

Modulation of cadmium stress responses in wheat by putrescine pre-treatment under blue and white light

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Blue light is an essential environmental factor that regulates various plant functions, including morphology, photosynthesis, and both primary and secondary metabolism. While some studies suggest that blue light may enhance stress tolerance, its precise mechanisms remain unclear. Polyamines are well known as being involved in stress adaptation, but their interactions with light dependent processes are not well comprehended. Polyamine metabolism could be influenced by light quality, which might affect its relationship with other protective compounds. According to these, the main question of the present work was that whether blue light induces different responses during Cd stress, especially which are related to polyamine metabolism, and whether it may be able to modify the protective effect of exogenous putrescine compared to white light conditions in wheat. The results indicated that Cd stress was less severe under blue light than under white light. Metabolite and gene expression levels were independently affected by blue light, which resulted in reduced Cd uptake, phytochelatin content, and higher levels of conjugated polyamines. Pre-treatment with putrescine provided protection, particularly under white light, and emphasized differences between the effects of blue and white light under Cd stress—especially in phytochelatin synthesis, polyamine metabolism, and the accumulation of phenolic compounds and plant hormones. B light exerted stronger effects on methylation than PUT, while PUT treatment induced more alterations under W light. The gene ontology study revealed that differentially methylated genes are involved in a wide range of cellular processes, such as stress responses, hormone signalling and stress responses. Our results indicate that blue light increases Cd tolerance in wheat and changes the defense mechanisms, particularly when putrescine is present in excess.

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Exploiting somaclonal variability to increase drought stress tolerance in grapevine

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Global warming has enhanced the frequency and severity of drought events, hence calling for a better management of water resources in the vineyard and for an improvement of breeding platforms. Somatic embryogenesis (SE) is a morphogenetic process in which the plant regenerative potential is exploited to replicate a whole organism starting from somatic explants. Moreover, SE process and *in vitro* culture can generate somaclonal variability, i.e. genetic variability resulting from gene mutations, changes in epigenetic marks, or phenotypic alterations, which can represent a powerful green biotechnological tool for genetic improvement purposes. The aim of this work was to deepen the somaclonal variation phenomenon and demonstrate whether vines *in vitro* regenerated through SE, namely somaclones, can tolerate water deprivation better than the mother plant. Physiological trials of water stress and recovery were conducted on eleven somaclone lines of *Vitis vinifera* "Nebbiolo" CVT 185. During the experiments, dynamic changes in the main eco-physiological parameters (gas exchange and stem water potential) were evaluated daily on target somaclones compared to the mother plant. Alterations in biometric and anatomical traits and in xylem hydraulic conductivity were also inspected. The observed responses were further deepened by analyzing differences in the accumulation of defense secondary metabolites, non-structural carbohydrates (NSC), starch, osmoprotectant solutes, hormones and in the transcription of stress-responsive genes. In parallel, sequencing analyses of the

genomes of the best and worst performing lines are ongoing to inspect genetic alterations potentially affecting specific physiological modifications. The integration of physiological, biochemical, and molecular data proved that "Nebbiolo" somaclones are more tolerant to drought. The integration of physiological, biochemical and molecular data proved that grapevine somaclones are more tolerant to drought. The exploitation of somaclonal variability can therefore represent an effective and ready-to-use genetic improvement approach for implementing clonal selection and breeding programs in grapevine.

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Genetic and physiological control of early vigor and transpiration efficiency in rice

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In the current context of water scarcity and global warming, the transition of rice cultivation from anaerobic to aerobic system is crucial to reduce water consumption and greenhouse gas emissions. Early vigor to better compete with weeds and transpiration efficiency (TE) for improved water use are two target traits for breeding new varieties better adapted to aerobic rice agrosystems. We previously identified a genetic locus located on chromosome 5 involved in the control of these traits in African rice (*Oryza glaberrima*) using association genetics. This locus colocalized with QTL previously reported for early vigor and lateral root development in *O. sativa* (Cui *et al.*, 2002; Dinh *et al.*, 2023). A gene named *OgFPS1* encoding the Farnesyl Diphosphate Synthase 1 was identified as an interesting candidate. Here, we further

characterized the role of this locus in the control of early vigor and TE and investigated the function of *FPS1*. To this end, we first performed a Linkage Disequilibrium analysis to define genetic locus into a QTL region and identify different haplotypes for this QTL. A 109 kb QTL region containing 23 candidate genes and two major haplotypes were identified. Expression studies in 8 rice genotypes belonging to the two main haplotypes showed that *OgFPS1* was the only gene significantly more expressed in leaves and roots of the haplotype associated with greater vigor and TE. In parallel, we found that the *Arabidopsis thaliana fps1* mutant shows defects in early vigor and TE. Altogether, these results suggest that *OgFPS1* and his homologous *AtFPS1*, are potentially involved in the control of these traits. Ongoing work aims to validate the QTL region using a biparental population, while examining the functional role of *FPS1* in early vigor and TE through gene editing in *O. sativa*.

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