flow diagram.

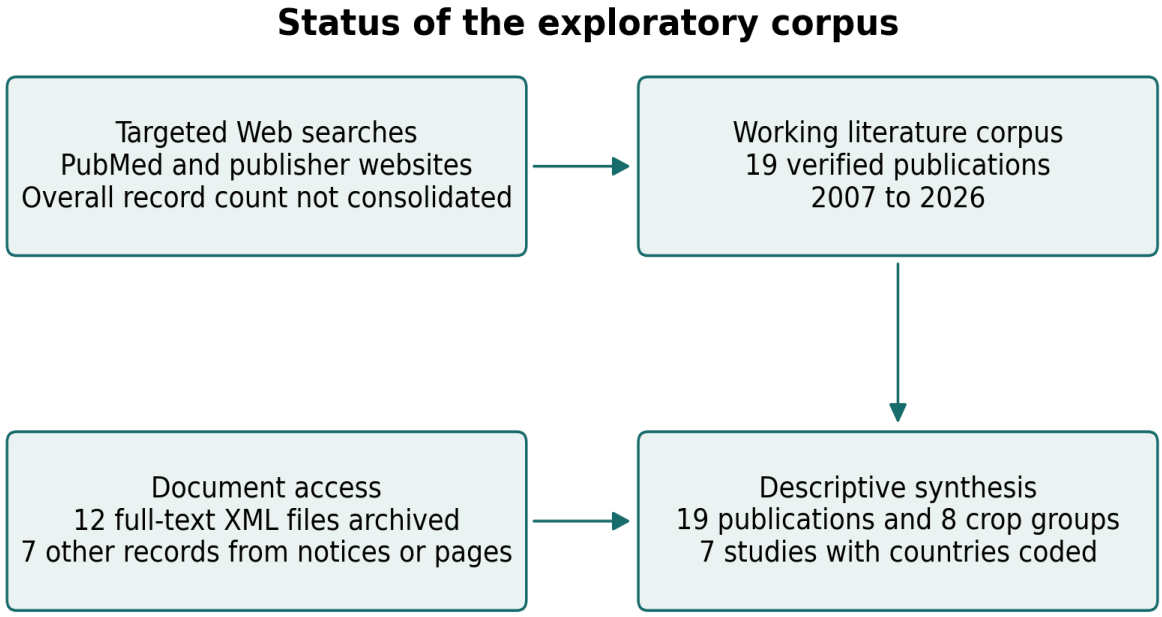


Figure.2 Annual distribution and cumulative number of the 19 selected publications. Years with no articles describe this targeted corpus; the curve does not measure the growth of the entire research literature.

