International Journal of Integrated Science and Technology (IJIST)
Vol. 3, No. 12 December 2025: 2485-2504

Genetic Variability of Rhizobium and its Correspondence with Plant Genotype Response: A Systematic Review

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ARTICLEINFO

Keywords: Genetic Variability, Genotype × Genotype Interaction, Plant Responsiveness, Rhizobium, Systematic Review

Received : 20, October
Revised : 25, November
Accepted: 20, December

ABSTRACT

Rhizobium-legume symbiosis is a cornerstone of sustainable agriculture, yet the integrated understanding of how bacterial genomic variation determines phenotypic outcomes across different host genotypes remains fragmented. This systematic review aims to synthesize the correspondence between *Rhizobium* genetic variability and plant genotype responses. Using a structured PRISMA framework, 86 studies were selected to analyze genomic diversity patterns, host responsiveness, and Genotype × Genotype (G×G) interactions. The synthesis reveals that rhizobial diversity is shaped by variations in housekeeping genes, symbiotic islands, and plasmid-borne *nod* and *nif* clusters, which drive nodulation competitiveness and environmental adaptation. Correspondingly, host plant responsiveness is actively modulated by specific genetic architectures, such as *Rj* genes in soybeans and immune receptors in *Medicago*, creating a selective filter for bacterial partners. The results demonstrate consistent G×G specificity, ranging from strict compatibility in specialized systems to flexible interactions in woody legumes, all of which are influenced by environmental pressures. A conceptual framework is proposed, describing symbiosis as an emergent system where microbial genomic modules interact with plant regulatory networks to determine nitrogen fixation efficiency. The study concludes that optimizing agronomic performance requires coordinating microbial genomic traits with host plant genetics, emphasizing the need for genotype-matched inoculants and molecular breeding strategies to enhance biological nitrogen fixation stability.

DOI: https://doi.org/10.59890/ijist.v3i12.243

INTRODUCTION

Rhizobium represents one of the most ecologically significant groups of soil bacteria due to its unique capacity to form nitrogen-fixing symbioses with legumes. Through the establishment of root nodules, *Rhizobium* converts atmospheric nitrogen into ammonia via the nitrogenase enzyme complex, supplying host plants with accessible nitrogen and simultaneously receiving carbon substrates for its metabolism. This mutualistic association accounts for nearly half of the biologically fixed nitrogen in terrestrial ecosystems, making it essential for maintaining soil fertility and supporting global food production (Huang, 2024). In agricultural systems, effective Rhizobium legume partnerships substantially reduce dependency on synthetic nitrogen fertilizers, thereby lowering environmental costs, enhancing sustainability, and improving crop productivity under diverse climatic and edaphic conditions (Abd-Alla et al., 2023). Given its dual ecological and agronomic importance, understanding the biological determinants of symbiotic efficiency has become a major scientific priority.

Genetic variability within *Rhizobium* plays a central role in shaping its symbiotic performance. This diversity is observed not only in the conserved core genome, comprising essential housekeeping genes used for species delineation such as *16S rRNA, recA,* and *atpD*, but also in highly dynamic symbiotic regions carried by large plasmids or chromosomal islands. These symbiotic elements harbor key determinants of nodulation (*nod*) and nitrogen fixation (*nif* and *fix*) whose structural and regulatory variability profoundly influences the molecular dialogue between bacteria and host plants. As shown in comparative genomic studies, variations in Nod factor–synthesizing genes shape host recognition specificity, while polymorphisms within *nifH, nifD,* and *fixABCX* modulate nitrogenase function and energy allocation (Nichio et al., 2025). Horizontal gene transfer and environmental selection further accelerate genomic diversification, producing strain-level differences in competitiveness, tolerance to abiotic stress, and symbiotic potential even within a single Rhizobium species.

Complementing bacterial variability, plant genotypes also display a wide range of responses to different *Rhizobium* strains. Legume hosts deploy receptor-like kinases and signaling components that decode specific Nod factor structures, resulting in genotype-dependent compatibility outcomes. Consequently, phenotypic responses such as nodule number, nodule dry weight, nitrogenase activity, biomass accumulation, and grain yield frequently differ between cultivars inoculated with the same strain or among strains tested on the same cultivar (Mendoza-Suárez et al., 2021). This selective responsiveness highlights the importance of genotype × genotype (G×G) interactions, where the symbiotic performance is determined not by either partner alone but by the molecular compatibility between them. Such specificity has major implications for breeding programs, inoculant design, and the deployment of microbial technologies across agroecosystems.

