MICROBE training sheet

Keystone Taxa for microbiome engineering

Introduction and summary

The successful application of simplified microbial consortia is context-dependent, often limited by the fact that the needed microorganisms often remain uncultured due to their specific physiological conditions or the need for a minimal microbial consortium for their successful establishment. Thus, current microbiome research aims to develop targeted isolation approaches, using new -omics techniques to identify “the most important” microorganisms to be prioritized. Overall, this approach provides a reproducible and systematic pathway from co-occurrence network analysis to simplified microbial consortia design by linking network influence, functional potential, and culturing feasibility to the assembly of simplified microbial consortia.

Overview and background

The idea of one species having a stronger ecological influence than others was first discussed in the 1960s[1]. Since then, the term “keystone species” has been widely used in ecology, particularly in studies of macro-organisms' food webs. In microbiology, however, the application of this concept has begun more recently, in line with the development of sequencing technology and computational infrastructure that has opened the possibility of more ambitious microbiome studies.

The extension of the “keystone species” concept to microbiology faces several challenges, requiring even rethinking its definition. But applying this concept may help prioritize microorganisms for culturing and integration into representative simplified microbial consortia. Currently, a microbial keystone taxon refers to a specific taxa playing critical roles in maintaining the overall structure, function, and stability of its community[2].

HMGU applied a trait-based 8-component framework (Fig. 1) that characterizes the ecological significance of microbial keystone taxa and an operational 4-step approach (Fig. 2) to recover these taxa from complex omics data. We consider microbial keystone taxa to be specific microorganisms within a community that exert a disproportionately large impact on ecosystem structure, stability, and function relative to their abundance. They may regulate community dynamics through specialized metabolism, interactions, or ecological engineering, shaping nutrient cycling and microhabitats. Keystone traits may vary across strains, and the keystone status can shift from one taxon to another in response to environmental conditions[3].

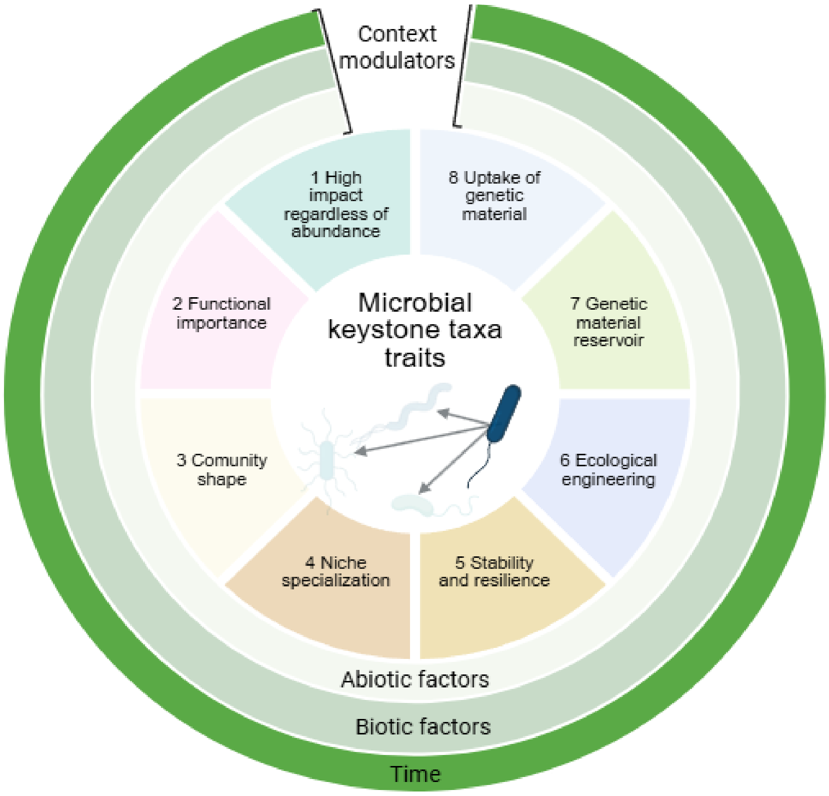


Figure 1: Trait-based frameworking for defining microbial keystone taxa[3] *- created with in BioRender:* *LINK*

