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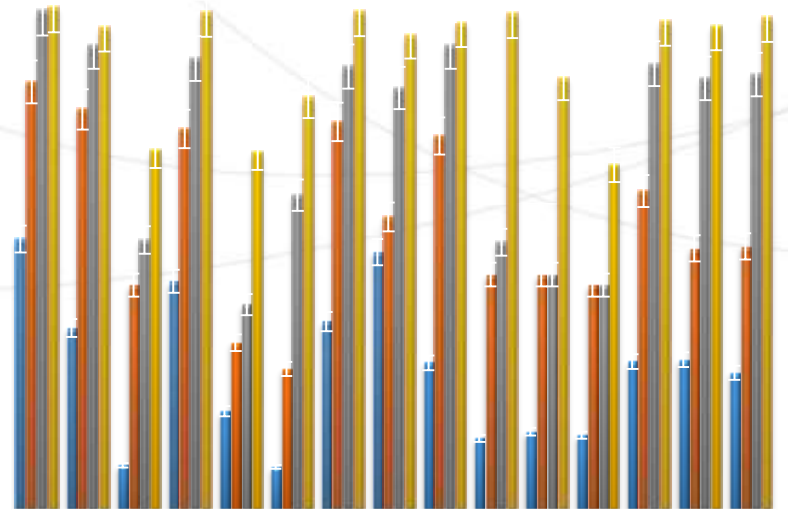
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GLOBAL SYMPOSIUM ON SOIL BIODIVERSITY | 19-22 April 2021



PCB agricultural soils  
(Italy)  
range: 2-10 ppm



Diverse PCB congeners

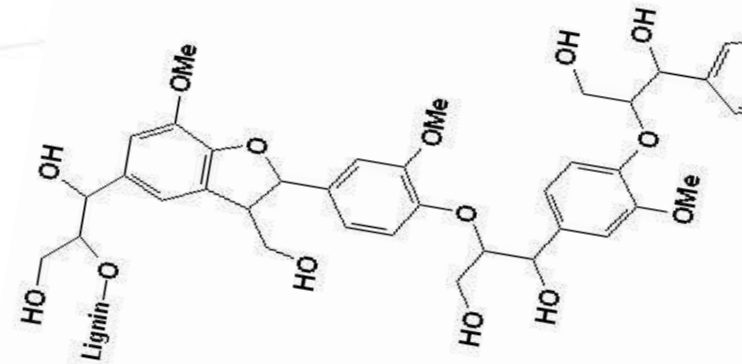
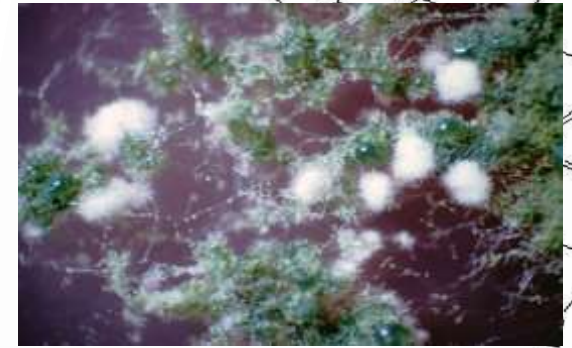




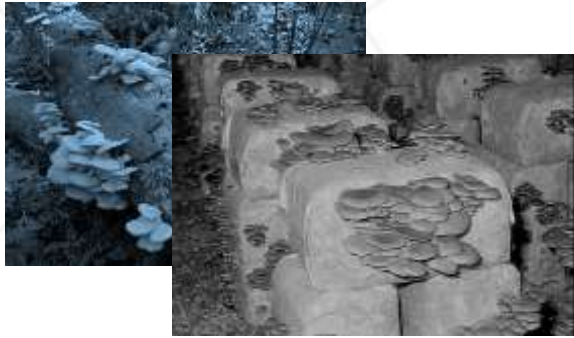
**White rot fungi  
produce  
extracellular  
enzymes**

**ASPECIFICITY  
OF THE  
ENZYMATIC  
BACTERY**

- Peroxidases (polyphenol oxidases)
- Laccases



# Biostimulation of the indigenous microbial community

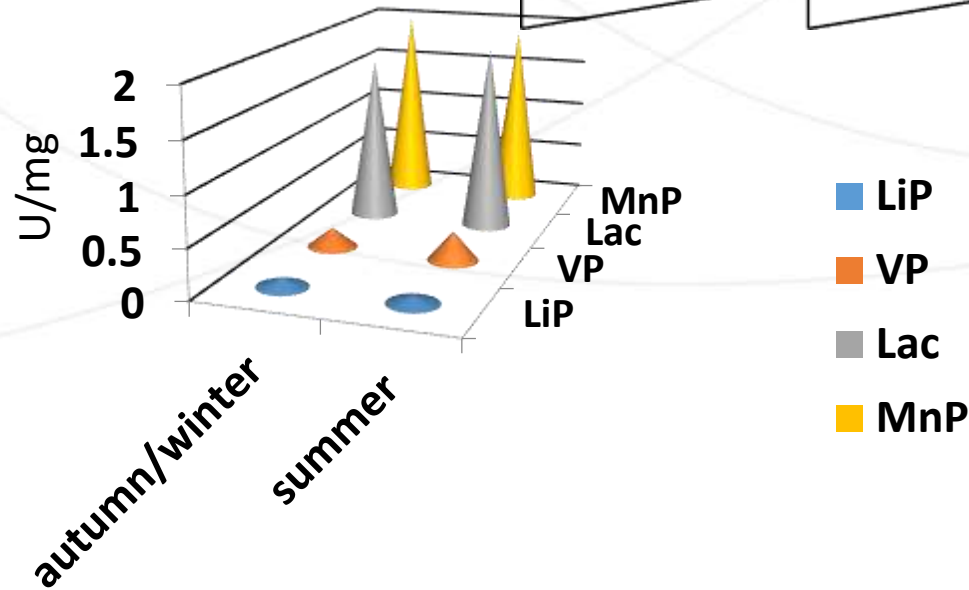


*Pleurotus ostreatus*: second position in the context of edible mushroom industrial production in the world

