

ARBUSCULAR MYCORRHIZAL SYMBIOSIS PROMOTES THE TRANSCRIPTION OF ANTIOXIDANT GENES IN A WHITE POPLAR CLONE TOLERANT THE HEAVY METALS

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Poplar (*Populus spp.*) represents one of the tree species of greatest interest for phytoremediation because of high biomass production, high growth vigour and the economic importance.

The exposure to heavy metals, HM, triggers in the plant a complex network of responses. They include mobilization of the antioxidative protection and switching on the synthesis of metal-binding phytochelatins and metallothioneins, MT, in the cytoplasm. Under natural condition, roots of many tree species are associated with mycorrhizal symbionts. This significantly modifies the response of plants to HM and it has convincingly been shown to alleviate HM-induced stress.

The aim is to study how the exposure to HM and the symbiosis with two arbuscular mycorrhizal (AM) fungi, *Glomus mosseae* or *Glomus intraradices*, could affect the transcription of the antioxidant and MT genes in a tolerant white poplar clone so that to deep on the knowledge on interrelated networks of the different antioxidant and detoxification systems activated by the plant in response to stress.

Accordingly, it was performed the expression analysis of genes coding for antioxidant enzymes and proteins induced by heavy metals (SOD, CAT, APX, DHAR, GR, MT).

Total RNAs was extracted from leaves of cuttings grown both on polluted and on non-polluted soil (high concentration of Cu and Zn), in the presence or absence of the AM symbionts, cDNA obtained after retro-transcription was used for gene expression analysis through a reverse northern approach.

In leaves of non-mycorrhizal plants, only few genes were activated in a significant manner in response to HM. Two *Sod* genes, encoding for a chloroplastic FeSOD and for a mitochondrial MnSOD, the catalase (CAT2) and a dehydroascorbate reductase (DHAR) genes. On the other hand, the colonization with *G. intraradices* or *G. mosseae* resulted in a strong expression increase of many of the genes considered. In fact, we observed the increased transcription of all CAT, SOD (chloroplastic and mitochondrial proteins) and MT genes as well. In addition, our data point out the different effect of *G. intraradices* and *G. mosseae* on gene transcription. In fact, AM colonization with *G. mosseae* resulted in a higher transcript level of one CuZnSOD, of one catalase (*Cat3*) and of two MT genes in comparison with *G. intraradices*. These results suggest a more effective response to the oxidative stress imposed by HM in the presence of the AM symbionts and particularly of *G. mosseae*.

Previous studies about the interaction of poplar clones and these two AM fungi, in the presence of copper or zinc, revealed that they, and especially *G. mosseae*, improved the plant tolerance to HM stress, affecting some biochemical mechanisms of stress response, like polyamine biosynthesis and conjugation.

In conclusion our results indicate that the AMF colonization resulted in a general up regulation of antioxidant genes and that colonization with *G. mosseae* resulted in enhancement of specific defence genes demonstrating the specificity of interaction poplar clone/AM fungi in the response to HM. stress.