Comparison of abiotic stress response systems between Arabidopsis thaliana and Fagopyrum esculentum

N.V. Demidenko , M.D. Logacheva, A.A. Penin

M.V. Lomonosov Moscow State University, Moscow, Russia, demidenkonatalia@gmail.com, maria.log@gmail.com, alekseypenin@gmail.com

Common buckwheat, *Fagopyrum*, is a widely cultivated pseudocereal and melliferous plant belonging to the family *Polygonaceae* (order Caryophyllales). Despite of its significance in food industry its cultivation area is restricted by environmental conditions. Buckwheat is sensitive to various abiotic stresses but there is a lack of any information about systems underlying stress response in buckwheat. Comparison of expression data between buckwheat and the most well-studied plant object *Arabidopsis thaliana* can reveal some evolutionally conservative pathways and therefore provide the information about stress response systems in common buckwheat.

We performed RNA-seq analysis of some essential stress series such as cold, heat and wounding for both studied plant species. For cold and heat stress series total RNA was extracted at the following time points: 1, 3, 6, 12 and 24 hours of treatment with consequent recovery into normal conditions at 1, 3, 6, 12, 24 and 72 hours after the end of treatment series. For wounding series such time points as 1, 3, 6, 12, 24 and 48 hours after treatment were considered. cDNA was sequenced using Illumina HiSeq2000 platform. After sequencing reads from buckwheat samples were mapped on reference genome of Fagopyrum tataricum, close relative of common buckwheat. Differentially expressed genes identification was provided by DESeq R package [1].

A set of differentially expressed genes were obtained for all series on every time point and consequent analysis between Arabidopsis and buckwheat was focused on searching of genes with similar expression pattern. Search was provided as between direct orthologs identified by bidirectional BLAST analysis and between groups of genes clustered into orthogroups by OrthoMCL algorithm [2]. Obtained data will promote the further analysis of abiotic stress

response systems in buckwheat and understanding the evolution of mechanisms underlying adaptation processes to environmental conditions.

1. S.Anders, W.Huber (2010) Differential expression analysis for sequence count data, *Genome Biology,* **11(10):**R106.

2. Li L, Stoeckert CJ Jr, Roos DS (2003) OrthoMCL: identification of ortholog groups for eukaryotic genomes, *Genome Res*, **13(9):**2178-89.