Microbial inoculants for soil restoration: A Practical Framework for Risk-Governed stewardship

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Abstract

Global soil degradation and increasing reliance on chemical inputs threaten agricultural sustainability, driving interest in microbial inoculants as tools for soil restoration. These biological products have the potential to enhance nutrient cycling, improve soil structure, and support plant resilience, but their environmental release raises important safety and stewardship considerations. Here, we propose a risk-proportional framework for the responsible deployment of microbial inoculants grounded in release-based stewardship. The framework integrates genome-resolved strain identification, exclusionary hazard screening, bioassay-based risk triage, ecological testing under realistic conditions, and monitored field deployment. Drawing on evidence from microbial ecology and invasion biology, we highlight how inoculants can alter resident microbial communities, influence ecosystem function, and, in some cases, facilitate gene flow, underscoring the need for context-dependent risk assessment. We further outline a federated, genome-informed data infrastructure to support traceability, cross-jurisdiction learning, and adaptive management. Together, this approach provides a scalable and scientifically grounded pathway to balance innovation and safety, enabling microbial technologies to contribute to soil restoration and climate-resilient agriculture.

Sustainability Statement

This work primarily supports SDG 15: Life on Land by advancing a risk-governed framework for the responsible use of microbial inoculants in soil restoration. The approach is designed to help recover degraded soils, protect ecosystem functions, and support biodiversity by integrating genomic screening, ecological testing, and post-release monitoring. By enabling safer adoption of biological alternatives to intensive chemical inputs, the framework may contribute to more sustainable land stewardship and regenerative agriculture. Additional relevant SDGs: SDG 2 (Zero Hunger) and SDG 13 (Climate Action).

1. A New Paradigm for Risk Assessment in Soil Restoration

The degradation of global soil systems has reached a critical point. Conventional management practices, characterized by heavy chemical fertilization and intensive tilling, have disrupted natural microbial processes and degraded soil structure (Albright et al., 2022). Projections suggest that without intervention, global topsoil may be largely lost by 2050 (Kaminsky et al., 2019). This urgency is driving rapid interest in microbial inoculants as a tool that may contribute to soil restoration efforts.

Continued reliance on intensive chemical inputs carries well-documented cumulative risks including, soil acidification, nutrient runoff and eutrophication, and suppression of beneficial soil microbiota and meiofauna, that are difficult to reverse (Li et al., 2024; Baquero et al., 2013). Microbial inoculants offer an alternative strategy. By introducing living, soil-associated organisms (typically not genetically modified), microbial inoculants have the potential to restore or reinforce core biological functions such as nutrient cycling, root-microbe interactions, and soil aggregation (Santos et al., 2019; Mawarda et al., 2020; Albright et al., 2022).

However, the intentional release of living organisms into complex ecosystems raises legitimate safety and stewardship questions. Past biological introductions (intentional or not) have caused substantial ecological harm, e.g., the spread of the chytrid fungus *Batrachochytrium dendrobatidis*, which decimated amphibian populations worldwide (Schulz et al., 2019), as well as numerous non-microbial examples where biocontrol measures have failed (Schulz et al., 2019). These precedents underscore that microbial technologies cannot be assumed to be risk-free and require rigorous, context-appropriate oversight. In 1975, the landmark Asilomar Conference established a precedent for managing biological risk (Berg, 2008). That framework was developed in response to the containment of recombinant DNA. Fifty years later, the 2025 "Spirit of Asilomar" summit recognized that many emerging biological applications, including microbial soil amendments (Beattie et al., 2025; Marken, 2025), are intended for open environmental deployment and therefore require an expanded safety toolkit. While the more recent summit continued to emphasize containment-based biosafety, it also addressed the release pathogens or GMOs, with what we term release-based stewardship (Chemla et al., 2025).

Release-based stewardship treats environmental release of beneficial microorganisms as the operational context for certain biological technologies and strives to ensure safety through strain-resolved genomic screening, ecological testing, confined and traceable field evaluation, and post-release monitoring. This is not a move away from containment-based biosafety, rather, it extends traditional containment and pre-release controls with open-system stewardship practices, strain-resolved screening, confined/traceable field evaluation, and post-release monitoring that is appropriate for the environmental deployment of beneficial microorganisms.

However, implementing such a risk-proportional approach is complicated by the present regulatory landscape. Oversight of microbial inoculants is fragmented across agricultural, environmental, and public health authorities, resulting in widely varying requirements across

jurisdictions and countries. This fragmentation can lead to duplicate testing, limited data portability, and slower evidence accumulation. We therefore propose a unified, genome-informed risk assessment and monitoring framework designed to support rigorous yet scalable stewardship of microbial inoculants for soil restoration. Achieving this in practice will also require policy alignment and standards-setting to enable data portability, reduce redundant testing, and support cross-jurisdiction reciprocity.

While parallel discussions in the field are examining broader governance models and policy gaps for environmental release of microbial technologies (Kaminsky et al., 2019) this perspective takes a complementary approach. Rather than focusing primarily on regulatory theory, we present a practical, implementation-oriented framework grounded in strain-resolved genomics, ecological testing, and field-level stewardship. Our goal is to translate ecological and regulatory principles into actionable guidance for developers, regulators, and practitioners working at the interface of research and real-world deployment.

