

(META)GENOMIC CHARACTERIZATION OF A BIOREACTOR WITH POLYHYDROXYALKANOATES (PHA) AND BIOCHAR AS BIOMATERIALS TO PROMPT REDUCTIVE DECHLORINATION

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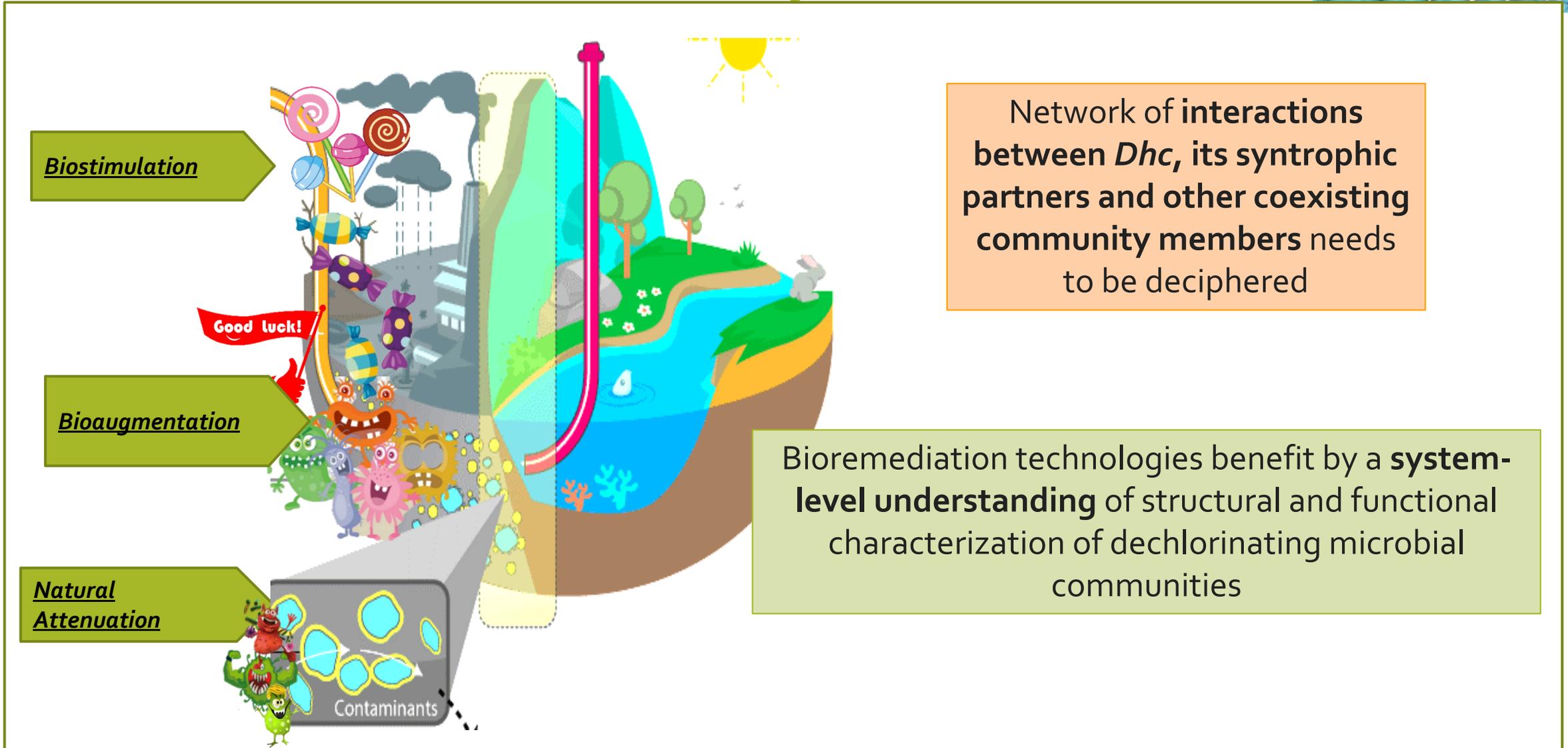
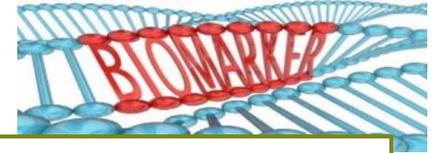
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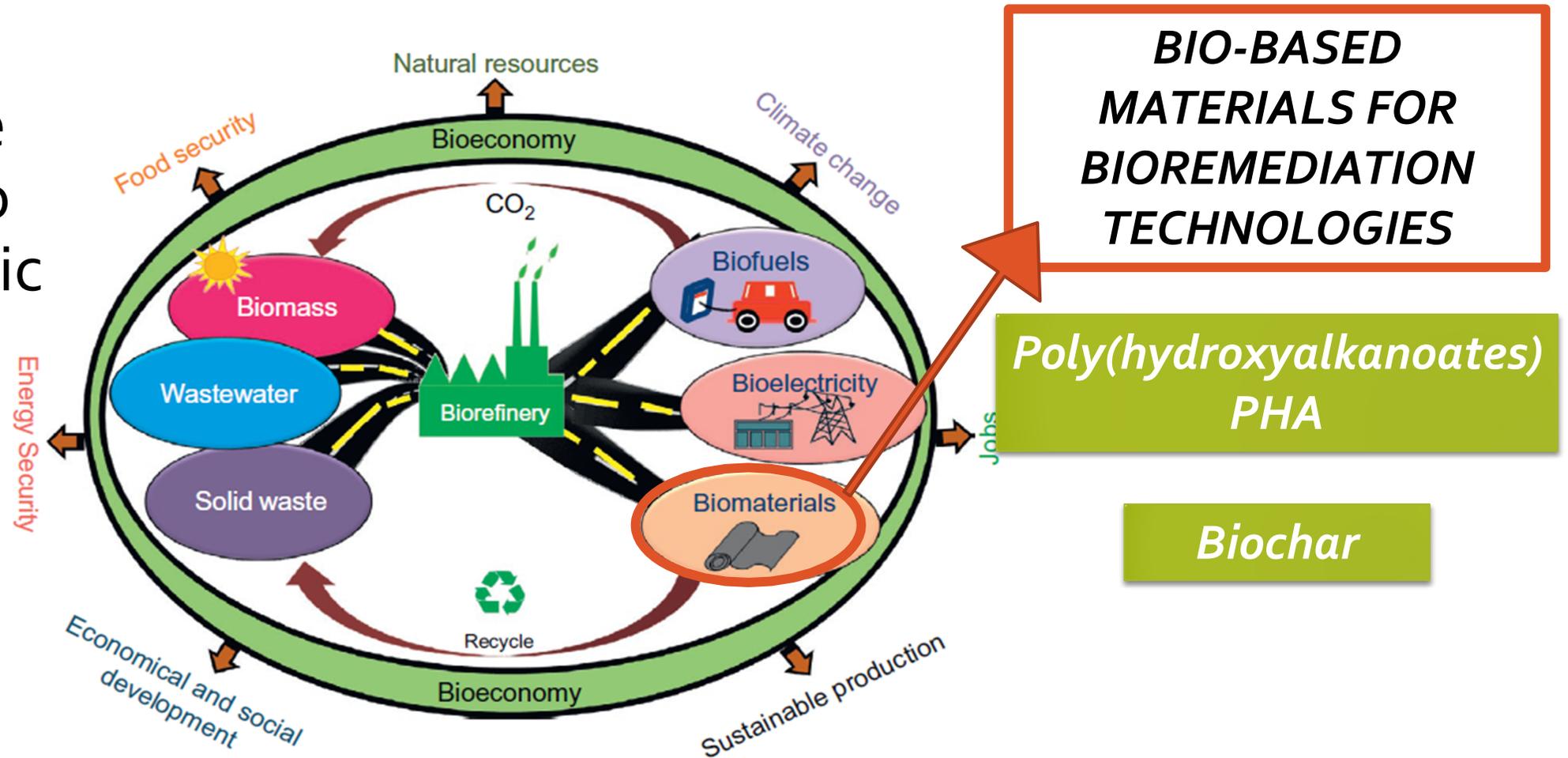
Sixth International Symposium on Bioremediation and Sustainable Environment Technologies
Austin, Texas | May 8-11, 2023

Dehalococcoides mccartyi (*Dhc*) and RD



Bioremediation technologies in a circular bio-based economy perspective

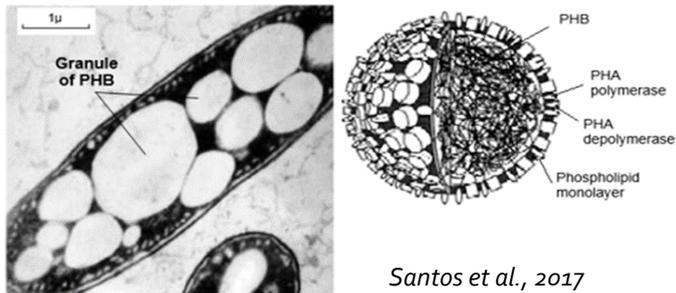
- Exploit the capacity to turn organic waste into valuable products



Adapted from Prasad, 2016 Bioremediation and bioeconomy

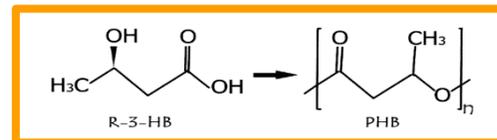
Bio-based materials for bioremediation technologies: Poly-Hydroxybutyrate (PHB)

- Polyhydroxyalkanoates (PHA) are biodegradable and biocompatible aliphatic polyester with linear polymer chain **accumulated intracellularly** by many **microorganisms under unfavorable growth conditions** and used as carbon and energy reserves

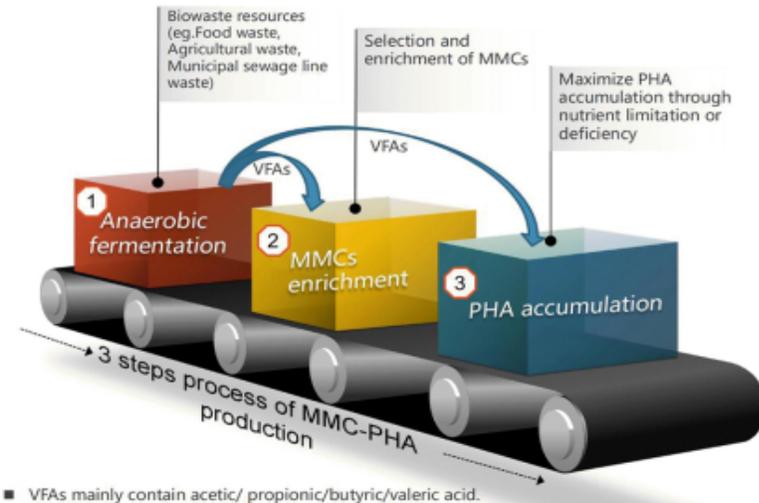


Santos et al., 2017

- Poly-β-hydroxybutyrate (PHB): member of PHA family with a methyl functional group (CH₃) and an ester linkage group (-COOR). It is composed of 3-hydroxybutyrate monomers strung together by β-bonds.