Despite substantial empirical evidence describing genetic variation in *Rhizobium* and plant-specific responses, integrated syntheses linking these two components remain scarce. Existing reviews are typically focused on either

Rhizobium genomics or legume physiology but seldom address how specific genomic attributes correlate with plant phenotypes across diverse systems. There is also limited synthesis of how high-resolution genomic markers, such as average nucleotide identity (ANI), single nucleotide polymorphism (SNP) profiling, multilocus sequence typing (MLST), and whole-genome phylogenetics map onto measurable host responses such as nitrogen fixation efficiency and yield. This fragmentation limits the development of a unified framework describing how genetic determinants shape symbiotic outcomes. As global agriculture increasingly relies on precision microbial technologies, the absence of such integrated knowledge represents a notable research gap.

Therefore, this systematic review aims to provide a comprehensive synthesis of Rhizobium genetic variability and its correspondence with plant genotype response. Specifically, the review seeks to: (i) summarize dominant patterns of genomic diversity across *Rhizobium* lineages; (ii) identify which plant genotypes exhibit enhanced responsiveness to particular Rhizobium strains; (iii) evaluate the extent and consistency of genotype × genotype (G×G) specificity across experimental systems; and (iv) construct a conceptual framework that links molecular variation to phenotypic performance, with relevance for sustainable agriculture, molecular breeding, and the development of genotype-matched microbial inoculants. By integrating molecular, physiological, and ecological perspectives, this review contributes to advancing the design of more efficient Rhizobium–legume partnerships in both natural and managed ecosystems.

MATERIALS AND METHODS

The analysis of genetic variability in *Rhizobium* and its correspondence with plant genotype response was conducted through a qualitative systematic literature review. This review employed a structured protocol adapted from the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework, which consisted of four major stages: Identification, Screening, and Include. These stages ensured the rigorous selection of studies that reported molecular variation in *Rhizobium* and measurable phenotypic responses in host plants. The complete PRISMA flow diagram summarizing the study selection process for this review is presented in Figure 1.