2. Inoculant Impacts and Ecological Constraints

Microbial inoculants can alter the composition and function of recipient soil communities, sometimes beneficially, often transiently, and in some cases with effects that persist beyond the intended window of application (Zhang et al., 2026; Zhang et al., 2025; Mawarda et al., 2020; Li et al., 2024; Francioli et al., 2025; Wang et al., 2021; Papin et al., 2024; Baquero et al., 2013). At the same time, many soils exhibit strong biotic resistance, where established microbial communities limit invasion and constrain long-term establishment of introduced strains, particularly in healthy, undisturbed systems, where high microbial diversity hinders potential impacts (Van Elsas et al., 2012; Ye et al., 2025; Timmis et al., 2025; Klümper et al., 2024).

Together, these observations indicate that measurable shifts in the composition or function of soil microbial communities can occur even when inoculant persistence is limited. Recognizing this distinction is central to responsible stewardship because it underscores the need to evaluate both short-term functional outcomes and potential longer-term ecological effects when assessing inoculant performance and risk (Mallon et al., 2018).

2.1 Inoculants Reshape Microbial Community Composition and Genetic Diversity

The deliberate introduction of microbial inoculants frequently alters resident soil microbial communities. In a meta-analysis of 108 studies (Mawarda et al., 2020), 86% showed that inoculants modified the composition of resident microbial communities. Sometimes these shifts appeared to be beneficial. For instance, application of a biofertilizer containing *Bacillus amyloliquefaciens* W19 and *Trichoderma guizhouense* NJAU4742 increased the abundance of taxa with potential antagonistic activity toward plant pathogens (Xiong et al., 2017). Other times, potentially less desirable effects were noted. For instance, the release of *Sinorhizobium meliloti* L33 into the rhizosphere reduced the diversity of beneficial *Pseudomonas* species (Schwieger & Tebbe, 2000).

Beyond compositional changes, inoculants can influence the genetic structure of resident microbial populations through horizontal gene transfer (HGT). Because HGT is a well-known route for the dissemination of antimicrobial resistance and other high-consequence traits, it is appropriately viewed as a potential risk mechanism and warrants explicit, strain-resolved scrutiny. For example, repeated large-scale inoculation of soybean with commercial *Bradyrhizobium* strains in Brazil resulted in extensive horizontal transfer of symbiotic genes to resident rhizobia (Barcellos et al., 2007; Batista et al., 2007; Hungria & Mendes, 2015). These observations show that inoculants can act as vectors of functional trait movement, sometimes beneficial (e.g., spreading symbiotic capacity), but potentially harmful if mobile elements carry antimicrobial resistance, toxin, or virulence-associated loci. Accordingly, HGT risk should be treated as feature-

and context-dependent: prioritized for strains with mobility-associated machinery or flagged loci during genome screening and verified through targeted field monitoring in pre-market trials.

In many cases, shifts in community composition translate into measurable changes in soil functioning. Across multiple studies, inoculation was found to increase activities of phosphatase, sulfatase, chitinase, esterase, urease, and other enzymes thus favorably impacting nutrient cycling, fertilization, decomposition, and biocontrol (Mar Vázquez et al., 2000; Wu et al., 2005). For example, in one study, the introduction of *Paenibacillus mucilaginosus* 3016 was correlated with increased soil phosphatase enzyme activity (Ma et al., 2018), which resulted in increased phosphate mobility and availability for plant growth. In other studies, inoculation was associated with the emergence of disease-suppressive soils (Shen et al., 2015; Xiong et al., 2017), even if the inoculant does not survive or drops below levels of detection (Deng et al., 2021), underscoring the potential for inoculants to steer functional outcomes by driving microbial community reassembly through secondary succession.

2.2 Constraints on Inoculant Persistence

While inoculants can initially reach elevated abundances following application, their relative abundance in soil microbial communities typically declines over time and often stabilizes at low levels (<1% of the total community) within weeks (Čaušević et al., 2024). Because most soil taxa naturally occur at low relative abundance, this pattern suggests that introduced strains may integrate into existing microbial communities rather than persist as dominant members capable of broadly restructuring community composition. Functional influence may still occur at low abundance through metabolic interactions, resource competition, or signaling. Under a release-based stewardship model, these ecological pressures are not merely hurdles to efficacy, but also inherent constraints that can limit long-term establishment. However, biotic resistance and post-application decline cannot be relied upon as safety controls on their own; they are context-dependent and must be verified empirically within the broader risk framework described below.

A variety of mechanisms appear to restrict inoculant persistence. Generally, inoculants are unlikely to be locally adapted to the soils into which they are introduced. Resident microbiota can produce antibiotics or toxic compounds that can inhibit newcomers (Berg, 2008). Inoculants may also be susceptible to predation, such as grazing by protists and nematodes and lysis by phages (Dong et al., 2024). Further, resident microorganisms will already occupy many of the available functional niches, making it difficult for newcomers to find a foothold (Dong et al., 2024; Marken, 2025).

Importantly for unintended spread risk, inoculant establishment is strongly context dependent. Consistent with invasion ecology, disturbed soils (e.g. tilled or otherwise degraded systems) may offer reduced biotic resistance and increased niche opportunity, facilitating establishment during restoration (Hibbing et al., 2010; Beattie et al., 2025). In a field setting, the fumigation of diseased soils prior to introduction of organic fertilizers enriched with Bacillus strains led to the development of disease suppressive soils (Deng et al., 2021). In contrast, intact, less disturbed soils may be more resistant due to habitat filtering and resident community constraints (Deng et al., 2021; Klümper et al., 2024; Cheng et al., 2024); these expectations should be verified empirically within the monitoring framework.

