

**Poster 5.0.98****Plasmid bearing rhizosphere *Pseudomonas* bacteria for biodegradation of organic pollutants in the plant rhizosphere**

V.V. Kochetkov<sup>1,2,\*</sup>, T.V. Siunova<sup>1</sup>, T.O. Anokhina<sup>1</sup>, O.I. Sizova<sup>1</sup>, A.M. Boronin<sup>1,2</sup>

<sup>1</sup> Institute of Biochemistry and Physiology of Microorganisms, Russian Academy of Sciences, 5 Prospect Nauki, Pushchino, Moscow Region, Russia

<sup>2</sup> State Educational Institute of Natural Sciences, 3 Prospect Nauki, Pushchino, Moscow Region, Russia

Plant growth promoting *Pseudomonas* (PGPP) rhizobacteria possess, jointly with plants, a significant bioremediation potential for combating mixed scattered contaminations of soils. The capability of degrading various pollutants is often determined in *Pseudomonas* by plasmids. The ability of these bacteria to transfer and receive most diverse plasmids by conjugation, biodegradation plasmids including, enables them to accelerate biodegradation of organic pollutants in the plant rhizosphere.

*Pseudomonas* plasmids were used to produce multifunctional bacterial strains and to develop biopreparations on their basis for soil cleanup from polycyclic aromatic hydrocarbons (PAHs) under conditions of co-contaminations with heavy metals and arsenic. The obtained multifunctional PGPP strains *P. aureofaciens* BS1393 (pBS216, pBS501), BS1393 (pBS216, pKS1) and *P. chlororaphis* PCL1391 (pBS216, pBS501), PCL1391 (pBS216, pKS1) were resistant to heavy metals and arsenic, degraded PAHs and efficiently protected plants from the phytotoxic action of these compounds. Bacterial population and plant biomass were observed to be increased significantly and efficiency of naphthalene/phenanthrene biodegradation to rise by 30% on average in the occurrence of co-contaminations with heavy metals and arsenic. It is important to note that these rhizosphere plasmid bearing *Pseudomonas* strains preserved all their key properties, such as stimulation of plant growth and protection of plants from phytopathogens.

Use of the potential of novel plasmid bearing multifunctional PGPP strains is a promising trend in protection of the environment.

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**Poster 5.0.99****Proteomic investigation of compatible interaction between wheat and yellow rust**

Yahya Emin Demirci<sup>1,\*</sup>, Cihan İnan<sup>2</sup>, Zafer Mert<sup>3</sup>, Dilara Maytalman<sup>4</sup>, Ahmet Tarık Baykal<sup>5</sup>, Aslıhan Günel<sup>6</sup>, Şenay Vural Korkut<sup>1</sup>, Semra Hasançebi<sup>5</sup>

<sup>1</sup> Yıldız Technical University, Faculty of Arts and Science Department of Molecular Biology and Genetics, Istanbul, Turkey

<sup>2</sup> Istanbul University, Faculty of Science Department of Molecular Biology and Genetics, Istanbul, Turkey

<sup>3</sup> Field Crop Research Institute, P.O. Box: 226, Lodumlu, Ankara, Turkey

<sup>4</sup> Istanbul University, Faculty of Science, Department of Biology, 34118 Vezneciler, Istanbul, Turkey

<sup>5</sup> TUBITAK Marmara Research Center, Genetic Engineering and Biotechnology Institute, Gebze, Kocaeli, Turkey

<sup>6</sup> Ahi Evran University, Faculty of Science and Letters, Department of Chemistry, Kirsehir, Turkey

The largest portion of yield loss in wheat harvesting results from the diseases caused by various pathogens. One of the most devastating diseases is the yellow rust (*Puccinia striiformis* f.sp. tritici-Pst) that causes high losses in efficiency and quality. Fungicide using and conventional agricultural methods are not effective as expected. Elucidation of the compatible interaction between the host and pathogen, especially identification of the differentially expressed proteins during infection provides to develop new strategies for disease control. Recently, genomic and transcriptomic studies have been reported about compatible interactions and disease development in plant tissue. However, as known, all processes in a biologic system is being formed by the contribution of various proteins and proteomic is accepted as a powerful tool for elucidation of complex cellular responses such as susceptibility and resistance.

In this study, aimed to identify differentially expressed proteins during disease development in susceptible Turkish bread wheat cultivar (Seri82). For this purpose, total proteins were extracted from either infected or mock inoculated susceptible wheat leaves and these proteins were separated by using ProteomeLab PF2D that is a two dimensional liquid chromatography system. After separation, proteome maps of pathogen inoculated and mock inoculated plant leaves were created and compared by using software. Selected differentially expressed proteins were digested by proteases and analysed by nanoLC-ESI-MS/MS. Obtained mass spectra data were processed with ProteinLynx Global Server V2.4 and searched against wheat and fungal reviewed protein database from Uniprot. Identified proteins were assessed about their roles in disease development in wheat.

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