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GENOREM: IMPROVING BIOREMEDIATION OF POLLUTED SOILS THROUGH ENVIRONMENTAL GENOMICS

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Abstract

Mining activities, oil and gas extraction, industrial processes, and most forms of modern agriculture all contribute to soil contamination, creating a significant problem world-wide. Efforts are underway to reduce the production of industrial and agricultural pollutants at their source, but this does not address the enormous legacy sites containing trace metals and organic pollutants that can remain in the soil. Pollution is not only threatening the quality of life in terms of human and environmental health, but also the future availability of essential resources, such as agricultural land and clean water. If we do not intervene promptly, repercussions on the ecological balance on our planet may be either irreversible or most costly to remediate. GenoRem project proposes an innovative phytoremediation approach to decontaminate polluted sites, employing scientifically controlled, most effective associations of plants, fungi and bacteria. Yet, the decontamination process itself is due to complex interactions of plants with soil microbes. Major objectives of the GenoRem project are therefore: (i) isolation of soil microbes that are most effective in decontamination, either by degradation of organic materials such crude oil, or in case of toxic trace metals, take-up and concentration by plants; (ii) developing combinations of the most effective plants fungal and bacterial symbionts, and other microbes, which will be outperform current phytoremediation practices without these selected microbes.

A large-scale (0.5 h) phytoremediation trial was set up in summer 2011, in the field of an old oil refinery in Montreal region (Quebec, Canada), to submit 11 willow cultivars to a soil contaminated with a mixture of organic and inorganic pollutants. In total, about 10 000 trees were planted using split-plot design. We collected soil and root samples in May, August and October 2011 and isolated a broad range of free living fungi and bacteria, arbuscular mycorrhizal fungi (AMF), endophytes and rhizosphere microorganisms. We used novel cultivation strategies such as high-throughput dilution-to-extinction on low nutrient content media amended with crude oil and other organic pollutants. Fungal and bacterial isolates have been molecularly identified using the ITS and 16S rRNA genes, respectively. Endophytes and AMF were trapped using indigenous plants. Metagenomics approaches were also used to investigate microbial diversity and community structures associated with willow cultivars and their analyses are in progress.
