#### 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.



Amirova Aigul Kuzembayevna

Associated professor, Candidate of Biological Science

aigul\_amir@mail.ru



# Aim of the lesson: familiarization with the plant microbiomes.

## Main questions:

- 1. The microbial communities or microbiomes.
- 2. Plants with their root system provide unique ecological niches for soil microbiota
- 3. Factors affecting plant microbiota.
- 4. Functions of plant microbiota.
- 5. The application of microbial consortia.



Nowadays, crop production is facing many challenges such as climate change, the demographic development, and there is an increasing demand of sustainable production.

As microorganisms have shown the potential to be applied as biofertilizers or biopesticides there is increasing interest to integrate them as alternatives to chemical products in agricultural practices [7], [8]. Since the 80's, many researchers have addressed the topic of microbial inoculants [9], however, with limited success in the field. Having more information on plant microbiota in regard to biotic and abiotic stresses, plant genotype, and environmental conditions, it might be feasible to find better suitable candidates or approaches for inoculation in a given environment [7].

Plant microbiota consist of different types of organisms including fungi, archaea and bacteria.

Due to the wealth of information available on bacteria and interest from the industry, this review focusses on the bacterial component of plant microbiota and discusses functionalities as well as challenges and concepts in regard to the application of plant-associated bacteria.

Plants actively recruit their microorganisms from surrounding microbial reservoirs such as the soil/rhizosphere, the phyllosphere (i.e. the aerial plant habitat sensus lato or the leaf surface in relation to the external environment), the anthosphere (the external environment of flowers), the spermosphere (the exterior of germinated seed) and the carposphere (the external fruit environment) [3].

Root microbiota are mostly horizontally transferred, i.e. they derive from the soil environment, which contains highly diverse microorganisms, dominated by Acidobacteria, Verrucomicrobia, Bacteroidetes, Proteobacteria, Planctomycetes and Actinobacteria [10]. However, bacteria may be also vertically transmitted via seeds. Seeds also represent an important source of microorganisms, which proliferate in the roots of the developing plant [11], [12].

## \* Plants with their root system provide unique ecological niches for soil microbiota

Plants with their root system provide unique ecological niches for soil microbiota which colonize the rhizosphere, roots and to a certain extent above ground parts [13]. The narrow layer of soil under the direct influence of plant roots, i.e. the rhizosphere, is considered as a hot spot of microbial activity and represents one of the most complex ecosystems [14].

Recently, Donn et al. [15] showed root-driven changes in bacterial community structure of the wheat rhizosphere and found a 10-fold higher abundance of actinobacteria, pseudomonads, oligotrophs, and copiotrophs in the rhizosphere as compared to bulk soil.

Moreover, the authors also reported that rhizosphere and rhizoplane communities were altered over time, whereas the bulk soil population remained unaffected. Similarly, Kawasaki et al. [16] reported that the Brachypodium distachyon (a model for wheat) rhizosphere was dominated by Burkholderiales, Sphingobacteriales and Xanthomonadales, while the bulk soil was dominated by the order Bacillales. Root exudates such as organic acids, amino acids, fatty acids, phenolics, plant growth regulators, nucleotides, sugars, putrescine, sterols, and vitamins are known to affect microbial composition around roots, the so-called rhizosphere effect [8], [17].

Plant roots are colonized also internally (root endosphere) by a diverse range of bacterial endophytes. The entry of bacterial endophytes inside root tissues often occurs through passive processes or root cracks or emergence points of lateral roots as well as by active mechanisms [21].

The colonization and transmission of endophytes within plants depend on many factors such as the allocation of plant resources and the endophyte ability to colonize plants. Diverse range of bacterial taxa can gain entry in root tissues, for example, the most abundant phyla often found in grapevine roots were *Proteobacteria*, *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Verrucomicrobia*, *Planctomycetes*, *Chloroflexi*, *Firmicutes and Gemmatimonatedes* [22], [23], [24], [25]. In the roots of rice, *Rhizobiaceae*, *Comamonadaceae*, *Streptomycetaceae*, and *Bradyrhizobiaceae* were found as most dominant families [26].

As another example, Correa-Galeote et al. [27] found *Proteobacteria, Firmicutes*, and *Bacteroidetes* as predominant phyla inside the maize roots and the abundance of these phyla was influenced by soil cultivation history.

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 interactions 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

## Questions for monitoring the material being studied:

- 1. The microbial communities or microbiomes.
- 2. Plants with their root system provide unique ecological niches for soil microbiota
- 3. Factors affecting plant microbiota.
- 4. Functions of plant microbiota.
- 5. The application of microbial consortia.

#### Recommended list of references:

- 1. Шулембаева К.К., Токубаева А.А. Реконструкция генома мягкой пшеницы на основе хромосомной инженерии и отделенной гибридизации: монография. КазНУ им. аль-Фараби. Алматы: Қазақ ун-ті, 2019. 240 с.
- 2. Огурцов А.Н., Близнюк О.Н., Масалитина Н.Ю. Основы генной инженерии и биоинженерии. Учебное пособие. Часть 1.: Молекулярные основы генных технологий. Харьков: НТУ "ХПИ", 2018. 288 с.
- 3. Нефедова Л.Н., Применение молекулярных методов исследования в генетике: Учебное пособие. М.: НИЦ Инфра-М, 2012. 104 с.
- 4. Муминов Т.А., Куандыков Е.У. Основы молекулярной биологии : курс лекций. Алматы : ССК, 2017. 222 с.
- 5.Varshney Rajeev K. Plant Genetics and Molecular Biology. London: Springer, 2018. - 298 p.
- 6. Halford Nigel G. Crop Biotechnology: Genetic Modification And Genome Editing. - London: World Scientific, 2018. - 218 p.
- 7. Glick Bernard R. Molecular biotechnology: principles and applications of recombinant DNA. - 4th ed. - Washington, 2010. - 1200 p.

