Al-Farabi Kazakh National University (KazNU)

Faculty of Biology and Biotechnology



DISCIPLINE: «Modern Problems of Plant Genetics»

Lecture 7

The plant microbiome: ecology, functions, and emerging trends in microbial application.



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Aim of the lesson: familiarization with the plant microbiomes.

Plan of the lesson:

- 1. The microbial communities or microbiomes.
- 2. Factors affecting plant microbiota.
- 3. Functions of plant microbiota.
- 4. The application of microbial consortia.





Microbes are fundamental to the maintenance of life on Earth, yet we understand little about the majority of microbes in environments such as soils, oceans, the atmosphere and even those living on and in our own bodies.

Culture-based techniques have allowed isolated microbes to be studied in detail, and molecular techniques such as metagenomics are increasingly allowing the identification of microbes in situ.

The microbial communities, or microbiomes, of diverse environments have been studied in this way, with the goal of understanding their ecological function.

The plant microbiome is a key determinant of plant health and productivity and has received substantial attention in recent years.

A testament to the importance of plant-microbe interactions are the mycorrhizal fungi.

Molecular evidence suggests that their associations with green algae were fundamental to the evolution of land plants about 700 million years ago.

Plants have evolved with a plethora of microorganisms having important roles for plant growth and health. A considerable amount of information is now available on the structure and dynamics of plant microbiota as well as on the functional capacities of isolated community members.

Due to the interesting functional potential of plant microbiota as well as due to current challenges in crop production there is an urgent need to bring microbial innovations into practice. Different approaches for microbiome improvement exist.

On the one hand microbial strains or strain combinations can be applied, however, field success is often variable and improvement is urgently required. Smart, knowledge-driven selection of microorganisms is needed as well as the use of suitable delivery approaches and formulations.

On the other hand, farming practices or the plant genotype can influence plant microbiota and thus functioning.

Therefore, selection of appropriate farming practices and plant breeding leading to improved plant microbiome inter actions are avenues to increase the benefit of plant microbiota.

In conclusion, different avenues making use of a new generation of inoculants as well as the application of microbiome-based agro-management practices and improved plant lines could lead to a better use of the plant microbiome.

Plant microbiota and their interactions are highly diverse and multiple factors shape community assembly and functioning.

While recognized since the 19th century, the investigation of and interest in plant-associated microbiota only started to bloom since the 800s.

Due to the high potential of microorganisms to improve plant growth, stress resilience and health, numerous microbial inoculants have been developed, but many of them show poor performance in the field.

Several approaches may lead to improved field success such as designing smart microbial consortia, the selection of agricultural management practices favoring microbiota with beneficial functions or a new generation of plant breeding approaches.

Last but not least the development of suitable formulations and delivery approaches is highly important for any field application.

Our understanding of plant microbiota, its functionality and its exploitation has substantially increased in the last years.

However, a better understanding is needed on how inoculants modulate the resident microbiome, how complex microbiota and the holobiont affect the activity of the applied strain or how microbial inoculants colonize the plant environment in the field.

Microbes in a community interact with each other and the host plant, so it is important to capture as much of the diversity of a microbiome as possible.

To do so requires the use of global analyses such as metagenomics, metatranscriptomics and metaproteomics, which allow simultaneous assessment and comparison of microbial populations across all domains of life.

Metagenomics can reveal the functional potential of a microbiome (the abundance of genes involved in particular metabolic processes), whereas metatranscriptomics and metaproteomics provide snapshots of community-wide gene expression and protein abundance, respectively.

Metatranscriptomics has revealed kingdom-level changes in the structure of crop-plant rhizosphere microbiomes.

The relative abundance of eukaryotes in pea and oat rhizospheres was fie-fold higher than in plant-free soil or the rhizosphere of modern hexaploidy wheat.

***** Factors affecting plant microbiota

In any plant organ microbial composition is influenced by a range of biotic and abiotic factors. These factors may include soil pH, salinity, soil type, soil structure, soil moisture and soil organic matter and exudates, which are most relevant for belowground plant parts, whereas factors like external environmental conditions including climate, pathogen presence and human practices influence microbiota of above- and below-ground plant parts.

The plant species and genotype recruit microorganisms from the soil environment where root morphology, exudates, and type of rhizodeposits play a significant role in the recruitment of plant microbiota.

The members of plant microbiome comprise beneficial, neutral or pathogenic microorganisms.

Plant growth-promoting bacteria (PGPB) can promote plant growth by either direct or indirect mechanisms.

Some PGPB produce phytohormones like auxin, cytokinin, and gibberellin which affect plant growth through modulating endogenous hormone levels in association with a plant.

Moreover, some PGPB can secret an enzyme, 1aminocyclopropane-1-carboxylate (ACC) deaminase, which reduces the level of stress hormone ethylene in the plant.

Strains of *Pseudomonas spp.*, *Arthrobacter spp.* and Bacillus spp. and others have been reported to enhance plant growth through the production of ACC deaminase.

Some bacteria can cause disease symptoms through the production of phytotoxic compounds proteins and phytohormones. For

example, Pseudomonas syringae is a well-known plant pathogen having a very broad host range including tomato, tobacco, olive and green bean. Another well-known pathogenic bacterium is Erwinia amylovora that causes fire blight disease of fruit trees and ornamentals plants. Xanthomonas species, Ralstonia solanacearum, and Xylella fastidiosa are also associated with many important diseases of crops like potato and banana

Rascovan et al. found a diverse range of bacteria

including *Pseudomonas spp.*, *Paraburkholderia spp.* and *Pantoea spp.* in wheat and soybean roots that showed important plant growth promotion properties like phosphate solubilization, nitrogen fixation, indole acetic acid and ACC deaminase production, mechanisms involved in improved nutrient uptake, growth and stress tolerance.

* The application of microbial consortia

The application of microbial consortia is an emerging approach to overcome lab to field hurdles.

The rationale of this approach may be the combination of microorganisms with different traits, either complementing each other to combine different mechanisms needed for different effects such as plant growth enhancement and biocontrol of pathogens.

Microbial consortia may also comprise strains showing the same mode of action but tolerate different environmental conditions or plant genotypes.

Various studies on grapevine, potato, tomato, Arabidopsis and maize have shown that microbial combinations have the potential to increase plant growth-promoting (PGP) effects as compared to single inoculants

- Home tasks:
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GOOD LUCK!

