

induced pluripotent stem cells, with their unique capacity for self-renewal and differentiation, offer the potential to generate stable and productive lines expressing insulin. Genetic modification of stem cells aims to achieve optimal insulin gene expression and controlled production regulation. The use of such cells opens up the possibility of post-translational modifications similar to those that occur in natural cells, which can influence the functionality and structure of recombinant insulin and reduce the likelihood of immune rejection. Despite the potential benefits, the use of stem cells in recombinant insulin production faces challenges such as ethical issues, cell line stability and process optimisation. Nevertheless, this approach is attracting the attention of scientists as a promising direction for expanding the possibilities of producing recombinant biological medicines.

Expression systems for insulin production have become diverse and innovative. However, each system has its challenges and limitations, such as ethical issues, production sustainability and the need for process optimization. Overall, the combination of scientific research and technological development is contributing to the further improvement of expression systems for insulin production and defining progress in the production of this important drug.

Cooperative synergies between members of the plant microbiota

Petrashenko A., Soloviova A.

Biotechnology department, National University of Pharmacy, Kharkiv, Ukraine

soloviova.alina@gmail.com

Since the ancestral plant lineages inhabited the land 450 million years ago, plants and their associated microbes have interacted with each other to form a collection of species often referred to as the holobiont. Microbial synergies are presented on an evolutionary scale, showing that interactions between plants and microbes are relatively recent compared to older interactions between bacteria or between different microbial kingdoms. It is generally recognized that the formation

of bacterial communities on plants is not random, but rather controlled by certain rules of assembly.

Despite the wide variety of bacterial phyla described in nature and the numerous factors affecting these communities, three main phyla (Proteobacteria, Actinobacteria, and Bacteroidetes) dominate the bacterial microbiota of plants in both aboveground and underground plant tissues. Although archaea represent a large proportion of the plant microbiota, they are less well understood than their bacterial counterparts, most likely because no pathogenic isolates have been described to date.

The plant endophytic archaea mainly belong to *Thaumarchaeota*, *Crenarchaeota*, and *Euryarchaeota*, but their functional significance for host plants remains to be determined. Although less attention has been paid to the fungal microbiota of plants, culture-independent community profiling has revealed a stunning diversity of fungi colonizing both aboveground and belowground plant tissues, mainly belonging to two major phyla: *Ascomycota* and *Basidiomycota*.

In roots, although arbuscular (*Glomeromycota phylum*) and ectomycorrhizal fungi have been mainly studied, recent community profiling data indicate that other endophytic fungi also represent an important fraction of the fungal microbiota of roots. These interactions refer to the reciprocal exchange of metabolites between nutrient-dependent microorganisms to compensate for metabolic deficiencies. Using this strategy, microbes can expand their fundamental niches to survive in low-nutrient environments, gain access to complex compounds.

The combination of both empirical approaches and computational association networks will be crucial for understanding the ecology of microbial interactions during plant microbiota formation, for better predicting the formation and stability of natural or synthetic microbial communities, and for better defining the dynamics of microbial community formation in time and space.