1kg of *P. ostreatus* on the mkt

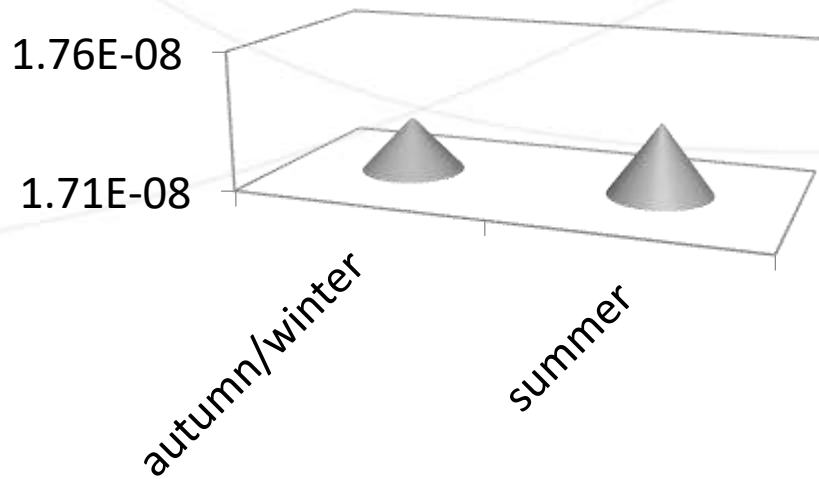
5 kg SMS

that has to be disposed off

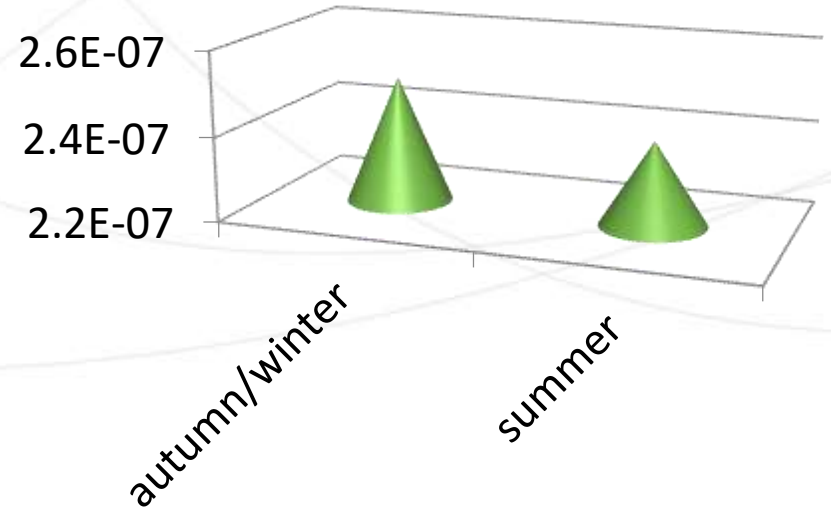




**Bacterial load**  
**[CFU /g dw SMS]**



**Fungal load**  
**[CFU/ g dw SMS]**



contaminants	ppm	Public area ppm	Industrial area ppm
PCB	9,28 ± 0,08	0,5	25
SMS % fresh weight			
<ul style="list-style-type: none"> <li>▪ 0.1</li> <li>▪ 1</li> </ul>			