2.3 Legacy Effects

While inoculant persistence is often limited over the longer term, an important finding for risk assessment is that inoculation-induced effects on community composition often persist even after the strains decline to low abundance or become undetectable. Numerous studies have reported lasting shifts in resident communities despite rapid decreases in inoculant population size (Kozdrój et al., 2004; Mallon et al., 2018). In a field study using luciferase-tagged *Sinorhizobium meliloti* L33, the inoculant was detected in adjacent non-inoculated plots following release, and

rhizosphere community composition shifted, with reductions in *Acinetobacter calcoaceticus* and *Pseudomonas* spp. and enrichment of rhizobia, interpreted as a replacement of generalist taxa by specialists (Schwieger & Tebbe, 2000). These findings showcases that microbial inoculants can disperse into other sites as well as reorganize resident soil microbiomes in ways that may underpin not only desired outcomes (e.g., improved nutrient cycling or disease suppression) but also unintended consequences (e.g., altered diversity or gene flow), underscoring the need to evaluate community-level responses in risk assessment.

3. Risk Assessment: A Multi-Tiered Framework for Safety

Figure 1 summarizes the proposed risk-proportional release-based stewardship framework as two sequential phases: (I) pre-release risk screening, comprising genome-resolved strain identification and hazard/bioassay triage, and (II) environmental stewardship, comprising ecological testing and monitored field deployment. The sections below follow this structure and outline how each component can be implemented in practice.

A proactive safety framework is non-negotiable for the rapidly expanding bioinoculant sector (now estimated at ~1,000–1,200 companies globally). Moving beyond the "containment-based" limits of 1975, we propose a framework that treats risk not as inherent to the category, but as strain- and context-dependent. A practical framework must therefore distinguish (i) immediate biosafety risks (pathogenicity/toxicity) from (ii) long-term ecological risks (establishment, spread, and impact), and it must do so with strain-resolved genomics and standardized, scalable testing. A prerequisite to the Proposed Release-based Stewardship Framework is that the bioinoculant actually contains the microbial species stated by the manufacturer, and without the presence of other non-disclosed microorganisms or other plant growth enhancing products such as fertilizers. For example, the arbuscular mycorrhizal fungal (AMF) inoculum industry represents an almost annual 1 billion US$ market. Of the AMF products commercially available, many do not contain the fungal species stated by the manufacturer and most are produced in non-sterile substrate that

contains an undefined microbiome composed of other diverse bacterial and fungal species (Vahter et al., 2023; Koziol et al., 2025; Boussageon et al., 2025). There is clearly a need for strict product quality control of commercial products before further risk assessment steps are undertaken.

The stewardship framework presented in Figure 1 follows four sequential components: (1) genome-resolved strain identification, (2) bioassay-based risk triage, (3) ecological testing under realistic conditions, and (4) monitored field deployment. The sections below describe the implementation of each component.

