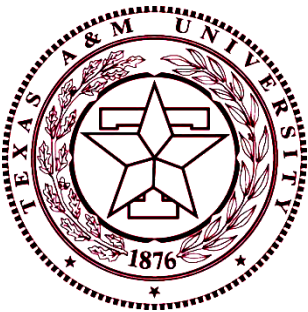


Stable Isotope Probing (SIP) of Rhizosphere Bacteria in 6:2 Fluorotelomer Sulfonic Acid (6:2 FTSA)-Contaminated Soil



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May 9, 2023

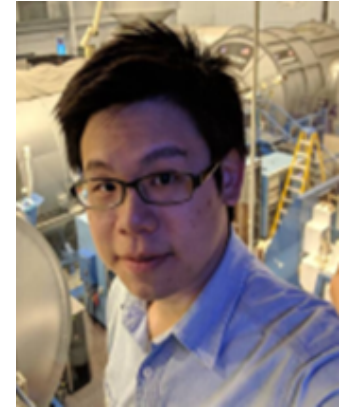


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Per- and Polyfluoroalkyl Substances (PFAS)

- PFAS are a group > 3,000 man-made fluorinated chemicals as of 2018

(10.1021/acs.est.6b04806)

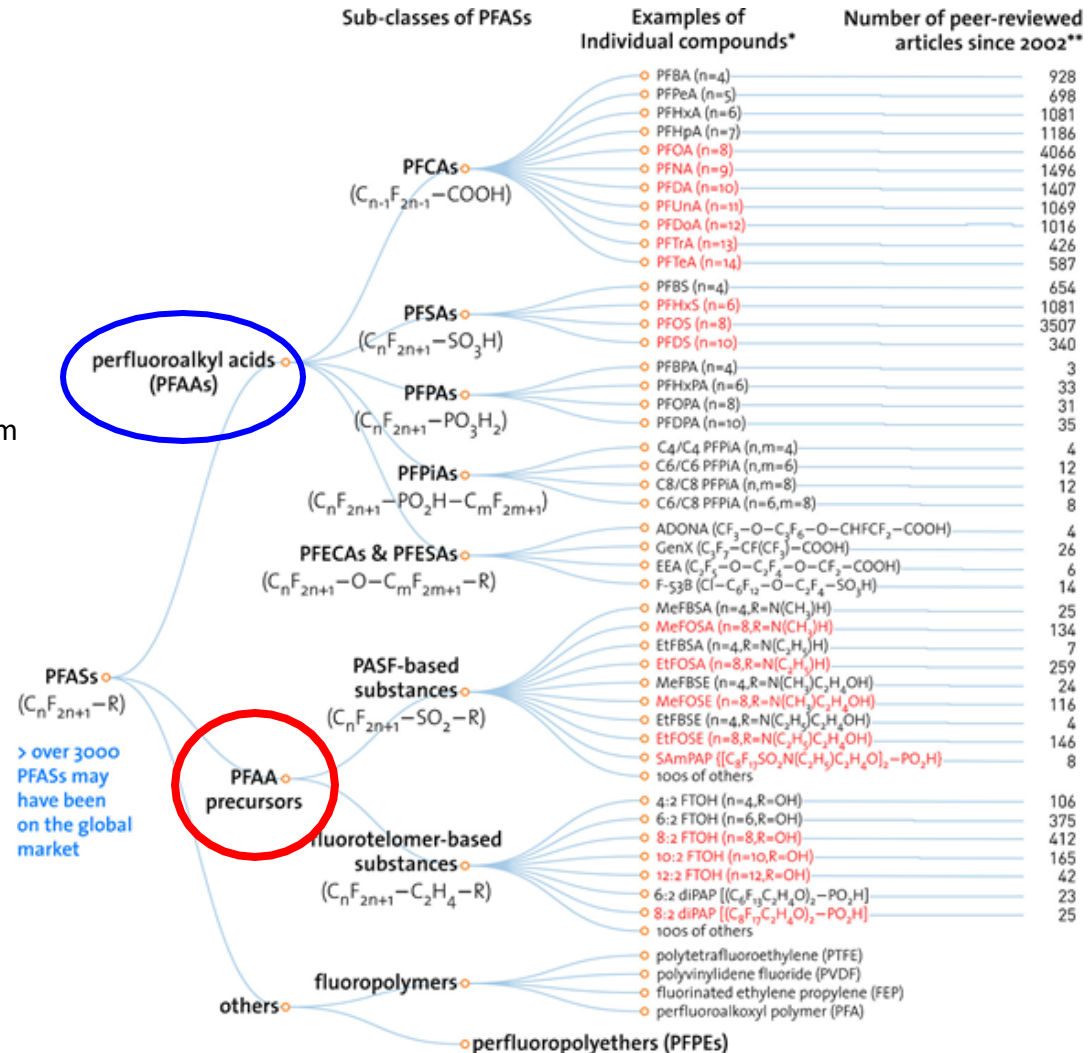
- > 9000 PFAS has been identified (source: CDC)

(<https://www.cdc.gov/niosh/topics/pfas/default.htm>)

Precursors



Various chain-length
PFAS



* PFASs in RED are those that have been restricted under national/regional/global regulatory or voluntary frameworks, with or without specific exemptions (for details, see OECD (2015), Risk reduction approaches for PFASs. <http://oe.cd/iAN>).