No SMS

0.1% SMS

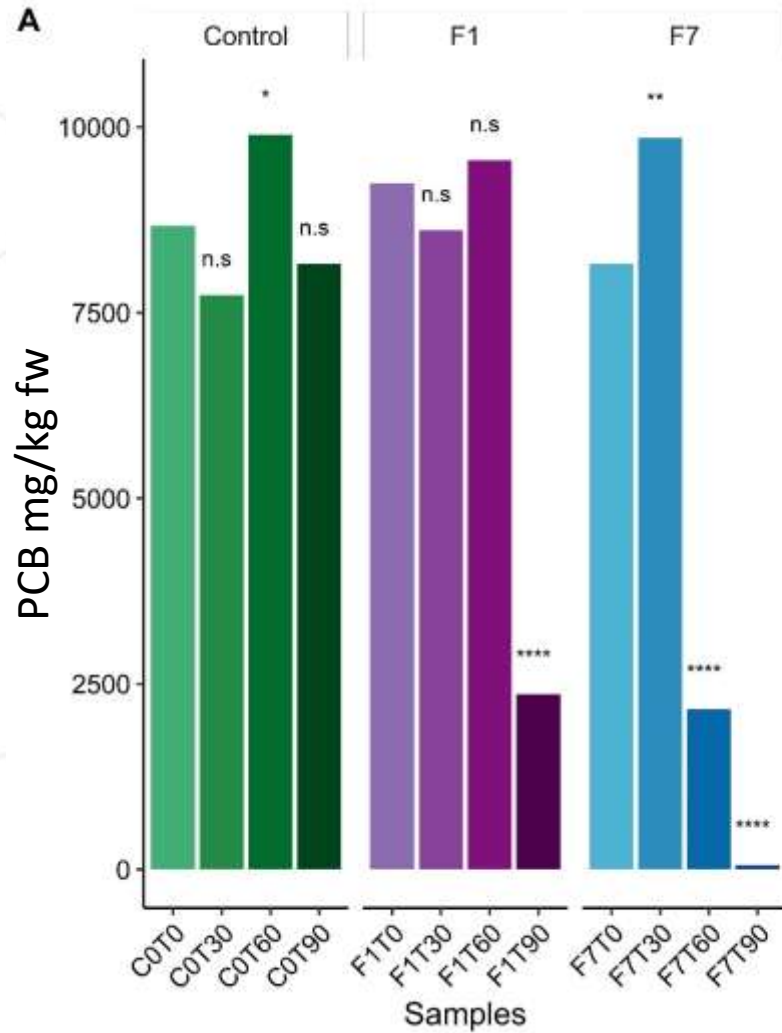
1% SMS

No SMS

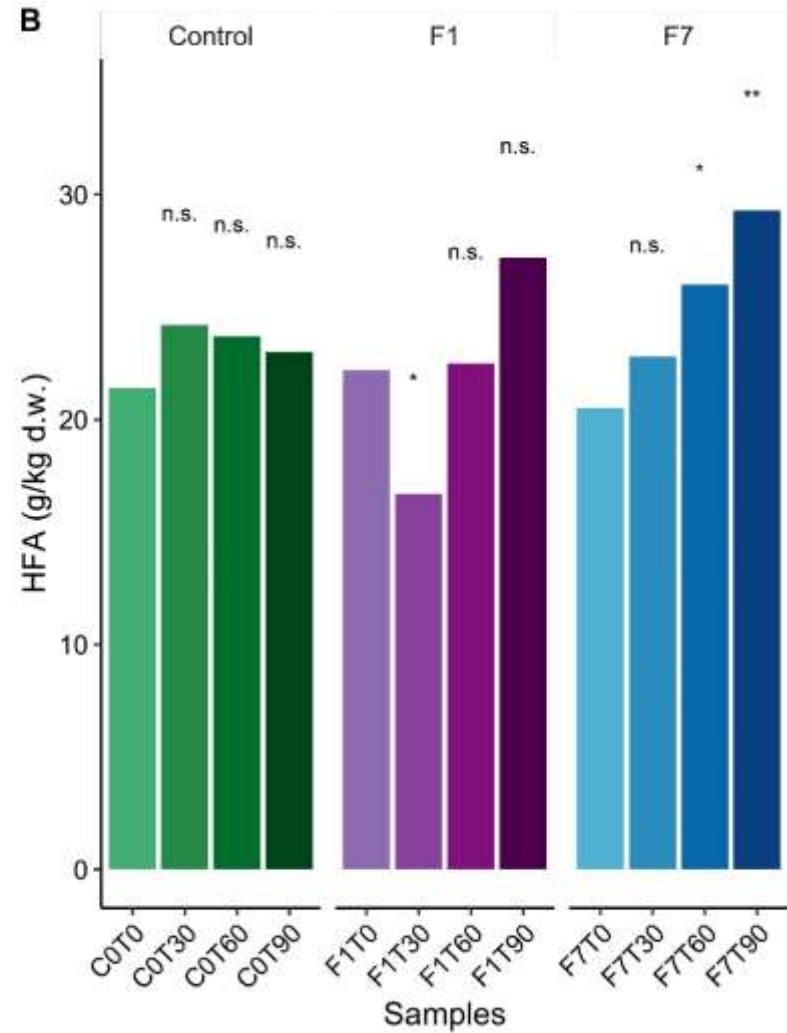
0.1% SMS

1% SMS

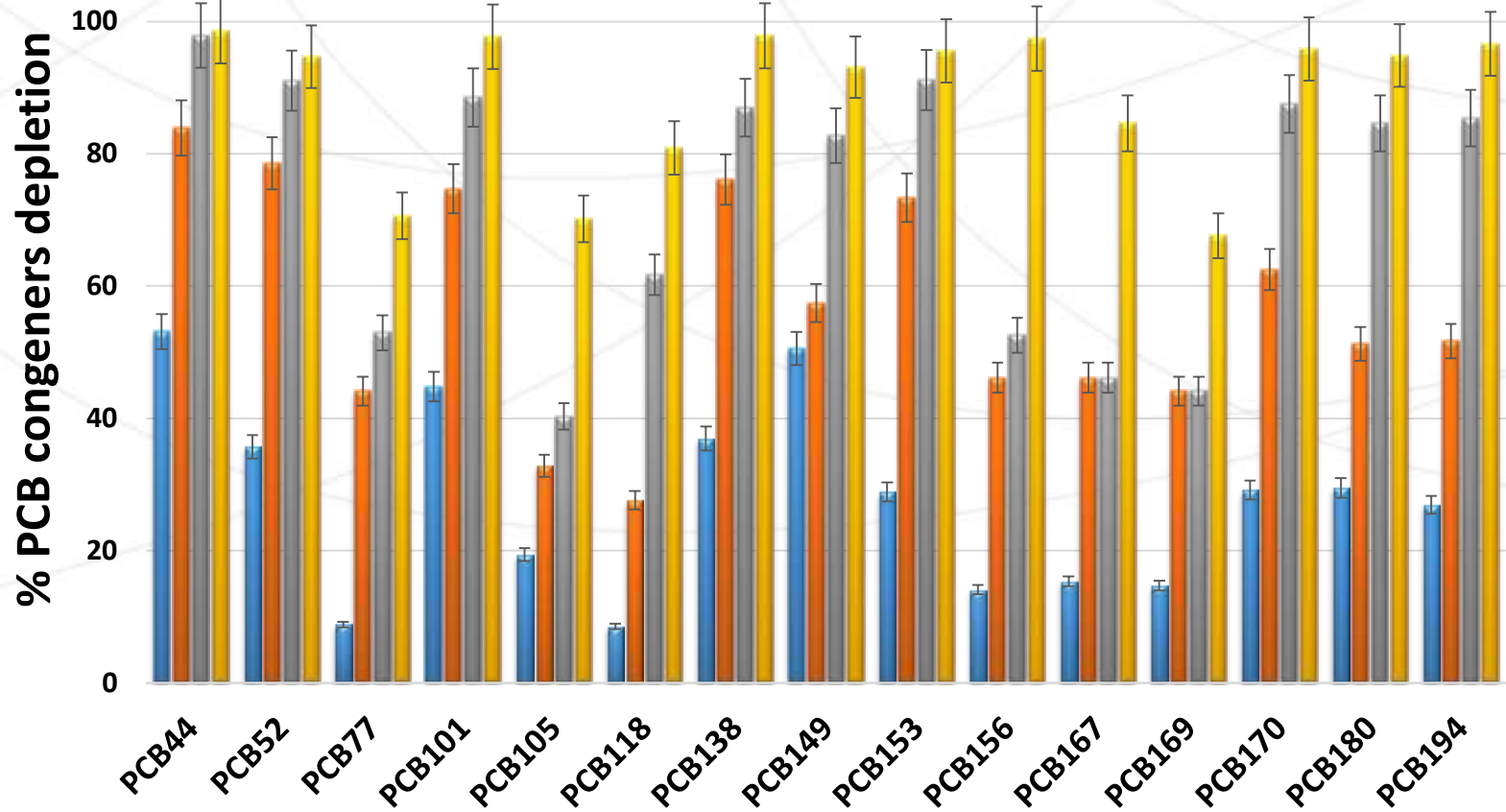
**A**



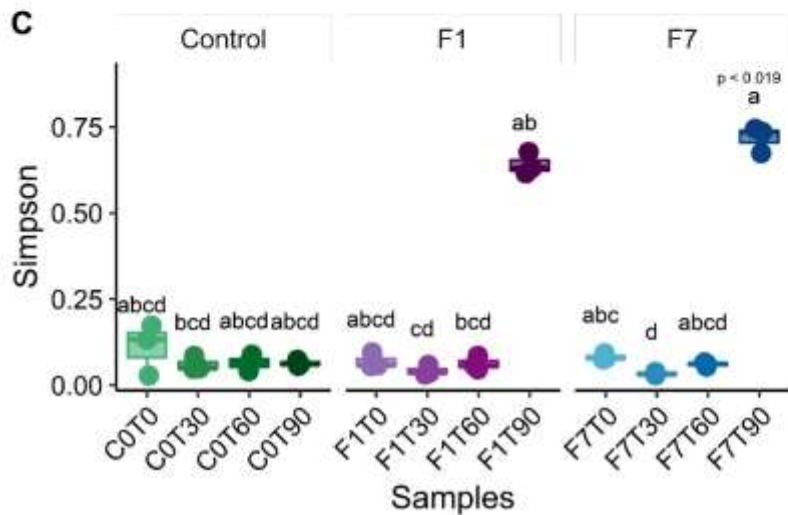
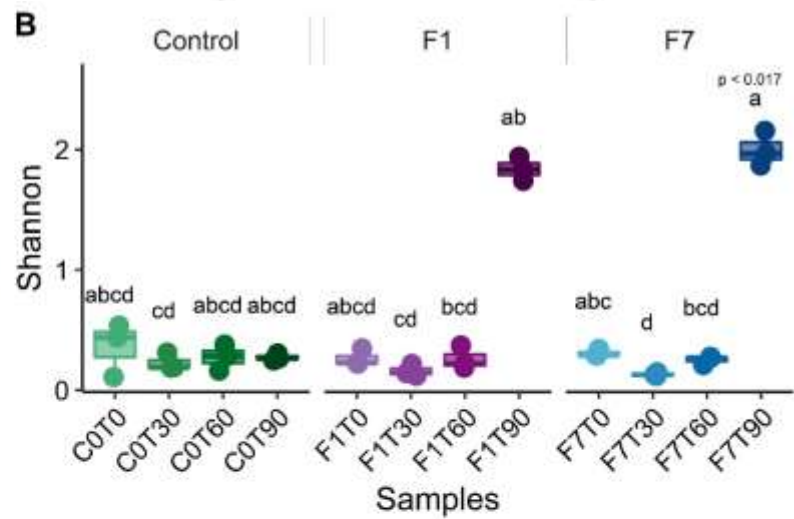