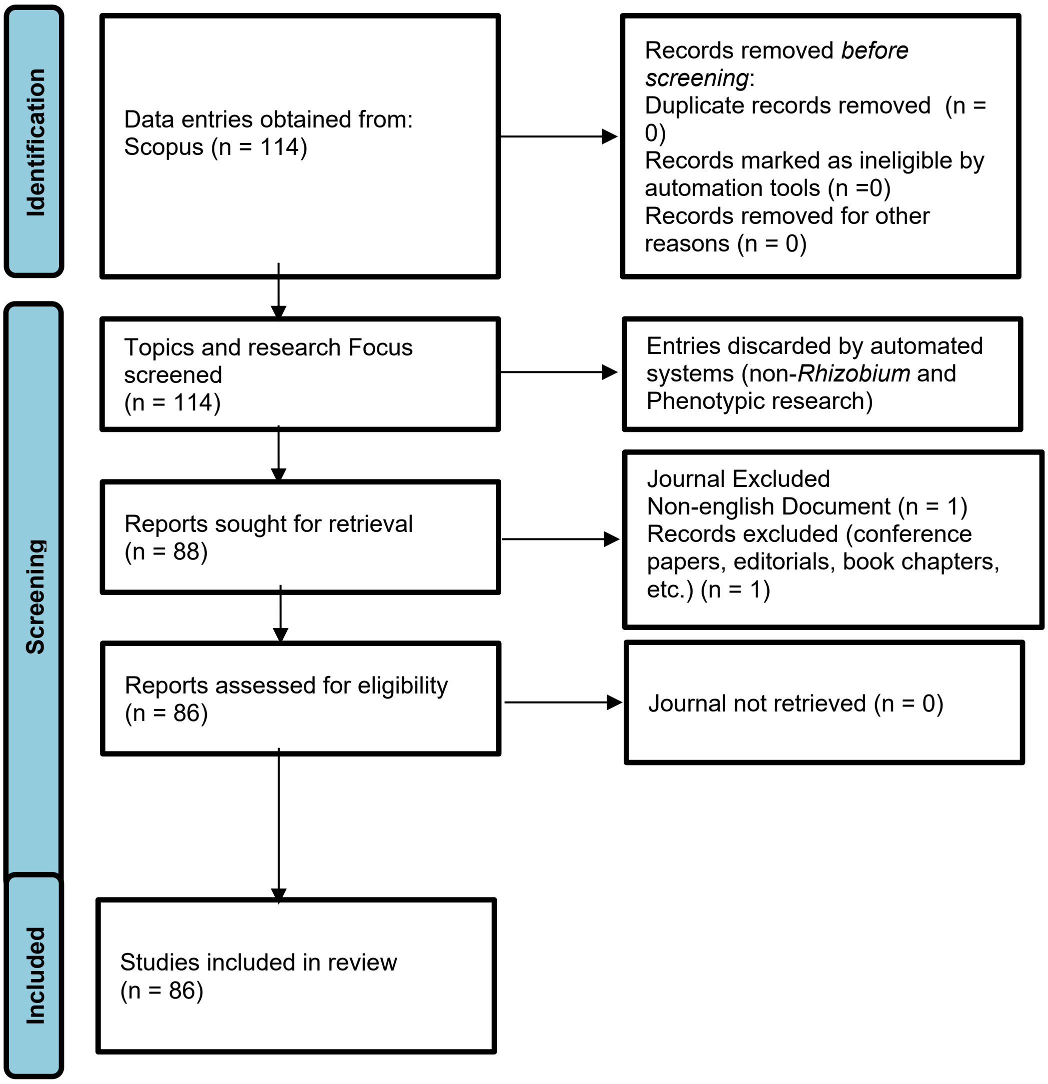

Figure 1. PRISMA Flow Diagram

The PRISMA flow diagram presented in Figure 1 describes the systematic and transparent process used to identify, screen, and select studies included in this review on the genetic variability of *Rhizobium* and its correspondence with plant genotype responses. The review began with the retrieval of 114 articles from Scopus during the identification stage. At this phase, no duplicate entries were found and no records were removed by automated tools, indicating a clean initial dataset. The subsequent screening phase involved examining titles and research focus, which led to the exclusion of studies that did not address *Rhizobium* or phenotypic responses relevant to plant hosts. This step refined the dataset to 88 articles deemed appropriate for retrieval. During the eligibility assessment, two articles were excluded because one was published in a non-English language and the other did not meet the criteria for peer-reviewed journal publications, such as conference papers or book chapters. All remaining articles were successfully retrieved without loss. Ultimately, 86 studies fulfilled the inclusion criteria, which required the presence of molecular or genomic data on *Rhizobium* and measurable responses in host plants. The structured approach illustrated in the PRISMA diagram enhances the methodological rigor of this review and ensures that the final body of literature reflects both relevance and scientific reliability.

RESULTS AND DISCUSSION

Publication Output and Subject Area Distribution

The “Document by Subject Area” in Figure 2 demonstrates a predominant focus on life sciences. Agricultural and Biological Sciences represents the most significant portion of the dataset, accounting for 28.0% of the total output with 46 documents. This is closely followed by Immunology and Microbiology (25.0%, 41 documents) and Biochemistry, Genetics, and Molecular Biology (20.1%, 33 documents). Moderate contributions are observed in Medicine (6.1%, 10 documents) and Environmental Science (4.9%, 8 documents), while the remaining disciplines, including Chemistry, Computer Science, and Multidisciplinary fields, comprise smaller fractions of the overall research landscape.