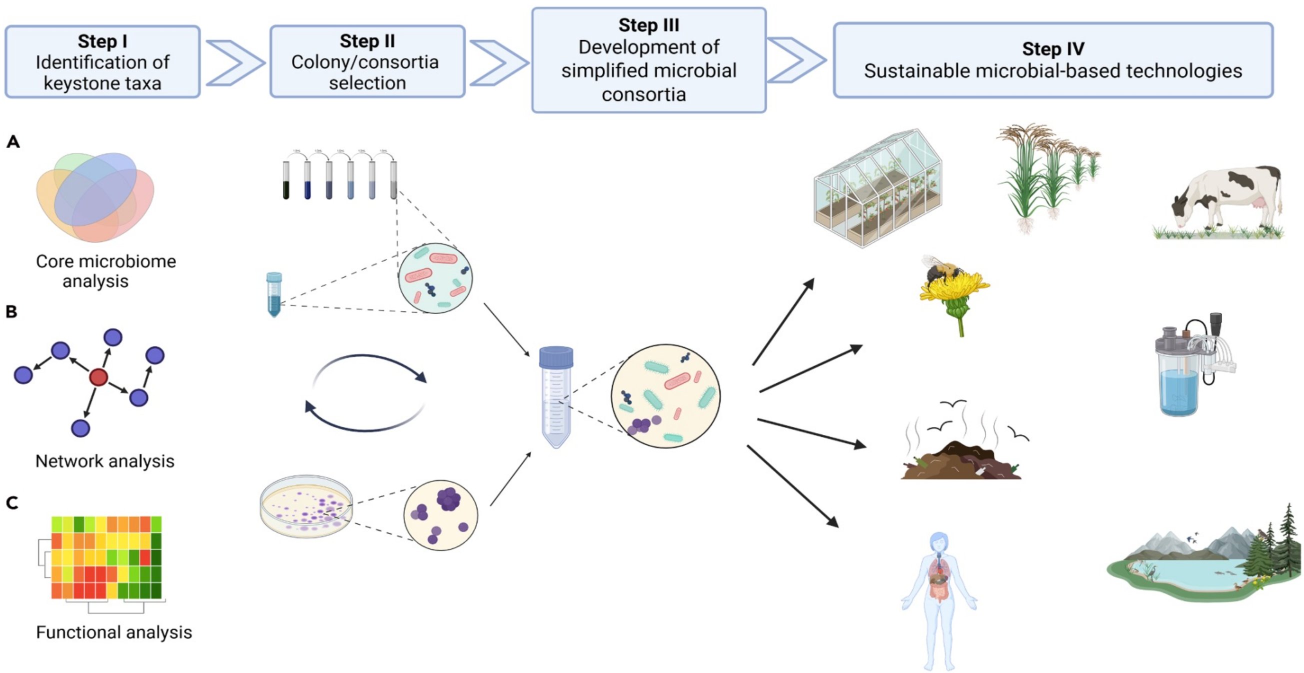
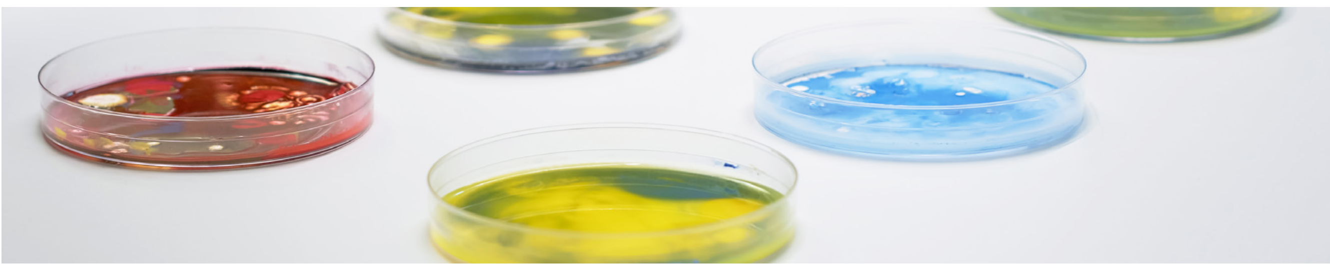


Figure 2: Identification of microbial keystone taxa and simplified microbial consortia assembly for microbiome sulutions[3] *- created with in BioRender:* *LINK*



Advantages for users and stakeholders

The main users of simplified microbial consortia are scientists, developers of microbial applications, farmers, plant experts, and medical experts.

Users of MICROBE results benefit from simplified microbial consoria applications in the following way:

- Agriculture: Disease suppression,improved nutrients use efficiency, enhanced crop productivity,increased resilience to climate stress
- Environmental Health: Enhanced degradation of pollutants in soil and wastewater, detoxification of contaminated environments, and recovery of ecosystem functions
- Forestry / Agriculture: Microbiome restoration in degraded ecosystems, improved plant establishmen and productivity
- Human Health: Restoration of gut microbiota (e.g., post-antibiotics), development of next-generation probiotics, improved host health
- Industrial Biotechnology: Increased efficiency in bioproduction processes, metabolic division of labor, improved system stability
- Food & Nutrition: Improved fermentation processes, enhanced food quality, safety, and nutritional value
- Marine & Aquatic Systems: Improved water quality, disease prevention in aquaculture, enhanced sustainability of aquatic systems

Involved experts

Helmholtz Center Munich, HMGU
MICROBE Consortium

Links & further information

1. Paine, R.T. (1969). The Pisaster-Tegula Interaction: Prey Patches, Predator Food Preference, and Intertidal Community Structure. Ecology 50, 950–961. LINK
2. Banerjee, S. et al (2018). Keystone taxa as drivers of microbiome structure and functioning. Nat Rev Microbiol 16, 567–576. LINK
3. Espíndola-Hernández et al. (2026) A trait-based framework to identify microbial keystone taxa for microbiome engineering. Cell Reports Sustainability. https://doi.org/10.1016/j.crsus.2025.100615. LINK
4. MICROBE Workshop on Keystone taxa and Core Microbiome (Video - LINK)

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