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

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21th Symposium of the Serbian Plant Physiology Society

COST ACTION FA1106 QUALITYFRUIT Workshop

Petnica Science Center, June 17-20, 2015

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Molecular characterization of *Fusarium* spp. isolated from maize and cereals

PP8-36

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Fusarium spp. is one of the most damaging cereal pathogens that provokes serious economic losses worldwide. Also, this pathogen produces mycotoxins which pose severe danger to animal and human health. Thus, it is very important to control and eliminate risks caused by this fungus. For making improvement in overcoming these issues, accurate separation of *Fusarium* species is needed. Besides identification based on morphological and pathogenic characters, novel molecular genetic methods are available nowadays. The aim of this research was characterization of fifty *Fusarium* spp. isolates from maize and cereals and possible detection of recently discovered species *F. gerlachii* and *F. vorosi*. Characterization was done by DNA sequence-based analysis using two specific primer pairs (ITS/ITS4, ef1/ef2). Specific genome fragments were sequenced and analyzed. Sequences were compared to the data from GeneBank, NCBI (National Center for Biotechnology Information). Genetic similarities between sequences were determined using software MEGA, version 6.06. All tested isolates appeared to represent *F. graminearum sensu stricto* species. Molecular detection, sequencing and phylogenetic analysis provide more accurate classification of fungi species, identification of unknown isolates, establishment of relationships between species and determination of toxogenic profiles.

Keywords: cereals, DNA sequencing, *Fusarium* spp., maize, molecular characterization

Application of Tempo EPR spin probe for *in vivo* detection of salt-induced oxidative stress in *Centaurium erythraea* Rafn

PP8-37

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Electron paramagnetic resonance spectroscopy (EPR) was applied for *in vivo* detection of oxidative stress induced by high ionic strengths in *Centaurium erythraea* Rafn (*Gentianaceae*), a herbaceous perennial often found on saline soils. Shoots of *C. erythraea* were cultured *in vitro* for 4 weeks on solid 1/2 MS medium, or 1/2 MS medium supplemented with 200 mM NaCl to induce salt stress and thus stimulate the production of reactive oxygen species (ROS), which is a common response of plant cells subjected to various types of biotic or abiotic stresses. The reduction of a stable cell-permeable aminoxyl radical spin probe, Tempo, was measured to assess the oxidative status of the control and salt-treated samples. In both types of samples, the reduction of Tempo showed zero-order kinetics. After one hour, the control reduced only 9% of the initial amount of the spin probe, whereas the sample grown with 200 mM NaCl reduced it by 20%. This may indicate that the plants grown in the presence of 200 mM NaCl produced higher amounts of ROS which are able to reduce the aminoxyl radical. The obtained results indicate that EPR can be used as a method for *in vivo* evaluation of the redox state of plants under stress conditions, and could also be useful in determining the salt-stress tolerance of plants. Further studies, including different salt concentrations, and plant species, have to be conducted to verify these findings.

Keywords: *Centaurium erythraea*, EPR, Tempo, oxidative stress, salt stress

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Prospective protein markers for heat tolerance screening in potato, *Solanum tuberosum* L.

PP8-38

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Potato, *Solanum tuberosum* L. ssp. *tuberosum*, is the fourth most important food crop in the world and major vegetable crop in Serbia. Most of the commercially important cultivars of potato are well adapted to cool climates, whilst adversely affected by high temperatures. In order to develop a procedure for efficient screening of potato cultivars/genotypes regarding heat tolerance, we were investigating expression and accumulation of heat stress-related HSP18, HSP21, HSP101 and eEF1A proteins by immunobloting in six potato cultivars. Potato was grown in the irrigated field in Zemun Polje (randomized complete-block experimental design) and leaf samples for protein analyses were collected after high temperature incidents in summers 2011 and 2012. Besides, relevant agronomic yield parameters were determined each year. Years 2011 and 2012 were extremely hot; summer 2012 was the warmest since records began in Serbia. Positive, linear correlation has been determined between yield per plot and accumulation of HSP18, HSP101 or eEF1A under heat stress (HS) in examined potato cultivars. Negative correlation has been determined between height of primary shoots, as well as above-ground biomass, and accumulation of HSP18, HSP101 or eEF1A. Explicitly, potato genotypes/cultivars which accumulated higher amounts of HSP18, HSP101 and eEF1A under HS in the field, also had shorter primary shoots, lower above-ground biomass and higher tuber yield. HSP21 abundance under HS, however, did not correlate with any of the measured agronomic parameters. Our results indicate that among investigated proteins, HSP18, HSP101 and eEF1A might be considered as prospective protein markers for selection of high-productive potato genotypes under HS.

Keywords: potato, heat tolerance, HSP, eEF1A

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