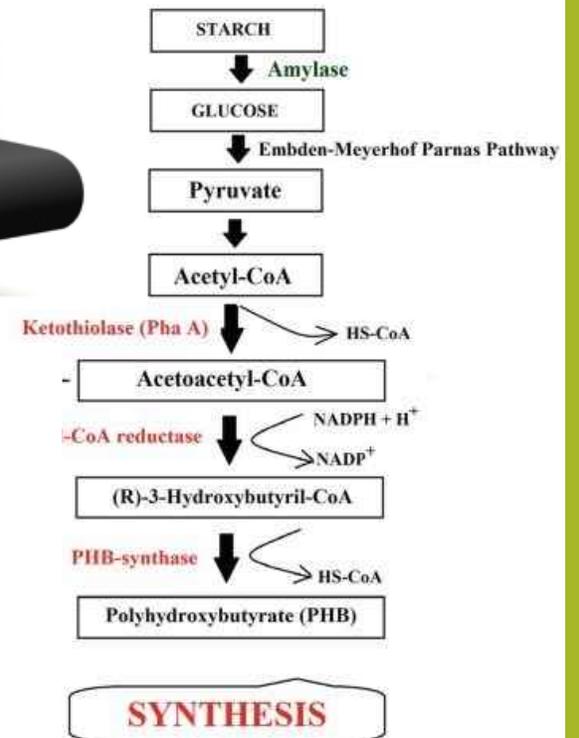


- Produced as Pure or Mixed Microbial Cultures (MCC)



■ VFAs mainly contain acetic/ propionic/butyric/valeric acid.

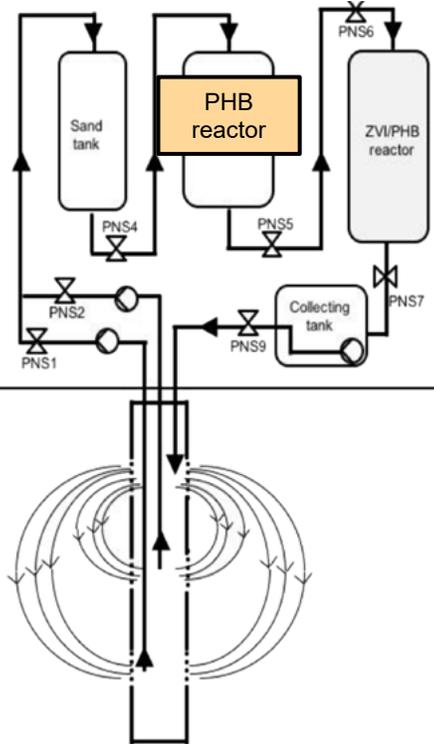
Wei and Fang, 2022



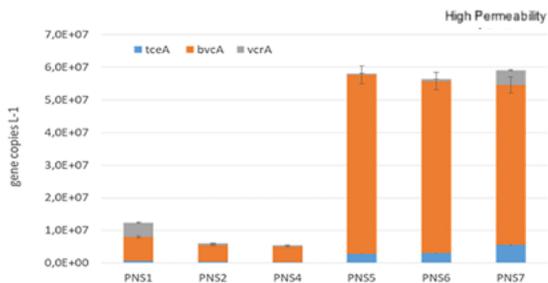
SYNTHESIS

PHB as slow release carbon source for RD: previous experiences

Groundwater Ricirculation Well system at field scale

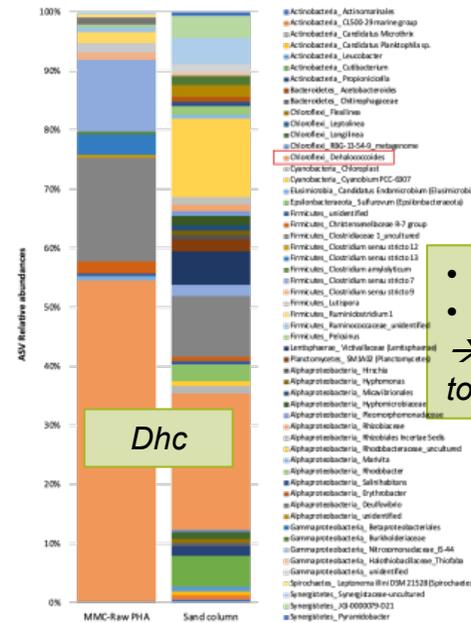
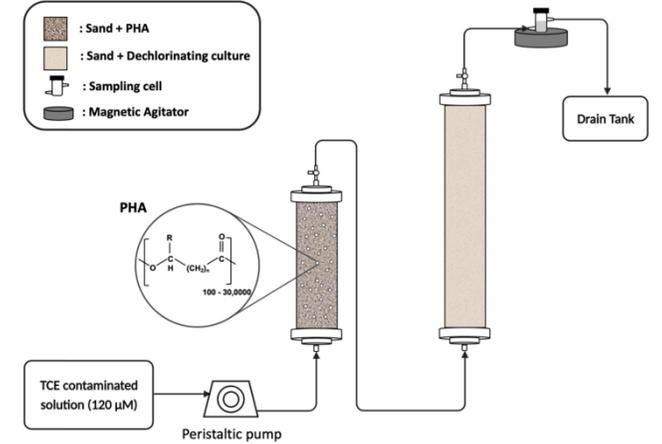


- *Dhc* growth after PHB reactor unit;
- Increment of chlorinated solvents biodegradation

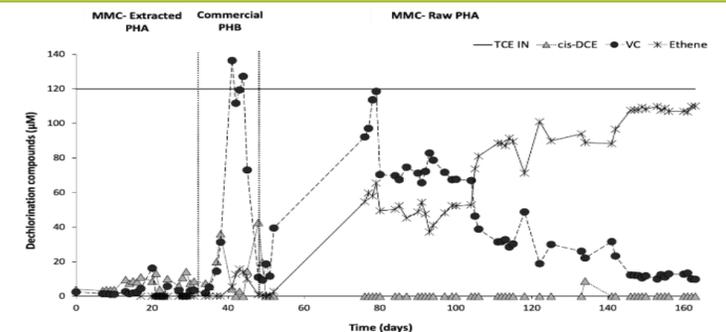


Pierro et al., 2017; Matturro et al., 2018

Column system at lab scale with PHA from pure and MMC cultures

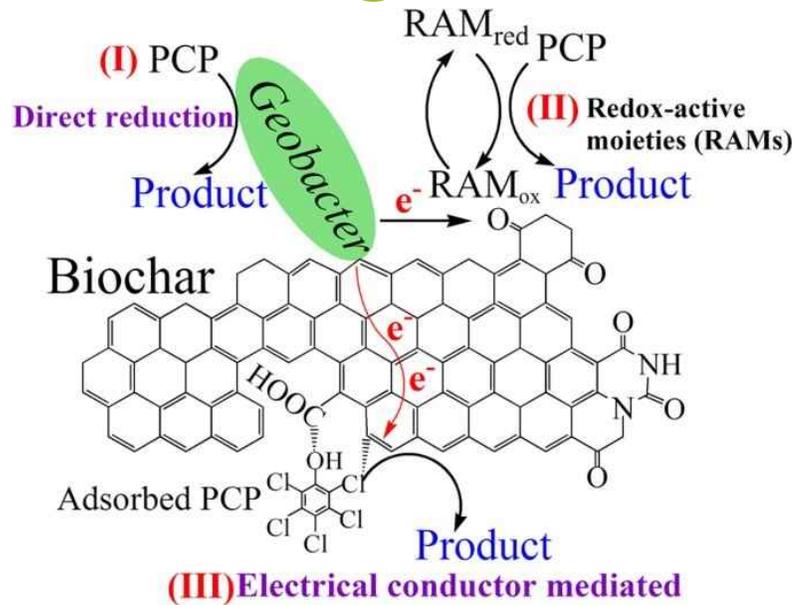


- PHA from a municipal foodwaste treatment plant
- Enhanced TCE biodegradation
- Microbial interactions during the fermentation need to be clarified

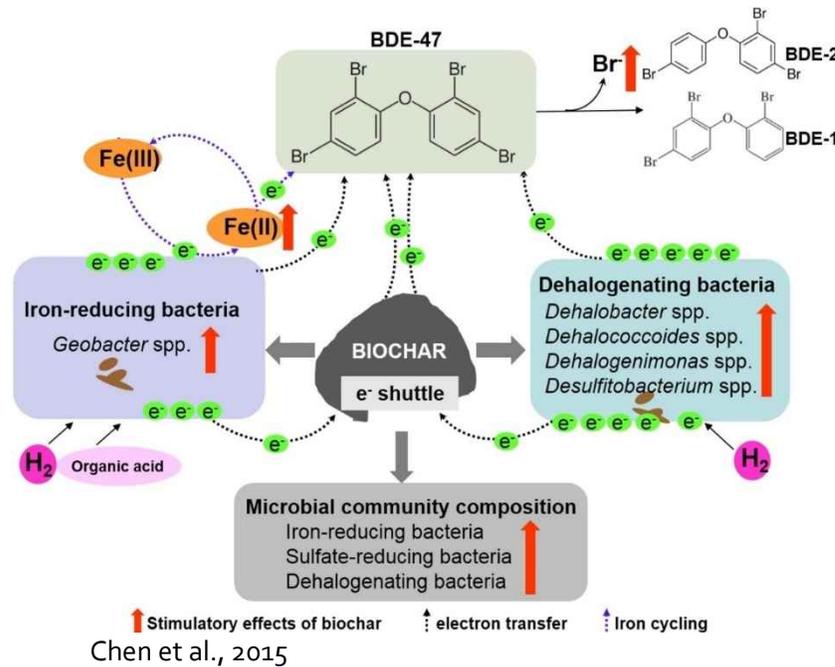


Amanat et al., 2021; Amanat et al., 2022

Bio-based materials for bioremediation technologies: **BIOCHAR**



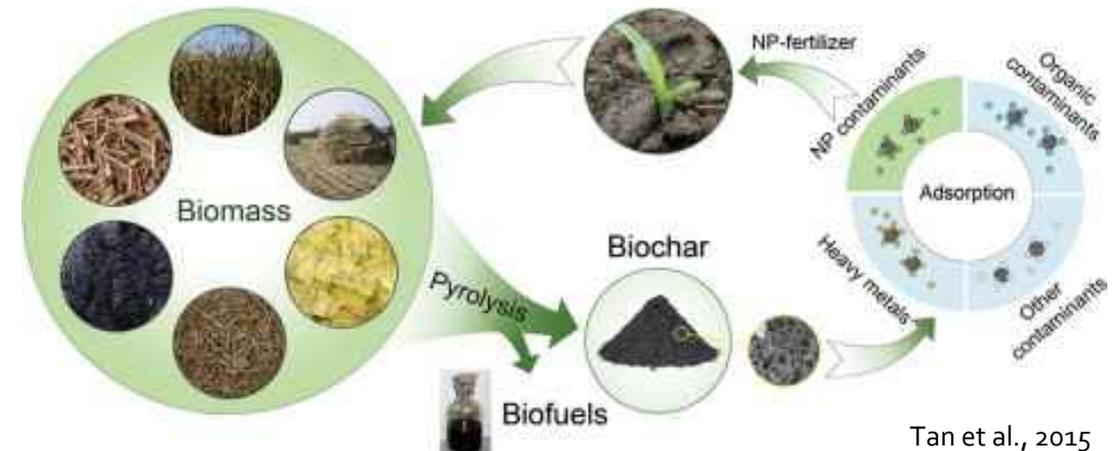
Yu et al., 2015



- Biochar selectively enriched microbial communities involved in halogenated pollutant degradation, mostly aromatic compounds
- Few studies report for chlorinated solvents biodegradation