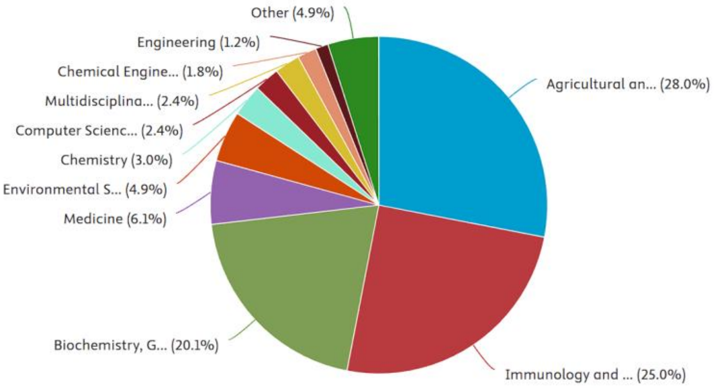

Figure 2. Documents by Subject Area

Author Productivity Analysis

The “Documents by Author” diagram (Figure 3) reveals the leading contributors within the scrutinized research domain. Abdelmoumen, H. emerges as the most prominent author, recording the highest individual output with 3 documents. Following this leading position, the data exhibits a uniform distribution pattern among the subsequent top-tier researchers. Specifically, a cluster of nine authors, including Batstone, R.T., Courty, P.E., El Idrissi, M.M., and others listed demonstrates identical productivity, each contributing 2 documents. This plateau in publication frequency among the top ten authors suggests a balanced research landscape where scientific contribution is shared among multiple key scholars, rather than being heavily monopolized by a single researcher.

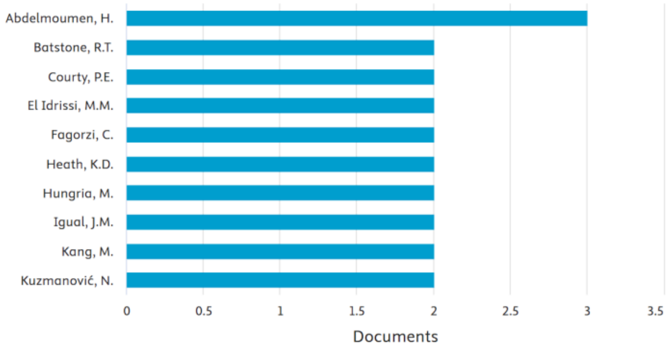

Figure 3. Documents by top 10 Author

Institutional and Affiliation Analysis

The "Documents by Affiliation" visualization (Figure 4) reveals a diverse network of contributors, primarily dominated by specialized research organizations and academic institutions. INRAE occupies the premier position as the most productive affiliate, leading the dataset with 7 documents. Trailing closely is a competitive second tier of contributors, where Faculté des Sciences Rabat, the Consejo Superior de Investigaciones Científicas, and Mohammed V University in Rabat each account for 5 documents, indicating a significant concentration of research output within French, Spanish, and Moroccan spheres. The analysis further highlights a substantial and uniform cohort of institutions sharing the third rank; prominent entities including CNRS, Embrapa, CSIC - IRNASA, the Chinese Academy of Agricultural Sciences, IRD Centre de Montpellier, and CIRAD all recorded an identical output of 4 documents. This distribution underscores a global research landscape with strong participation from national research agencies across Europe, South America, and Asia.

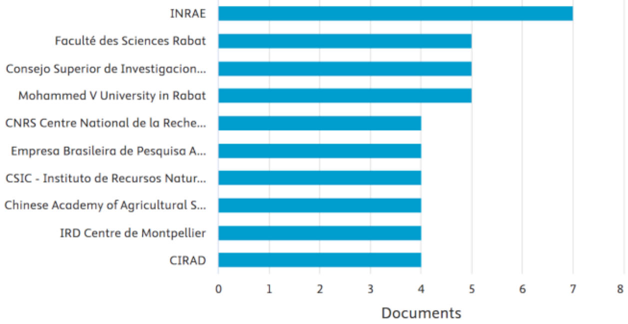

Figure 4. Documents by top 10 Affiliation

Qualitative Analysis of Genetic Variability of Rhizobium and Its Correspondence with Plant Genotype Response

The qualitative analysis of genetic variability in *Rhizobium* and its correspondence with plant genotype response was conducted through a systematic literature review using a structured protocol adapted from the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework, which included the sequential stages of Identification, Screening, Eligibility, and Inclusion to ensure the methodological robustness of the selected studies. This procedure enabled the precise extraction of research that reported molecular variation in *Rhizobium*, including polymorphisms within nod, nif, and fix gene clusters, variation in housekeeping genes, and differences in symbiotic plasmid configurations, along with measurable phenotypic responses of host plants such as nodule formation, nitrogenase activity, shoot and root biomass, and final yield. The combined evidence facilitated a qualitative synthesis that highlights genotype by genotype (G×G) specificity, demonstrating how distinct bacterial genomic features correspond to differential plant performance across various legume genotypes. The consolidated patterns emerging from this synthesis are presented in Table 1, which summarizes the key relationships between *Rhizobium* genetic attributes and host phenotypic responses to provide a coherent interpretation of symbiotic compatibility.