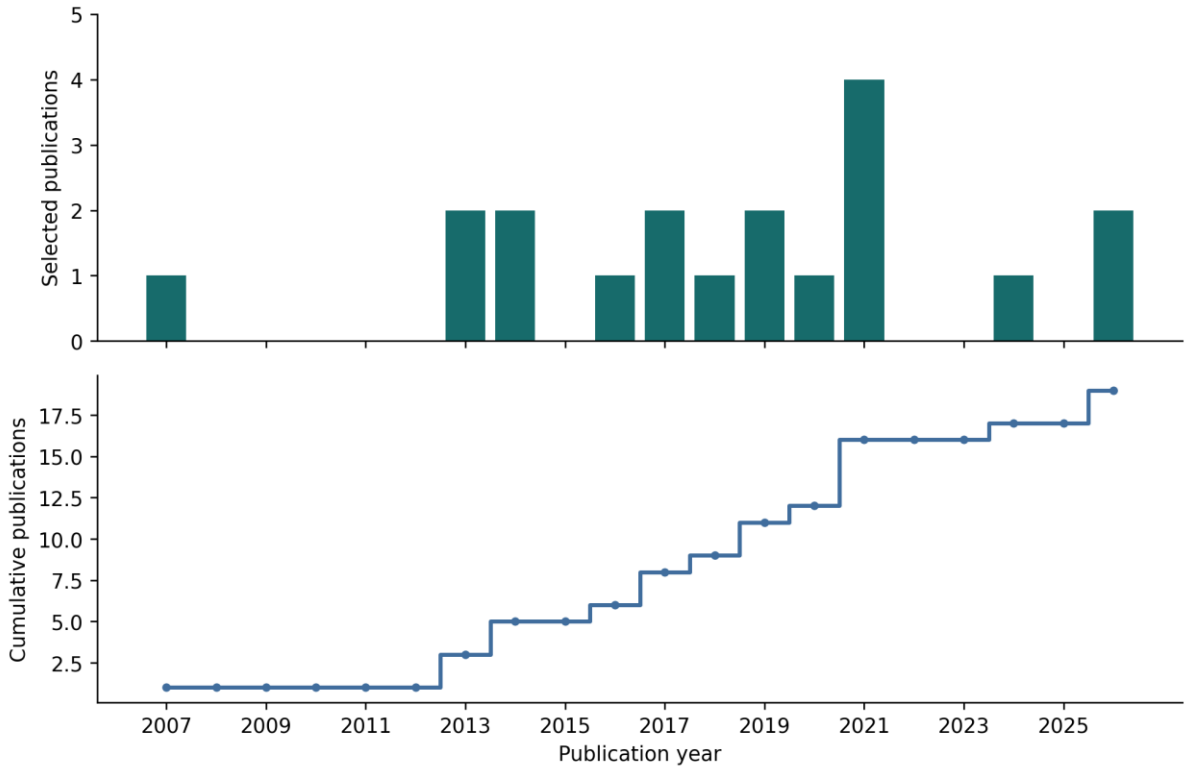


Figure.3 Distribution by crop. Each publication is counted once; taxonomic groups are retained at the level used in the synthesis.

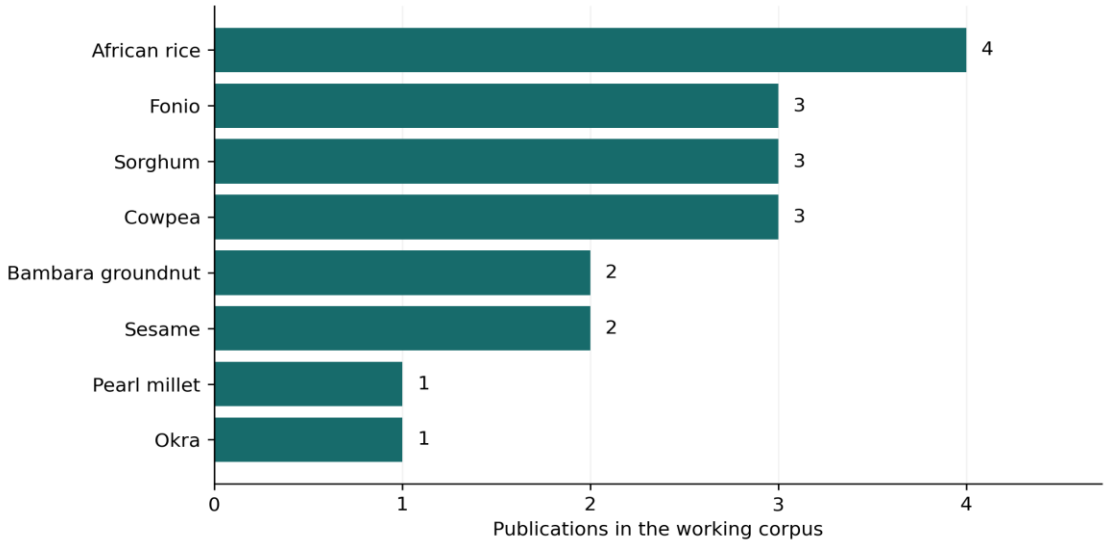


Figure.4 Explicitly verified countries of origin in seven corpus studies: F01, F03, S03, B02, E01, E02 and O01. A study may contribute to several countries. Grey indicates uncoded countries. Basemap: Natural Earth, public domain.