APPLICATIONS FOR POLLUTANTS REMOVAL

- Immobilization of different classes of pollutants, thanks to the carbon structure and functional groups present on the surface
- **Electron transfer capacity** which made biochar responsible for the degradation of several pollutants

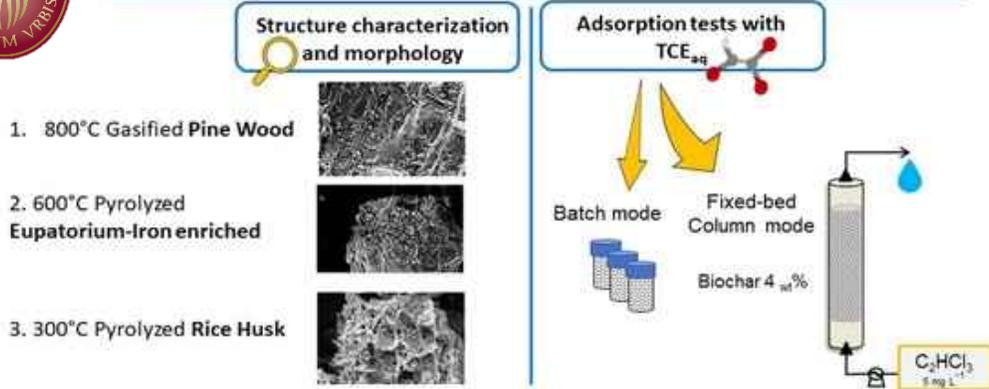


Tan et al., 2015

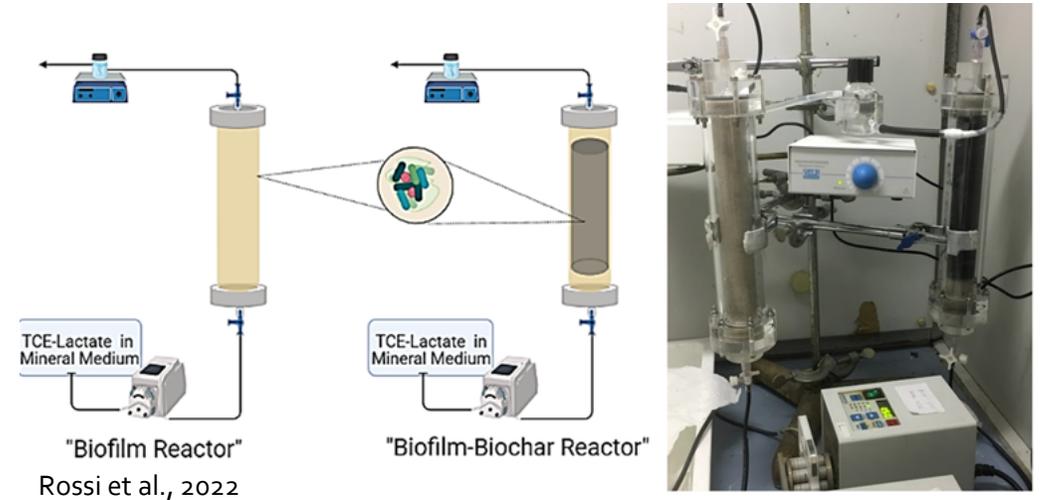
Biochar in bioremediation technologies: previous experiences



Characterizing Biochars for TCE Removal from Water



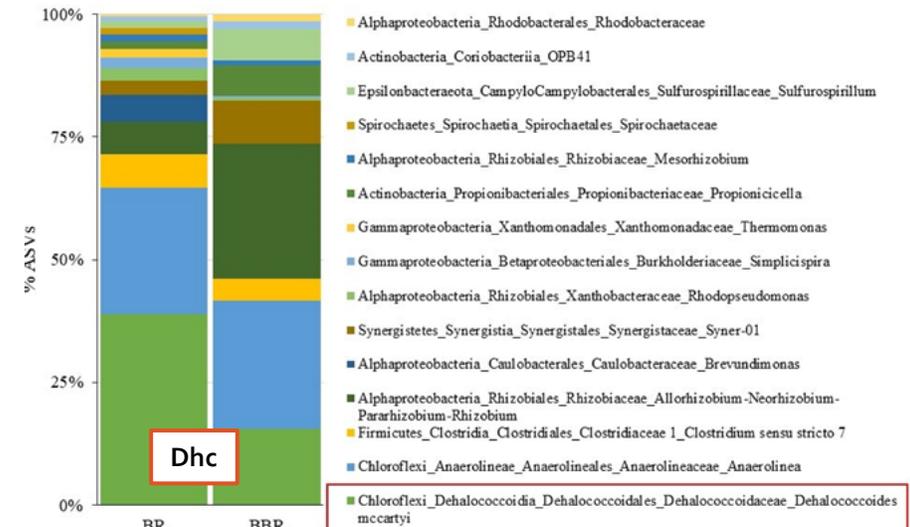
Rossi et al., 2021



Coupled Adsorption and Biodegradation of TCE on Biochar



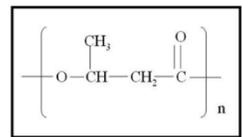
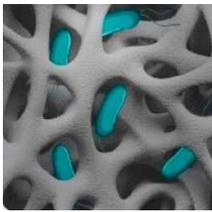
- TCE-dechlorinating consortium as inoculum
 - Lactate as electron donor
 - Biochar as bio-based material to sustain/enhance RD
- *The role of Biochar for Dhc growth needs to be clarified*



PHB/BIOCHAR Mini-pilot scale reactor to prompt TCE dechlorination

BIOCHAR

- Adsorbent material;
- Sustain growth/activity dechlorinating biomass



Hydrolysis

3-hydroxy butyrate

hydrogenation → Butyrate
 → Acetate
 β-oxidation → hydrogen

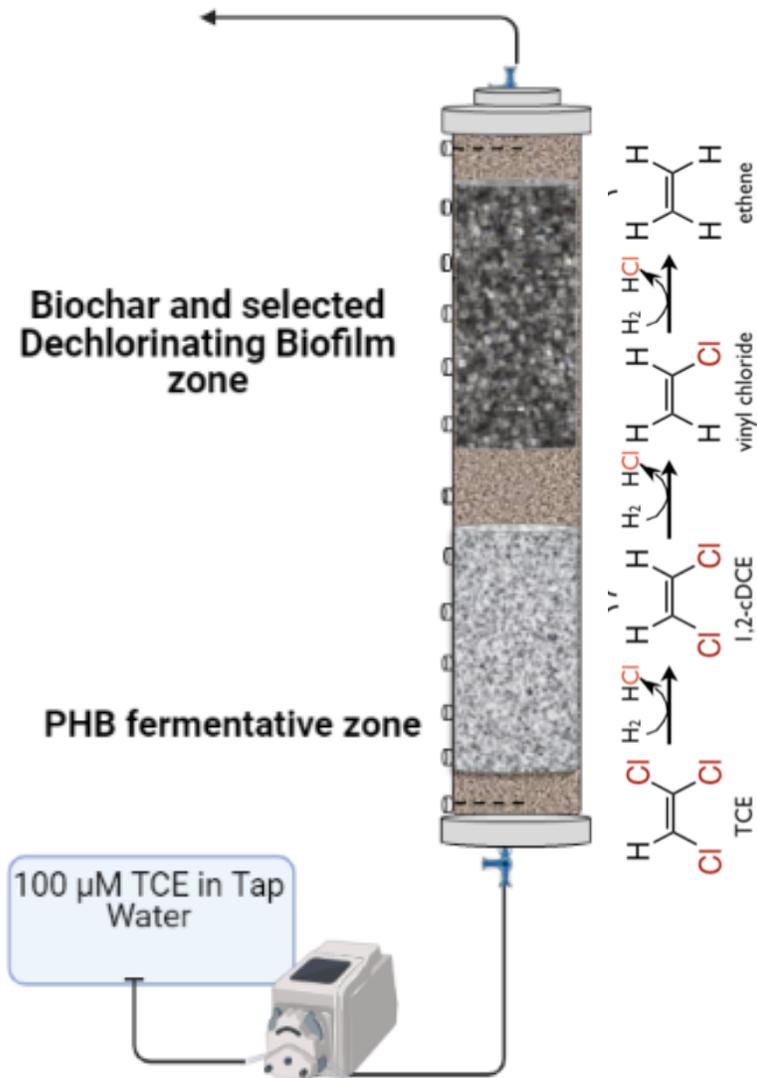
PHB
 Source of
 electron
 donor



**Biochar and selected
 Dechlorinating Biofilm
 zone**

PHB fermentative zone

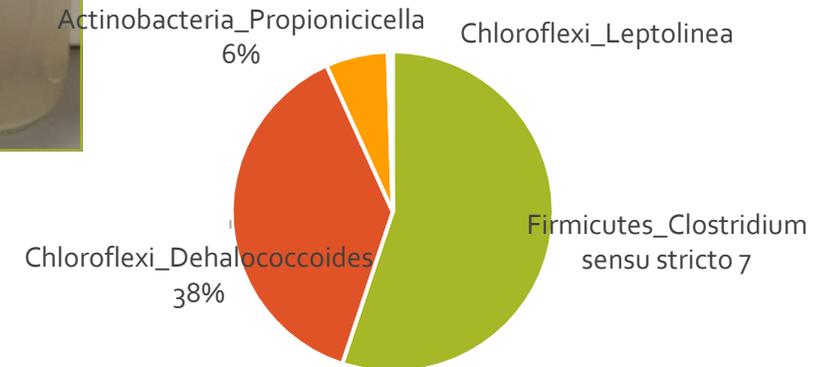
100 μM TCE in Tap
 Water



Reactor Working Conditions

Flow rate (L/day)	6
HRT (day)	1.8
TCE in (mM)	0.1
Pore water velocity (cm/day)	76.4
Length (cm)	144

