

Phytoremediation capacity of black poplar clones and dynamic of rhizosphere microbiome in relation to Zn soil pollution and/or compost amendment.

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Remediation of environments, polluted by heavy metals (HMs), needs ecologically and economically sustainable strategies, such as phytoremediation, in order to restore quality levels well-suited for health and survival of living organisms, possibly relying on the best available methodology. To obtain an efficient HM soil phytoremediation, a promising strategy should include the modulation of some factors influencing the efficiency of HM removal, like bioavailability of the metals in the soil, soil properties, metal speciation, plant species and rhizosphere community. Poplars are of great interest for their useful phytoremediation traits among them we highlight: its ability to grow on nutrient-poor soil, a deep and/or wide-spreading root system, a fast rate of growth, and a relevant metal-resistance. In addition, the application of compost is an excellent way of recycling both nutrients and organic matter contained in the waste organic fraction, but also to improve quality of the polluted soil (e.g., fertility, texture, acidity, water content, CEC, etc.). The application of compost introduces new organic matter, nutrients, as well as microorganisms (bacteria and fungi). These microorganisms not only can promote plant growth, but they have an influence on the mobility and on bioavailability of HMs, in soils and rhizosphere, and can either enhance or repress HM transfer from soil to the harvestable epigeous part and therefore the efficiency and rate of phytoremediation, and they can also protect plants from toxicity. The aims of this study are to compare the phytoremediation capabilities of two different black poplar clones, one tolerant and one HMs sensitive, grown on Zn spiked soil (450 mg kg⁻¹ soil dry weight), in the presence or not, of compost, and to investigate the effects of different growth conditions on bacterial communities of rhizosphere. The N12 tolerant poplar clone, belonging to an Italian poplar collection, and the Jean Pourtè, a commercial poplar clone, were grown in greenhouse on Zn spiked soil with/without compost for three months. Root, stem and leaf samples were collected and stored separately for DW measurements and for determination of element concentrations. Therefore, in order to evaluate the dynamics of soil microbial communities in response to treatments (metal contamination and/or compost amendment), root rhizosphere soils were harvested at the end of the trial, and the collected microorganisms were analysed using a metagenomic approach. To assess the composition and diversity of microbial communities, the hypervariable regions from small-subunit ribosomal RNA (16S rDNA) gene and from ITS (Internal Transcribed Spacers) were sequenced with NGS (Next Generation Sequence) procedure. Metal addition did not significantly influence the growth of plants; while compost amendment significantly improved the growth and biomass production of both clones. The NGS analysis revealed a consistent biodiversity (in terms of richness and abundance of identified taxa) rhizosphere microbiomes, in relation to clone, metal and/or compost addition to soil.