

## Transcriptomic changes underlying partial albinism in barley nearly isogenic line

Shmakov N.A.<sup>1\*</sup>, Glagoleva A.Yu.<sup>1</sup>, Doroshkov A.V.<sup>1</sup>, Afonnikov D.A.<sup>1</sup>, Khlestkina E.K.<sup>2</sup>

<sup>1</sup>*Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

<sup>2</sup>*N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia*

\* e-mail: [shmakov@bionet.nsc.ru](mailto:shmakov@bionet.nsc.ru)

Chlorophyll is a plant pigment involved in photosynthesis. Abnormalities in chlorophyll synthesis lead to albinism and premature death of the plant. However, cases of partial albinism are known. Such plants are a perfect model to investigate specific details of chlorophyll biosynthesis, plastid development, and interaction of plastid and nuclear genomes. An example of plant with partial albinism is a *Hordeum vulgare* nearly isogenic line i:BwAlm which contains a mutant allele of gene *Alm* located in the short arm of chromosome 3H. However, neither structure of the gene nor its functions are currently known. Microscopic analysis was implemented for phenotypic characterization of i:BwAlm line. Total mRNA of the i:BwAlm line and control Bowman isogenic line was sequenced using IonTorrent platform, and computational analysis was performed in order to identify genes involved in the process. Most of the differentially expressed genes are down-regulated in i:BwAlm line. Among these are genes that take part in chlorophyll biosynthesis, photosynthesis and nitrogen utilization. Down-regulation of genes located in plastid genome was observed. Additionally, *de novo* transcriptome assembly was performed, and putative new barley genes were predicted.

*Acknowledgements:* This work was supported by RSF project 18-14-00293.