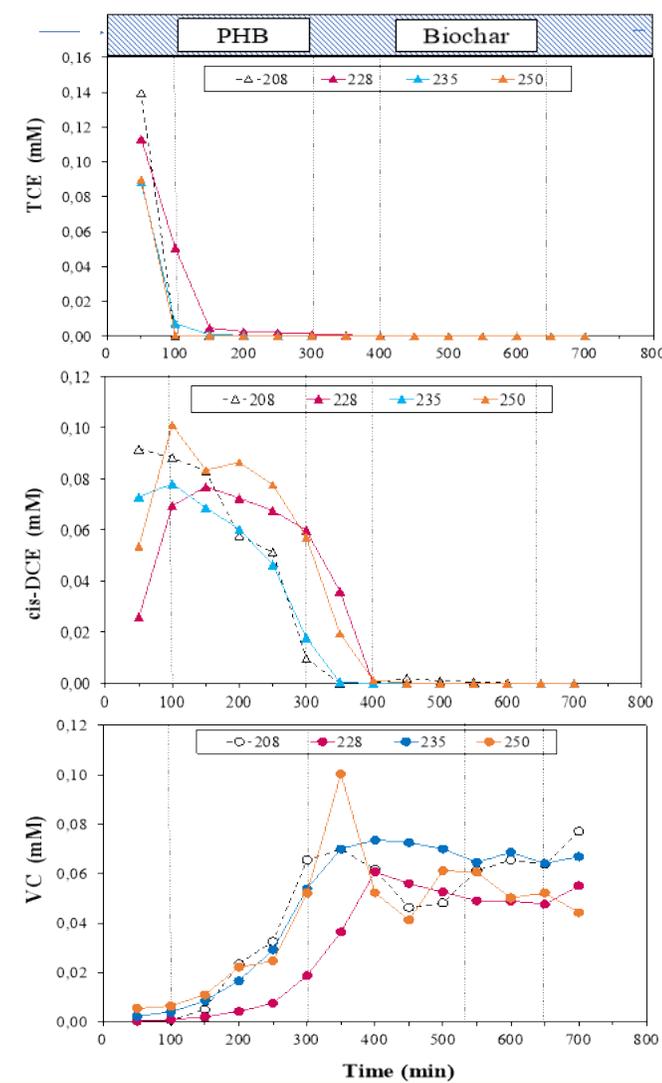
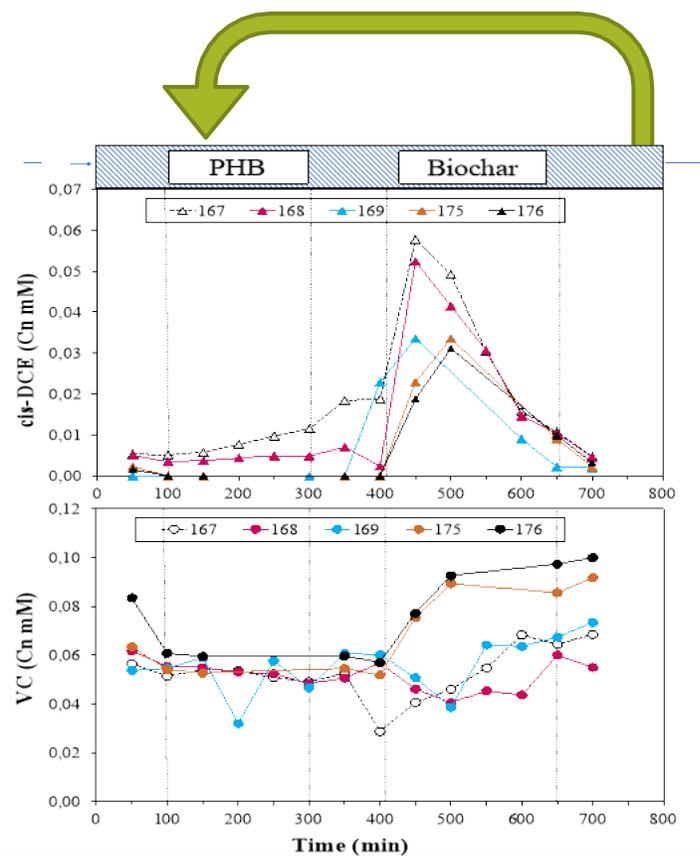
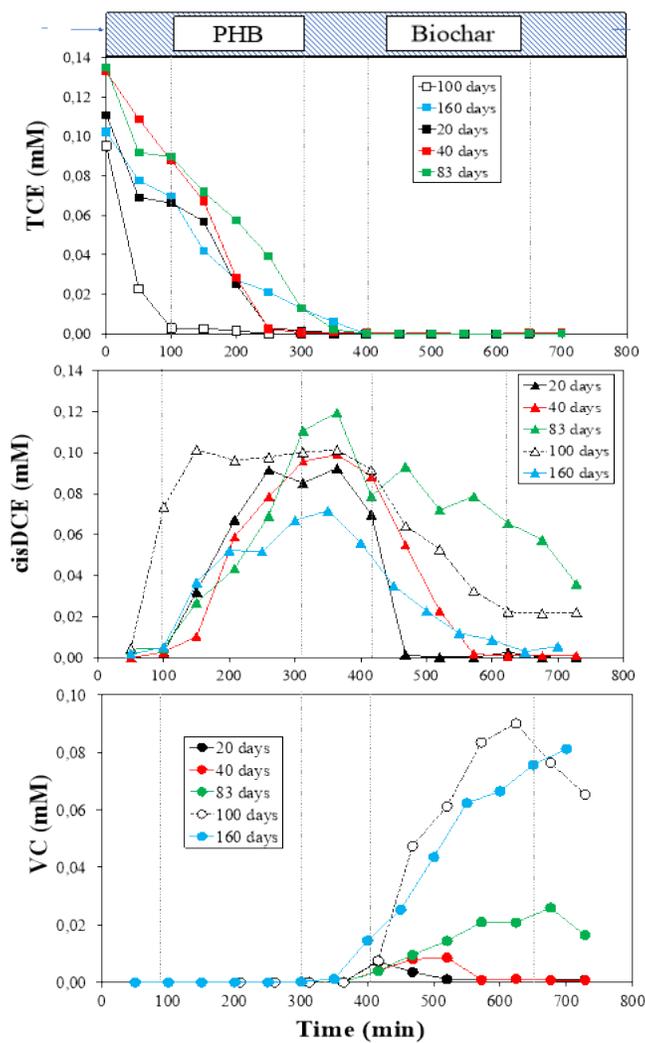
**START UP with A TCE-
 dechlorinating consortium
 inoculated in the Biochar zone**



TAP WATER + TCE

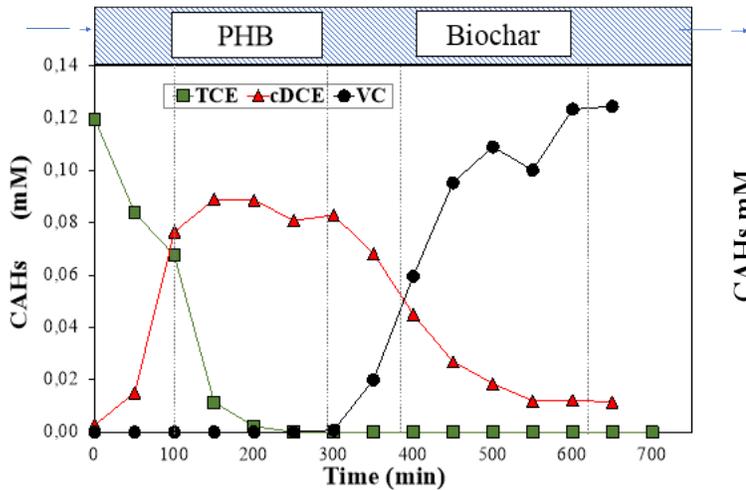
OUTLET RICIRCULATION

ANAEROBIC MINERAL MEDIUM + TCE



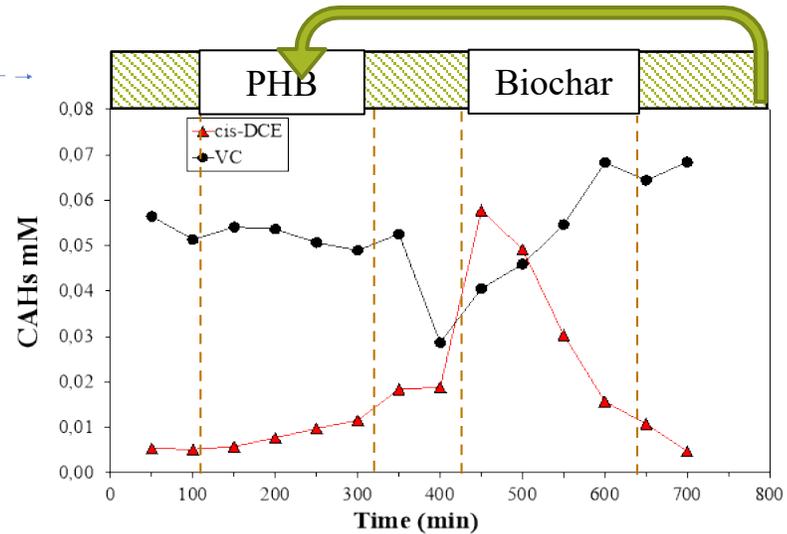
T₁
(160 days)

TAP WATER + TCE



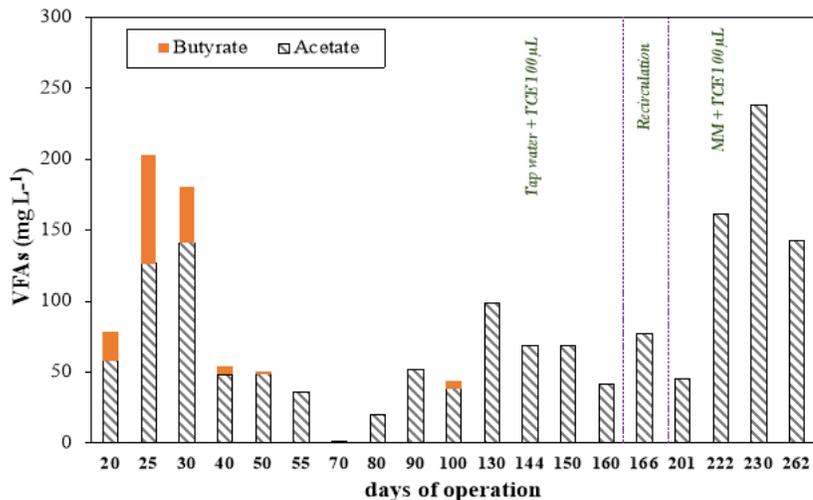
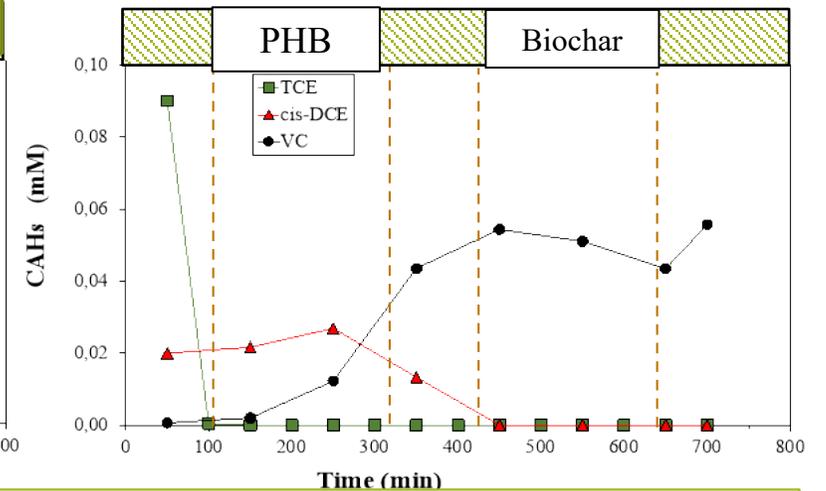
T₂
(180 days)

OUTLET RICIRCULATION



T₃
(250 days)