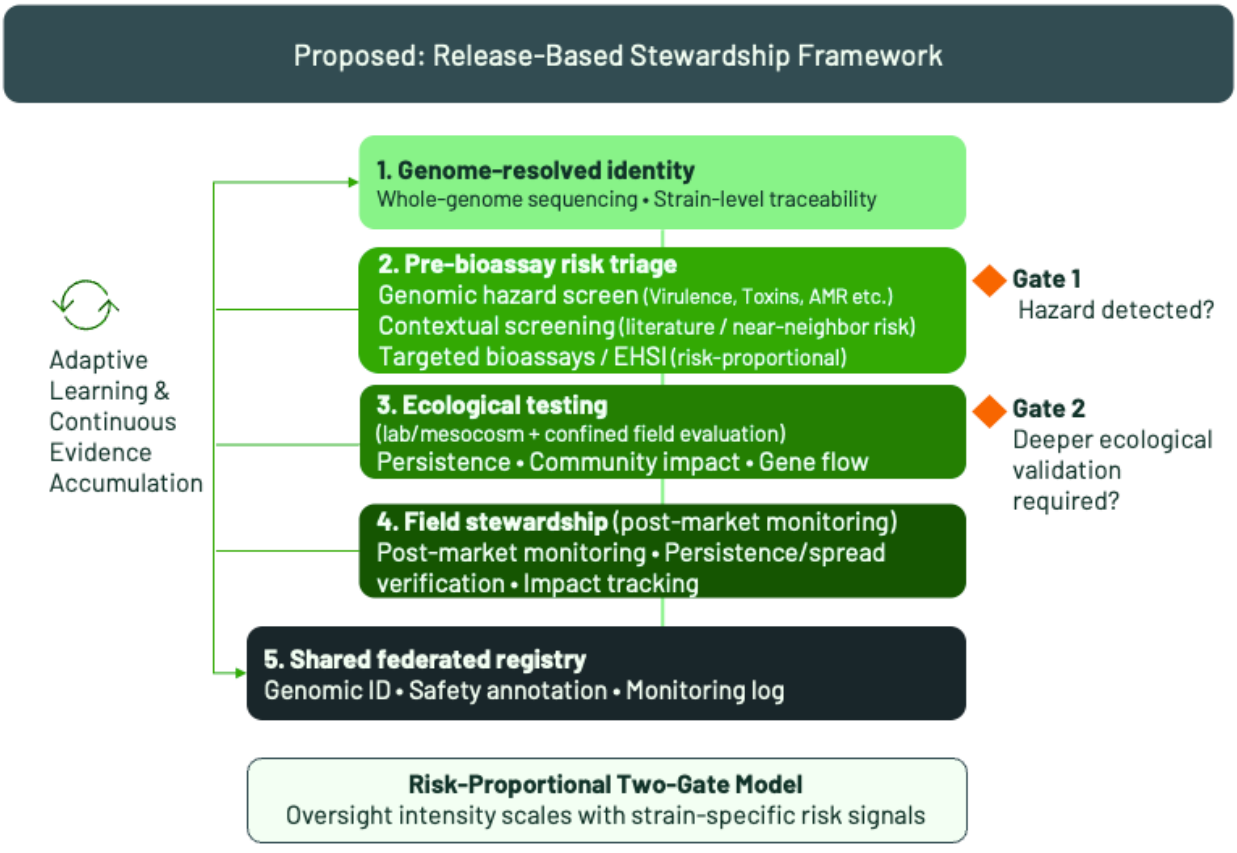

Figure 1. Risk-proportional release-based stewardship framework for microbial inoculants. The proposed framework integrates genome-resolved strain identification, exclusionary hazard

screening, ecological testing, and monitored field stewardship within a structured, risk-proportional decision pathway. Candidate strains first undergo whole-genome–based identity confirmation and exclusionary screening for virulence factors, toxins, antimicrobial resistance (AMR), and mobility-associated elements (Gate 1). Strains that pass this stage proceed to contextual ecological evaluation and monitored field trials to assess establishment, community impacts, and gene-flow risk (Gate 2). Oversight intensity scales with strain-specific risk signals rather than taxonomic category alone. A federated global registry links genomic identifiers, safety annotations, ecological performance, and regulatory outcomes to enable traceability, cross-jurisdiction learning, and adaptive stewardship over time.

3.1 Pre-release risk screening: genome identity and hazard/bioassay triage (Steps 1–2, Figure 1)

The most consequential failure mode for the entire field would be an inoculant linked to disease in crops, livestock, wildlife, and humans. Even rare events would disproportionately damage public trust and regulatory confidence. Immediate-risk assessment should therefore begin with exclusionary screening - a set of criteria that, if triggered, disqualifies a candidate strain regardless of efficacy.

