

Understanding microbiomes in agroecosystems: A challenge to address in the era of sustainable development

Comprender los microbiomas de agroecosistemas: un reto a enfrentar en la era del desarrollo sostenible

Among the 17 Sustainable Development Goals (SDGs) defined by the United Nations General Assembly in the 2030 Agenda, with the purpose of meeting current needs without affecting future generations, eradicating hunger is included as a priority (Tremblay *et al.*, 2020; United Nations Environment Programme, 2015). It is for this reason that there is widespread recognition of the need for available, accessible, innocuous, nutritionally and organoleptically acceptable food, with a reduced environmental impact on its production. It has been estimated that resource-intensive agricultural practices occupy 43% of non-desert and non-ice-covered land, of which 87% is devoted to the production of crops of agronomic interest (Poore & Nemecek, 2018). Within the environmentally safe strategies to produce food, the exploitation of biological functions of microorganisms is identified, including nitrogen fixation, phosphate solubilization, production of indole acetic acid and siderophores, transformation of complex carbon sources, in addition to protection against pathogens and tolerance to abiotic stress in plants, among others. These capabilities have awakened a growing interest in knowing and understanding the microbial ecology of agricultural soils, especially through the analysis of microbiomes.

The microbiome, understood as a characteristic microbial community occupying a defined habitat with distinctive physicochemical properties (Berg *et al.*, 2020), such as the soil of a given location or a plant, is a valuable opportunity to search for potential exploitable traits for the maintenance of agroecosystems. Within these, there is a remarkable variability of habitats that host microorganisms in the soil-plant continuum, including bulk soil, rhizosphere and rhizoplane, as well as endophytic and epiphytic microorganisms on stems and leaves (Xiong & Lu, 2022).

In the case of Colombia, a primary analysis of published studies on microbiomes in agricultural soils in the Scopus

database, using the general search equation “microbiome” AND “soil” AND “Colombia” and excluding articles related to the field of medicine, revealed 15 articles published between 2017 and 2024. These studies focused primarily on the taxonomic diversity of rhizospheric fungi and bacteria associated with crops such as coffee, avocado, and tomato. In a megadiverse country like Colombia, it is essential to face the challenge of knowing not only the composition of microbial communities in multiple agroecosystems but also their functional diversity, to explore their possible biotechnological applications, providing new options for the sustainable management of agricultural production.

Given the current availability of metagenomics, meta-transcriptomics, and metabolomics techniques, it might seem that understanding the microbial ecology of soils in agroecosystems is a simple task, however, there are limitations that must be recognized. At the most basic level, the definition of a prokaryotic species as an ecological unit is an ongoing topic of discussion. Likewise, the analysis of core microbiomes, understood as those microbial taxa shared between more than two samples from the same particular host or habitat (Neu *et al.*, 2021), represents *per se* an essential challenge in an ecosystem as heterogeneous as the surface soil of any agroecosystem. This difficulty becomes especially relevant when recognizing that native species have specific niches that contribute to the cycling of elements and the development of their hosts.

It is widely recognized that microbial communities in an ecosystem as complex as agricultural soil have a direct or indirect impact on its functioning and stability. This is mainly due to the wide metabolic capacity of taxa that can carry out, in a unique way, processes of hydrolysis of complex polymers and oxidation/reduction of chemical elements, enabling the development of biogeochemical cycles. Despite recognizing this role, knowledge of the functional

attributes of the soil microbiome remains restricted, especially due to technical limitations, such as the impossibility of culturing taxa with unique metabolic characteristics (Fierer, 2017). This makes the development of new techniques for cultivation and isolation of microorganisms, based on the use of ecological and genomic information, a valuable strategy for obtaining cost-effective and efficient bioinoculants. However, this type of biotechnological products is also a challenge, especially due to the cost of their production, their ability to colonize and express functions in the application habitat, as well as their effect on native microbial communities.

The interdisciplinary study of the taxonomic and functional composition of native microorganisms in the rhizosphere, rhizoplane, and phyllosphere, as well as the analysis of the topology and structure of microorganism-microorganism and microorganism-plant interaction networks, represents a potential opportunity to propose viable alternatives for the development of products such as biofertilizers or biocontrol agents. The use of cutting-edge techniques to address these investigations can generate a large amount of information, but it is the comprehensive and interrelated analysis of these data that can generate answers to contribute to establishing successful strategies for integrated management of agronomic practices that ensure the preservation of biodiversity and the well-being of our and future generations.

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XIMENA PEREZ-MANCILLA, MSc.

Auxiliary Professor

Universidad Nacional de Colombia, Facultad de Ciencias Agrarias,

Departamento de Agronomía, Bogotá (Colombia)

Email: xcperez@unal.edu.co