** The numbers of articles (related to all aspects of research) were retrieved from SciFinder® on Nov. 1, 2016.

Per- and Polyfluoroalkyl Substances (PFAS)

- Man-made fluorinated chemicals
- Unique property
 - Thermally stable and chemically inert
 - High surface activity
 - Water- and oil-repellent

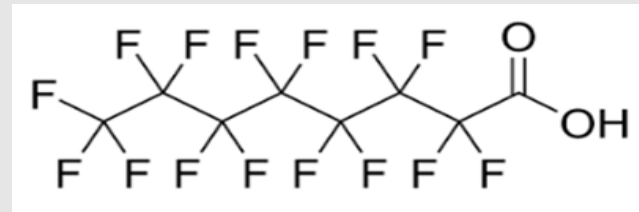
Per – fully fluorinated

Poly – partially fluorinated



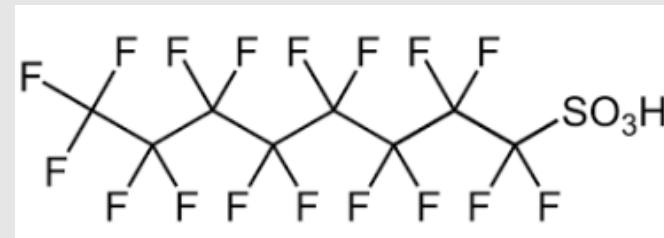
8:2 FTOH

Fluorotelomer alcohol



PFOA

Perfluorooctanoic acid



PFOS

Perfluorooctanesulfonic acid

6:2 Fluorotelomer Sulfonic Acid (6:2 FTSA)

- **1H,1H,2H,2H-Perfluorooctanesulfonic acid**

Molecular weight = 428.17 g/mol

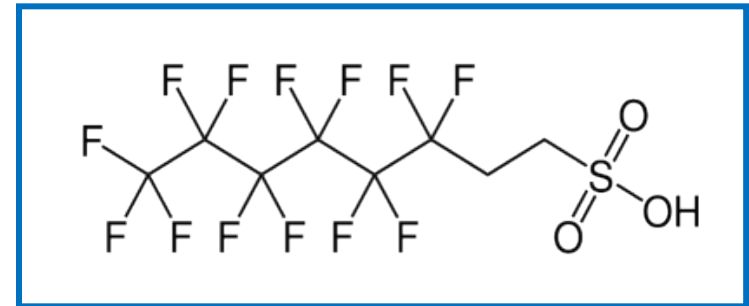
log water solubility (mol/L, 25 °C)= -2.51

log K_{OC} (pH 7, 25 C)= 1.0

log K_{OW} = 4.44

Density = 1.68 g/mL

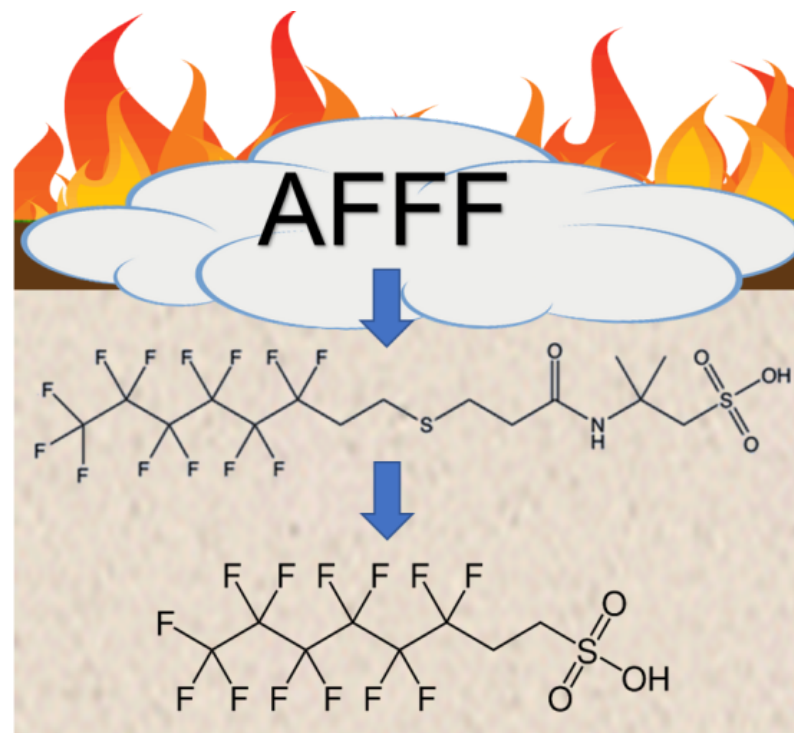
Boiling point = 219 - 272 °C



- **Resistant to heat, acids, and bases**
- **Alternative to perfluorooctane sulfonate (PFOS)**
- **Persistent, bio-accumulative, toxic**

