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 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). 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 (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, 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; Mawarda et al., 2020; Li et al., 2024). 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; 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). 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 (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., 2014; 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 may initially reach high abundance, they typically decline over time and stabilize at low levels (<1%) within weeks (Čaušević et al., 2024). This suggests integration into existing communities rather than long-term dominance, although functional effects can still occur at low abundance through metabolic interactions or signaling. These ecological constraints can limit persistence but should not be assumed as safety controls, as they are context-dependent and require empirical validation.

Inoculant persistence is restricted by multiple factors, including lack of local adaptation, competition with resident microbiota, antimicrobial interactions, predation, and niche saturation (Berg, 2008; Dong et al., 2024; Marken, 2025). Establishment is therefore highly context-dependent: disturbed or degraded soils may facilitate colonization, whereas intact systems often exhibit stronger resistance (Hibbing et al., 2010; Klümper et al., 2024). These dynamics should be evaluated within a structured monitoring framework.

2.3 Legacy Effects

Even when inoculant populations decline, their ecological effects can persist. Studies show lasting shifts in community composition despite rapid decreases in inoculant abundance (Kozdrój et al., 2004; Mallon et al., 2018). For example, Sinorhizobium meliloti L33 altered rhizosphere

communities and dispersed beyond treated plots (Schwieger & Tebbe, 2000). These findings highlight that inoculants can reshape microbial communities and spread beyond target sites, with both beneficial and unintended consequences, underscoring the need to assess community-level responses in risk evaluation.

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.

We propose a framework that treats risk 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 (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.**

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

The most serious failure for the field would be an inoculant linked to disease in crops, livestock, wildlife, or humans. Even rare events would undermine public trust and regulatory confidence, so risk assessment should begin with exclusionary screening that disqualifies strains with high-consequence hazard traits regardless of efficacy. Although consortia can in principle generate emergent behaviors through microbial interactions, hazards such as virulence, toxin production, and clinically relevant antimicrobial resistance are largely strain-encoded and can usually be identified through genome-resolved screening. Still, because interactions within consortia may affect persistence and ecological function, the framework includes consortia-level ecological testing and monitored field evaluation to verify that no unintended risks emerge under realistic conditions (Section 3.2).

>Figure 2.

Step 1: Strain-resolved identity and placement relative to high-concern clades (beyond 16S, 18S and ITS). Whole-genome sequencing (WGS) should be the baseline for commercial candidate strains because marker genes such as 16S, 18S, and ITS often lack the resolution to distinguish lineages with different hazard potential. WGS enables strain-level identification and placement relative to known pathogenic or regulated clades using curated reference databases and genome-to-genome comparisons such as Average Nucleotide Identity (ANI) (Konstantinidis and Tiedje,

2005). Lineage-aware tools can further improve classification in high-concern groups (Zhang et al., 2026). However, phylogenetic distance from known pathogens should not be taken as evidence of safety, since distantly related strains may still carry virulence-, toxin-, resistance-, or mobility-associated traits that require further screening.

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., 2015) 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 spread through mobile genetic elements, candidate genomes should be screened for mobility-linked hazard potential, not just evidence of past HGT (Partridge et al., 2018). Screening should identify mobile elements such as plasmids, integrative elements,

transposons, integrons, and prophages, and determine whether they carry clinically or agriculturally relevant resistance, virulence, or toxin genes. It should also assess evidence of active mobility. Candidates carrying mobile elements with high-consequence traits should be excluded or subjected to heightened scrutiny, whereas those lacking such traits may proceed with documentation and monitoring.

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) (Vílchez et al., 2016). 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, microbial inoculants may still cause unintended ecological effects, particularly in multi-strain consortia where interactions can alter persistence, functional expression, or impact relative to single strains. We therefore apply an invasion-ecology framework in which risk is evaluated as a progression from introduction to establishment, spread,

and impact (Mallon et al., 2015). Here, impact refers specifically to unintended ecological disruption rather than intended agronomic or restoration benefits. Ecological stewardship should therefore assess whether deployment leads to adverse outcomes such as displacement of native beneficial taxa, unexpected persistence, altered nutrient-cycling trajectories, destabilization of disease-suppressive communities, horizontal transfer of high-consequence traits, or off-site movement into non-target habitats.

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 realisticconditions 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.**

1. Establishment and Persistence.

Strain-resolved detection (e.g., qPCR or genome-resolved omics) should confirm establishment and track abundance over time. Monitoring should assess whether persistence aligns with the intended functional window and identify unexpected long-term dominance. This represents the baseline for all monitored releases and provides insight into ecological integration within the resident microbiome (McMullen & Lennon, 2023).

2. Community Structure and Stability.

Microbiome profiling should assess shifts in resident communities following inoculation. Changes in diversity, stability, and taxa can indicate unintended ecological disruption, particularly under repeated applications, in sensitive systems, or where products aim to restructure the microbiome.

3. Functional Ecosystem Processes.

Indicators such as soil respiration, nutrient cycling (e.g., nitrogen dynamics), soil structure, and pathogen suppression should be evaluated to distinguish beneficial functional shifts from unintended changes.

4. Gene Flow and Mobility

Gene-flow monitoring is most relevant for strains with mobility-associated elements or flagged resistance, toxin, or virulence genes. Genome screening should identify such features, while field monitoring verifies that they do not expand, mobilize, or transfer under agronomic conditions.

Recognizing practical constraints, we propose a tiered, risk-proportional approach where baseline monitoring is broadly applied and additional measures are triggered by genomic features, deployment context, or claim requirements. At minimum, trials should include strain-resolved tracking and a targeted mobility watchlist. Monitoring can escalate where elevated risk signals are detected. All trials should include appropriate controls to distinguish inoculant effects from 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)

Effective stewardship requires knowing exactly which strain is being released and what evidence already exists about its safety and ecological behavior. Yet current oversight is fragmented across jurisdictions, leaving safety and performance data siloed, duplicating studies, and slowing responsible deployment. To address this, we propose a federated global registry that links strain-resolved genomic identifiers with risk screening, ecological testing, field monitoring, and regulatory outcomes (Table 1). Such a system would make safety data discoverable and portable across projects and regions, reducing redundant testing and improving traceability. A federated model, with shared standards but distributed data ownership, could support cross-jurisdiction learning, adaptive stewardship, and more efficient scaling of microbial technologies.

> Table 1.

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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460

461 **Figure legends**

462 **Figure 1. Risk-proportional release-based stewardship framework for microbial inoculants.**
463 Candidate strains undergo genome-based identity confirmation and hazard screening, followed
464 by ecological testing and monitored field evaluation. Oversight is scaled to strain-specific risk
465 signals, and a federated registry supports traceability, shared learning, and adaptive stewardship.

466 **Figure 2. Release-based stewardship framework for microbial inoculants in soil**
467 **restoration.** Steps: (1) genome-resolved strain identification and hazard screening, (2) bioassay-
468 based risk triage, (3) ecological testing under realistic conditions, and (4) monitored field
469 deployment.
470

471 **Figure 3.** Conceptual framework for tiered environmental monitoring of microbial inoculants after
472 field release.