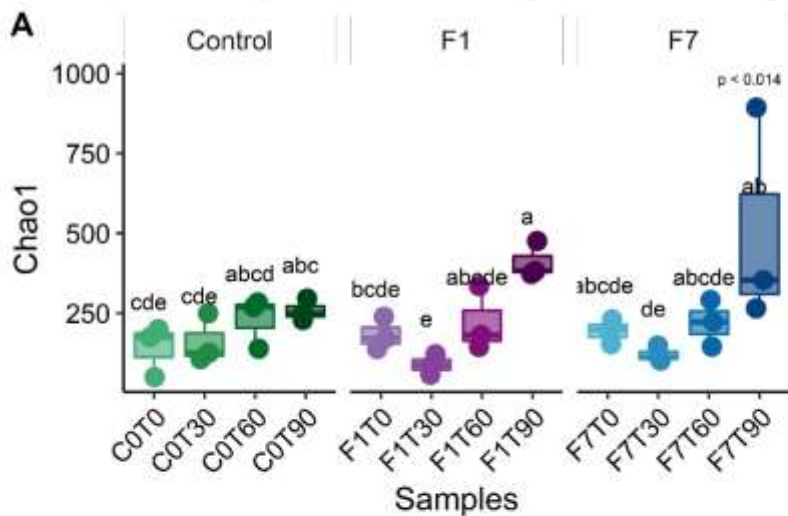
**B**



# Spent mushroom substrate: 1% on a weight base ratio





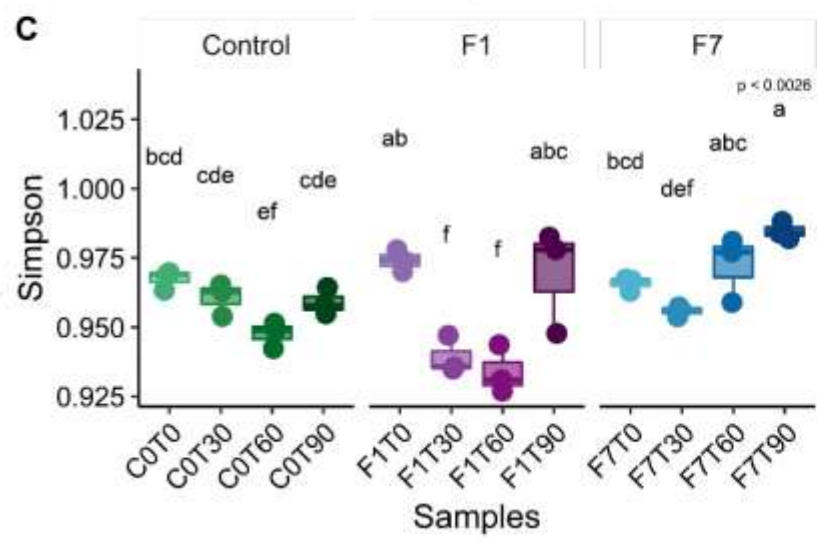
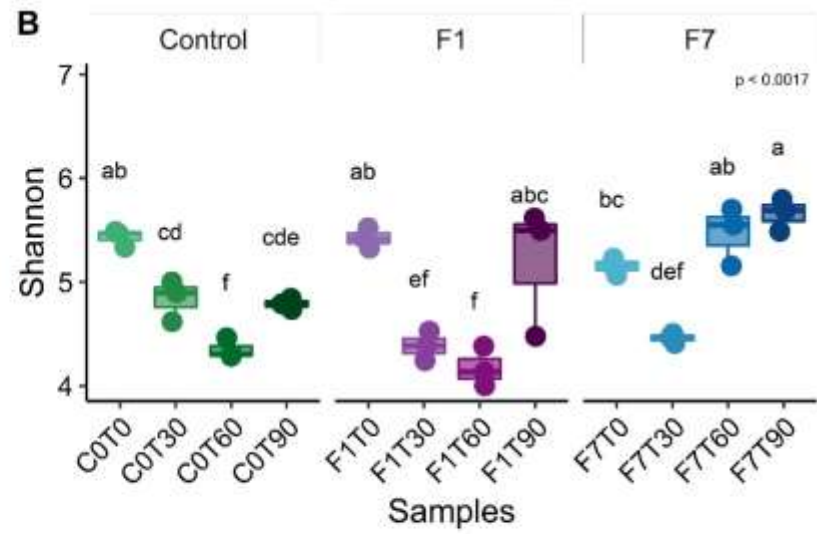
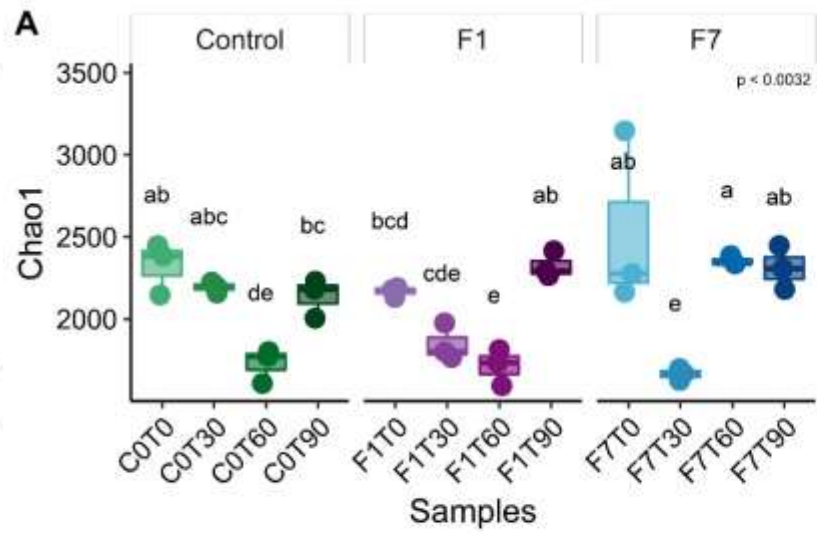