Occurrence, Source, and Fate

- Fluorotelomer sulfonates
 - as ingredients in aqueous film-forming foams (AFFFs)
 - as transformation metabolites from precursors in AFFFs
- Known Precursors to fluorotelomer sulfonates
 - fluorotelomer thioether amido sulfonate (FtTAoS)
 - fluorotelomer sulfonamide betaines (such as 6:2 FTBA)



- 6:2 FTSA found in high levels in AFFF-impacted soils and groundwater
 - AFFF-impacted soil: 612-2,101 µg/kg
- 6:2 FTSA is also detected in
 - River, groundwater and wastewater: 1.6-37.9 ng/L
 - Landfill leachate: 582 ng/L

Biodegradation of 6:2 FTSA

Degradation of 6:2 FTSA in activated sludge

- Formation of similar biodegradation metabolites as those observed during 6:2 fluorotelomer alcohols (6:2 FTOH) biodegradation.
- Slow biotransformation. ~ 63.7% remaining on day 90
- Half life: ~ 2 years

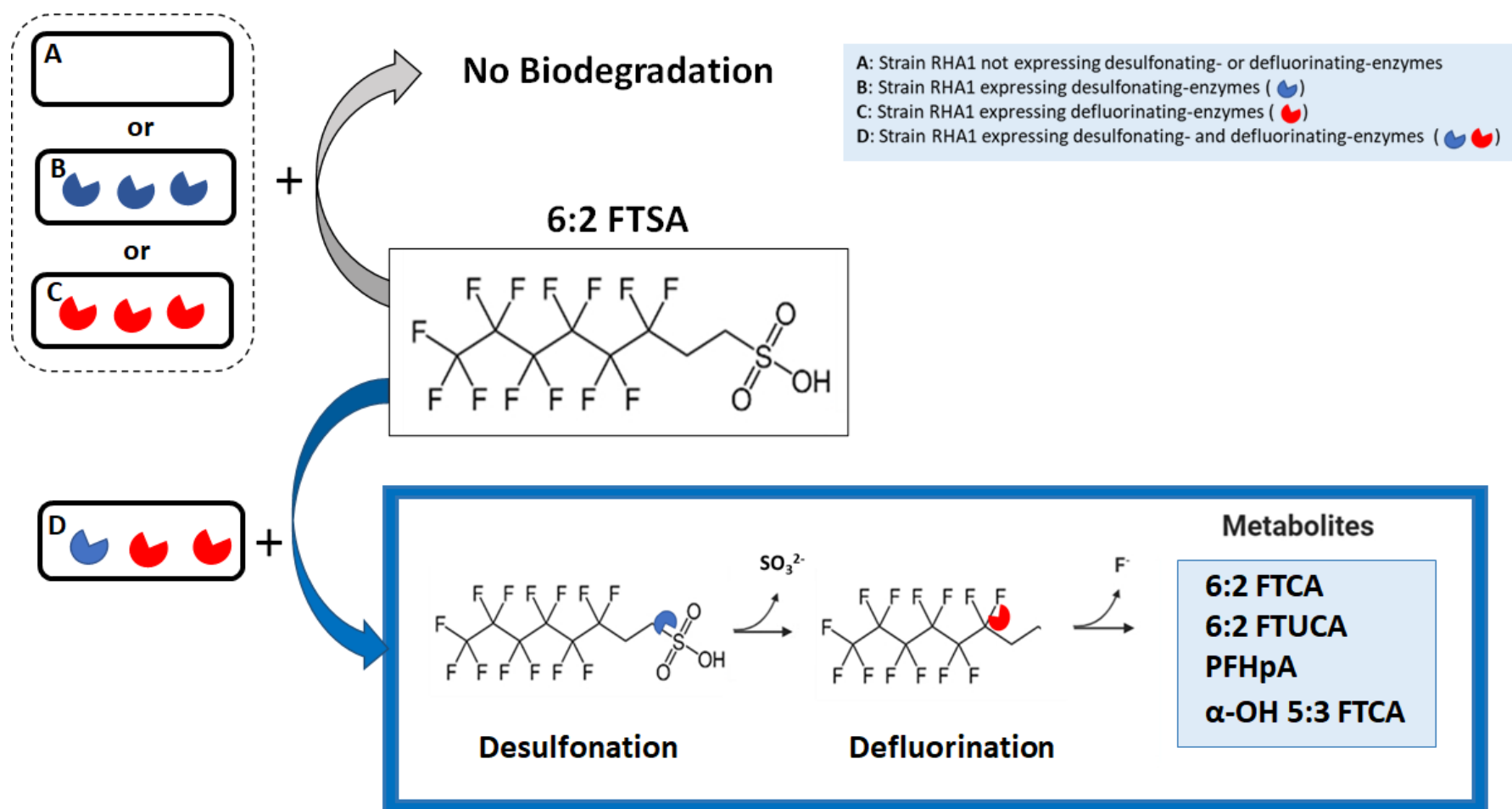
Aerobic River Sediments

- Rapidly biotransformed.
- Half life: ~ 5 days

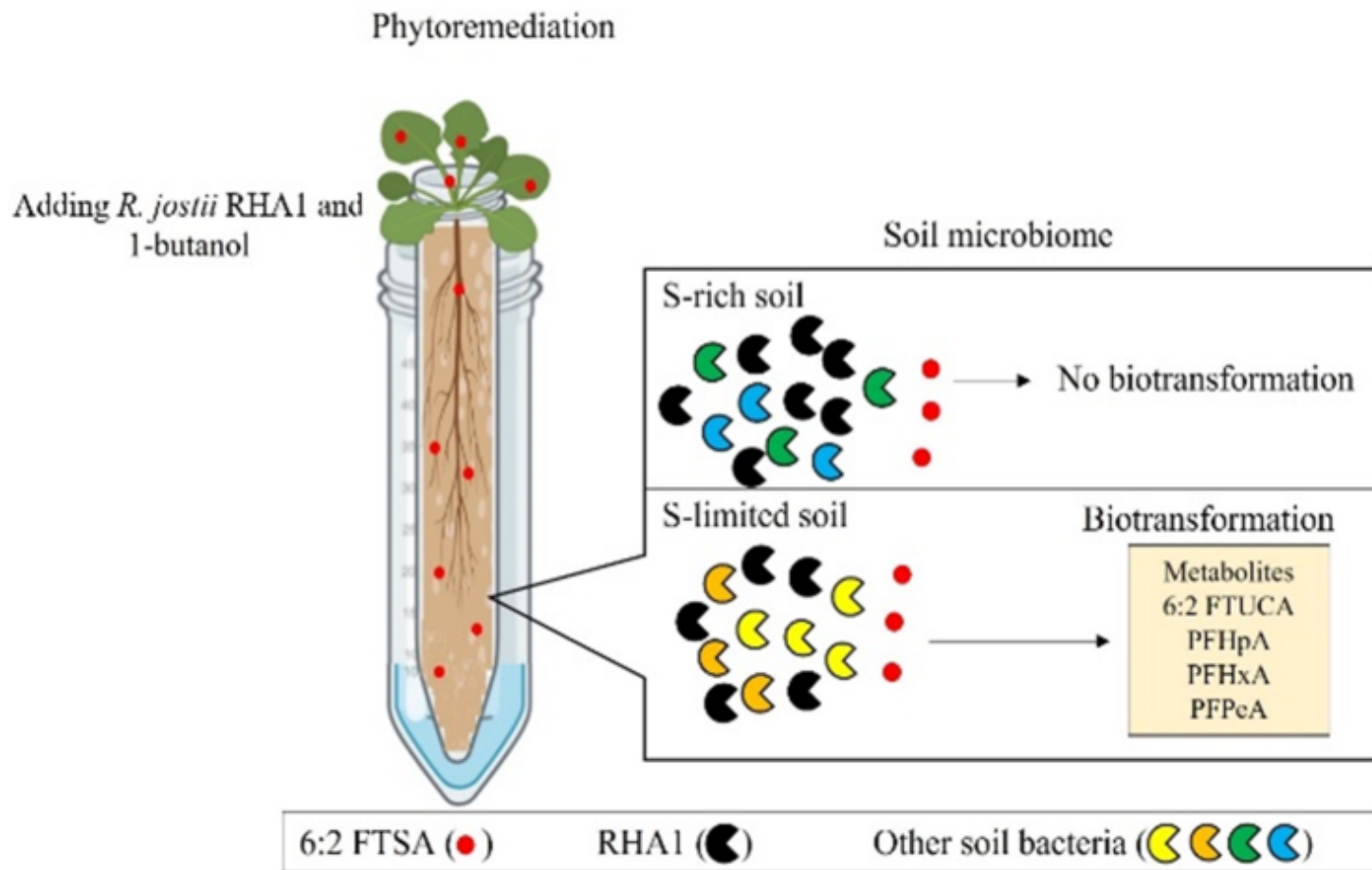
Anaerobic River Sediments

- No evidence of biodegradation or biotransformation over 100 days

Carbon and sulfur sources affected biodegradation of 6:2 FTSA by *Rhodococcus jostii* RHA1

