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Effect of arsenic on gene expression in an elite Arundo donax L. clone, particularly suitable for assisted phytoremediation.

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Arsenic (As) toxicity of soil and water is an increasing menace across the globe. Among the 1.4 million worldwide contaminated sites, 41% are in the USA, and US Environmental Protection Agency has recognized that As concentration in some Australian soils was greater than 10,000 mg kg^{-1} (Smith et al. 2002). Heavy use of pesticides, containing As, is considered the main source of this kind of pollution (Chopra et al. 2007). Considered the global scale of the problem, we approached the remediation process of contaminated soils using a global spread species the Arundo donax L., a plant able to thrive in diverse and environmental tricky habitats producing very high amount of biomass. This study aimed to estimate the remediation capacity of A. donax grown on sandy soil in the presence or not of a Plant Growth Promoting Bacteria (PGPB) consortium, and under increasing concentrations of As, in order to identify and quantify gene expression related to As uptake, transport, accumulation and plant stresses.
Although the A. donax transcriptome has been already sequenced, it is not completely annotated, then a preliminary bioinformatics study was conducted to identify the candidate sequences involved in the investigated processes. We focused our attention on several transporter gene families such as: ABC, Phosphate, Phytochelatin, etc, and also on stress-related genes. Ramets of an elite A. donax genet were grown in green house on sand spiked every three days with a solution containing 2, 10, 20 mg L-1 of $NaAsO_2$, combined (or not) with a bacteria consortium constituted by two strains of Stenotrophomonas spp. and one of Agrobaterium sp., previously isolated and characterized as PGPB (Cicatelli et al. 2016). Leaf samples were collected each five days and stored in liquid nitrogen for the following molecular analyses. At the end of the experimentation biomass, As, phosphorus, and other elements were evaluated in the different plant organs. Sand As content was analysed at the start of the experiment, one week after the As last addition, and at the end of the trial. No visible toxic effects were observed in the different experimental theses, although some differences in As accumulation were detected in the plant organs in relation on treatments. Bioinformatics analysis retrieved putative gene sequences, within the A. donax transcriptome, related to As transport, and plant stress. The molecular results demonstrated, for the first time, that, in A. donax leaf, several transporter and enzyme are involved in As accumulation and detoxification.

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