Table 1. Qualitative Analysis of Genetic Variability of *Rhizobium* and Its Correspondence with Plant Genotype Response

No	Theme/Category	Genetic Variability of Rhizobium	Plant Genotype Response	Mechanism/Correspondence	References
1	Bradyrhizobium & Soybean Interaction	High variability is observed in Bradyrhizobium japonicum and B. diazoefficiens strains (e.g., USDA110 vs USDA123). Genetic variation encompasses housekeeping genes, genomic islands, and Type III effector domains (such as Bel2-5) that determine symbiotic efficiency and nodulation competitiveness.	Soybean (Glycine max) cultivars exhibit specific responses to inoculation, where certain plant genotypes (controlled by Rj genes) actively select or restrict specific bacterial strains. Plant response is evident in enhanced nitrogen metabolism, yield, and seed quality when inoculated with compatible strains or through co-inoculation.	Correspondence is mediated through the recognition of specific molecular signals (Nod factors) and the secretion of effector proteins via the bacterial Type III Secretion System (T3SS) which modulates plant immunity. The genetic complexity of nodule occupancy indicates that this interaction is highly selective and influenced by plant growth regulators.	Araya et al. (2023); Chen et al. (2023); Hsouna et al. (2023); Ratu et al. (2021); Tu et al. (2021)
2	Genetic Diversity in Phaseolus (Bean) Symbionts	Remarkable genetic diversity is found in Phaseolus vulgaris symbionts (including Rhizobium etli, R. leguminosarum, R. phaseoli, and new species like R. croatiense).	Common bean genotypes show variation in biological nitrogen fixation (BNF) capability and response to biotic stress (e.g., viruses). Different cultivars	Interaction is driven by root exudates (flavonoids) triggering bacterial nod gene expression. Plant transcription factors regulate nodule development in response to bacterial signals. Bacterial phenotypic plasticity and novel small molecules play crucial roles in adaptation to competitive	Andrade-Domínguez et al. (2021); Ayra et al. (2021); Belousova et al. (2021); Castellano-Hinojosa et al. (2021); Chen et al. (2022); Darrington et al. (2022); Ford et al. (2021); Hug et al. (2021); Kouki

		High phenotypic plasticity and horizontal gene transfer (HGT) on symbiotic plasmids cause extensive variation in acid tolerance and competitive ability between native strains and inoculants.	recruit distinct bacterial communities from the soil, influenced by transcription factors (such as MADS/AGL domains) that control nodule formation and symbiosis.	and acidic rhizosphere environments.	et al. (2022); Mechan-Llontop et al. (2023); Moura et al. (2023); Rajnović et al. (2022); Rodríguez-Navarro et al. (2022); Schumacher et al. (2023); Sofla et al. (2023); Suproniene et al. (2021); Tesfaye et al. (2023); Youseif et al. (2021); van Cauwenberghe et al. (2021)
3	Mesorhizobium & Chickpea Symbiosis	Genomic characterization of Mesorhizobium (e.g., M. ciceri, M. amorphae) reveals phylogenetic diversity linked to geographic adaptation. Variations in symbiotic islands (ICEs) carrying nif and nod genes critically determine symbiotic effectiveness. The presence of strains with variable Type III secretion systems affects host compatibility.	Cicer arietinum genotypes (Desi and Kabuli types) and wild relatives display distinct nodulation responses. Some genotypes are restrictive (accepting only specific strains), while others are promiscuous. Plant response also includes ecological adaptation and biomass enhancement on different soils.	Correspondence is mediated by signaling pathways dependent on Nod factors and T3SS. Bacterial cytoskeletal proteins (MreB, FtsZ) are involved in cell morphology during bacteroid differentiation. Genetic compatibility between plant LysM receptors and bacterial signals is vital for infection initiation in indeterminate nodules.	Basbuga et al. (2021); Chhetri et al. (2021); Fahsi et al. (2021); Fall et al. (2021); Huo et al. (2021); Kawaharada et al. (2021); Kawaka et al. (2022); Khambani et al. (2023); Kuzmanović et al. (2022); Rahi et al. (2021); Rogato et al. (2021); Su et al. (2021); Zaw et al. (2021); Zhao et al. (2021)
4	Symbionts of Acacia & Woody Legumes	Isolates from Acacia, Mimosa, Prosopis, and Sonneratia reveal broad taxonomic diversity (Rhizobium, Paraburkholderia, Allorhizobium). These strains possess stress tolerance genes	Woody legumes show significant growth responses (root and shoot biomass) when inoculated with adaptive native isolates. These plants often possess a broad	Mechanisms involve high flexibility in nod gene regulation and the ability of endophytic bacteria to colonize root tissues. Abiotic stress tolerance at the bacterial level translates into increased host plant survival rates in extreme environments through stable nitrogen supply.	Lebrazi et al. (2023); Li et al. (2021); Li et al. (2023); Ma et al. (2023); Mavima et al. (2021); Protachevicz et al. (2023); Pulido Suarez et al. (2022); Shen et al. (2022); Shen et al. (2022)