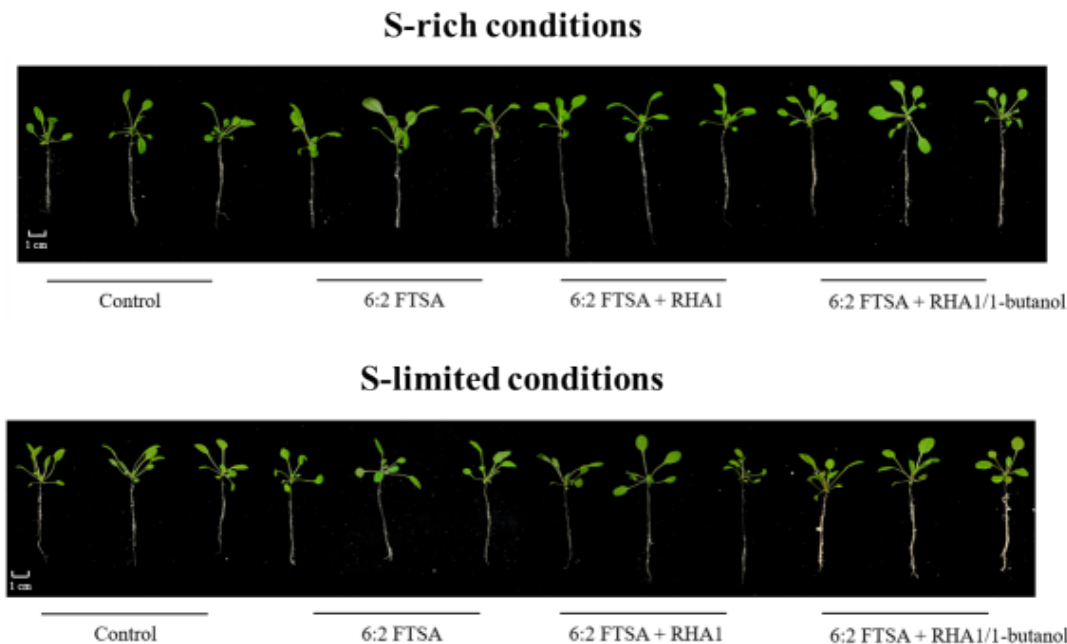


Fate and transformation of 6:2 FTSA affected by plant, nutrient, bioaugmentation & soil microbiome interactions

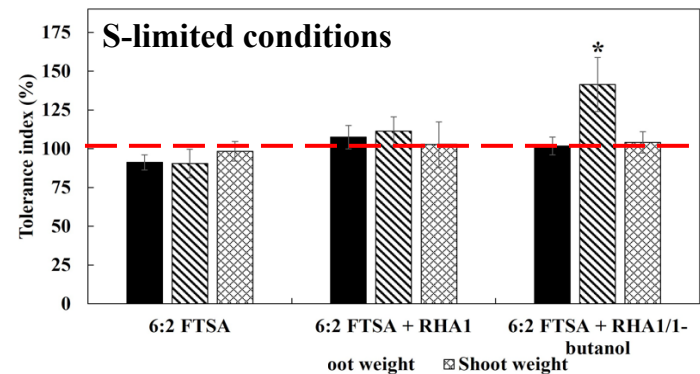
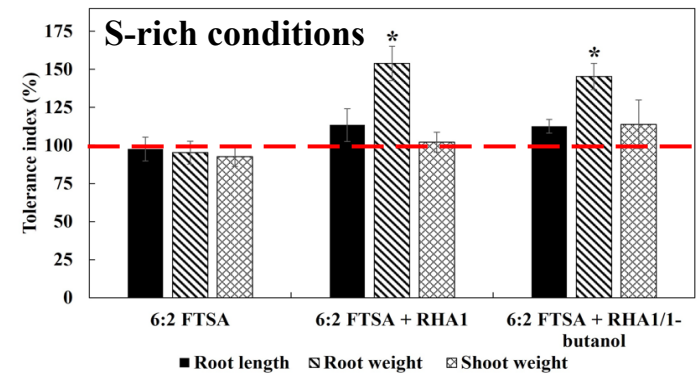


