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Spotlight

Naturally engineered plant microbiomes in resource-limited ecosystems

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Nature-designed plant microbiomes may offer solutions to improve crop production and ecosystem restoration in less than optimum environments. Through a full exploration of metagenomic data, Camargo *et al.* showed that a previously unknown microbial diversity enhances nutrient mobilization in stress-adapted plants.

There is a well-established relationship between biodiversity and ecosystem functioning based on hundreds of experimental studies performed with plants and animals [1,2]. This relationship, however, is complex and elusive for microorganisms, given the astonishing number of species and our limited understanding of their expressed functional traits. The challenge of identifying new microbial species and gaining insights into their ecological roles is exciting and unsettling at the same time. On one hand, it allows us to gain valuable information on the true extent of microbial diversity and the services they provide to our planet. On the other hand, it demands that we move rather fast, given the state of environmental degradation of the Earth's natural ecosystems and the alterations being caused by climate change. This is of particular concern for the tropics, owing to its disproportionately high number of plant species in comparison with any other ecosystem [3] and an estimated number of >40 000 tree species threatened to be extinct worldwide by 2050 [4]. With plants disappearing, there is

also the danger of losing their microbiomes, a particular microbial community with distinct properties and functions working in concert with the host plant species to optimize their reproduction and survival.

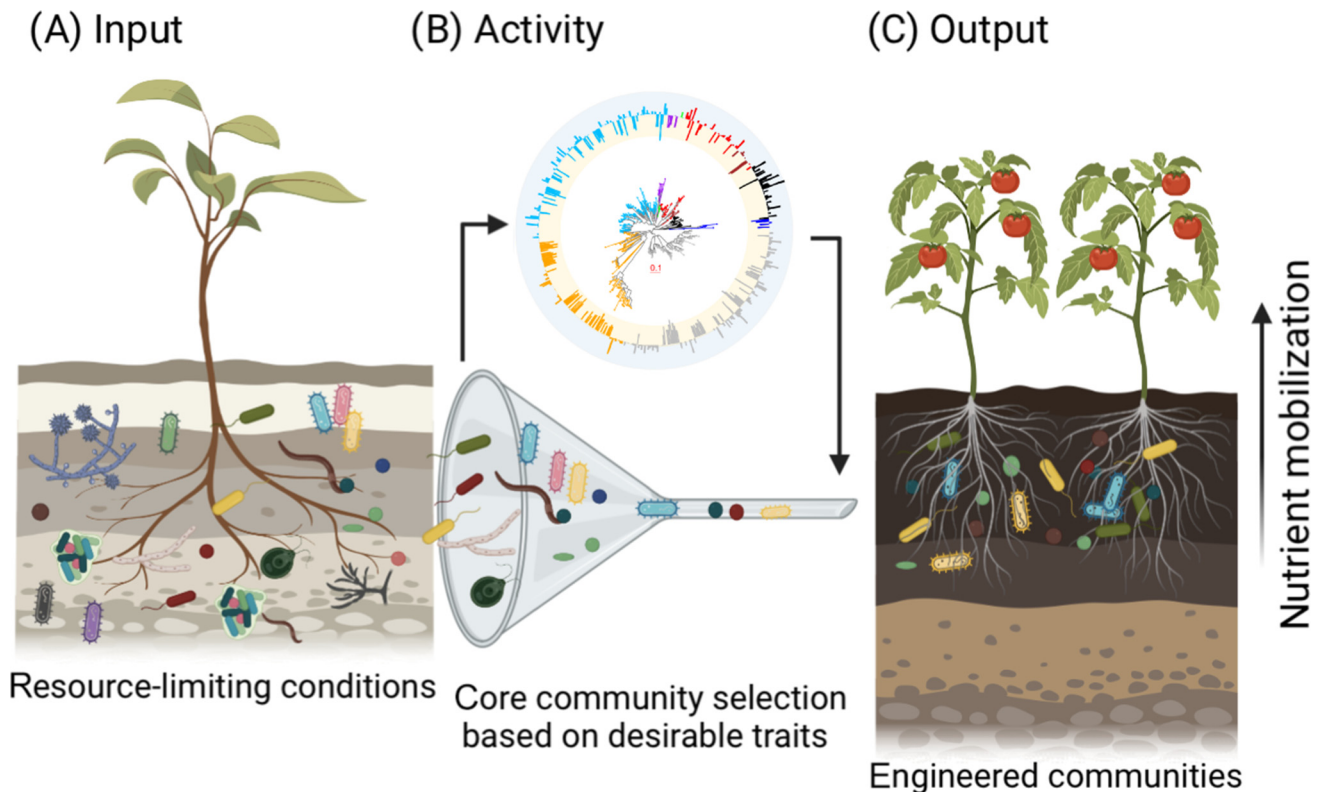
Camargo and colleagues explored the concept of nutrient acquisition dependency on microbiomes associated with plants growing under resource-limiting conditions of *Campos rupestres* [5]. This is a grassland ecozone, known to be a hotspot of endemic species, that consists of weathered and shallow soils formed at the edges of three large tropical biomes in Brazil: Cerrado, Atlantic Forest, and Caatinga [6]. Interestingly, unraveling the microbiome of only two species of the family *Velloziaceae*, a group of plants adapted to seasonally dry conditions and nutrient-impooverished soils, was sufficient for Camargo and collaborators to demonstrate that these plants share an organ-specific microbiome core capable of mobilizing phosphorus (P) and fixing nitrogen (N). These microbiome assemblages were far from being random, but well-orchestrated interactions that happened between the plant host and its recruited microbiome. More importantly, these microbiomes had significant taxonomic novelty, with 46.5% of the 16S rRNA genes and 77.5% of internally transcribed sequences lacking taxonomic assignment in prokaryotic and fungal databases, respectively. Indeed, this unprecedented high level of species taxonomic diversity required the development of the weighted average community identity (WACI) index as a new measure of taxa novelty among different communities. These plant microbiomes were dominated by members of new families and genera, raising interesting new questions about the extent of microbial diversity in this hitherto unknown ecosystem, the degree of coordinated interactions that might occur between a plant host species and its microbiome, the life history traits that allow for adaptation and survival, and/or the transferability of these microbiomes