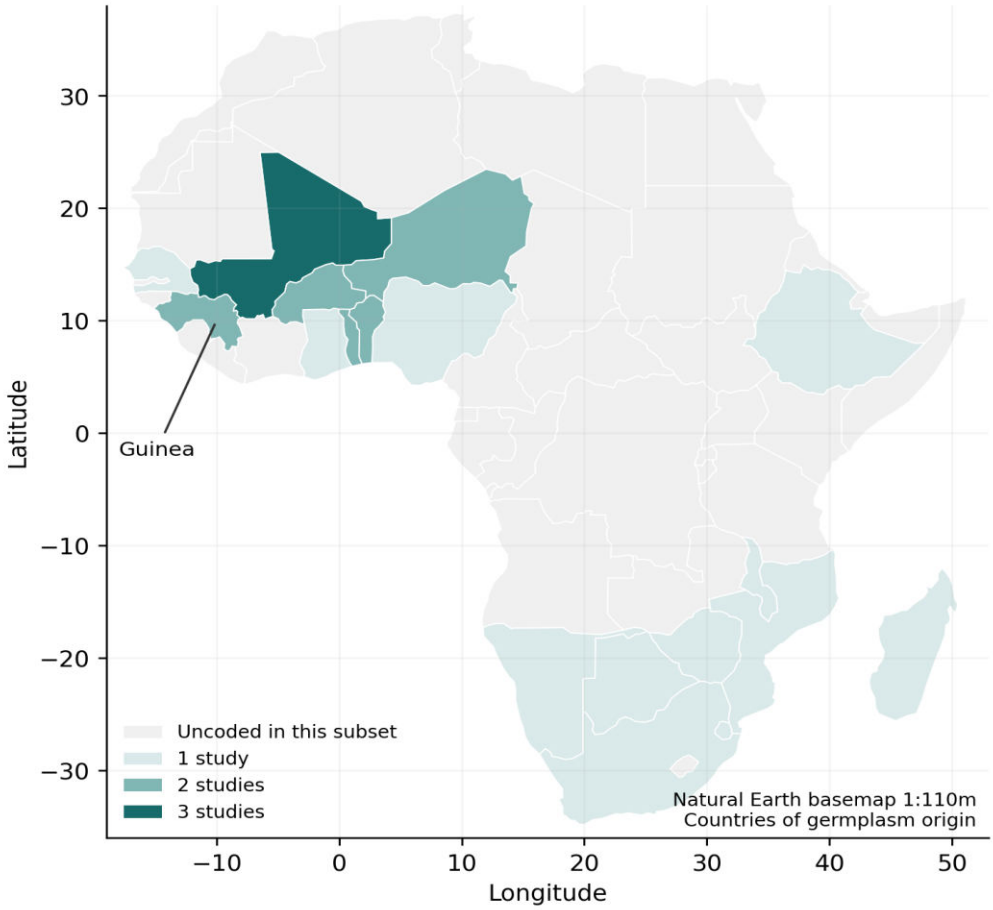


Figure.5 Country composition of fonio panel F03. Values are taken from the description of the plant material and total 259 accessions.

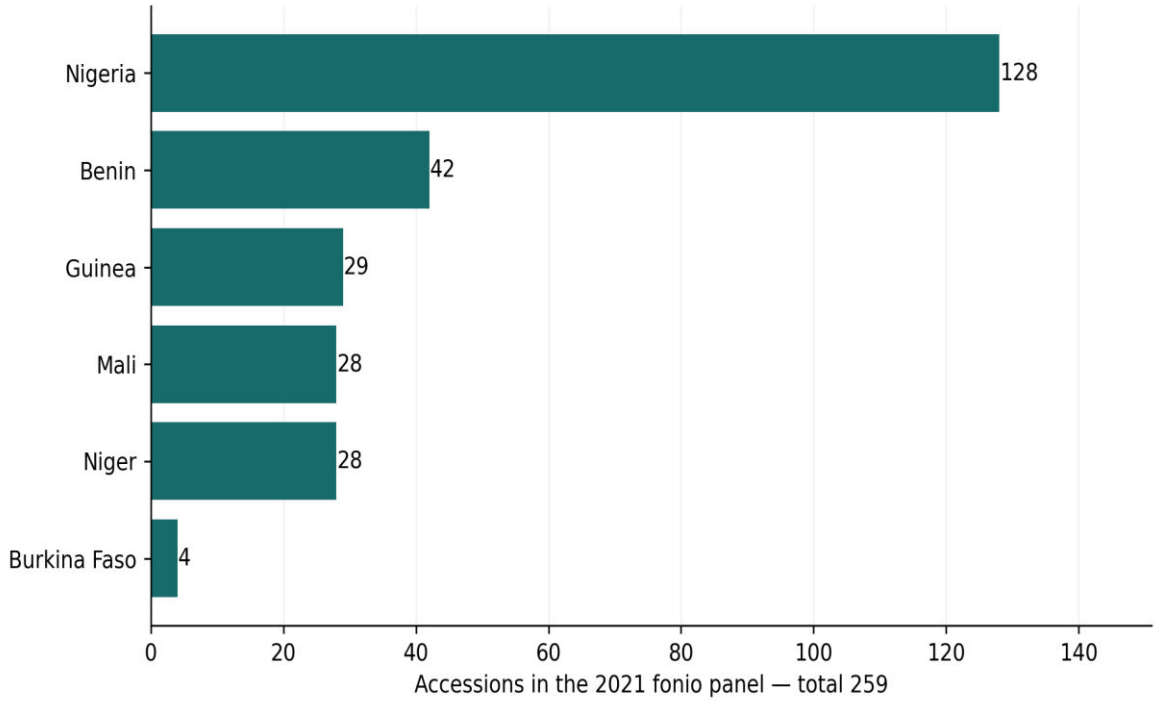


Figure.6 Main methods used in the 19 publications. Categories are mutually exclusive to avoid double-counting SNPs derived from resequencing.