6:2 FTSA had no effects on plant growth while RHA1 promoted the growth

No plant growth effect by 6:2 FTSA

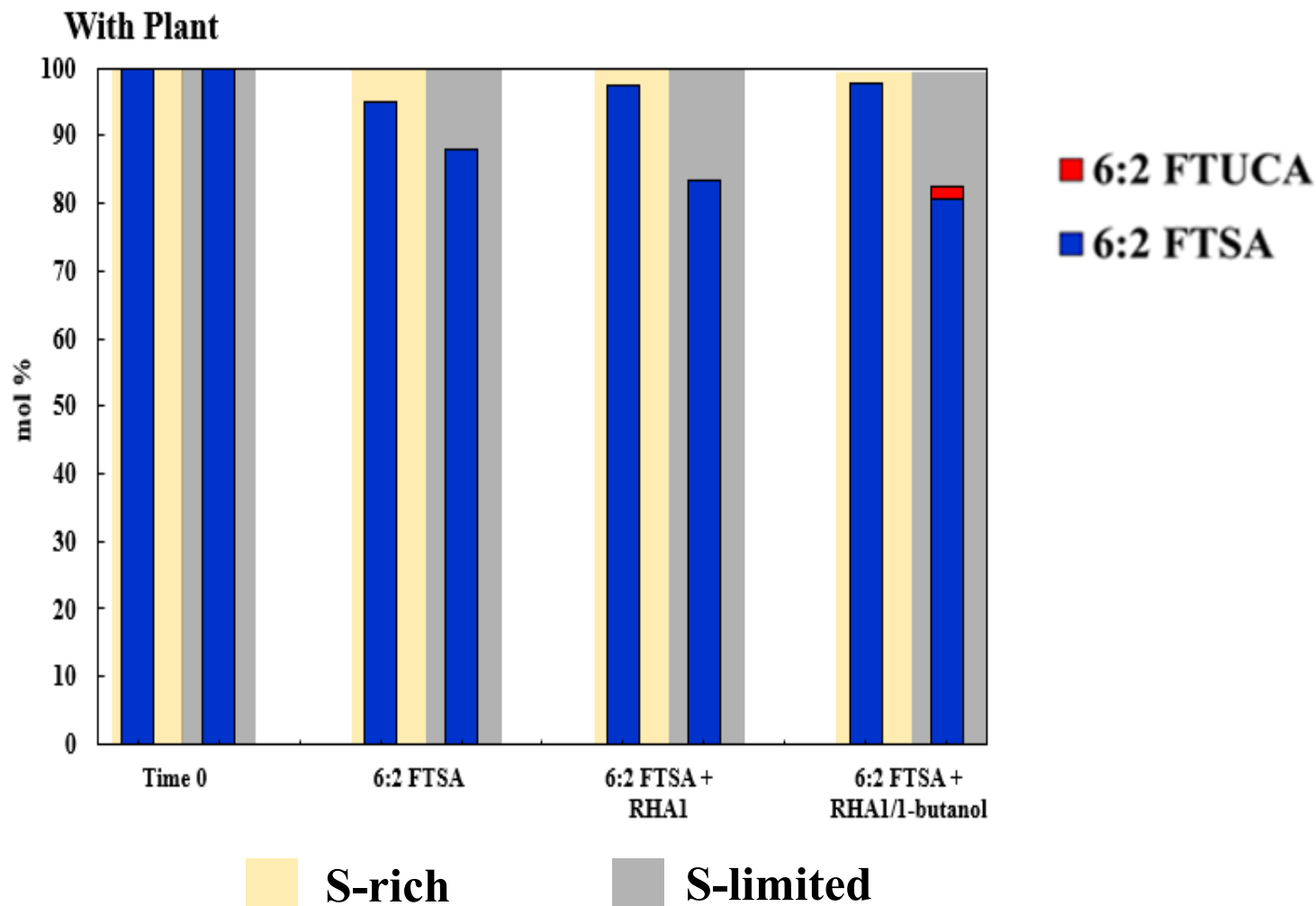


RHA1 promoted plant growth



$$\text{Tolerance Index (TI)} = \frac{\text{mean phenotype measurement of treatment}}{\text{mean phenotype measurement of control}}$$

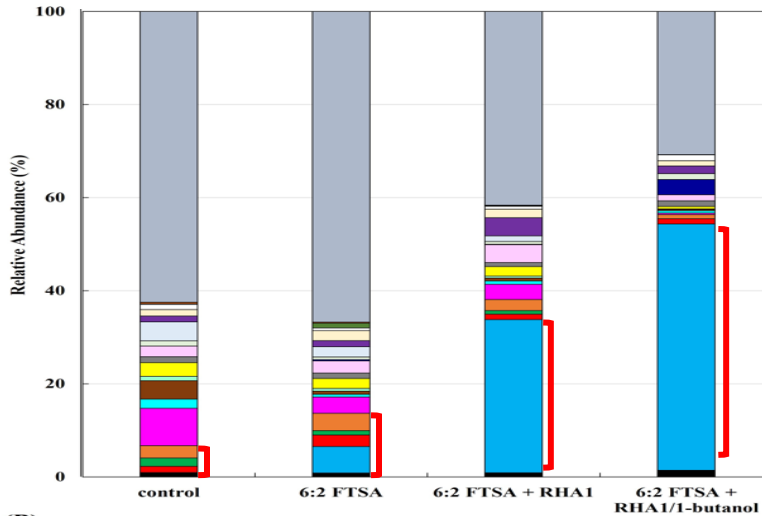
Degradation of 6:2 FTSA in the rhizosphere of plants amended with RHA1 and 1-butanol under S-limited conditions



