

Environmental genomics of willows and microorganisms applied to the decontamination of abandoned industrial sites

Michel Labrecque and collaborators

What is GenoRem?
GenoRem is a multidisciplinary research project launched in 2011 that brings together scientists from diverse disciplines to work on the development of innovative approaches to the decontamination of polluted sites. This research integrates genomics to study how plants (in particular, willows) and microorganisms interact to extract or degrade soil contaminants.

Research objectives

• Improve Salix phytoremediation using physiological and molecular approaches.
• Study the structure, function and activities of bacterial and fungal communities in contaminated soils.
• Isolate and characterize soil bacteria and fungi effective for bioremediation of organic and trace metal contamination.
• Evaluate the response of trace elements in soils and plants to phytoremediation treatments.
• Apply genome sequencing and bioinformatics.
• Analyze the normative framework leading to guidelines for policy makers.

To meet these objectives, three experiments were set up:

A large-scale (0.5 h) phytoremediation trial was set up in the summer of 2011 on the abandoned site of an old oil refinery in the Montreal region (Quebec, Canada). Eleven willow cultivars were planted in a soil contaminated with a mixture of organic and inorganic pollutants. In total, about 10,000 trees were planted using a split-plot design. The design includes a non contaminated sector used as a control.

Another site (800 m²), specifically contaminated by trace metals (Cd, Cu, Pb, Zn), was planted with three willow genotypes (S. miyabeana SX67, S. purpurea ‘Fish Creek’ and S. caprea S365). The trial includes eight replicates with control plots without willows.

A greenhouse experiment comprising six treatments in which the selected willow genotype (S. purpurea ‘Fish Creek’) was cultivated in contaminated or non contaminated soils (both type of soil taken from the old oil refinery site), with or without AMF inoculum (Glomus irregulare). Pots without plants (with contaminated and non contaminated soil) were used as control.

Anticipated deliverables

• Identification of best Salix genotypes for phytoremediation of sites contaminated with organic and/or inorganic contaminants.
• Comparison of physiological responses of several willow genotypes to contamination.
• Identification of potential molecular pathways involved in detoxification of contaminants.
• Salix purpurea transcriptome grown in contaminated soils.
• Metabolic database and protein-to-metabolite networks of willow.
• Isolation and identification of AMF and bacterial taxa associated to soils with high contaminant removal efficiency.
• Genome sequencing of the most promising fungal (AMF) and bacteria.