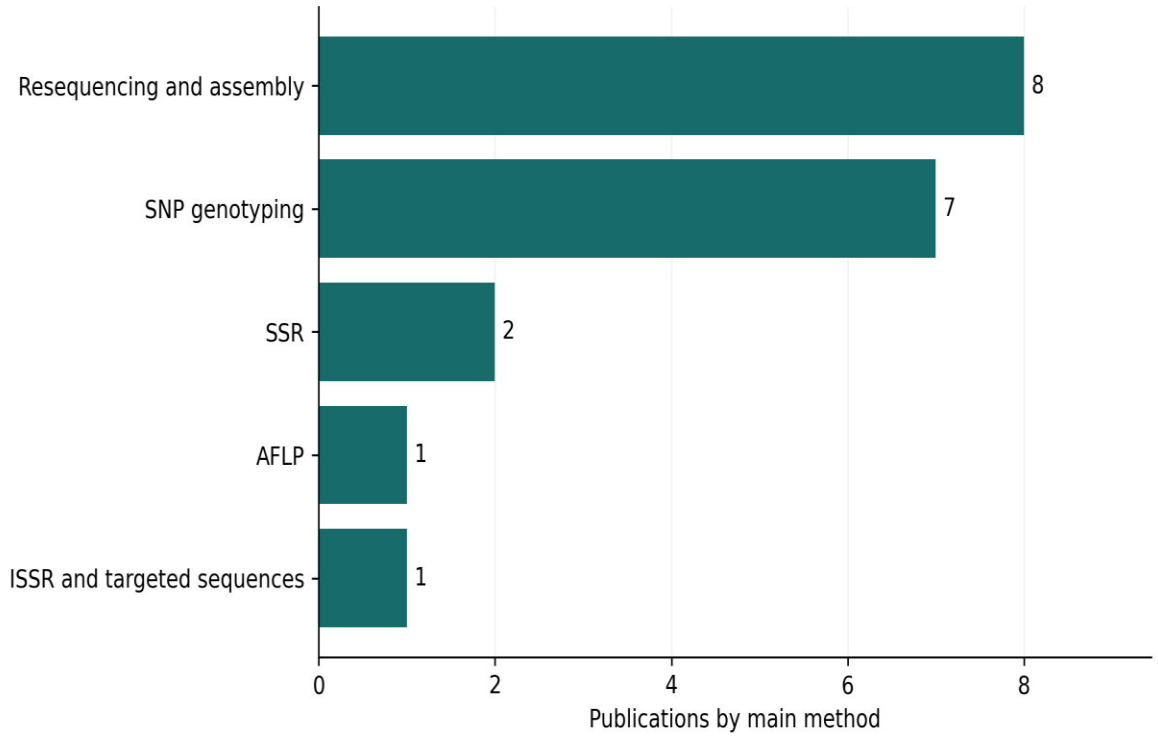


Figure.7 Crop–method matrix expressed as numbers of publications. Categories correspond to those in Figure 6.