**D**

value

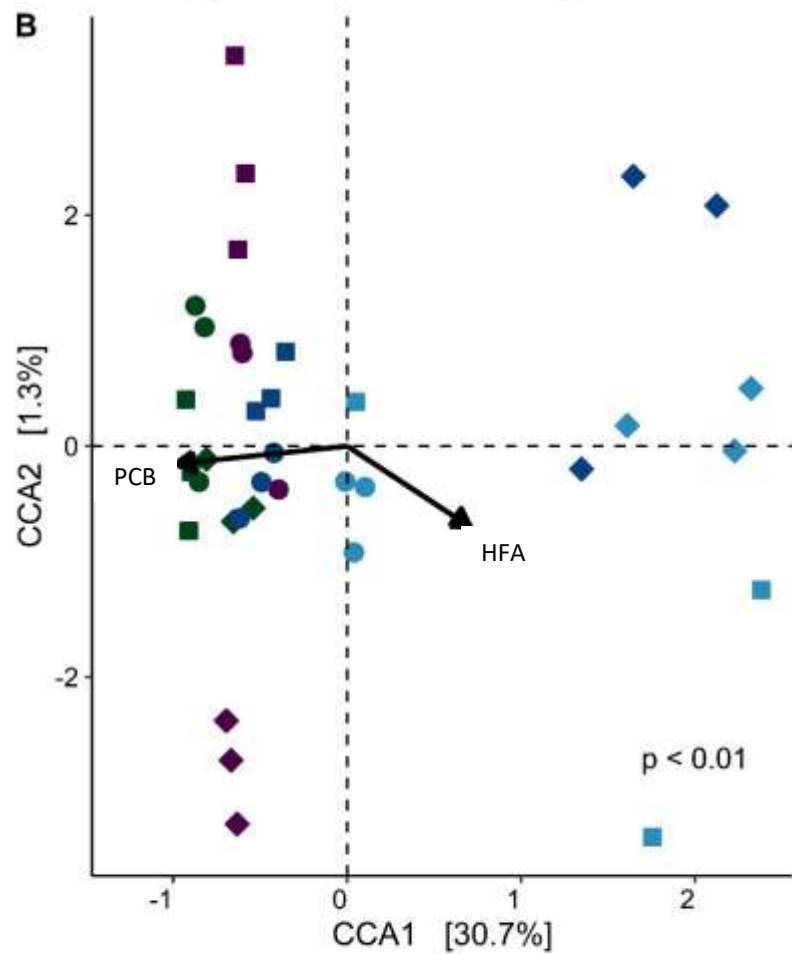
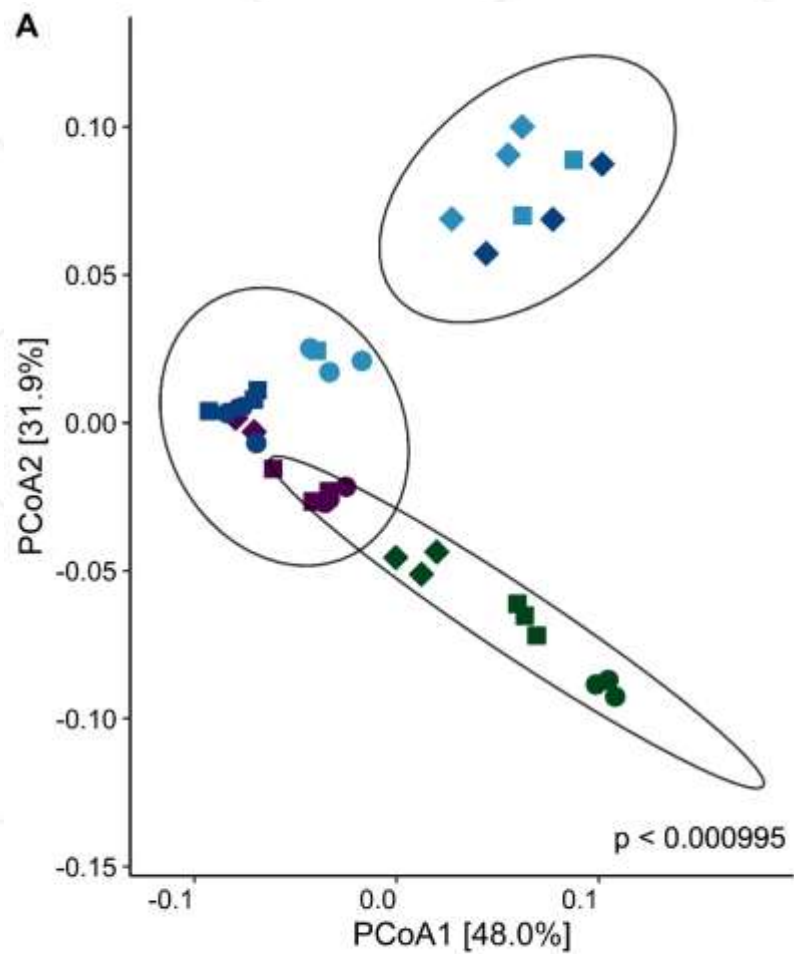
ANY SIGNIFICANT  
CHANGES IN THE  
FUNGAL ECOLOGY  
DURING THE  
PROCESS OF PCB  
DEPLETION





