Field-scale evaluation of the oil remediation capacity of the legume Galega orientalis

Lijuan YAN1
Miiro JÄÄSKELÄINEN1
Petr1 PENTTINEN1
Tuula PUHAKAINEN2
Kristina LINDSTRÖM1
Asko SIMOJOKI2
Fred STODDARD2
Departments of 1 Food and Environmental Science; 2 Agricultural Sciences; University of Helsinki, Finland

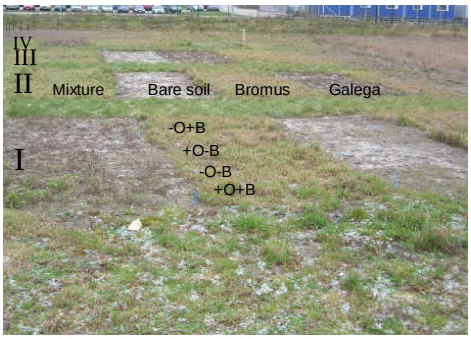
Background

•Glasshouse-based experiments have shown:
- Biological activity associated with *Galega* roots accelerates the degradation of oil contamination
- Plant growth promoting bacteria (PGPB) improved nodulation and plant yield

•This needed to be confirmed in the field
•Grass-legume mixtures often out-yield their components, and grasses have different root-associated bacteria
•Hence a multi-year trial was prepared using the legume *Galega orientalis* (forage goat's rue) and the grass *Bromus inermis* (smooth brome), singly and in combination, to remediate oil-contaminated soil
•This offered an opportunity to measure N_2O release

Aims

•Determine plant responses to the stress
•Follow changes in the bacterial community structure
•Determine the effects of the crops and treatments on N_2O release



Layout of the experiment, photographed in November 2010. Four replicates I-IV of 4 main plots (Galega, Bromus, Mixture, Bare soil) each of which has 4 subplots of ±O (oil) and ± B (PGPB) in factorial combinations

Materials and methods

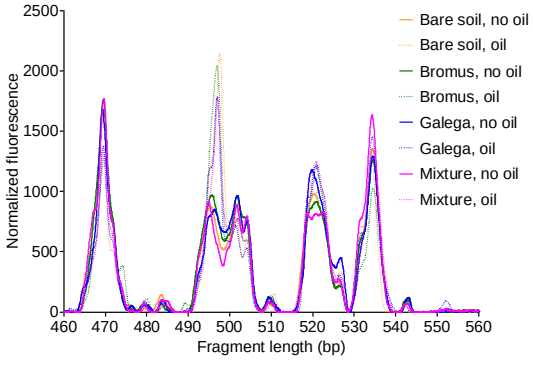
Plots were established in June 2009
•*Galega orientalis* cv Gale
•*Bromus inermis* cv Lehis
•Singly, in 75 grass:25 legume ratio, or bare soil as main plots in Randomized Complete Block Design
•Subplots ±fuel oil (6 kg per plot, 7000 ppm), ± PGPB, in factorial combinations
•60 kg/ha N fertilizer was given to the grass plots in 2009 but none subsequently
Soil samples taken 4 times: A: July 2009, B: May 2010, C: November 2010 and D: May, 2011
•Top soil (0-20 cm) passed through 5 mm sieve and stored in -20 °C freezer before analysis
•DNA extracted using standard techniques
•Soil bacterial community structures studied by length heterogeneity PCR (LH-PCR), using domain specific primers to amplify 16S rDNA (Mikkonen *et al.*, 2011).
Gas traps were installed in May 2011 on –oil-PGPB plots
•Samples were taken 6 times during 2011
•N_2O content of the collected gas was determined by GC

Results

Plants

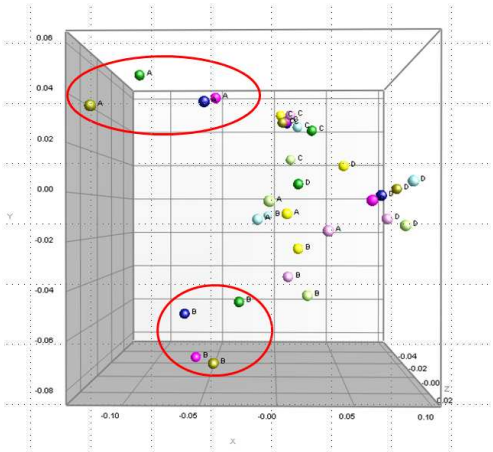
•In 2010, plant dry matter production was greatest in the crop mixture plots and in the +Oil +PGPB treatment
•In 2011, there was no significant difference in plant DM production among the main plot or subplot treatments
•% Galega in the mixtures declined through each growing season but recovered in spring

Bacterial community structure



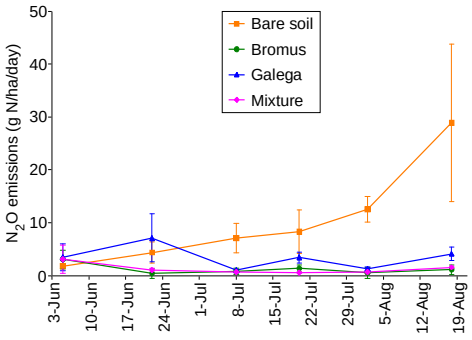
- At the start of the experiment, LH-PCR fragment lengths differed greatly between oil and no-oil plots, but showed few differences between crops

Bacterial community dynamics



- Multi-dimensional scaling ordination separates the LH-PCR profiles of bare soil (yellow), Bromus (green), galega (blue), and mixture (pink) (non-PGPB treatment only)
- Oil-treated plots at times A and B are clearly separated (red rings) from non-oil plots
- By time C, the oil plots cluster with the non-oil plots
- At time D, all treatments have shifted

Greenhouse gas release



- N_2O release was greatest from the bare soil except at the start of the season
- N_2O release from the Galega plots exceeded that from the grass and mixture plots
- Grass plots were not fertilized in 2011

Conclusions

•After the first year, yields were not affected by oil or bacteria treatments
•Changes in bacterial community structure followed oil contamination
•These alterations reduced with time
•The soil bacterial community can recover from oil contamination
•N_2O emission was very high from the fallow plots. Unfertilized grass released little N_2O
•Harvested biomass can be used for biomethane production

HELSINGIN YLIOPISTO
HELSINGFORS UNIVERSITET
UNIVERSITY OF HELSINKI

Legume Futures