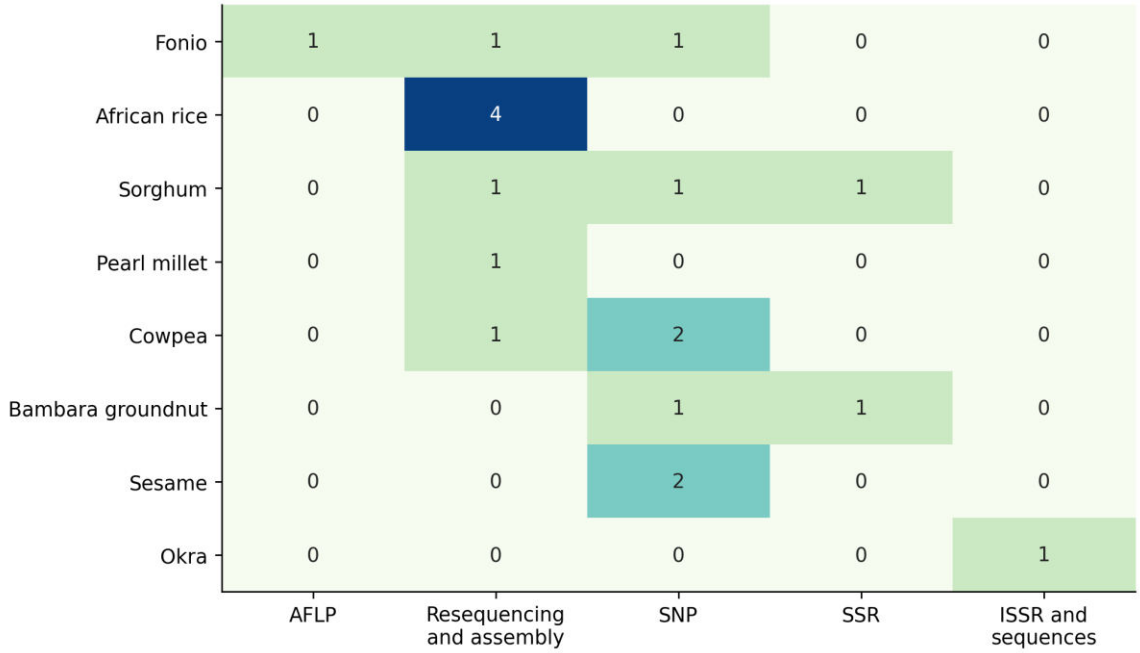


Figure.8 Reported sample sizes for 17 panels or genome datasets. A logarithmic scale facilitates reading. The units and exclusions associated with each sample size are specified in the supplementary file.

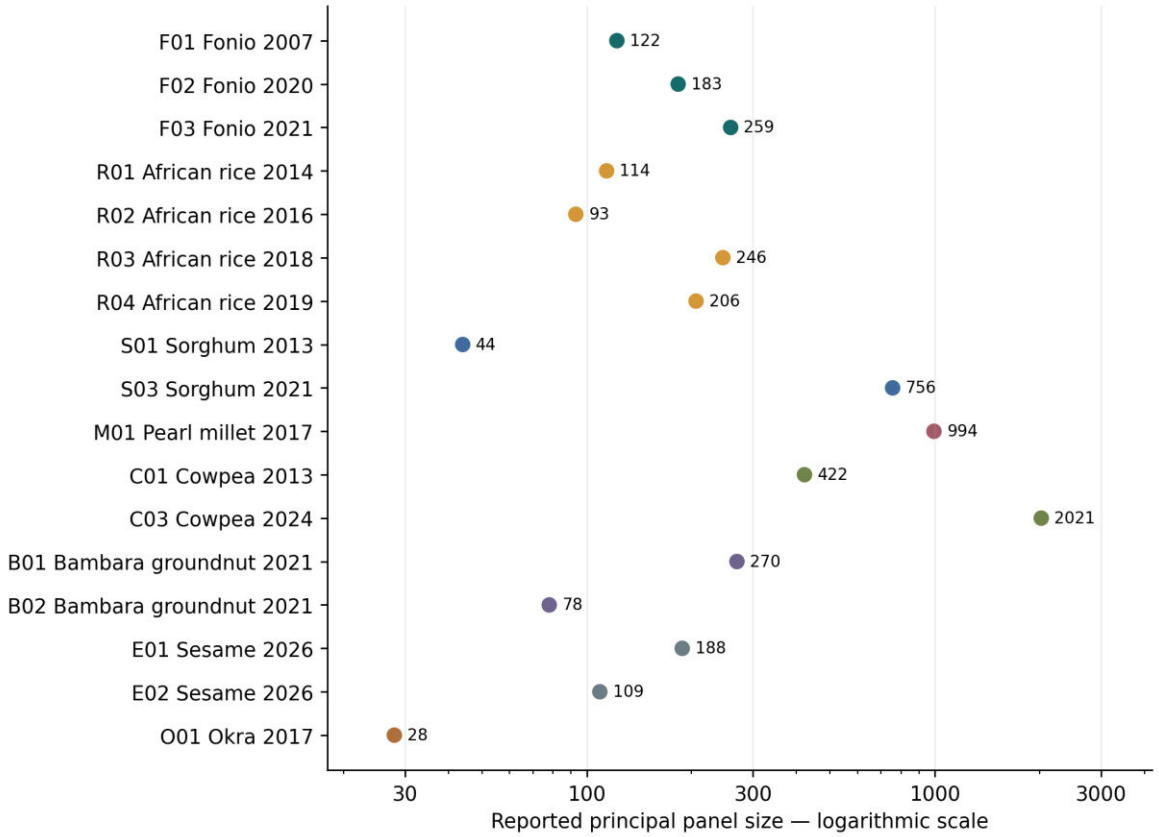


Figure.9 Published mean heterozygosity estimates for two sesame collections, E01 and E02. This is a descriptive comparison without a common variance estimate, confidence intervals or a statistical test between countries.