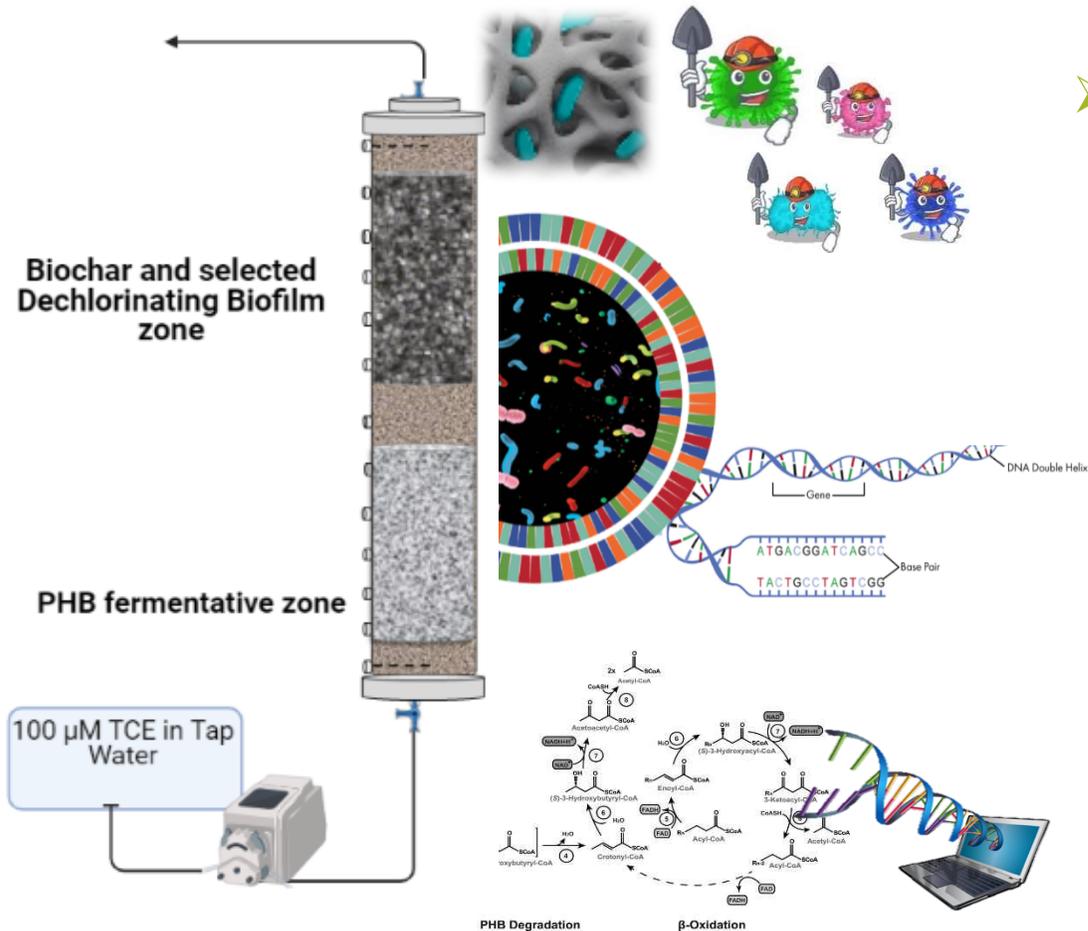
ANAEROBIC MINERAL MEDIUM + TCE



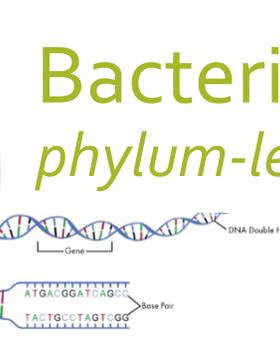
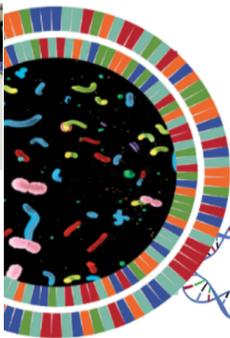
BIOMOLECULAR CHARACTERIZATION OF THE REACTOR

- 16S rRNA gene amplicon sequencing (MiSeq Illumina)
- Metagenomic analysis (MiSeq Illumina)
- Quantification of reductive dechlorination biomarkers' (digital droplet PCR)

Aim of the work

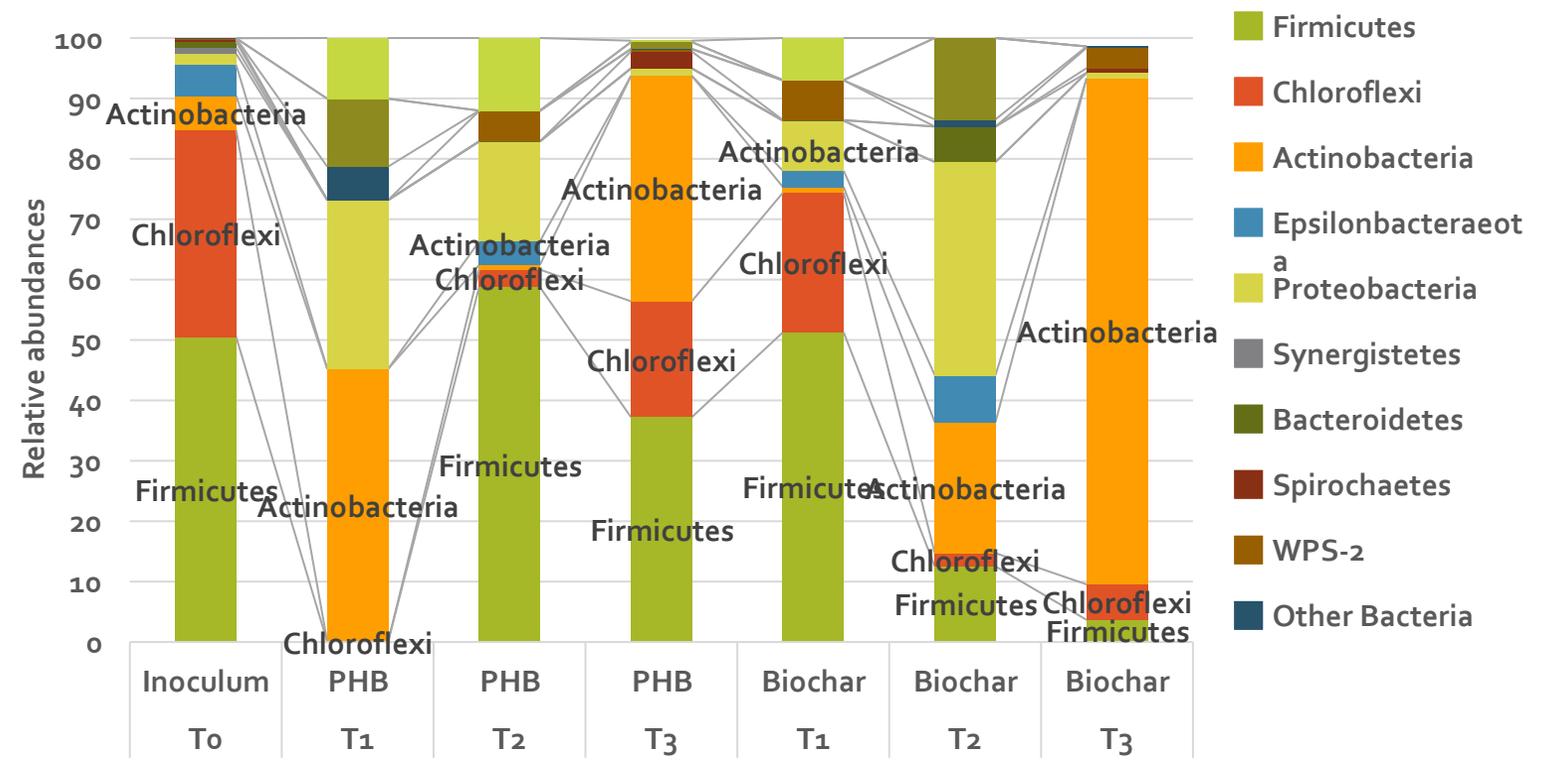
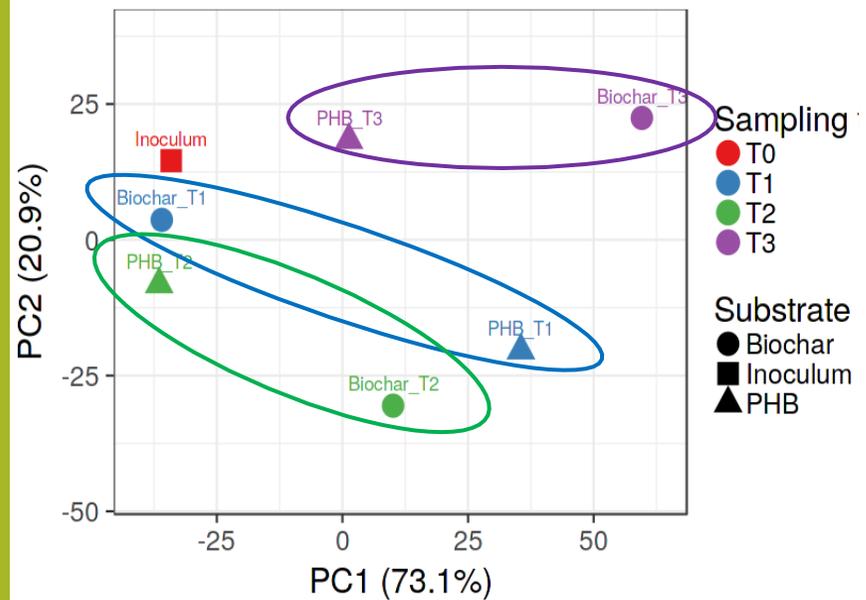


- Composition and dynamics of the bacterial communities established in the PHB and Biochar zone under various feeding conditions tested
- Shed light on the functional role of the main bacterial components in the system
 - Bacteria involved in the PHB-to-butyrate/acetate/ H_2 transformation
 - Role of Biochar for Dhc growth/activity
- Dhc biomonitoring overtime



Bacterial community composition and dynamics

phylum-level

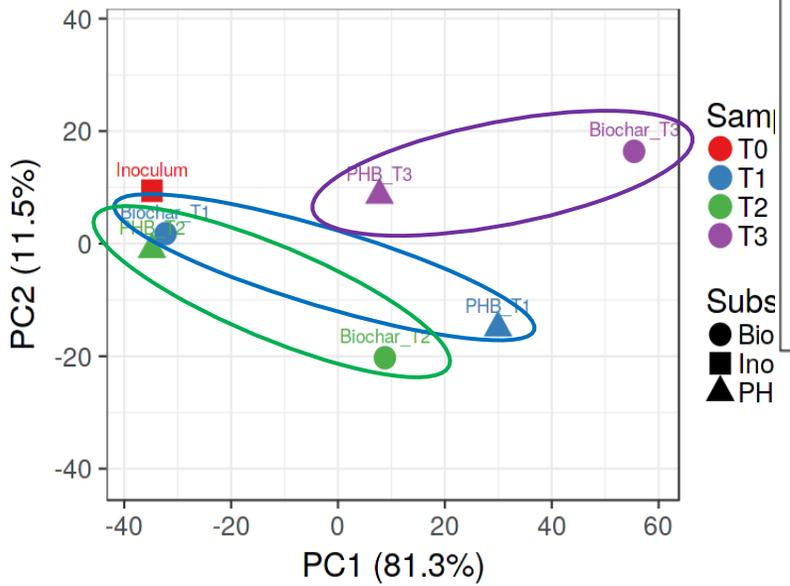


- **Inoculum:** core microbiome composed by *Firmicutes*, *Chloroflexi* → dominated the PHB/Biochar reactor fed with TapWater (and after ricirculation) at T1-T2
- **PHB zone:** effect of ricirculation on the microbial structure → fermentative *Actinobacteria* shifted to fermentative *Firmicutes* and *Chloroflexi* were introduced in the fermentative zone → T3 increment of dechlorinating *Chloroflexi* (effect of the anaerobic mineral medium feeding)
- **Biochar zone:** at T1 core microbiome of the inoculum → *Firmicutes* shifted to *Actinobacteria* that increased at T2 and then T3 in the biochar zone.



