



BOOK OF ABSTRACTS



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AGRONOMIC AND METABOLIC CHARACTERIZATION OF RICE UNDER COMBINED HEAT AND DROUGHT STRESS AND POST-STRESS RECOVERY DURING FLOWERING

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Global climatic models predict the occurrence of heat waves and drought spells to increase in the future. Heat and drought stresses, which are identified as constraints to sustainable rice production, invariably occur simultaneously under field conditions; however, little is known about the effects of their interaction in rice. In addition, recovery from stress has not been well studied. To address these, three cultivars with contrasting tolerance to heat and drought stresses were assessed for their agronomic and metabolic responses to this stress combination under field conditions during the critical flowering period and subsequent recovery from drought. Yield was significantly reduced under stress, which could be traced to decreased spikelet fertility and grain weight. Increased grain chalkiness and lower head rice yield were also observed. The heat- and drought-tolerant cultivar N22 exhibited the lowest reduction compared to the drought-tolerant but heat-sensitive Dular and heat- and drought-susceptible Anjali. Metabolic analysis revealed spatial differences in the metabolite profiles of the three cultivars, wherein flag leaves were more responsive to combined stress compared to spikelets. Levels of most metabolites under stress were maintained during recovery, while some metabolites showed altered levels. Metabolites with increased pool sizes under stress and during recovery relative to control conditions possibly function in conferring tolerance to N22. These responses are currently being validated with data from additional field trials. Potential metabolite markers will aid in establishing high-throughput molecular phenotyping to identify more tolerant cultivars for breeding to increase combined stress tolerance in rice.

COMPARATIVE STUDY OF XANTHINE DEHYDROGENASE IN SOFT WHEAT AND *BRACHYPODIUM* FOR INTRODUCTION OF THE LATTER INTO THE BREEDING PRACTICE

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Wheat main economically important cultivated crop in Kazakhstan, one of the world leaders for production of marketable grain, is strongly affected by the fungal diseases. Most dangerous and common pathogen of grain is brown leaf rust. Xanthine dehydrogenase (XDG) is considered as a water-soluble enzyme having physiological function in the metabolism of reactive oxygen species. It is known that the rate of purine degradation controlled by XDG increases during wheat infection with *Puccinia recondita*. From the literature search it was revealed that *Brachypodium* (Bd) halophyte now frequently used as a modern system for cereals research, which unlike *Arabidopsis* might also serve as a host for rust diseases caused by the pathogens from *Puccinia* genus [1, 2]. The aim of the current research is the comparative study of XDG enzyme in soft wheat and Bd.

Objects of research – two local varieties of spring wheat and Bd (line 21 seeds provided by RIKEN BioResource Center, Japan). Degree of resistance or susceptibility to leaf rust served as main reason for selection of wheat varieties. In two leaves growth stage, plants were subjected to experimental inoculation with rust urediniospores (provided by Kazakhstan SRI for Biological Safety); with untreated plants serving as control. Symptoms of plant infection were recorded on the 7th day. They appeared on the upper side of leaves, sometimes on leaf sheaths in the form of brown pustules with a diameter of 0.5–2.0 mm. Estimation of XDG activity was performed by the method of native gel electrophoresis. Leaves were extracted in an appropriate buffer (in ratio of 1:4 and 1:3 for leaves and roots, correspondingly), using a rotar, pestle and shaker vortexing. The buffer consisted of 250 mM Tris-HCl (pH = 8.48), 1 mM EDTA, 14 mM GSH, 4 mM DTT, 5 mM L-cysteine, 0.05 mM Na₂MoO₄·2H₂O solution, 0.1 mM PMSE, 0.001 mM pepstatin A and 250 mM sucrose. Extracts were centrifugated at 14,000 rpm under 40 °C for 20 minutes. XDG activity was evaluated by the relative intensity of formazan bands staining using the ImageJ processing of digital images of gels obtained on Epson Perfection V750 PRO scanner.

According to the results in Bd leaves a negative correlation by 36% between XDG activity and infection is observed, while for roots it is generally positive. This demonstrates that the main burden in halophyte adaption in terms of XDG activity is performed by roots. XDG inhibition may in turn lead to increased cell tolerance to bacterial pathogens.

References

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GENETIC ENGINEERING OF ABIOTIC STRESS RESPONSE IN PLANTS

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