**SIGNIFICANT  
CHANGES IN THE  
BACTERIAL ECOLOGY  
DURING THE  
PROCESS OF PCB  
DEPLETION**





○ Control □ F1 ◇ F7 ● 0 ● 30 ● 60 ● 90



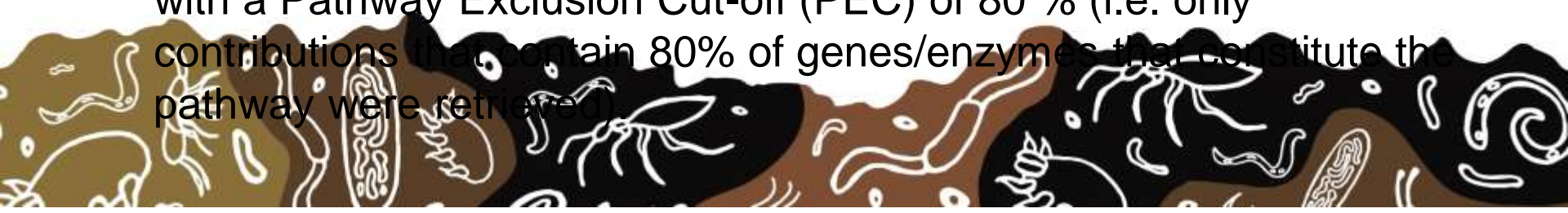
# PREDICTIVE METAGENOMIC FUNCTIONAL PROFILING

**To better evaluate the metabolic potential of the different bacterial taxa during the process of TPH degradation:**

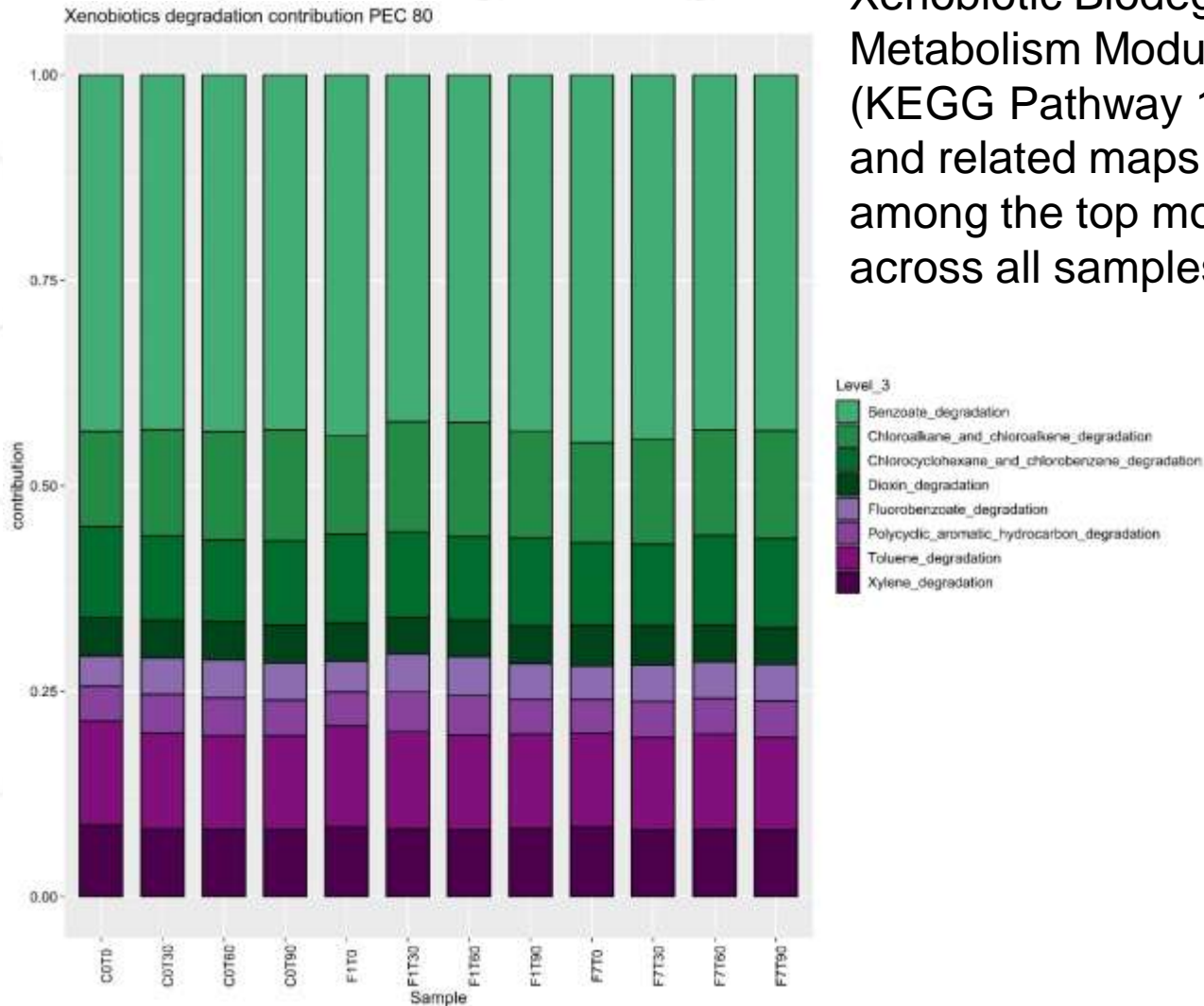
**The contribution of the different taxa to abundances of functional features of interest was evaluated**

Predicted proteins were classified by their Enzymatic Commission number (EC), resulting in the identification of 2313 ECs, and by KEGG orthology resulting in the identification of 7374 KOs, across all samples.

Metabolic reconstruction of pathways was carried out in iVikodak with a Pathway Exclusion Cut-off (PEC) of 80 % (i.e. only contributions that contain 80% of genes/enzymes that constitute the pathway were retrieved).