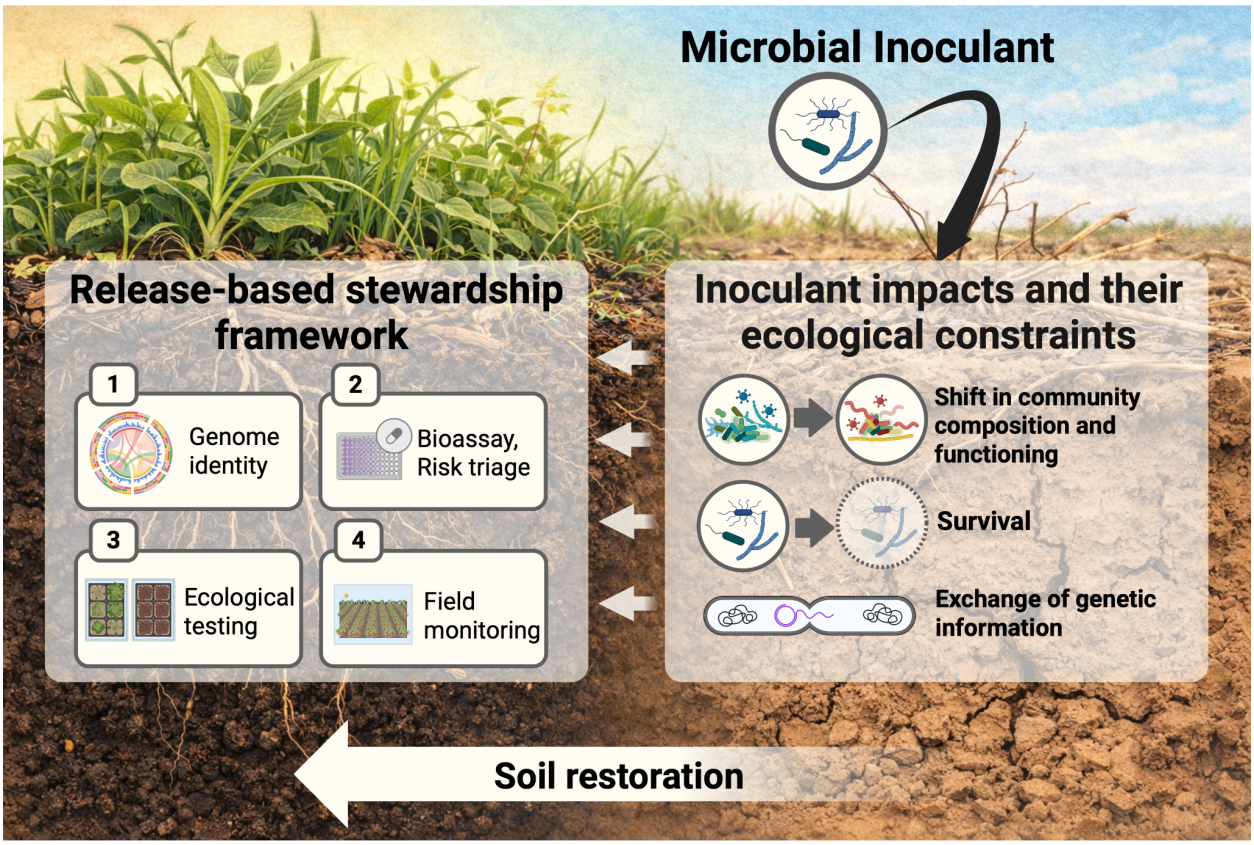

Figure 2. Release-based stewardship framework for microbial inoculants in soil restoration. Microbial inoculants can influence soil ecosystems through shifts in community composition and function, survival of introduced strains, and exchange of genetic information with resident microbiota. We propose a risk-proportional release-based stewardship framework to guide responsible environmental deployment, integrating four steps: (1) genome-resolved strain identification and hazard screening, (2) bioassay-based risk triage, (3) ecological testing under realistic conditions, and (4) monitored field deployment. Together, these components link ecological risk assessment with practical oversight to support safe and effective use of microbial inoculants in soil restoration.

An important consideration is whether risks that appear negligible when strains are evaluated individually could emerge when multiple strains are combined in a consortium. In principle,

245 microbial interactions can generate emergent behaviors through metabolic cross-feeding,
246 signaling interactions, or horizontal gene transfer. However, high-consequence hazard traits such
247 as virulence factors, toxin production, and clinically relevant antimicrobial resistance are
248 overwhelmingly strain-encoded and therefore detectable through genome-resolved screening. As
249 a result, exclusionary genomic and bioassay gates substantially reduce the likelihood that
250 hazardous phenotypes would arise de novo through strain combination alone.

251 Nevertheless, because ecological interactions can influence persistence, abundance, and
252 functional expression, the framework explicitly incorporates consortia-level ecological testing and
253 monitored field evaluation (Section 3.2) to verify that no unintended community-level or functional
254 risks emerge under realistic conditions. Empirical evidence suggests that the coalescence of
255 microbial communities follows similar patterns as those observed for individual strains, being
256 constrained by competition with the native microbiome and limited survival (Liu and Salles, 2024a
257 and b). Below we discuss the important steps to design stewardship framework for microbial
258 inoculants.

259 <u>Step 1: Strain-resolved identity and placement relative to high-concern clades (beyond 16S, 18S</u>
260 <u>and ITS).</u>
261 Whole-genome sequencing (WGS) should be treated as the baseline for commercial candidate
262 strains because conserved marker sequencing (e.g., 16S or 18S rRNA and ITS) often cannot
263 resolve within-species lineages that differ in hazard potential. WGS also provides the resolution
264 needed to identify genetic features relevant to both beneficial function and potential risk. The
265 purpose of Step 1 is to establish strain-resolved identity and near-neighbor placement relative to
266 known pathogenic or regulated clades. Raw or assembled DNA sequence reads should be
267 assigned to candidate taxa using curated genomic reference databases, and confirmed by
268 genome-to-genome comparisons using Average Nucleotide Identity (ANI; e.g., ≥95% as a
269 common species-level benchmark) (Konstantinidis and Tiedje, 2005) with higher-resolution

thresholds or complementary analyses applied when close relatives or regulated taxa require finer discrimination. Lineage-aware tools (Zhang et al., 2026) can further support strain-group classification in clades containing known hazards. Importantly, phylogenetic distance from recognized pathogenic clades should not be interpreted as evidence of safety on its own, because strains that are distantly related to known pathogens may still encode virulence-associated, toxigenic, antimicrobial-resistance, or mobility-linked traits that warrant concern and are therefore evaluated explicitly in subsequent screening steps.

Step 2: Evidence-based contextual screening to interpret Step 1 and triage downstream testing.

Step 2 is distinct from genomic feature screening (Steps 3–4): it is a targeted literature and evidence review conducted after identity is established to determine what is already known about the candidate taxon/strain group (and close relatives) with respect to disease associations, opportunistic pathogenicity, toxin production, antimicrobial resistance history, or high-risk ecological behaviors. This context is not sufficient alone to establish safety, but it informs how Step 1 placement should be interpreted (e.g., whether a clade has documented pathogenic members) and helps triage the depth of downstream genomic scrutiny and bioassays.

Step 3: Genome-informed virulence screening.

Candidate genomes should be screened against curated virulence databases such as the Virulence Factor Database (VFDB) (Zhang et al., 2023) and secretion-system resources such as SecReT6 (Li et al., 2016) and against curated antimicrobial-resistance gene databases (e.g., CARD, ResFinder, or AMRFinderPlus) (Jia et al., 2017; Bortolaia et al., 2020). This step functions independently of phylogenetic proximity to known pathogens: even strains that are distantly related to recognized pathogenic clades may still carry virulence-associated, toxigenic, resistance, or mobility-linked features that justify flagging the candidate as a strain of concern for deployment. In this way, genome-informed screening complements taxonomic placement by ensuring that trait-based hazards are not overlooked simply because a candidate falls outside a known high-risk lineage.

Step 4: Horizontal gene transfer (HGT) and mobility assessment.