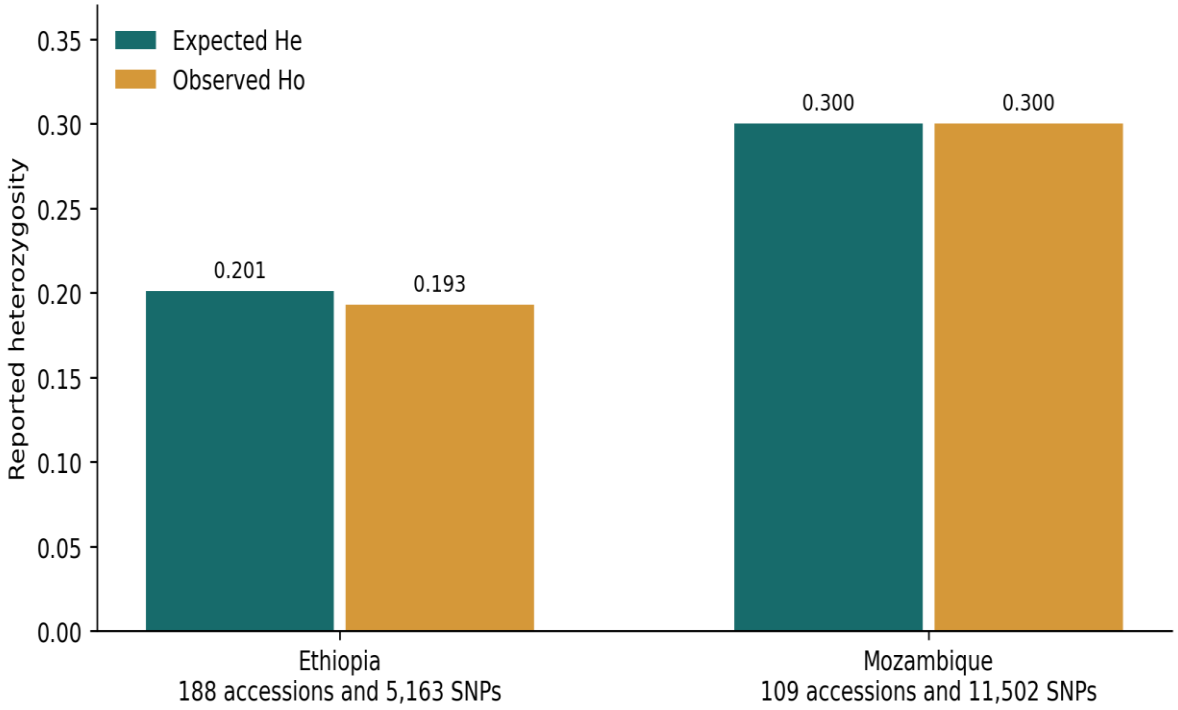


Figure.10 Document frequency of 12 controlled terms in the original titles. A publication contributes at most one occurrence per term. The dictionary is supplied with the data.