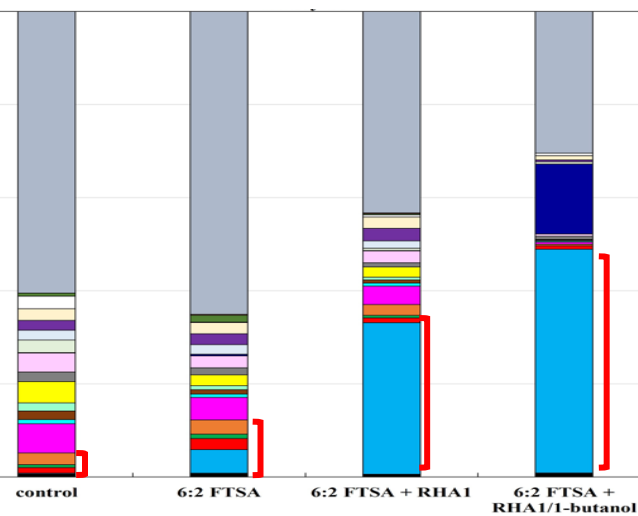
$$\text{Molar yield} = 100\% \times \frac{\text{Mass of PFAS species dected in soil (mole)}}{\text{Initial mass of 6:2 FTSA spiked in soil(mole)}}$$

Rhodococcus is one of the dominant species in RHA1- spiked treatments

S-rich rhizosphere sandy soil



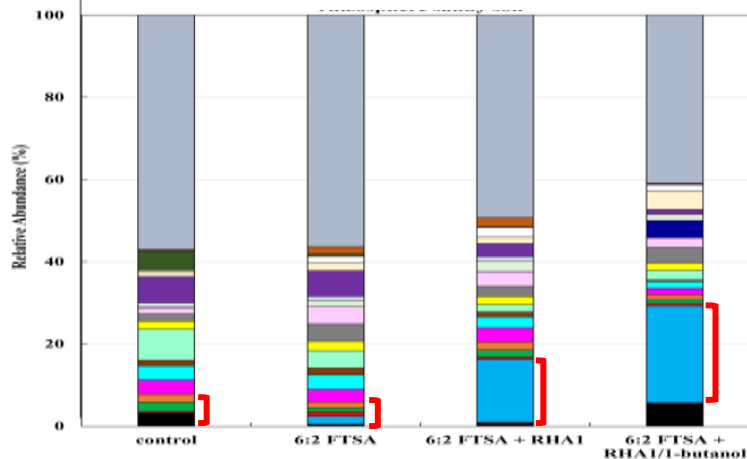
S-rich sandy soil



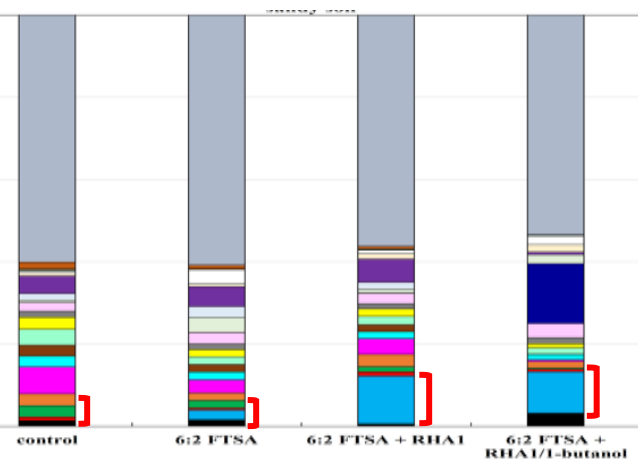
Genus

- Other
- Solimonas*
- Streptomyces*
- uncultured bacteria
- Luteimonas*
- Rhodanobacter*
- Nevskia*
- uncultured bacteria
- Zoogloea*
- uncultured bacteria
- Sphingomonas*
- uncultured bacteria
- uncultured bacteria
- uncultured bacteria
- Pseudonocardia*
- Nocardioides*
- Mycobacterium* Δ
- Pseudomonas* * Δ
- Rhodococcus* *
- Gordonia* *

S-limited rhizosphere sandy soil



S-limited sandy soil

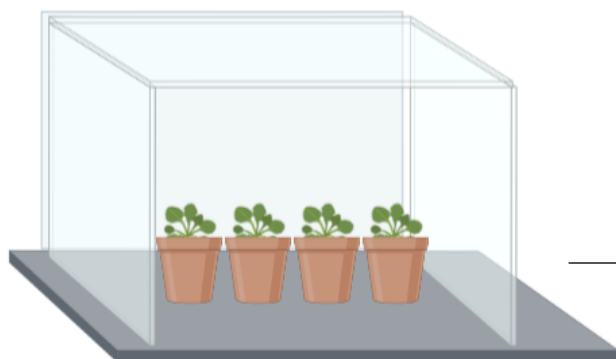


Q1: Which rhizosphere microbes were supported by the root exudate?

Q2: Was root-exudate-supported microbial community affected by 6:2 FTSA, carbon sources, and bioaugmentation?