		(salt, heat) and capabilities to degrade complex compounds, as well as unique genomic characteristics like in Rhizobium acaciae sp. nov.	host range (promiscuity) to ensure nodulation in forest environments or degraded, nutrient-poor soils.		
5	Rhizobial Tolerance to Abiotic Stress	Genetic variability in stress response genes (e.g., trehalose synthesis, heat shock proteins/HSPs, and hydrocarbon degradation in Acinetobacter). Certain strains (Rhizobium, Pseudomonas, Enterobacter) demonstrate phosphate solubilization and siderophore production capabilities that remain high even under drought, salinity, or soil contamination.	Plant genotypes inoculated with stress-tolerant rhizobacteria show improved physiological stability (chlorophyll content, proline, and water balance). Seedling growth and germination rates increase significantly compared to non-inoculated controls under environmental stress conditions.	Bacteria mitigate plant stress through ACC deaminase enzyme activity (lowering stress-induced ethylene levels) and phytohormone (IAA) production. This enables the plant to maintain root architecture and nutrient uptake despite osmotic pressure or environmental toxicity.	Dwivedi et al. (2023); Hemmerle et al. (2022); Kang et al. (2022); Kuzmanović et al. (2023); Mahnert et al. (2021); Mansour et al. (2023); Pang et al. (2021); Rios-Galicia et al. (2021); Santos-Torres et al. (2021); Silva et al. (2021); Sondo et al. (2023); Taha et al. (2022); Wang et al. (2022); Wang et al. (2023)
6	Sinorhizobium & Medicago Symbiosis	Populations of Sinorhizobium (Ensifer) meliloti and the new genus Fererhizobium exhibit variation in plasmids (pSym) and exopolysaccharide (exo) genes. GWAS (Genome-Wide Association Studies) reveal complex genetic architecture related to symbiotic phenotypes and non-additive	Medicago species (e.g., M. sativa) show strict specificity. Strong Genotype x Genotype (GxG) interactions exist where specific plant genotypes optimize only with specific bacterial genotypes. Plants can "sanction" ineffective nodules by	Correspondence is strictly regulated by molecular signal exchange during infection initiation. Variations in bacterial exopolysaccharides are crucial to avoid host defense responses. Plant genes (like MsSPL9) modulate nodulation based on nutrient status (nitrate), integrating symbiotic signals with plant nutrient status.	Azib et al. (2022); Batstone et al. (2022); Batstone et al. (2022); Borhani et al. (2022); Fagorzi et al. (2021); Missbah El Idrissi et al. (2021); Missbah El Idrissi et al. (2021); Nasrollahi et al. (2023); Romanenko et al. (2023)

