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## Structure, diversity and density of the protocatechuate-degrading bacterial community - Impact of long-term organic amendments

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# Impact of long-term organic amendment on *pca* bacterial community

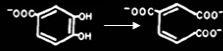
## Structure – Density – Diversity

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### Background

*pca* bacterial community: bacterial guild involved in the ring fission of the protocatechuate.



**Protocatechuate:** key intermediate of the degradation of aromatic compounds (deriving from complex organic matter)

**Molecular marker used:** *pcaH* coding the  $\beta$  sub-unit of the protocatechuate 3,4-dioxygenase

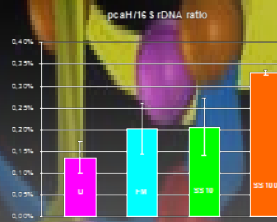
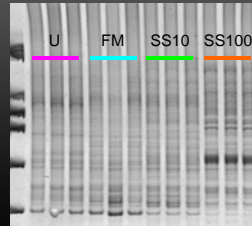
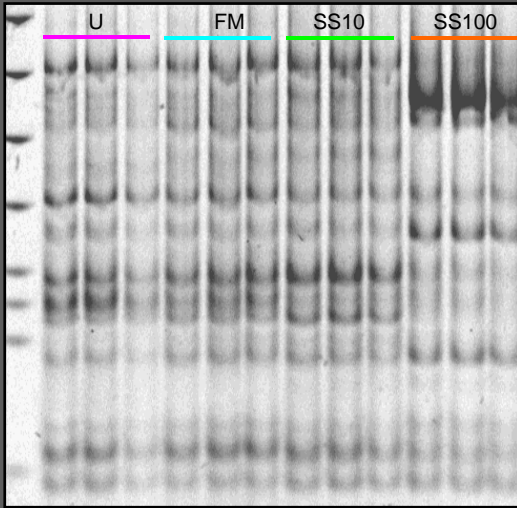
### Experimental design

17 years of amendment – maize cropped

4 conditions

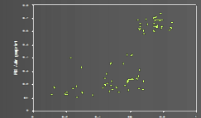
- U:** Un-amended, control NPK fertilised
- FM:** Farmyard manure, 10 ton/ha/year
- SS10:** Sewage sludge, 10 tons/ha/year
- SS100:** Sewage sludge, 100 tons/ha/2years

### Results



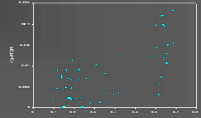
### Structure:

- Ribosomal Intergenic Spacer Analysis (RISA): assessing the global community structure) performed for each experimental condition by triplicates.
- Comparison of **RISA vs *pcaH* fingerprints**: mantel correlation test based on Bray & Curtis dissimilarity matrices
- Fingerprints significantly correlated** ( $r=0.702$ )
- Global and functional communities similarly impacted** by organic input, particularly SS100 treatment.



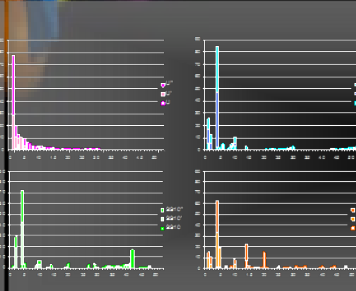
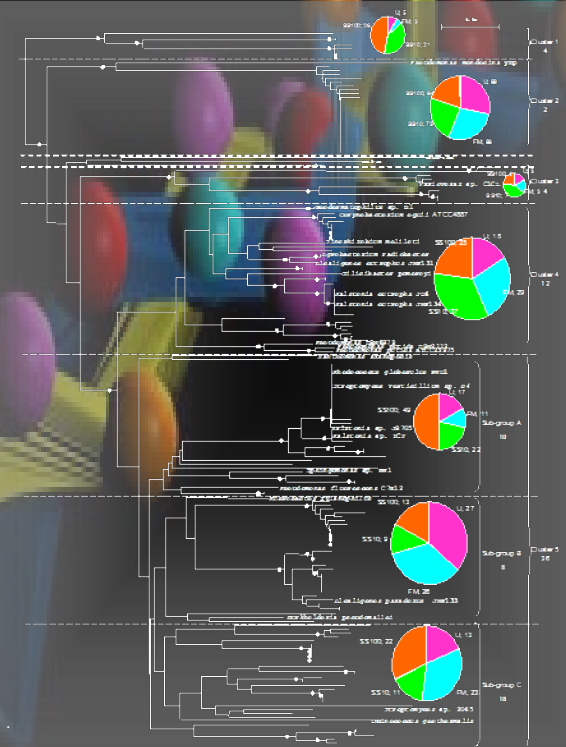
### Density:

- Abundance evaluated by q-PCR: *pcaH/16S rDNA ratios*.
- pca* community is significantly more abundant in **SS100**
- Comparison of density vs *pcaH* fingerprints: mantel correlation test based on Euclidian and Bray & Curtis dissimilarity matrices
- Matrices significantly correlated ( $r=0.764$ )
- Density and structure of *pca* community similarly impacted by organic input



### Structure:

- pcaH* PCR- RFLP performed for each experimental condition by triplicates.
- SS100 significantly different from the control (U), FM and SS10
- Important impact** of high organic matter input on *pca* bacterial community (i.e. SS100)



### Diversity

- Phylogenetic tree of PcaH amino-acid sequences
- Important diversity** of PcaH sequences in all experimental conditions
- Speciation** according to the treatment (i.e. Cluster 5 subgroup B, SS100 dominates)
- Distribution of RFLP profiles: Same dominant profile in FM, SS10 and SS100.
- Different dominant profile for U** but grouped in same cluster

### Conclusion

- Impact of organic amendment on Structure – Density – Diversity of *pca* bacterial community
- Impact increased for high carbon input (i.e. SS100)
- Tendency respected for structure – density and diversity

**Carbon input changes the genetic potential of the protocatechuate degrading community therefore changing soil functioning**

### Acknowledgement

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Laurent Philippot for scientific input and guidance for correlation tests