Transcriptional activity of genes involved in the metabolism of abscisic acid in *Quercus robur* L. under drought conditions

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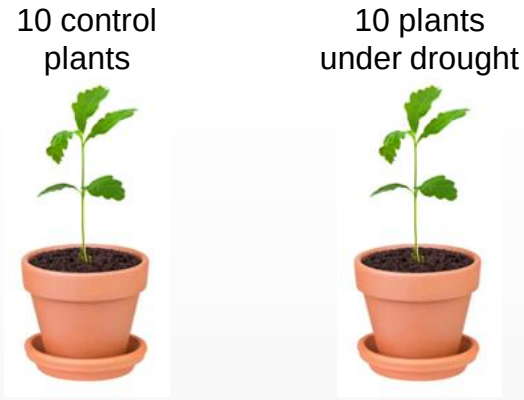
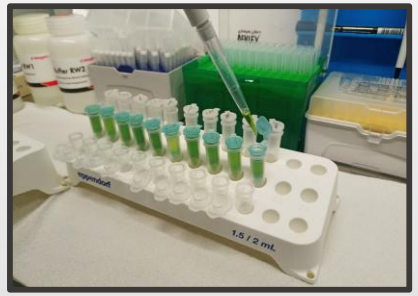
The aim of the study:

Evaluation of the transcriptional activity of genes involved in the abscisic acid metabolism in *Quercus robur* L. under soil drought conditions



① *Q. robur* seedlings were divided into two groups of 10 plants each: **control** (75-80% moisture-holding capacity – MHC) and **drought** (8-12% MHC)

② Sampling of leaf blades after **2 weeks**



③ RNA extraction with DNase treatment

Evaluation of the quantity and quality of RNA

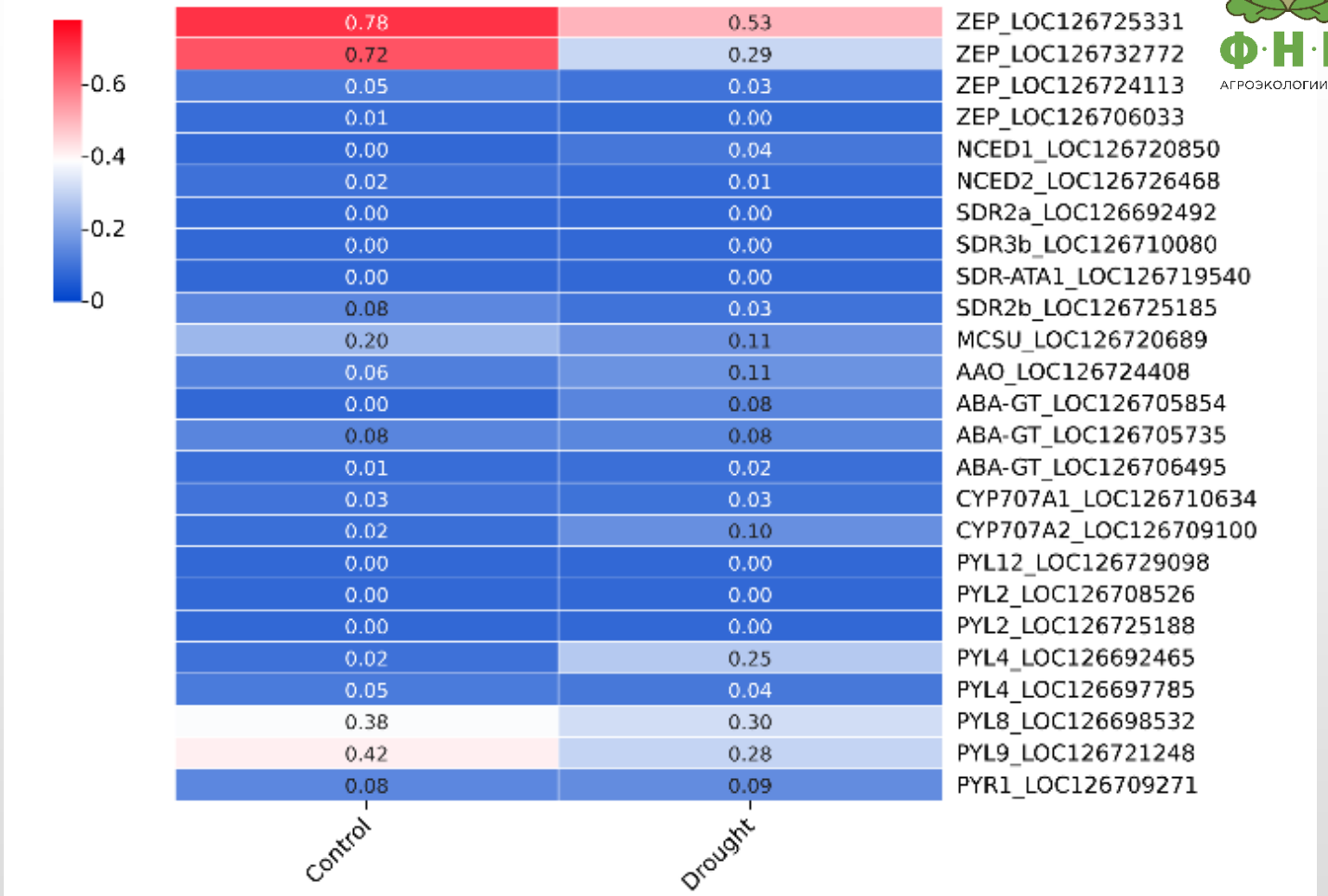
④ Preparation of the sequencing library

⑤ Nanopore RNA-sequencing on a MinION device

Base calling and read mapping with the Dorado software

Results:

- the **ZEP** (zeaxanthin epoxidase) gene family exhibited high transcriptional activity in control group, particularly ZEP_LOC126725331 and ZEP_LOC126732772, with notable decrease under drought stress
- **NCED1** and **NCED2** (9-cis-epoxycarotenoid dioxygenase) showed low transcriptional activity in both groups
- the oxidation-stage enzymes **SDR** (short-chain dehydrogenase/reductase) and **AAO** (abscisic-aldehyde oxidase) demonstrated generally low expression levels, though **AAO** activity was nearly two-fold higher under drought conditions
- **ABA-GT** (abscisate beta-glucosyltransferase) genes displayed enhanced activity during drought
- **CYP707A1/2** (abscisic acid 8'-hydroxylase) remained weakly expressed in both conditions
- among **ABA receptors**, only PYL2_LOC126725188 showed increased transcriptional activity under drought



Transcriptional activity of genes involved in the metabolism of abscisic acid in *Q. robur* under drought conditions, which were identified using ONT long-read RNA-Seq technology

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Conclusions:

The study revealed drought-induced changes in ABA metabolism-related gene expression in *Q. robur*, including decrease of **ZEP genes** activity and increase of **AAO** and certain **ABA inactivation genes** activity. These results demonstrate complex regulation of ABA biosynthesis and catabolism under drought conditions, though further research is needed to fully understand drought adaptation mechanisms, particularly through investigating ABA dynamics at different stress stages.

The research was carried out within the state assignment of Ministry of Science and Higher Education of the Russian Federation No. FNFE-2025-0013 «Regulation of gene expression involved in the adaptation to adverse environmental factors to improve economically valuable traits of woody and cultivated plants used in agroforestry».

Thank you for your attention!