Because virulence and antimicrobial resistance traits can be acquired and disseminated through mobile genetic elements, candidate genomes should be screened for mobility-linked hazard potential **(**not merely evidence of historical HGT) (Partridge et al., 2018) Specifically, screening should (i) identify plasmids, integrative conjugative elements, transposons, integrons, and prophages, (ii) assess whether these elements carry clinically or agriculturally relevant resistance genes, virulence factors, toxin genes, or secretion-system islands, and (iii) evaluate evidence for recent or active mobility (e.g., intact conjugation machinery, relaxases/oriT, transposition modules, or clustered resistance cassettes). Candidates with mobile elements carrying high-consequence traits should be excluded or subjected to heightened scrutiny, whereas genomes with mobile elements lacking such traits may proceed with documentation and appropriate monitoring. This step is especially important for taxa known to exchange pathogenicity islands or rapidly acquire resistance under selection.

Step 5: Environmental and Human Safety Index (EHSI).

Genomics can identify hazard potential, but bioassays are needed to evaluate organism-level effects under realistic exposure conditions. A pragmatic approach is to integrate results from existing standardized ecotoxicology and biosafety assays (e.g., impacts on representative soil fauna, beneficial insects, aquatic proxies, non-target plants, and small mammals) into a composite interpretive framework such as the Environmental and Human Safety Index (EHSI) (Zhang et al., 2023; Mawarda et al., 2020). Importantly, this does not propose a new universal testing battery; rather, it provides a structured way to synthesize outcomes from assays that are already widely used in microbial biopesticide and biostimulant evaluation (e.g., OECD/EPA guideline tests). Under a risk-proportional model, only the subset of assays relevant to the candidate strain, use pattern, and exposure pathway would be required. The resulting index provides an interpretable “go/no-go” gate aligned with emerging biostimulant regulatory philosophies while remaining feasible for large-scale screening.

3.2 Environmental stewardship: ecological testing and monitored field deployment (Steps 3–4, Figure 1)

> *Decision rule:* Candidate strains must pass both exclusionary genomic/bioassay screening (Section 3.1) and structured ecological field evaluation before commercial release.

Even when acute biosafety risks are excluded, there is still a potential for undesirable ecological consequences. This includes the possibility that interaction effects within multi-strain consortia could alter persistence, functional expression, or ecological impact relative to single-strain behavior, and therefore warrants explicit evaluation under field-realistic conditions. One would adopt an invasion-ecology framework in which risk is conceptualized as a progression: introduction → establishment → spread → impact (Mallon et al., 2015). Field stewardship must therefore critically evaluate each stage empirically.

In this context, impact refers specifically to unintended ecological disruption, not intended agronomic or restoration benefits. While beneficial impacts (e.g., yield increase, improved soil aggregation, enhanced nutrient use efficiency) are often desired outcomes, ecological risk assessment focuses on detecting adverse consequences such as displacement or suppression of native beneficial taxa, persistent dominance beyond expected functional windows, altered nutrient-cycling trajectories (e.g., excess N mineralization or immobilization), destabilization of disease-suppressive communities, horizontal transfer of high-consequence traits, off-site movement into non-target habitats. Distinguishing intended functional outcomes from unintended ecological disruption is central to responsible deployment. This includes the possibility that interaction effects within multi-strain consortia could alter persistence, functional expression, or ecological impact relative to single-strain behavior, and therefore warrants explicit evaluation under field-realistic conditions.

3.2.1 Ecological Testing (confined but realistic)

Prior to commercial authorization or broad agricultural deployment, we recommend that pre-market field trials should be conducted under realistic agronomic conditions while remaining geographically and operationally bounded to allow traceability and monitoring. “Contained” in this context does not imply physical enclosure, but rather controlled deployment within defined spatial and management parameters, as well as the monitoring of non-target functions and microbiomes to infer potential undesired impacts. This includes plot-level application, spatial separation from sensitive habitats where appropriate, strain-resolved traceability, and a predefined monitoring window aligned with the intended functional duration of the inoculant.

These trials should evaluate both intended agronomic performance and potential ecological risk indicators. Monitoring should be structured around four core domains as follows (Figure 3):

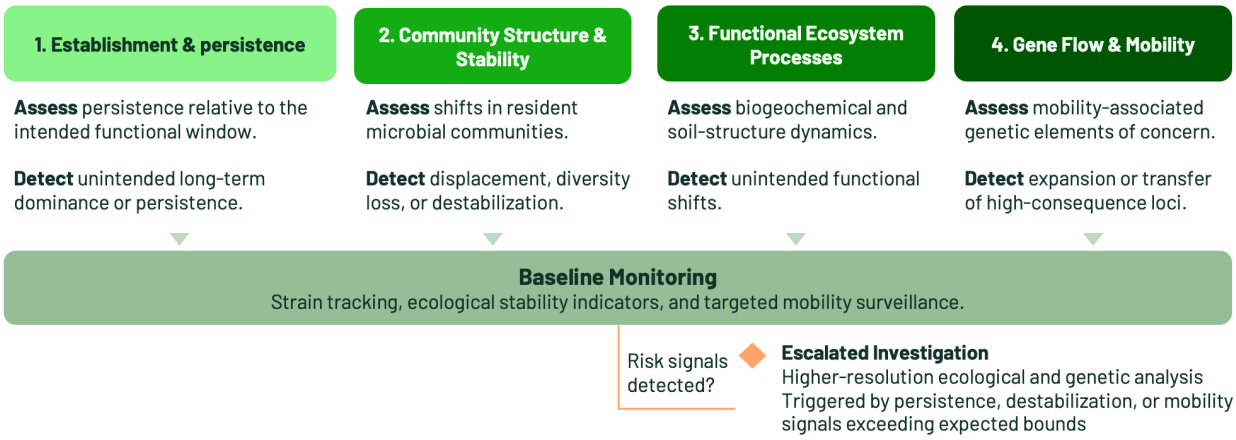

Figure 3. Conceptual framework for tiered environmental monitoring of microbial inoculants after field release. Monitoring is organized into four domains: establishment and persistence of inoculant strains, community structure and stability of resident microbiomes, functional ecosystem processes, and gene flow and mobility. Baseline monitoring includes strain tracking, ecological stability indicators, and targeted surveillance of mobility-associated loci. Detection of persistence, destabilization, or mobility signals beyond expected bounds triggers

escalated investigation using higher-resolution ecological and genetic analyses. This risk-proportional approach is designed to provide scientifically defensible and operationally feasible monitoring aligned with genomic features, deployment context, and product claims.

