

POSTER PRESENTATION

Open Access

Mitochondrial iron-sulfur cluster genes in *Eucalyptus*

Luisa de Oliveira*, Giancarlo Pasquali, Jeverson Frazzon

From IUFRO Tree Biotechnology Conference 2011: From Genomes to Integration and Delivery
Arraial d'Ajuda, Bahia, Brazil. 26 June - 2 July 2011

Iron-sulfur [Fe-S] clusters are prosthetic groups required to maintain life processes including respiration, photosynthesis, metabolic reactions, sensing, signaling, and gene regulation. In plants the biogenesis of Fe-S proteins is compartmentalized and adapted to specific needs of the eukaryotic and photosynthetic cell. Although critical to so many fundamental metabolic pathways and drastically affecting plant adaptability and productivity, Fe-S proteins were never investigated in woody species. *Eucalyptus grandis* is an important economical tree widely cultivated in subtropical regions which suffers under low temperature stress. Here we describe a transcriptional analysis of the *E. grandis* *NFS1*, *ISU1* and *ISA1*, three genes involved in the biogenesis of [Fe-S] clusters. Microarray analyses were carried out for the comparison of global gene expression in leaves and vascular tissues (xylem) of *E. grandis* and vascular tissues of *E. globulus*. In general, leaves from *E. grandis* demonstrated higher expression of these genes than xylem. *EgrISU1* had a constitutive expression in *E. grandis*, but its expression pattern was higher in this species than in *E. globulus* xylem. Differences observed in the relative gene expression profile between xylem tissues from the two *Eucalyptus* species suggest that these genes may be implicated in the contrasting phenotypic characteristics of their wood. The response of these genes to a series of hormonal and stress signals over *E. grandis* seedlings was also evaluated by RT-qPCR. After the chilling treatment of seedlings, *EgrNFS1* and *EgrISU1* showed 6 to 8-fold and 0.6 to 1.7-fold increase respectively; and *EgrISA1* exhibited a drastic 69 to 114-fold increase. These data are the same observed in *Arabidopsis* microarrays available in GeneVestigator database. These results suggest that (i) *NFS1* and *ISA1* may be related to the cellular

response to stress caused by chilling, and (ii) the increase in the expression is probably due to sulfur metabolism. A time-course chilling experiment was also carried out. The *ISU1* gene expression was higher in the first two hours of treatment and decreased right after that period. The *ISA1* gene, which showed the highest expression in the previous experiment, didn't show significant differences in the expression pattern during the 16 hours of chilling, as well as the *NFS1* gene. Our data indicated that Fe-S proteins are possibly involved in the recovery of plants after chilling stress.

Published: 13 September 2011

doi:10.1186/1753-6561-5-S7-P160

Cite this article as: de Oliveira et al.: Mitochondrial iron-sulfur cluster genes in *Eucalyptus*. *BMC Proceedings* 2011 5(Suppl 7):P160.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

 **BioMed Central**

* Correspondence: lu_abruzzi@yahoo.com.br
Biotechnology Center, Federal University of Rio Grande do Sul, Porto Alegre, RS, Brazil