to ecosystems that require conservation and recovery.

While some of the above questions remain unsolved, Camargo and coauthors advanced knowledge on two fronts. First, they investigated the ability of the two plant hosts to actively recruit their microbial partners. Instead of using a direct, but still unresolved, metabolomics approach to identify plant root exudates [7], the authors performed metagenomics of the rhizosphere microbial community and the surrounding soils and evaluated the differential abundances of organic substrate transporter genes. Not only the overall abundance of transporter genes increased in the rhizosphere, but also the substrate specificity of their putatively encoded proteins changed, indicating an active recruitment of amino acids and organic acids secreted by the root system. Secondly, the study explored the coordinated potential for P turnover in nutrient-limited soils. Specifically, Camargo *et al.* elegantly explored three alternatives for P metabolism, transport, organic mineralization, and inorganic solubilization, and observed significant increases of 14 P turnover processes in the rhizosphere in comparison to those in adjacent soils. It is noteworthy that different microbial taxa were involved in distinct P turnover processes. These results have profound implications for our future endeavors of managing P as a nonrenewable resource [8] for agricultural settings and ecosystem restoration practices. Theoretically, one could design microbial communities containing life-history traits associated with exopolyphosphatase and pyrophosphatase activities to respond to conditions in which inorganic P release is needed, while developing a different community for maximizing organic phosphate solubility (Figure 1).

To evaluate the contribution of *Vellozia epidendroides* and *Barbacenia macrantha* microbiomes to the N cycle, Camargo *et al.* examined metagenomes and 522





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Figure 1. Trait-based microbiome design for increasing nutrient turnover in agricultural and ecosystem restoration settings. (A) Plant–microbe interactions are key for thriving systems in resource-limiting conditions, nonetheless poorly explored. (B) Identification of microbial species and screening of their specific functional traits (e.g., P mobilization, biological N₂ fixation, and nitrification) can be used to enhance ecosystem processes. These functional traits should have a certain degree of phylogenetic conservation to ensure robustness of the selected function. (C) Delivering engineered microbial communities could enhance metabolic processes in resource-limited environments (e.g., agricultural soils and degraded ecosystems).

metagenome-assisted genomes (MAGs). The authors found evidence of sequence enrichments for genes encoding subunits of the nitrogenase complex in the plant rhizospheres and stems, suggesting the establishment of both microbial free-living and endophytic partnerships with the plant species. Furthermore, many of these potential interactions have yet to be fully described, such as the identification of four novel MAGs of the *Isosphaeraeae*, a family of the *Planctomycetota*, carrying *nifHDK* and *hao* genes for nitrogen fixation and oxidation of hydroxylamine, respectively. The concurrent presence of these genes in the same MAGs indicates a duality of metabolic roles associated with N turnover in this impoverished ecosystem.

Historically, breeding practices have unintentionally selected for specific plant-associated microbiota that thrives in intensive agricultural systems. Camargo *et al.* uncovered novel functions of pristine microbiomes which have potential for incorporation in microbiome-assisted breeding (recently reviewed by Mueller *et al.* [9]). Plant breeders have long sought genes and traits of wild relatives to improve crops. Similarly, identifying and reintroducing ancestral microbiota with desirable traits [10] is an exciting opportunity to engineer novel plant–microbe partnerships for agricultural productivity and ecosystem restoration.

Concluding remarks

This study by Camargo *et al.* brought us a step closer to find microbiome-based

solutions to improve agricultural systems under suboptimal environmental conditions. The study also highlights how little we know about the functional diversity that exists in nutrient-deficient soils and the tremendous potential for developing nature-based solutions for today's challenges.

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Declaration of interests

No interests are declared by the authors.

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