1. Establishment and Persistence.

Inoculant strain-resolved detection (e.g., strain-specific qPCR or genome-resolved omics) should be used to confirm establishment and track abundance over time. Monitoring should assess whether persistence aligns with the intended functional window and whether unexpected long-term dominance occurs. This domain represents the recommended baseline for all monitored releases. Conceptually, introduced inoculants can be viewed as ecological invaders entering an established microbial community, where success depends on overcoming sequential filters such as colonization, competition with resident taxa, and environmental constraints. Tracking population trajectories of introduced strains over time therefore provides critical information on invasion success, persistence dynamics, and ecological integration within the resident microbiome (McMullen & Lennon, 2023).

2. Community Structure and Stability.

Community profiling using marker-gene sequencing or other microbiome-resolved methods should be used to assess shifts in resident microbial communities, including potential changes in the relative abundance or occurrence of native taxa following inoculant application ?". Diversity metrics, indicators of community stability, and evidence for changes in the presence or relative abundance of taxa with putative key ecological roles can provide early signals of unintended ecological disruption. This domain is particularly informative when the risk of community perturbation is plausible, such as under repeated applications, in sensitive ecosystems, or when novel taxa are introduced, and in cases where product claims depend on microbiome restructuring.

3. Functional Ecosystem Processes.

Trials should evaluate key biogeochemical and soil-structure indicators, such as soil respiration and carbon flux, nitrogen cycling dynamics (e.g., nitrification or denitrification potential), soil aggregate stability, and pathogen suppression capacity. These measurements help distinguish beneficial functional shifts from unintended trajectory changes. This domain is most relevant where claims depend on biogeochemical outcomes or where functional assurance is required by regulators or stakeholders.

4. Gene Flow and Mobility

Gene-flow surveillance is most relevant for candidate strains that (i) encode plasmids, integrative elements, or other mobility-associated machinery; (ii) contain resistance-, toxin-, or virulence-associated loci of regulatory concern; (iii) belong to taxa with documented horizontal gene transfer activity; or (iv) are intended for repeated or large-scale environmental deployment. Candidate strains should first undergo genome-level screening for mobile genetic elements, resistance loci, virulence factors, and associated transfer machinery (Section 3.1). Field surveillance then verifies that these elements do not expand, mobilize, or appear in new hosts under agronomic conditions.

Recognizing the practical constraints of field-based monitoring, implementing all domains at high resolution for every strain and deployment would rarely be proportionate in agronomic settings. We therefore emphasize a tiered, risk-proportional approach in which a minimum baseline is applied broadly and additional monitoring components are triggered by genomic features, deployment context, or claim requirements. The goal is not exhaustive environmental characterization, but decision-relevant monitoring that is scientifically defensible and operationally feasible.

At minimum, trials should include strain-resolved tracking of the inoculant (e.g., strain-specific qPCR/ddPCR or metagenomic read-mapping) together with a targeted mobility watchlist (e.g., integron markers such as intI1, mobility-associated loci, and any resistance or virulence genes flagged during genome screening). If genomic features or field signals indicate elevated concern,

such as mobile elements carrying high-consequence loci, unexpected persistence, or sustained increases in watchlist markers, monitoring can escalate to higher-resolution approaches capable of linking loci to mobile elements and hosts (e.g., targeted metagenomics or isolate-based confirmation where warranted).

To ensure interpretability, trials should include untreated and standard-management controls. This enables detection of deviations specifically attributable to inoculant deployment rather than background variability.

3.2.2 Post-market monitoring and adaptive stewardship Because soils are spatially and temporally dynamic, stewardship should extend beyond initial field validation. Post-market monitoring should verify that inoculant abundance trajectories align with the intended use profile of the product (e.g. transient vs. persistent), d, that no adverse ecological signatures emerge and that functional outcomes remain within expected bounds. Importantly, persistence is not inherently undesirable: for some applications (e.g., symbiotic or soil-structural functions), establishment may be necessary for efficacy, whereas for others a one-time application may be sufficient. Monitoring should therefore evaluate persistence relative to product intent and ecological context, rather than against a single universal expectation.

Similarly, while stewardship frameworks aim to minimize unintended spread, complete spatial containment of microorganisms in open agricultural systems cannot be assumed. Microbial movement via wind, water, biotic vectors, or soil transport is well established. The objective of post-market monitoring is therefore not to presume immobility, but to verify that any dispersal remains ecologically benign and consistent with upstream genomic and ecological risk assessments. Monitoring frameworks should be harmonized across regions to enable cross-site comparison and data sharing. However, standardized global ecological risk metrics for microbial

inoculants remain underdeveloped; establishing comparable indicators for establishment, spread, and ecological impact therefore represents an important priority for the field.

