BOOK OF ABSTRACTS

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(22nd SPPS Meeting)

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Institute for Biological Research "Siniša Stanković", University of Belgrade

Faculty of Biology, University of Belgrade

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Microbial-based inputs: opportunities and challenges for sustainable and resilient agricultural productions

IT5-2

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The interest and market for microbial-based biofertilizers and biopesticides is increasing worldwide due to improved production technologies, deeper knowledge about the mechanisms of activity of the inocula, isolation and selection of new beneficial strains, and the trend in reducing the impact of agricultural practices on the environment. Different kinds of soil microorganisms belonging to several taxa colonizing the rhizosphere or the plant tissues can be utilized for the production of these bioproducts. However, their application in agricultural practice is still hindered by several factors. The main reasons derive from not always consistent results (derived from the still limited understanding of the relationships among microorganisms and between them and the plants), problems in identifying and tracking the inoculated strains in the field, as well as the technology of production. After an excursus on the key microorganisms utilized to improve plant productivity and their mechanisms of action, a review of the factors affecting the efficacy of these bio-products on crop productivity will be presented. In particular, factors related to the effect of farmers' practices on products' efficacy, the formulation options (multifunctional products) and the persistence and traceability of inoculants in soil will be considered, since they are important to assure the future wider use of bio-products. Finally, the legal issues related to quality control and definition of biofertilizers will be considered. The data will be presented to discuss the role of biofertilizers and biopesticides in developing an integrated and sustainable agricultural management system.

Keywords: biofertilizers, biopesticides, plant growth promoting microorganisms

Old problems, new tools - Integrated approach to oil crop breeding

IT5-3

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Oil crop breeding and selection is a continual process designed to increase yield levels and improve resistance to biotic and abiotic stresses. Breeders have been successful in producing a large number of varieties using conventional breeding methods which vary depending on the species. Development of biotechnology, notably genetic transformations, and appearance of new techniques such as genome editing, paved the way for more efficient trait introduction. The last

three decades have also seen tremendous advances in the evolution of marker systems and the respective detection platforms. The most common application of these marker systems in oil crop breeding is marker assisted backcross breeding for gene introgression, as well as mapping of agronomically important traits. Novel approaches in genotyping and phenotyping enabled more efficient data collection for identification of quantitative characters and elucidation of the genetic basis of agriculturally important traits. Old and new tools found their place in oil crop breeding. However, there is still room for improvement, especially in data collection and integration. That is why further efforts should be made at better combining of phenotypic and -omics data and their integration into the breeding process and identification of traits and markers of real practical value for the breeders.

Keywords: breeding, phenotyping, molecular markers, oilcrops

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Plant terpenes and bioplastics

IT5-4

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Plants produce a large variety of highly functionalized terpenoids, in which the presence of, for example, partially unsaturated rings and carboxyl groups provides handles to use these compounds as feedstock for biobased commodity chemicals. Methylperillate, a monoterpenoid present in *Salvia dorisiana*, is useful for this purpose, as it carries both a ring and a methylated carboxyl group. By two mild chemical steps it can be converted to terephthalic acid, a precursor for PET plastic. In this work, we identified type VI-like trichomes from *Salvia dorisiana* as the site of biosynthesis and storage of methylperillate. mRNA from purified trichomes was used as a source to identify four genes that constitute the pathway towards methylperillate. This pathway includes a (-)-limonene synthase, a limonene 7-hydroxylase, and a perilla alcohol dehydrogenase. We also identified a terpene acid methyltransferase, perillic acid *O methyltransferase* (OMT), with homology to salicylic acid OMTs. Transient expression of these four genes, in combination with a geranyl diphosphate synthase to boost precursor formation, resulted in the reconstitution of the methylperillate pathway in *Nicotiana benthamiana*. This demonstrates the potential of these enzymes for metabolic engineering to produce a feedstock for biobased commodity chemicals.