



23rd International Congress on Sexual Plant Reproduction

Seeds for the future



Porto

13th to 18th July 2014

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Avenida da Boavista, 1466, Porto



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PS5-5

Comparative 2D-proteome analyses of non-pollinated, incompatibly and compatibly pollinated *thrum* and *pin* pistils of common buckwheat

Bojana Banović¹, Svetlana Dinić², Melita Vidaković², Jovanka Miljuš Djukić¹

¹Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia

²Institute for Biological Research "Siniša Stanković", University of Belgrade, Belgrade, Serbia

Common buckwheat (*Fagopyrum esculentum* Moench) is a self-incompatible dicot species with two morphologically different flower types: thrum (shorter style, longer anthers, larger pollen grains) and pin (longer style, shorter anthers, smaller pollen grains). In this species fertilization is allowed only between flowers of different morphology (compatible pollination), while it is prevented between flowers of the same morphology (incompatible pollination) through self-incompatibility (SI). Two flower morphs have different expression site of the SI response: in thrum pistil at the junction of stigma and style, and in pin pistil at 2/3 of style's length. It is well documented that SI response includes various protein-protein interactions in other studied plant SI species, but so far there are no such reports for buckwheat. The aim of our study was to track and compare changes in proteome profiles of thrum and pin pistils' upon their incompatible and compatible pollination. Total proteins extracted from non-pollinated, incompatibly and compatibly pollinated thrum and pin pistils were separated by 2D-PAGE and analyzed using Image Master 2D Platinum software v6.0. In each sample, proteome profiles revealed distribution over a wide mass range (10-130 kDa), with the prevalence of acidic to neutral proteins (pI 3.5-7) and only a few basic proteins (pI 7.5-9). The most abundant proteins were those shared by two morphs, which were present independently of pollination type (incompatible/compatible) (c. 90-95% of detected spots per sample). Proteins specific for morph and pollination type were also discovered (c. 5-10% of detected spots per sample) and will be identified by MS analysis.