		transcriptomic signatures.	reducing resource allocation.		
7	Symbiotic Efficiency & Plant Growth Promotion	Variability in PGPR (Plant Growth Promoting Rhizobacteria) traits such as phosphate solubilization, IAA production, and nitrogen fixation differs across isolates. Some strains (as in Aeschynomene) possess genetically unique Nod-independent symbiotic pathways.	Plant responses include root architecture modification, enhanced nutrient uptake, and nodule lipid polyester synthesis (e.g., in Lotus japonicus) to regulate oxygen permeability. Evolutionary trade-offs exist in symbiosis management to maximize growth.	Bacterial phytohormone production stimulates root cell division. Regulation of oxygen permeation by plant genes (nodule lipid synthesis) is essential to protect bacterial nitrogenase. Compartmentalization strategies allow plants to optimize symbiotic benefits while minimizing metabolic costs.	Chaddad et al. (2023); Da Silva et al. (2022); Mohd-Radzman et al. (2023); Quides et al. (2021); Quilbé et al. (2022); Rehling et al. (2021); Venado et al. (2022)
8	Phylogenetic Diversity & Taxonomy	Application of MLSA (Multilocus Sequence Analysis) and whole-genome sequencing has led to major reclassification and the discovery of new species (Rhizobium populisoli, R. quercicola, etc.) with distinct evolutionary lineages. Proteomic analysis shows protein conservation and divergence across phylogenies.	Accurate taxonomic identification predicts potential host range. Novel species often reveal specific symbiotic capabilities with native or wild plants previously unknown, indicating long-term co-evolution.	Bacterial phylogenetic distance often correlates with symbiotic compatibility. A selective bottleneck occurs during host entry, driving the evolution of new symbionts and ecological niche specialization between bacteria and host plants.	Rajkumari et al. (2022); Shin et al. (2021); de Moura et al. (2023); Łoś-Rycharska et al. (2021)
9	Rhizobia in Vigna & Peanut (Arachis)	Predominance of slow-growing Bradyrhizobium spp. with high genetic diversity in tropical soils, and the discovery of new species like B.	Vigna (Mung bean, Cowpea) and Arachis genera are generally promiscuous (accepting many partners), yet	A "loose specificity" mechanism allows nodulation by diverse soil populations. In Arachis, transcriptomic profiles show that histone deacetylase gene overexpression improves flavonoid/isoflavonoid metabolism, serving as key	Sadiq et al. (2023); Stella et al. (2021); Su et al. (2021); Zhang et al. (2023)

		zhengyangense. Some fast-growing Rhizobium strains are also found to nodulate these hosts.	yield response (pods and seeds) varies significantly depending on strain effectiveness. Inoculation enhances soil nitrogen dynamics and plant productivity.	signals to attract compatible rhizobia.	
10	General Genetic Variability & Host Interaction	Broad studies on drivers of rhizobial genome evolution, polyploidy impacts, and intraspecific competition. Microbiome analysis links plant secondary metabolites to bacterial community structure.	General host responses include regulation of invasion levels and resource competition. Non-symbiotic legumes are found to be more invasive if polyploid, indicating ecological costs and benefits of symbiosis.	Mutualism stability is maintained through partner choice mechanisms and ecological filtering. Plant secondary metabolites act as selection agents shaping rhizosphere microbiome composition, facilitating colonization by beneficial bacteria and inhibiting pathogens.	Parshuram et al. (2023)

Genomic diversity across Rhizobial lineages demonstrates a multilayered evolutionary architecture shaped by variation in housekeeping loci, symbiotic islands, and plasmid-borne nod and nif regions, as extensively shown in studies on Bradyrhizobium, Mesorhizobium, and Sinorhizobium. Comparative analyses reveal how genomic islands and Type III effector repertoires, such as the Bel2-5 domain in Bradyrhizobium japonicum (Araya et al., 2023; Chen et al., 2023), together with plasmid restructuring in Ensifer meliloti (Batstone et al., 2022), drive diversification in nodulation competitiveness, environmental tolerance, and nitrogen fixation efficiency. The emergence of new taxa, including Rhizobium populisoli and R. quercicola (Shin et al., 2021), underscores that genomic modularity functions as a dominant evolutionary mechanism generating novel symbiotic phenotypes. These findings collectively indicate that horizontal gene transfer, mobile symbiotic elements, and ecological filtering maintain a dynamic genomic landscape that directly influences symbiotic potential.