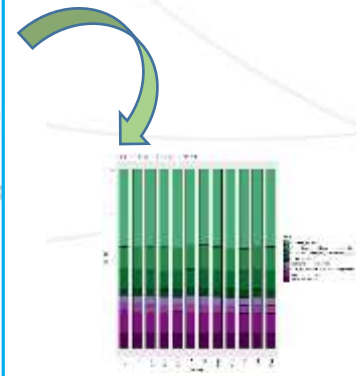
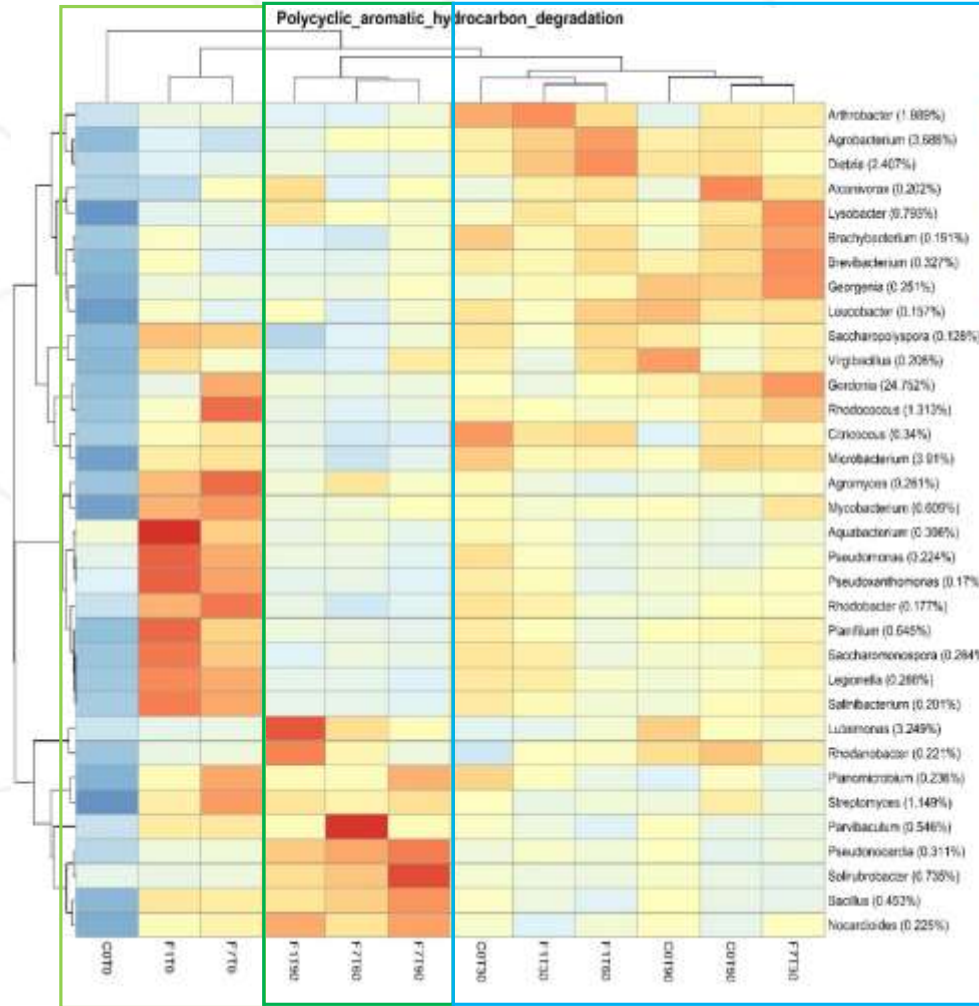


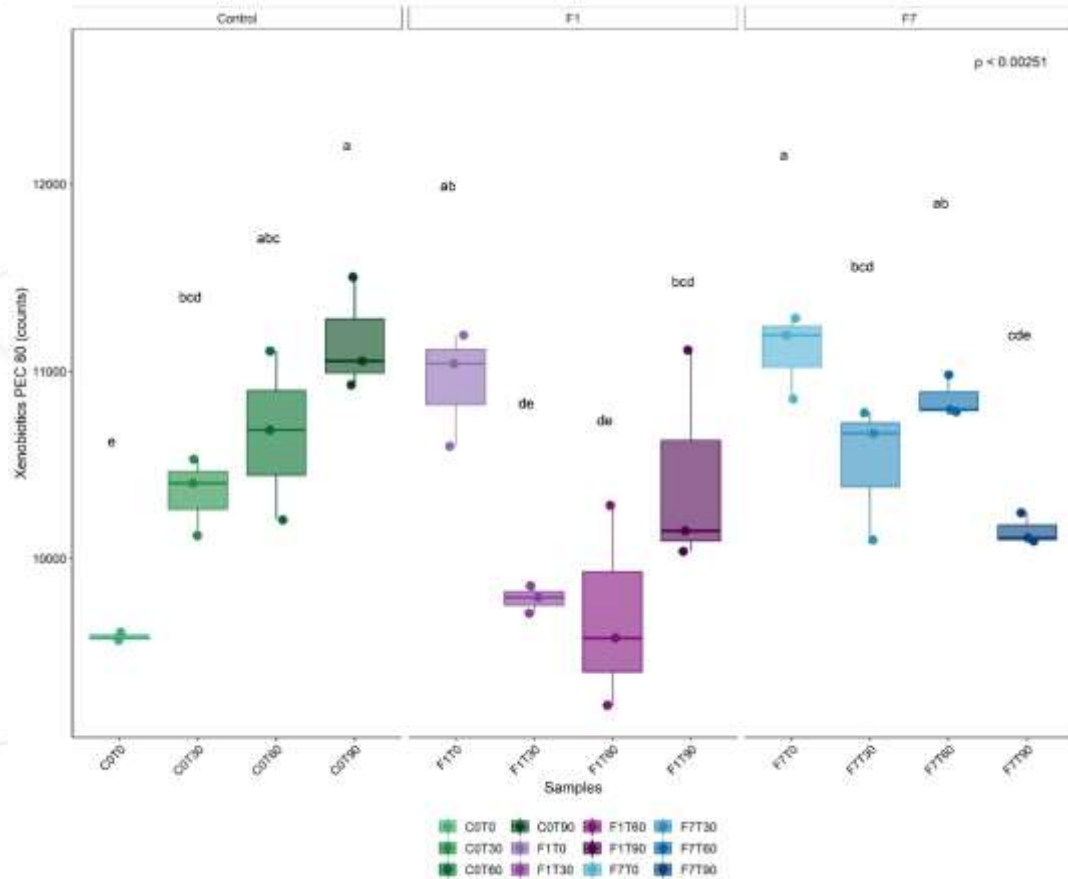
Xenobiotic Biodegradation and Metabolism Module (KEGG Pathway 1.11) and related maps resulted to be among the top modules recovered across all samples



3 groups:

1. the Time 0
2. The Time where PCB occurred
3. The transitional times



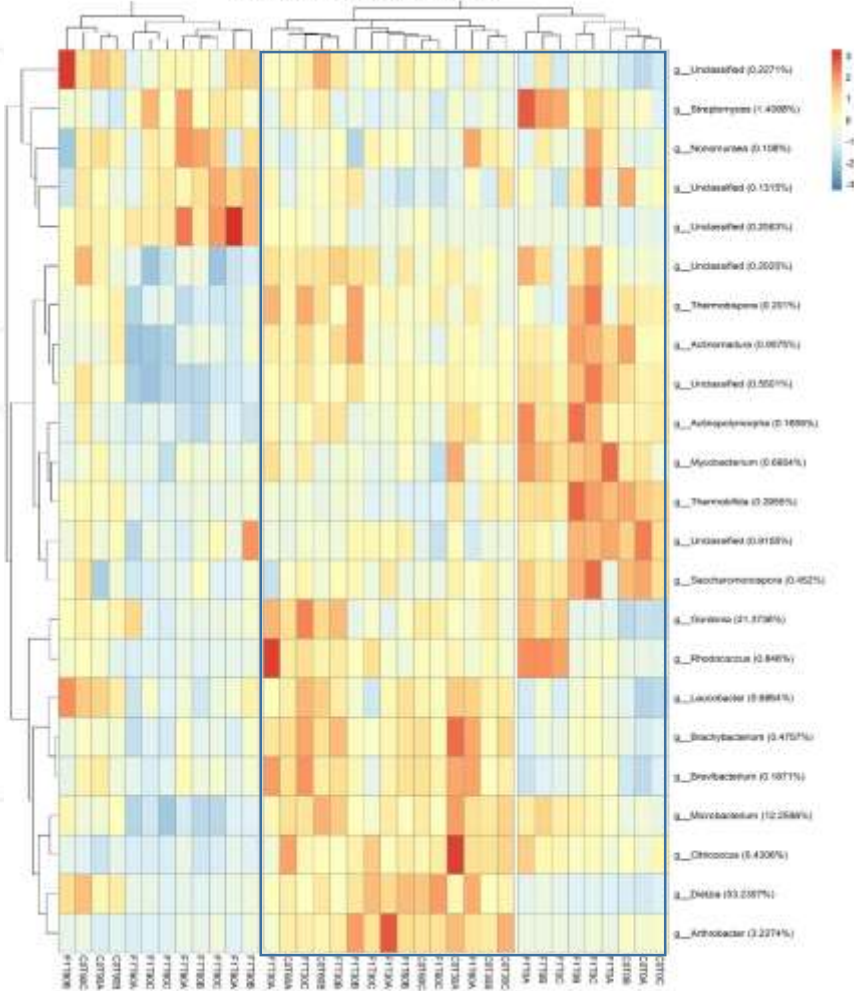


WHERE PCB DEPLETION OCCURRED

the diversified microbial community contributing to the PCB depletion decreased in diversity at the transitional time



Dye Decolorizing Peroxydase (EC:1.11.1.15)



Most of the *Actinobacteria* showing functional predominance in the **transitional times**, besides harbouring functional features for the transformation of the contamination, harboured also other functional feature that might be of interest for the process of PCB depletion.

the **Dye decolorising peroxidases**.

Bacterial DyP have a quite high redox potential that allows both the oxidation of phenolic and non-phenolic lignin model compounds.





# PREDICTIVE METAGENOMIC FUNCTIONAL PROFILING

## At T0 ACTINOBACTERIA:

*Agromyces,*  
*Mycobacterium,*  
*Saccharomonospora*  
,  
*Salinibacterium,*  
*Thermoactinomyces*  
*s,*  
*Saccharopolyspora,*  
*Gordonia,*  
*Rhodococcus,*  
*Citrococcus,*  
*Microbacterium,*  
**Streptomyces** sps.

## PROTEOBACTERIA:

**A:**  
*Rhodobacter,*  
*Acquabacterium,*  
*Pseudomonas,*  
*Pseudoxanthomonas,*  
*Thermomonas,*  
*Legionella,*  
**Parvibaculum** sps.

## FIRMICUTES:

**Planimicrobium**  
**m,**  
*Virgibacillus,*  
*Planifilium,*  
**Bacillus** sps.



TRANSITIONAL  
MESOCOSMS

## ACTINOBACTERIA:

**A:**  
*Arthrobacter,*  
*Dietzia,*  
*Brachybacterium,*  
*Brevibacterium,*  
*Georgenia,*  
*Leucobacter* sps.

## PROTEOBACTERIA:

*Alcanivorax,*  
*Lysobacter,*  
*Agrobacterium*  
sps.



MESOCOSMS  
WHERE  
PCB DEPLETION OCCURRED

## PROTEOBACTERIA:

**Rhodanobacter,**  
**ACTINOBACTERIA:**  
**Nocardioides,**  
**Pseudonocardia,**  
**Solirubrobacter**  
sps.

**BLOOMING**  
**OF**  
**SPECIALISTS**  
**TS**

Dy

MANDATORY FOR PCB DEPLETION  
not occurring in CONTROL field test



# PREDICTIVE METAGENOMIC FUNCTIONAL PROFILING

Spearman's rank correlation coefficient for combination of DyP total counts per sample and relative PCB concentrations

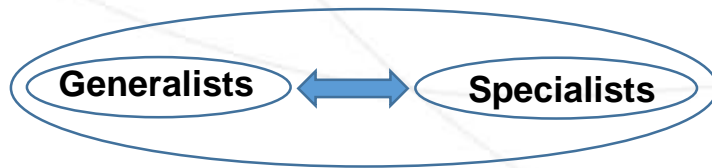
q	PCB/EC:1.11.1.19
Control	0.18
F1	0.32
F7	0.88

These evidences suggest that the **DyP** is associated to the **saprophytic metabolisms** of *Actinobacteria*, more than to their capacity to deplete the contamination.

**Carbon stabilisation = smoothly provide C**



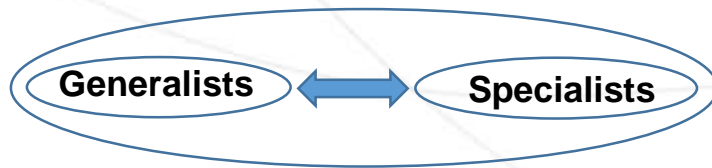
# CONCLUSIONS 1/2



The exploitation of *P. ostreatus* SMS in landfarming practices resulted to be a valuable management strategy for the re-utilisation of an organic waste deriving from food industry to recover PCB contaminated agricultural soils



# CONCLUSIONS 2/2



- Actinobacterial saprophytic metabolism mandatory for PCB depletion and preceded the establishment of specialist species
- The **saprophytic metabolism** is associated to **generalist species** and it is involved in the competition for nutrients in the environment NUTRIENT CYCLES (Carbon Cycle)
- the **saprophytic generalists** might result to be pivotal to prime the actual degradation of contaminants and the blooming of specialists **because of the low bioavailability of historical contamination = oligotrophic environment**





**Thank you for  
your attention**