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# Session V. Environmental Microbiology II

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## Opening Lecture

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### V.OL.1

#### Anhydrobiosis in yeasts and its possible applications

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Anhydrobiosis is a unique state of live organisms in which their metabolism is temporarily reversibly suspended as the result of their strong dehydration. This state helps the organisms to survive during the adverse climatic conditions of the environment connected with a strong heat and a drought. Microorganisms belong to those groups of organisms which actively use the state of anhydrobiosis for the survival during periods of unfavorable conditions. Already more than 300 years researchers try to reveal main mechanisms of this evolutionary developed state of life. Understanding of this phenomenon is very important for further development of our knowledge of essence of life and its limits. Besides that the earlier unknown intracellular protective reactions and their mechanisms which have been already revealed in conducted studies, as well as those which will be still found can be extremely important for the artificial increase of resistance of live organisms to various medical treatments. Studies of anhydrobiosis in yeasts have special interest because yeast cell is a unique model system of eukaryotic organisms and all results obtained in these researches can be easily transferred for animals and people. At the same time it is well known that anhydrobiosis is widely used already more than 70 years for the industrial production of active dry yeasts necessary for bread baking and production of wine. Last decades showed additional non-conventional possibilities for the applications of active dry yeasts. It has been shown that they can be used for the efficient protection, purification and bioremediation of the environment. High sorption activity of dehydrated yeasts is rather interesting tool in winemaking. Dry yeasts are already used as efficient feed for agricultural animals. Interesting application of yeast dehydration is linked with development of new cheap and efficient process for yeast cells' stable immobilisation on different carriers for various biotechnologies.

**Keywords:** Anhydrobiosis, Active dry yeasts, Non-conventional application

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## Oral presentations

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### V.OP.1

#### Bubbles/droplets-mediated assembly/ processing of cellular matter

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Experiments tracing bubbles rising in saline water and generation of jet/film droplets revealed that bubbles in motion separate ions and generate bi-ionic and oppositely spiraling motions. After separation both motions undergo bi-pirouette narrowing and splicing within a bubble vortex, which likely assembles double-helix stretches of matter of a RNA/DNA architectures. In addition, strong cationic vortex, that develops below a bubble attracts and collects anionic particles that are dispersed in the water column, transports them into the air/water interface and ejects them into the air with jet droplets. Next, the matter trapped in droplets undergoes electrostatic positioning in a positively charged air. This causes inner positioning of cationic domain with RNA/DNA, while anions are forced to compose an outer layer that then undergoes evaporation. Such processing may result in assembly of layered cellular features with anionic membranes. Thereafter, anionic particles dispersed in air may again condense water vapor and precipitate back to sea. The airborne processing may result in assembly of multi-membraned cells resembling bacteria or diatoms, which then are again scavenged and aerosolized by rising bubbles. For example, the abundance of bacteria or diatoms in a droplets may exceed their content in sea water by a factor of  $10^3$  and  $10^2$ , respectively. In general, laboratory and field evidences suggests that rising bubbles activate a set of synergistic processes that incorporates separation of ions, forcing them to rotate/spiral/splice within the sub-bubble vortex that assembles cationic RNA/DNA and ejects that matter into jet droplets. During the airborne processing of droplets, electric polarity between inner layers and outer anionic membranes is developed, activating a continuous bi-ionic rotational flow. Thereby, our observations suggests that processing of ions by rising bubbles and droplets may be responsible for assembly of cellular life that probably first occurred in droplets over oceans.

**Keywords:** cellular matter, ionic/rotational features, cellular configuration of droplets, cellular life

#### NOTES

## V.OP.2

### Investigation of pyridine degradation in actinobacteria

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Pyridine and its derivatives occur in nature as components of biological systems, however they are widely used in chemical, pharmaceutical and oil industries and are major environmental pollutants. Due to their heterocyclic structure, these compounds easily reach the biosphere in industrial waste waters and cause the danger for living organisms. The pyridine degradation has been investigated for more than 50 years. Although a number of bacteria capable of degrading pyridine have been described, little is known about degradation enzymes and their encoding genes.

*Arthrobacter* sp. 68b and *Rhodococcus rhodochrous* PY11 bacteria, belonging to class *Actinobacteria*, were isolated as capable of using pyridine as a sole source of carbon and energy. In both strains the degradation of pyridine was an inducible process. The synthesis of 40 kDa and 41 kDa proteins was induced in *Arthrobacter* sp. 68b and *R. rhodochrous* PY11 bacteria, pre-grown with pyridine, respectively. The proteins were sequenced *de novo* and the predicted sequences of peptides were used to identify target genes. In both strains it was revealed that genes are plasmid located. Further analysis revealed that both induced proteins are luciferase-like monooxygenases. Other genes and their proteins that could be involved in the degradation of pyridine were predicted as well.

**Keywords:** pyridine, luciferase-like monooxygenase, actinobacteria

## V.OP.3

### Soil microbial communities - super tights of ecosystems

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Global studies try to find general rules driving soil microbial communities composition. However, the microbial communities can be adjusted to their niches so closely that the number of co-occurring factors harden generalization between habitats. It seems crucial to describe each ecosystem in detail to pick the factors for multiple comparisons among ecosystems. During my PhD I was interested in microbial communities in the abandoned farmland. I performed a number of comparisons on structure and functioning of soil microbial communities in the two ecosystem types: fallows and meadows. Fallows were abandoned farmland in the initial stage of secondary succession and were counter-parted to meadows in the same area, with high plant diversity characteristic for older grasslands under sustainable management. Disappointingly, all of the comparisons showed no significant differences between the microbial communities. At that time the two ecosystem types had been initially chosen by the botanist in the field and I was waiting for his detailed community analysis. When the botanist did it, he included the third plant community: transitory fields between fallows and meadows. Taking the third, previously hidden group out revealed number of trends. The arbuscular mycorrhizal fungi (AMF) root colonization frequency was higher in the meadows than in the fallows. Meadow soils exhibited higher basal respiration rate, while cellulose decomposition and nitrogen mineralization were faster in fallows (Chmolarska et al. 2017a,b). My case points out how it is important for studying microbial component of ecosystem to be exact with the above community description. Communities adjust to temporary niches and fit them tightly.

**Keywords:** fallow; meadow; arbuscular mycorrhizal fungi, microbial niches

## V.OP.4

### Assessment of microbial community response to accidental release of oil into the Arctic marine ecosystem

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The aim of the study is to determine key bacterial species and metabolic pathways responsible for the degradation of different oil fractions in different compartments (aerobic and anaerobic water and sediments) of the Baltic Sea and the Northern Atlantic in the frame of the Horizon 2020 project GRACE. The biodegradation rates of different oil fractions in seawater and sediments are determined, and this data is related to environmental parameters and dispersant application. In order to maximize output from obtained data sets integrative knowledge discovery from multiple omics sources is applied. For this purpose, high-throughput sequencing datasets obtained during the current project and relevant public domain data are integrated. Information about microbial community taxonomic composition and metabolic markers together with abiotic factors are related to oil biodegradation kinetic parameters and oil remediation strategies using different modelling approaches. The main outcome of the project is the characterization of oil-degrading microbial community structure in geographically different marine environments and impact of dispersant, and environmental parameters on natural oil biodegradation capacity. Based on results of the meta-analysis of obtained omics datasets and modelling, metagenomics prediction platform for inferring oil biodegradation capacity in the marine environment will be established.

**Keywords:** oil pollution, microbial community, biodegradation, Arctic marine environment