Plant genotypes exhibit differential responsiveness to specific Rhizobium strains, demonstrating that host genetic architecture actively modulates partner compatibility. Rj-controlled selectivity in soybean cultivars determines whether strains such as USDA110 or USDA123 become effective nodule occupants (Tu et al., 2021; Hsouna et al., 2023), while Medicago genotypes enforce strict compatibility windows shaped by immune recognition receptors and nutrient sensing pathways (Azib et al., 2022). In chickpea, distinct responses of Desi and

Kabuli types to Mesorhizobium ciceri and M. amorphae reflect the importance of host receptor variation for infection efficiency (Basbuga et al., 2021; Huo et al., 2021). Even in more promiscuous hosts such as Vigna and Arachis, genotype specific yield improvements still depend on strain-level traits, including flavonoid-responsive nod gene activation and stress tolerance mechanisms (Sadiq et al., 2023; Zhang et al., 2023). These patterns highlight that plant responsiveness emerges through the integration of molecular perception pathways, transcriptional regulators of nodulation, and the biochemical environment of the rhizosphere.

Genotype × genotype specificity consistently appears across systems but varies in its ecological intensity and biological constraints. Highly specialized symbioses, including Sinorhizobium–Medicago and Bradyrhizobium–soybean, display strong G×G structuring driven by Nod factor chemistry, exopolysaccharide signatures, and Type III secretion system effectors that fine-tune plant immune responses (Batstone et al., 2022; Araya et al., 2023). In contrast, systems involving Phaseolus or woody legumes show more flexible yet still detectable G×G effects mediated by strain competition, phenotypic plasticity, and soil microbial background (Andrade-Domínguez et al., 2021; Lebrazi et al., 2023). Environmental factors such as acidity, drought, and salinity amplify or suppress specificity, particularly when stress-tolerant rhizobia influence plant physiology through ACC deaminase and auxin production (Dwivedi et al., 2023; Mansour et al., 2023). Despite methodological heterogeneity across studies, a central pattern emerges: symbiotic performance reflects the hierarchical interaction between microbial genomic variation, plant immune and developmental pathways, and local ecological pressures.

Synthesizing these insights, the review constructs a conceptual framework linking molecular variation to phenotypic performance with implications for sustainable agriculture and genotype-matched inoculant development. This framework conceptualizes the symbiosis as an emergent system in which microbial genomic modules such as symbiotic plasmids, T3SS clusters, and stress response genes interact with plant regulatory networks controlling recognition, nodule morphogenesis, and nutrient allocation. Integrating findings from Bradyrhizobium–soybean, Mesorhizobium–chickpea, Sinorhizobium–Medicago, and Phaseolus symbioses demonstrates that aligning specific microbial traits with plant genotypes enhances nitrogen fixation reliability, ecological resilience, and yield stability. Consequently, molecular breeding strategies can incorporate symbiosis-related alleles, while inoculant formulation can prioritize strains validated through G×G-based compatibility assays (Fagorzi et al., 2021; Mechan-Llontop et al., 2023). The resulting framework provides a biologically grounded route for designing next-generation microbial inputs optimized for specific host genotypes and agroecosystems.

CONCLUSION

The synthesis of current evidence demonstrates that genomic variability across Rhizobium lineages, coupled with plant genotype-specific responsiveness, forms a highly dynamic and selective symbiotic system in which molecular signals, effector repertoires, and host regulatory pathways collectively determine nitrogen fixation efficiency, ecological adaptability, and agronomic performance. The consistent yet context-dependent patterns of genotype × genotype specificity underscore that achieving optimal symbiotic outcomes requires aligning microbial genomic traits with host genetic architecture, particularly in systems such as Bradyrhizobium–soybean, Mesorhizobium–chickpea, and Sinorhizobium–Medicago. These findings suggest the need for developing genotype-matched microbial inoculants, integrating symbiosis-relevant alleles into plant breeding pipelines, and employing molecular screening tools to evaluate strain compatibility under variable environmental pressures. Taken together, this review reinforces that leveraging molecular diversity for sustainable agriculture requires a coordinated strategy combining genomic characterization, host genotype profiling, and ecological validation to enhance the reliability and scalability of biological nitrogen fixation across crop systems.

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