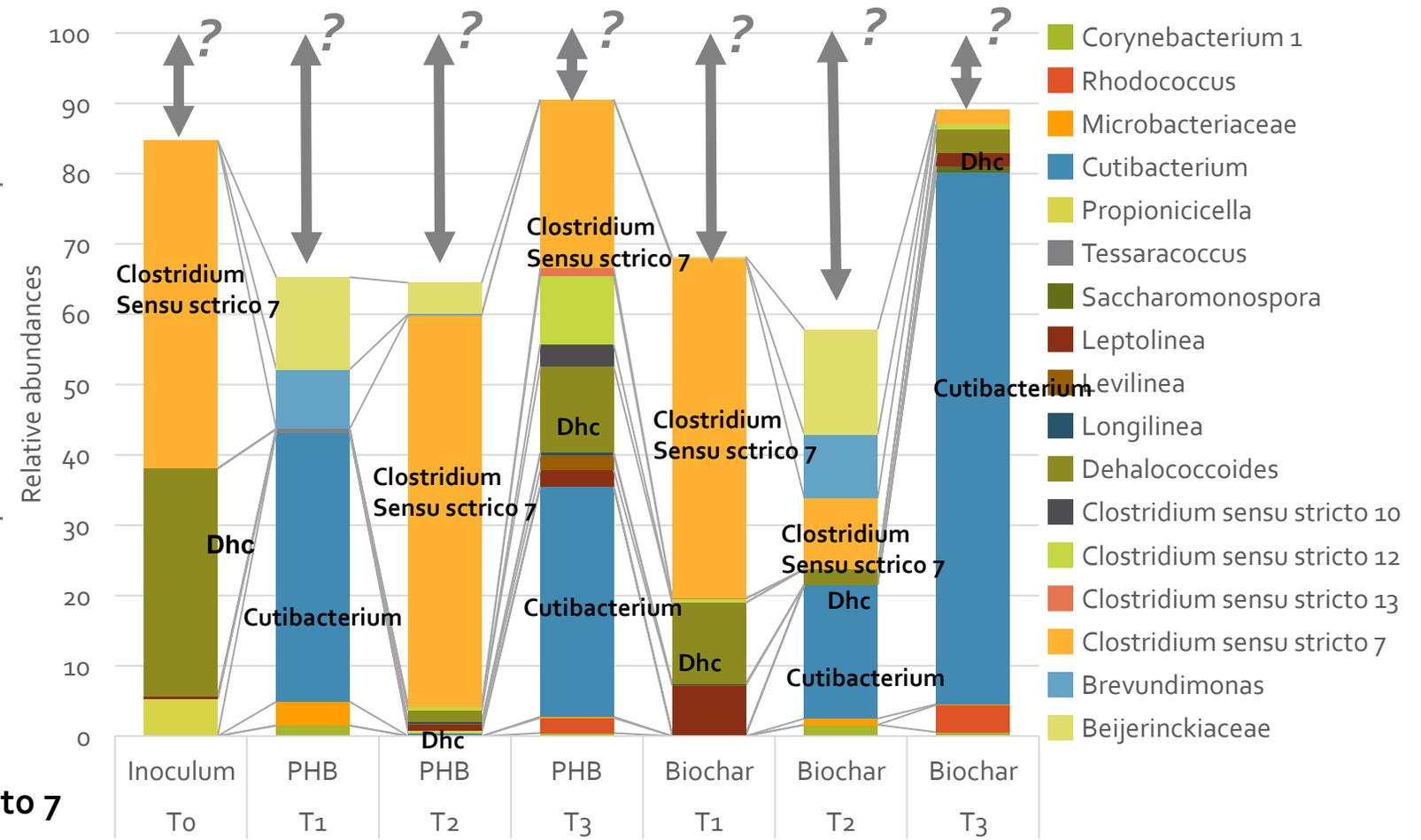
Bacterial community composition and dynamics

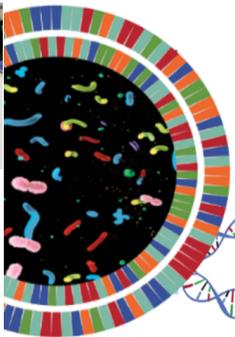
genus-level



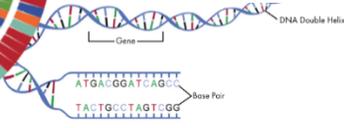
- **Most representative fermenters**
 - Firmicutes_Clostridium sensu stricto 7
 - Actinobacteria_Cutibacterium

- **Dechlorinating bacteria: Dehalococcoides mccarty**
 - **PHB zone:** Dhc established after the tap water recirculation and increased with the anaerobic mineral medium feeding (T₂, T₃)
 - **Biochar zone:** Dhc Established immediately but decreased both after the tap water recirculation (T₂) and feeding with the anaerobic mineral medium (T₃)