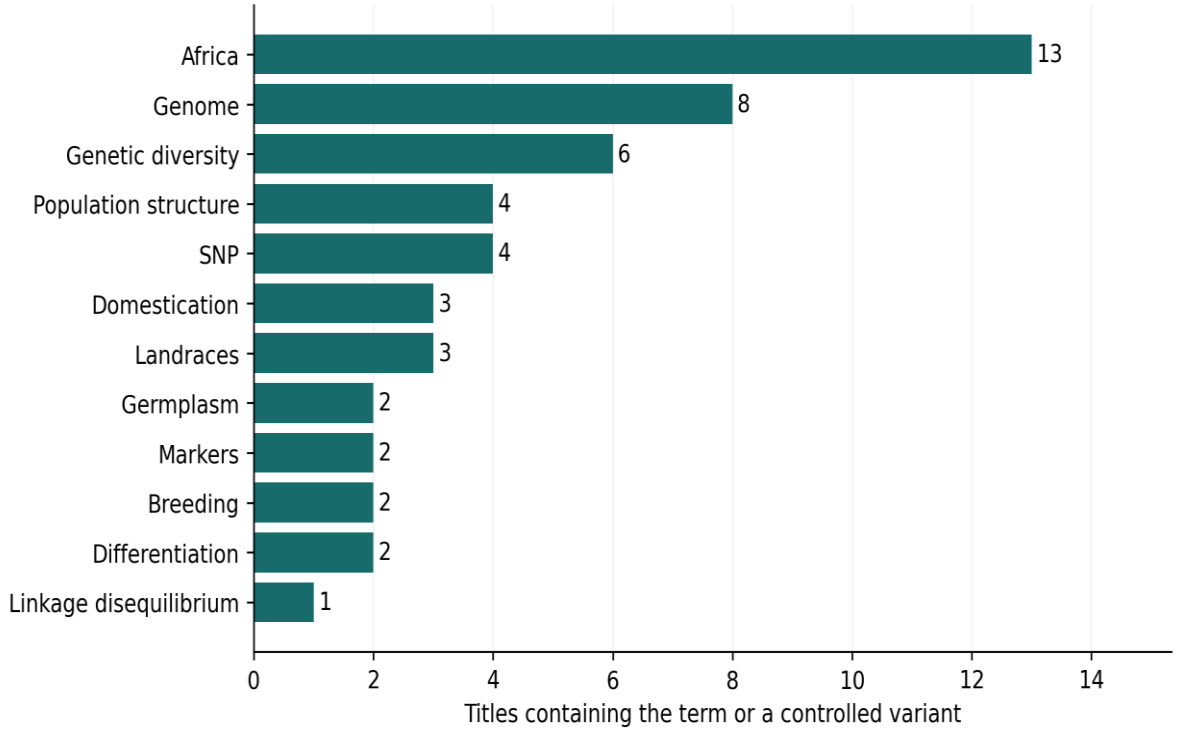


Figure.11 Network of term cooccurrences in titles. Node size reflects term frequency and link thickness reflects the number of shared titles. Up to 16 links are displayed among those observed in at least two titles. Colours are used solely for readability and do not represent algorithmically identified communities.

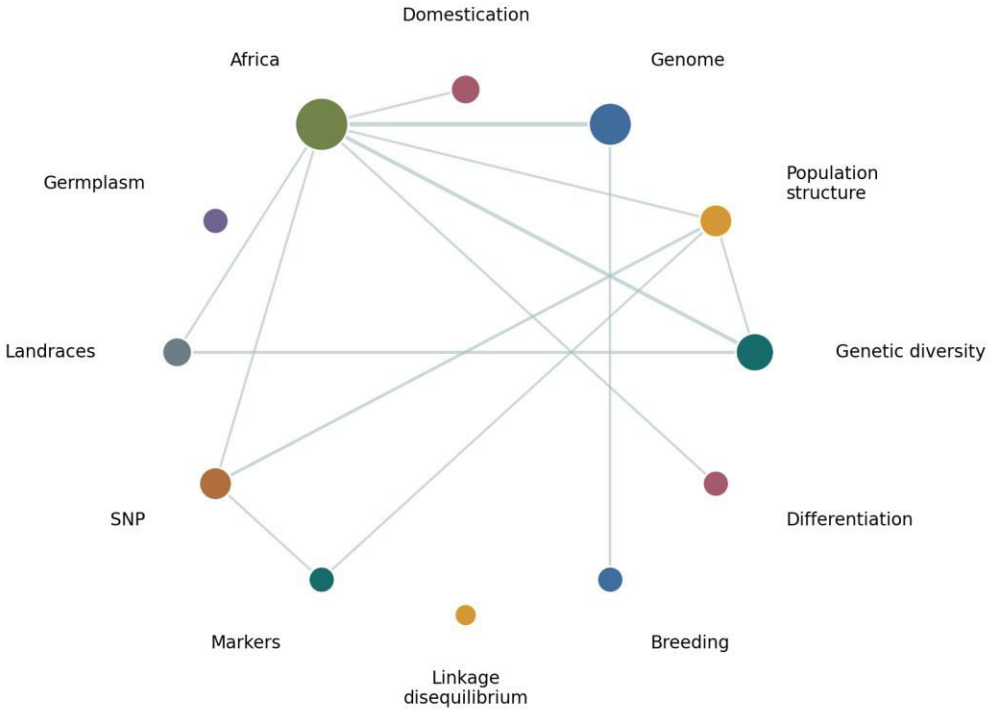
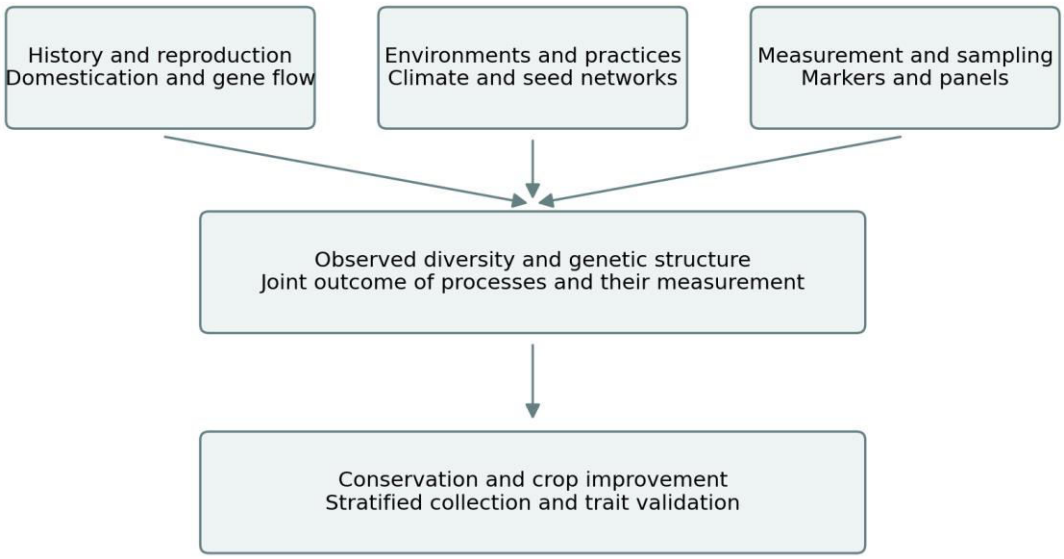