4. A Shared Database for Inoculant Stewardship (federated global registry)

If inoculant risk is contingent on strain identity and ecological context, then effective stewardship depends on two basic capabilities: (i) knowing precisely which strain is being released, and (ii) knowing what evidence already exists about its safety and ecological behavior. Achieving this at scale will require a shift from today's fragmented oversight, spread across agricultural, environmental, and public-health authorities, to a more harmonized, evidence-accumulating system that can share knowledge across companies, agencies, and countries.

The current fragmented landscape is not merely an administrative hurdle; it is a barrier to responsible scaling. Safety and performance data are often held in silos, and similar studies are repeated across jurisdictions because prior results cannot be easily discovered, compared, or trusted. The result is an efficiency trap in which developers and regulators repeatedly re-establish that a well-characterized strain lacks pathogenicity or toxin potential, slowing deployment of tools that could support soil restoration and climate resilience.

To address this, we propose a living, federated global registry for inoculant stewardship that links strain-resolved genomic identifiers to standardized risk screening, ecological testing, field monitoring, and regulatory outcomes. If a strain has already undergone whole-genome sequencing and rigorous exclusionary screening, those results should be discoverable and portable, so that the strain's safety profile can travel with it across projects and jurisdictions, subject to context-specific constraints and monitoring requirements. By enabling responsible knowledge transfer, the registry would reduce redundant testing, accelerate high-integrity deployment, and create a feedback loop in which academic research informs industrial standards and real-world monitoring improves scientific understanding.

A registry of this scope will require durable governance, resourcing, and incentives. We therefore envision a federated model in which the core strain identifier layer and minimum metadata standards are curated by a neutral steward (for example, a consortium involving regulators, standards bodies, and academic centers), while detailed datasets remain distributed across institutional or company repositories with controlled access where needed (Table 1). Maintenance could be supported through a mixed model of public funding (treating the registry as enabling infrastructure), membership fees from participating companies, and journal/funder requirements for deposition of standardized safety and monitoring outputs. Adoption would be accelerated by aligning the registry with regulatory submissions, so participation reduces duplicate testing and speeds cross-jurisdiction reciprocity, while offering clear value to contributors: faster review, clearer traceability, and a shared evidence base for responsible deployment.

Table 1. Proposed Federated Registry Architecture for Inoculant Stewardship

Layer	Purpose	Core Components	Why It Matters
1. Genomic Identifier Layer (Anchor)	Establish strain-resolved identity	• whole-genome sequencing (WGS) • stable strain IDs • reference genome / assembly version + QC metrics (coverage, contamination/completeness) • ANI thresholds • versioned taxonomy alignment (e.g., GTDB updates) • deposit/location of sequences (e.g., controlled-access link, accession IDs)	• prevents misidentification • enables exclusionary hazard screening • ensures traceability across jurisdictions • prevents “same strain ID, different genome” problems and makes the identifier portable
2. Stewardship & Provenance Metadata	Contextualize strain use	• strain origin • intended-use environment • intended functional duration (transient vs persistent) • formulation • deployment geography • prior use history • application method + dose + frequency	• risk is context-dependent — ecological behavior cannot be interpreted without use metadata

		• crop/host + soil type + management context (tillage, irrigation, etc.)	
3. Risk-Screening Repository	Archive exclusionary hazard screening	• virulence-factor screening (e.g., VFDB) • ARG database outputs (CARD/ResFinder/AMRFinderPlus) • toxin genes • AMR loci • mobility-linked elements (plasmids, ICEs, prophages) • bioassay outputs • decision rule / thresholds used (what triggers exclude vs monitor)	• provides transparent "go/no-go" documentation • reduces redundant testing across regions
4. Ecological Testing & Performance Data	Evaluate establishment and impact	• persistence/decline kinetics • baseline and controls definition (untreated, standard practice) • sampling design metadata (timepoints, replicates) • spread assessments; • community composition shifts; • nutrient-cycling indicators; • non-target effects; • functional outcomes	• distinguishes intended benefits from unintended ecological disruption • supports adaptive • stewardship • makes results comparable across jurisdictions and avoids "apples vs oranges
5. Regulatory & Monitoring Log	Enable reciprocity and adaptive governance	• prior regulatory decisions; • approval conditions; • post-market monitoring data; • time-stamped updates • adverse event reporting / incident log (even if rare) • versioning of regulatory status(approved/conditional /withdrawn + dates)	• allows safety profile to travel with strain; • supports cross-border harmonization and long-term oversight • provides an adaptive stewardship system rather than a static archive

Soil restoration cannot wait. Microbial inoculants offer real potential to improve crop resilience and accelerate ecosystem recovery, but that potential will only be realized through a more coherent, strain-resolved stewardship model. We call for a shift from fragmented regulation

toward a release-based, risk-proportional framework that combines genome-resolved identity, exclusionary safety screening, contextual ecological evaluation, and monitored field deployment. Safety data and field outcomes should be captured in shared infrastructure so knowledge can accumulate across projects and jurisdictions rather than restart each time. Microbial inoculants should be governed neither as inherently safe nor inherently suspect, but as context-dependent restoration tools whose responsible use depends on strain identity, ecological setting, and long-term stewardship. The urgent task now is to operationalize this framework so biological innovation can scale with rigor, reciprocity, and continuous learning.

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