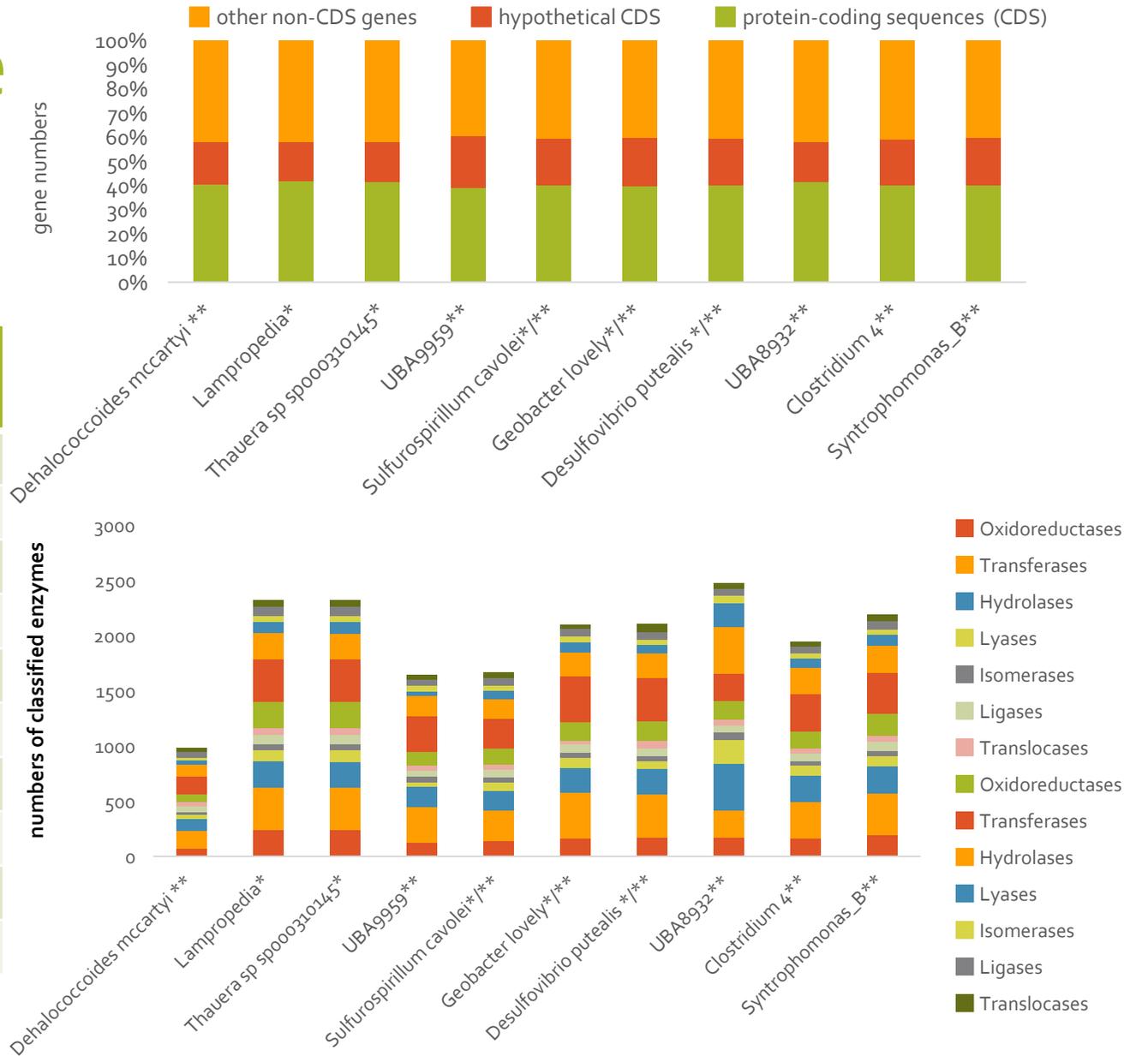




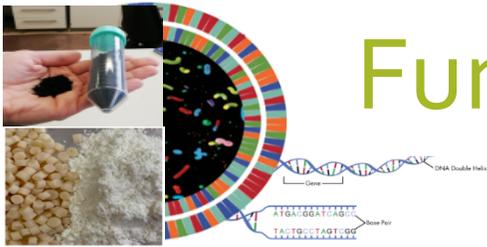
Metagenome



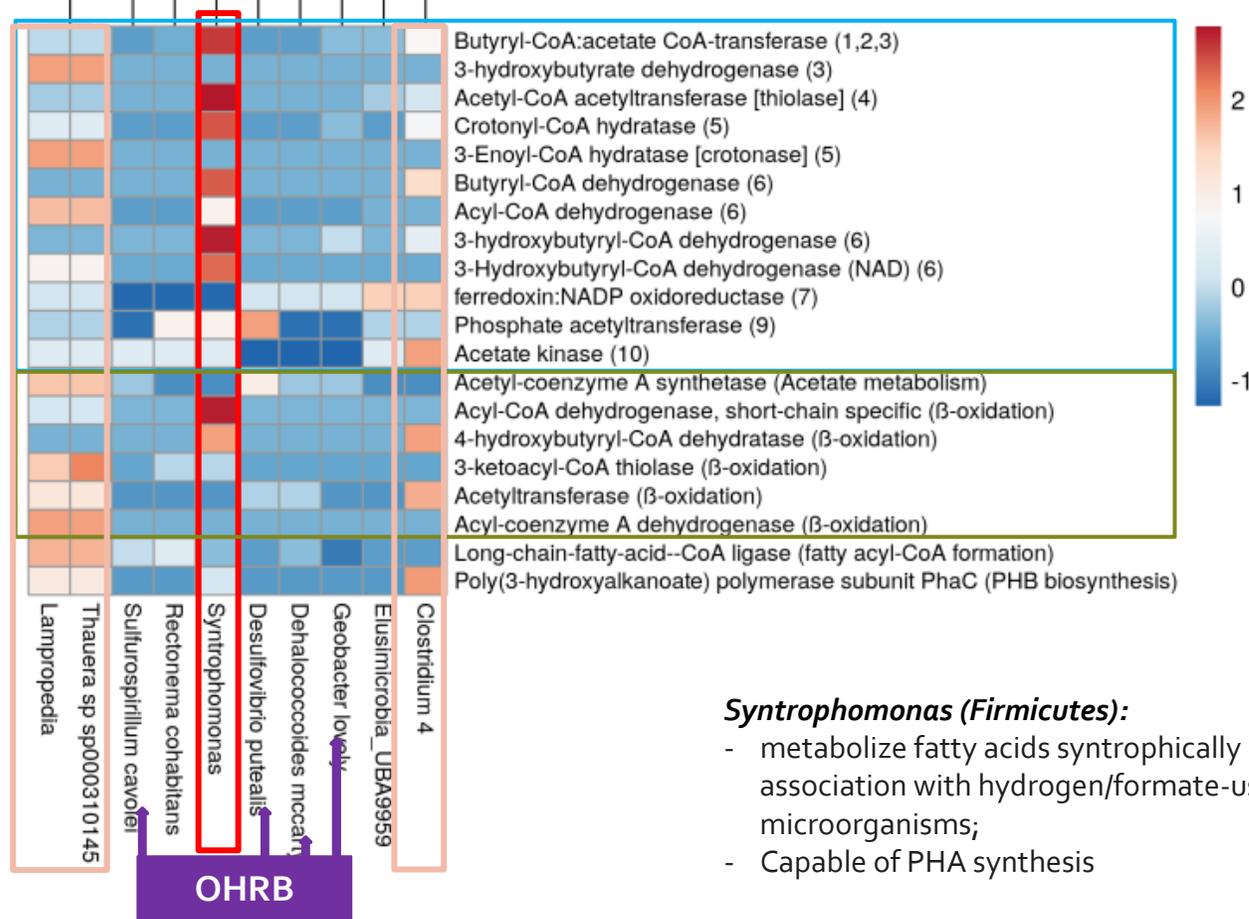
Bin	Affiliation	Coverage PHB*/Biochar**
Bin1	Dehalococcoides mccartyi	0/151
Bin2	Lamproedia	218/82
Bin3	Thauera sp sp000310145	274/46
Bin4	Elusimicrobia_UBA9959	16/56
Bin5	Sulfurospirillum cavolei	27/25
Bin6	Geobacter lovelly	10/8
Bin 7	Desulfovibrio putealis	26/28
Bin8	Rectonema cohabitans	2/28
Bin9	Clostridium 4	4/11
Bin10	Syntrophomonas_B	11/36



Functional prediction

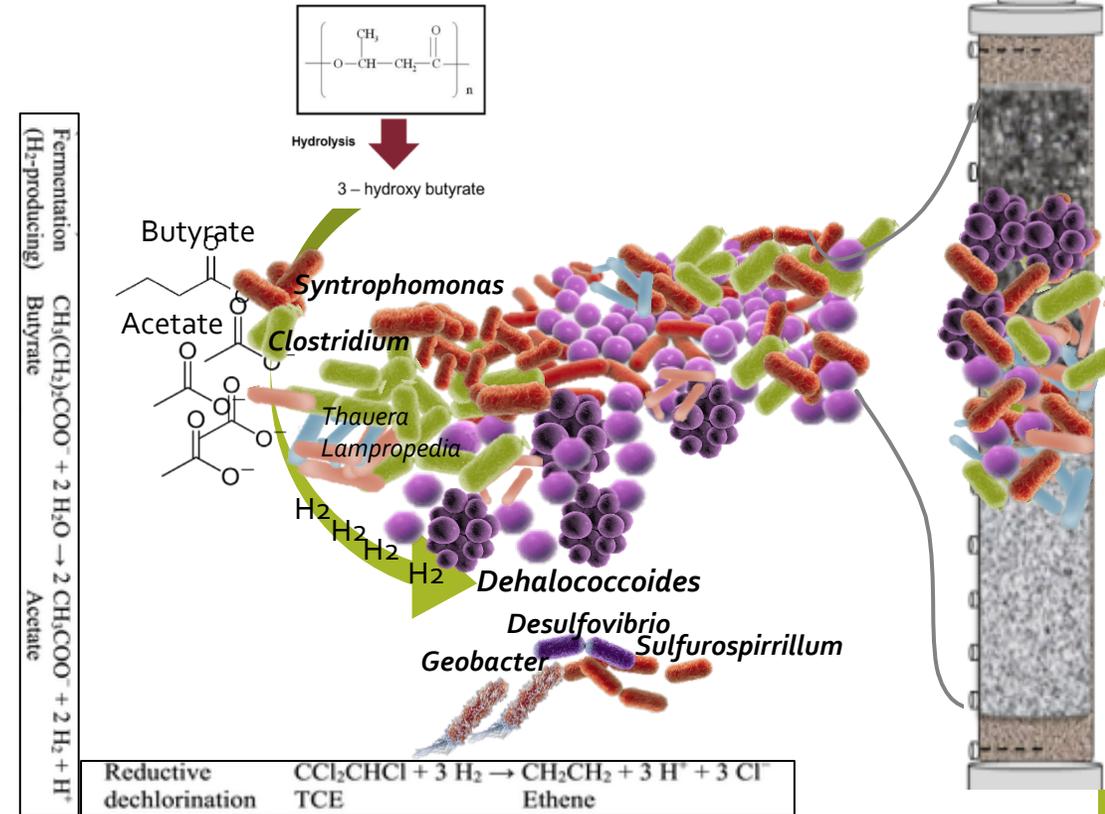
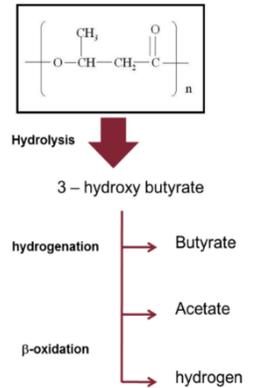
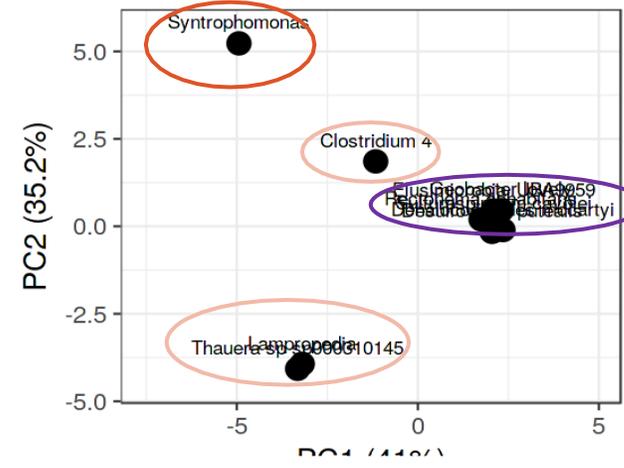


Genes involved in 3-HB hydrogenation and β -Oxidation

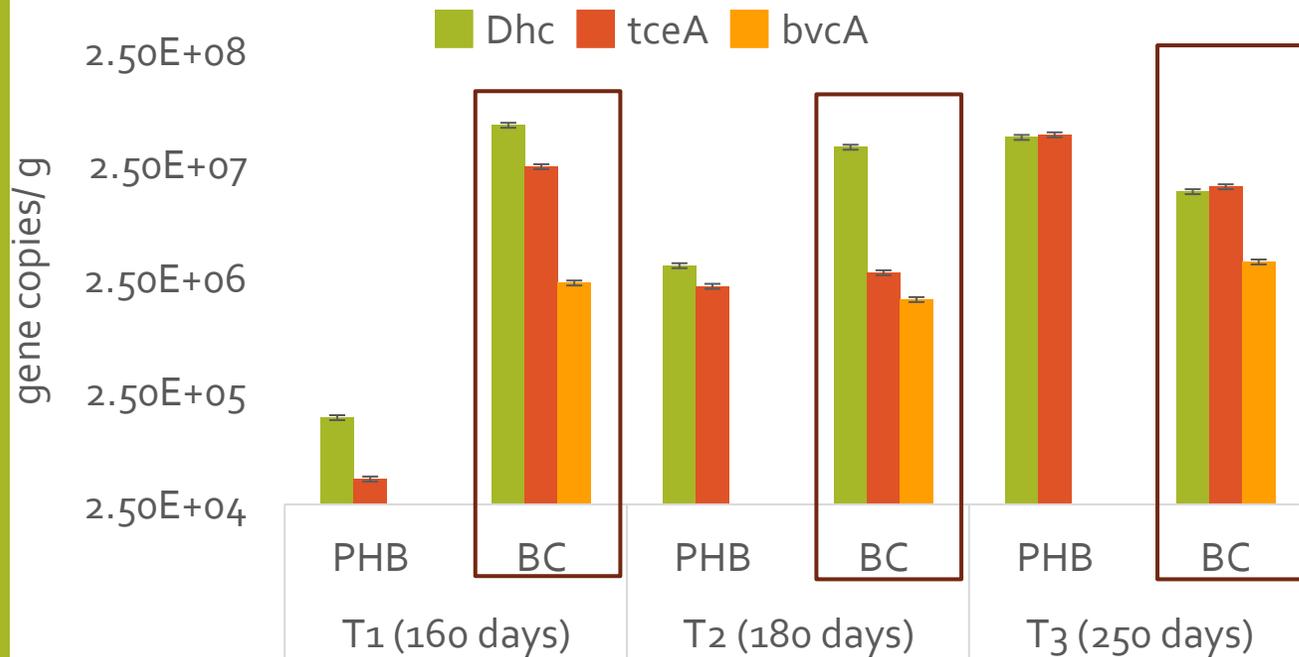


Syntrophomonas (Firmicutes):

- metabolize fatty acids syntrophically in association with hydrogen/formate-using microorganisms;
- Capable of PHA synthesis



Dhc quantification



Dhc also found in the PHB zone → probably some «backdiffusion» towards PHB zone (?)



After the ricirculation, *Dhc* increased in the PHB zone



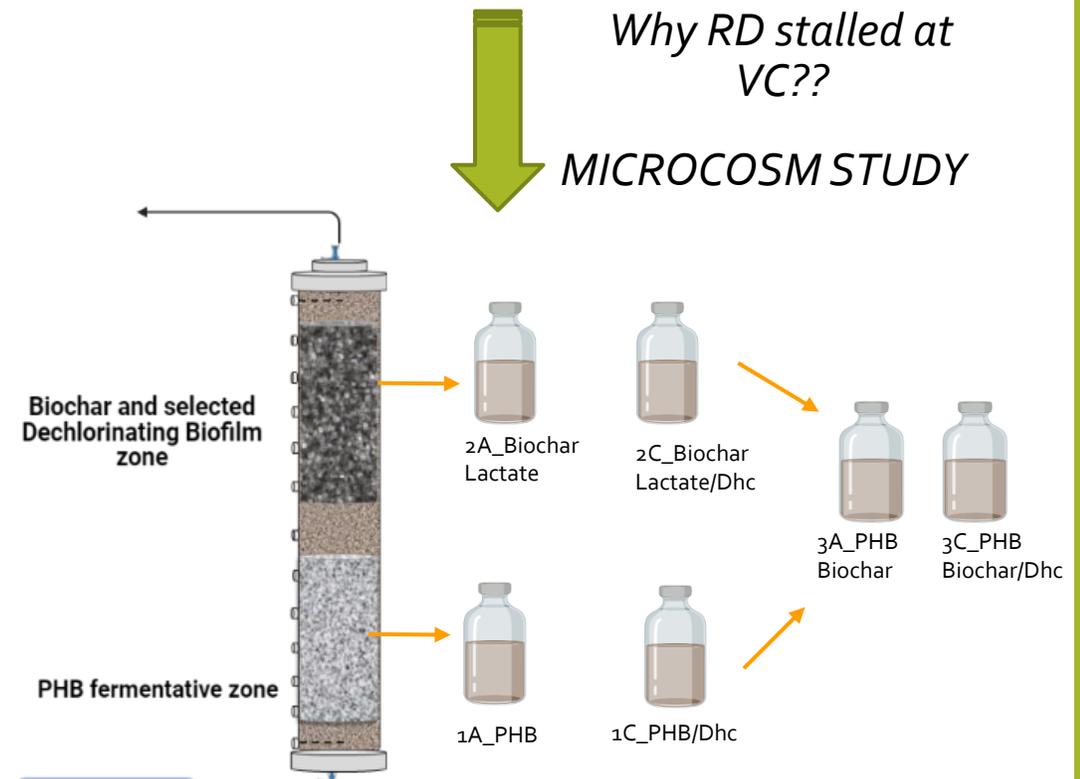
The anaerobic mineral medium positively affected *Dhc* abundance

➤ *Dhc* actively grows on Biochar → Biochar sustains biofilm-formation but does not provide nutritional requirements for growth and RD activity → no electron transfer systems known from biochar to *Dhc* cells!