Figure.12 Interpretative framework proposed by the manuscript's authors. Arrows express conceptual relationships and represent neither estimated causal effects nor measured coefficients.



What the figures can actually establish

The map provides an audit of the origins already extracted. Its partial coverage precludes interpreting grey areas as locations without research. The annual curve describes the assembled corpus rather than the exhaustive development of a scientific field. The lexical network depends on a dictionary and short titles; it complements qualitative reading but replaces neither thematic coding of full texts nor bibliometric analysis based on complete exports. These distinctions are essential if figures are to support valid conclusions.

The sesame comparison illustrates the difference between juxtaposition and meta-analysis. The two published mean He values can be plotted alongside their respective contexts. They cannot establish a country effect without comparable populations, harmonized definitions and appropriate uncertainty estimates. A forest plot pooling different species, estimates and markers would imply misleading precision. Likewise, a Manhattan plot or accession-level PCA requires genotypic data or usable original results; such plots cannot be derived from bibliographic records alone.

Limitations and priorities for literature coverage

The main limitation is the targeted nature of the searches. The eight groups represented do not cover all African annual crops: maize, wheat, barley, groundnut, soybean, common bean, several millets and many vegetable species remain to be screened. Their absence from this version reflects corpus construction rather than a demonstrated shortage of literature. Local studies, publication languages and less well-indexed documents may substantially change the final evidence map.

The absence of independent screening and of an appraisal framework applied to every study also limits the strength of cross-study conclusions. Access to 12 archived full texts does not mean that the other seven articles were examined in equal detail. No overall risk-of-bias score has been invented. The final version should distinguish information that is not reported, inaccessible or not applicable, and resolve extraction disagreements before any quantitative synthesis.

The priority next step is a multi-database search with dated exports and recorded reasons for exclusion. Analyses should then be organized by species, marker and population unit. In Guinea, a complementary investigation could combine stratified field exploration, provenance data and characterization of a core diversity collection. The selection of sites and species should follow a local assessment and seed-sector partnerships, rather than relying only on the bibliographic visibility of particular crops.

In conclusion, the 19 publications assembled show the value of integrating molecular tools, population history and seed management when studying African annual crops. They support documentary mapping and a considered comparison of approaches, but not a continental ranking of diversity or a common average effect across all species. Genetic findings must be interpreted in the context of their panel, mating system and filtering procedures.

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