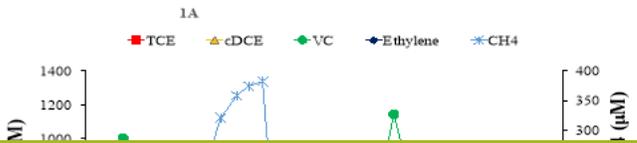
➤ *Dhc tceA*-carrying strains were the most abundant and *bvcA* was found only in the BC zone → in line with VC formation

Why RD stalled at VC??

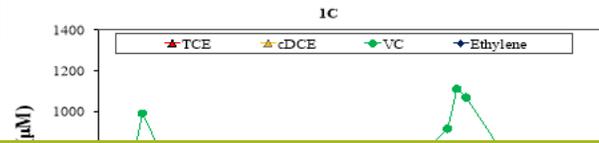
MICROCOSM STUDY



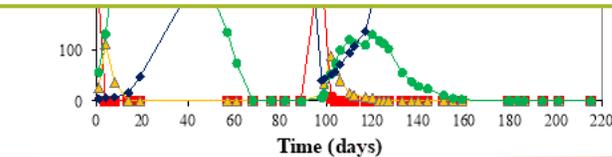
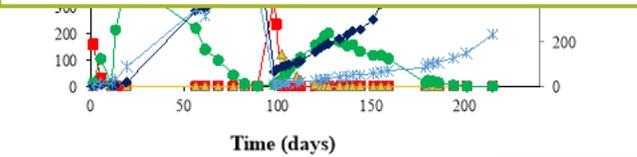
No Dhc bioaugmented



Dhc bioaugmented

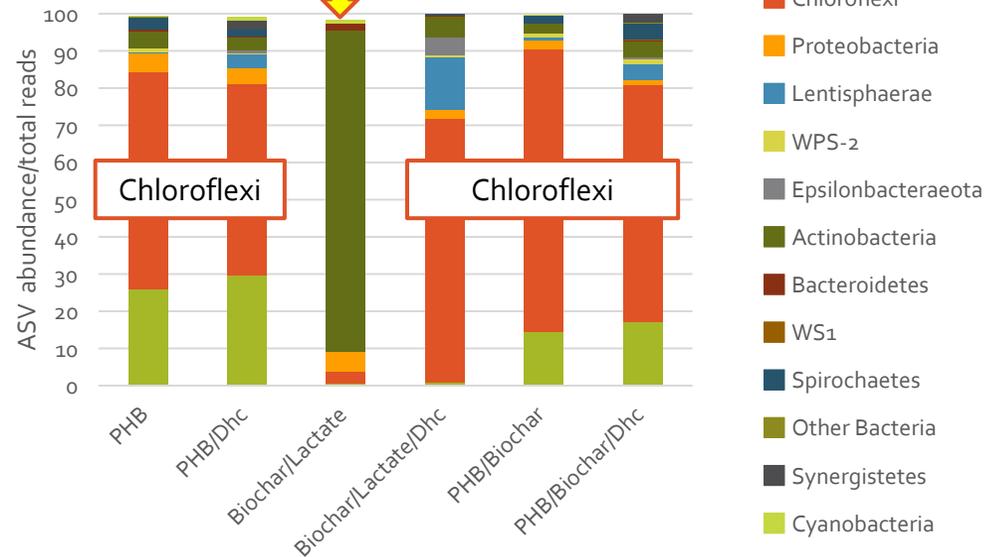


- ✓ TCE-to-ethylene was successfully completed in all the microcosms set-up from the mini pilot PHB/Biochar reactor;
- ✓ *Dhc* dominated the microbial community also in the non-bioaugmented microcosm;
- ✓ *Clostridium* as the main PHB-fermentative bacteria, except for Biochar microcosm (*Cutibacterium*);
- HRT of the mini pilot PHB/Biochar reactor lowered *Dhc* activity in VC-to-ethylene step
 - ❖ *Dhc* strains usually grow slowly with a doubling time of 1 to 2 days and have complex nutritional requirements!

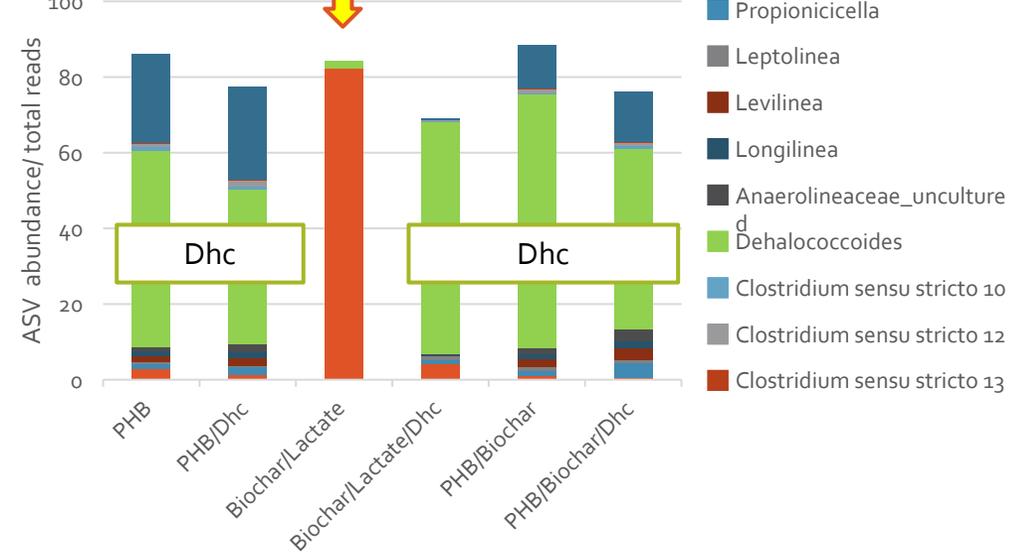


PHB/E

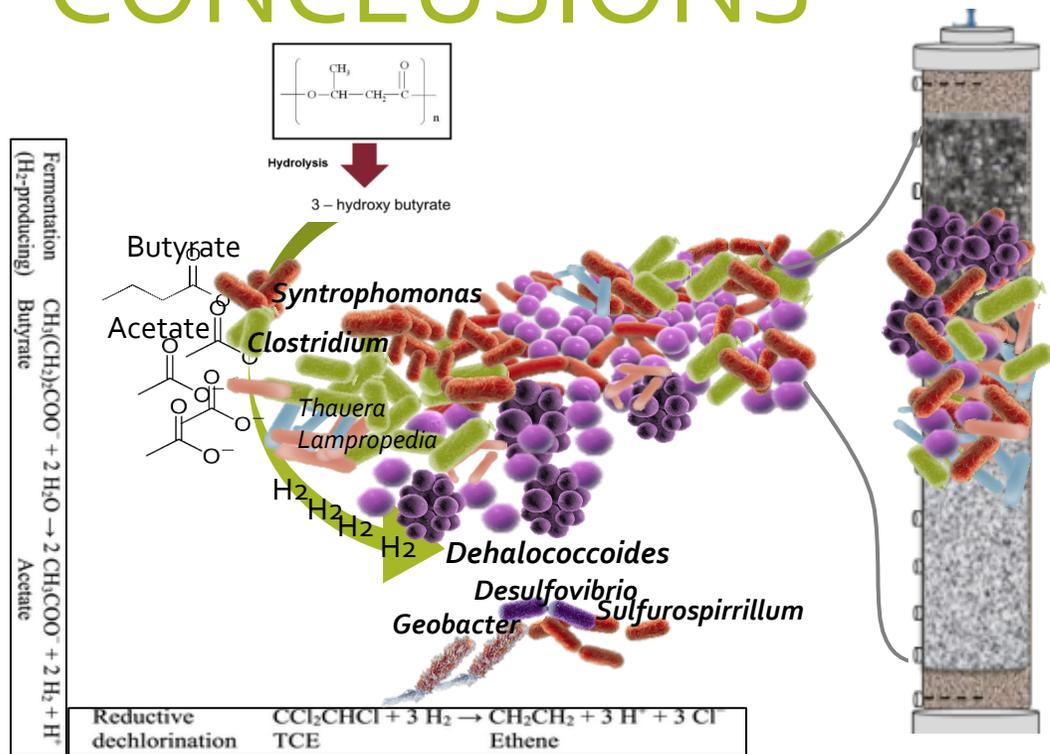
Phylum-level



Genus-level



CONCLUSIONS



❖ SOME ISSUES TO BE ADDRESSED IN THE NEXT ACTIVITIES

- Screening of the genes coding for hypothetical proteins in the extracted genomes
 - Reductive dehalogenases of the OHRB-community
 - PHB depolymerase
- Evaluation of the optimum HRT, by balancing reactor performances and management (e.g. volume of the feeding medium), with Dhc growth-requirements (e.g. doubling time, nutritional supply by the microbial community) to fulfill the complete TCE dechlorination to ethylene

- ✓ **Bio-based circular economy** spans various multidisciplinary areas, including the utilization of biological resources for bioremediation purposes → many efforts are still needed to fully exploit its **advantages in the bioremediation technologies.**
- ✓ **PHB and Biochar** have great potential as bio-based materials to sustain and support **Reductive Dechlorination processes**
- ✓ The mini-pilot scale PHB/Bioreactor successfully prompted RD processes:
 - **A core microbiome established in the PHB/Biochar reactor**
 - **PHB zone:** fermentation to butyrate/acetate/H₂ sustains the growth and activity of *Dhc* and other OHRB in the system (*Sulfurospirillum*, *Geobacter*, *Desulfovibrio*)
 - **Biochar zone:** biomaterials that support the “biofilm-formation” of *Dhc* → once *Dhc* colonized the PHB zone, it prefers the direct availability of electrons derived from fermentation products
 - The recirculation of tap water from Biochar to PHB zone and then the feeding with the anaerobic mineral medium, **prompted RD activity and growth of *Dhc*, the latter preferentially established in the PHB zone**
- ✓ In the reactor, RD stalled at VC probably because of the low HRT → microcosm study demonstrated the whole TCE-to-ethylene dechlorinating capability of the reactor-microbial community



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