Experimental Design

Grow the plant for 20 days



S-limited sandy soil

Control (no RHA1, no 6:2 FTSA)

RHA1

6:2 FTSA

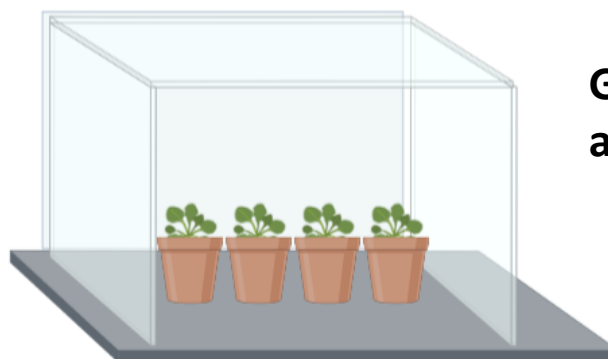
6:2 FTSA+RHA1

6:2 FTSA + RHA1 + 1-butanol

6:2 FTSA + n-octane

6:2 FTSA + 1-butanol

6:2 FTSA + DGBE



S-limited sandy soil

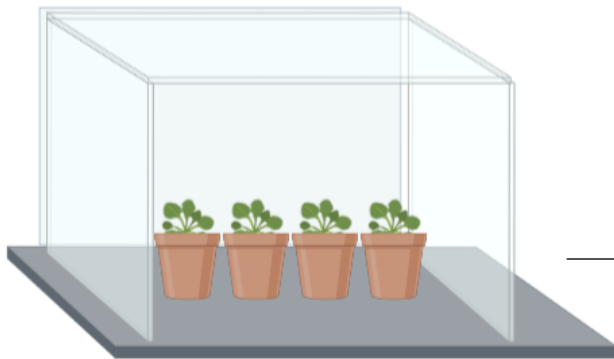
Grow the plant for another 10 days

- Purged the chamber with N_2 , then spiked O_2 to 21% and $^{13}CO_2$ to 500ppmv.
- Incubated with light intensity of $100 \mu E m^{-2} s^{-1}$ for 16 hours.

* Initial 6:2 FTSA concentration = 1.5 mg/kg.

Experimental Design (conti.)

$^{13}\text{CO}_2$ (30 days total)



S-limited sandy soil

Control (no RHA1, no 6:2 FTSA)

RHA1

6:2 FTSA

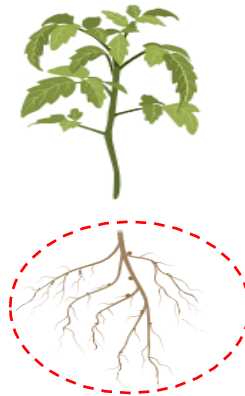
6:2 FTSA+RHA1

6:2 FTSA + RHA1 + 1-butanol

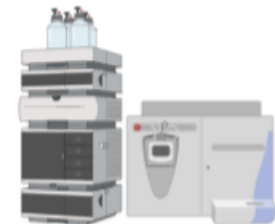
6:2 FTSA + n-octane

6:2 FTSA + 1-butanol

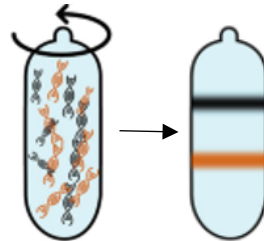
6:2 FTSA + DGBE



Phenotype:
Root length & Biomass



PFAS analysis



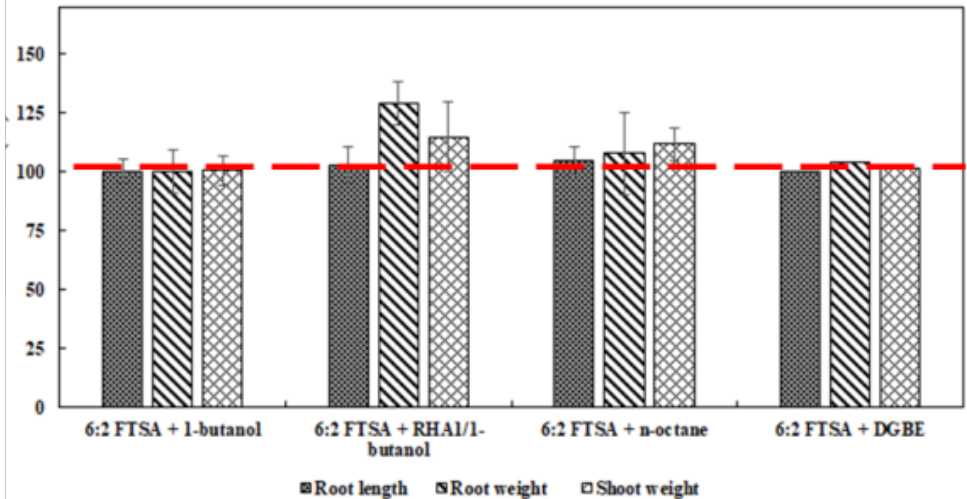
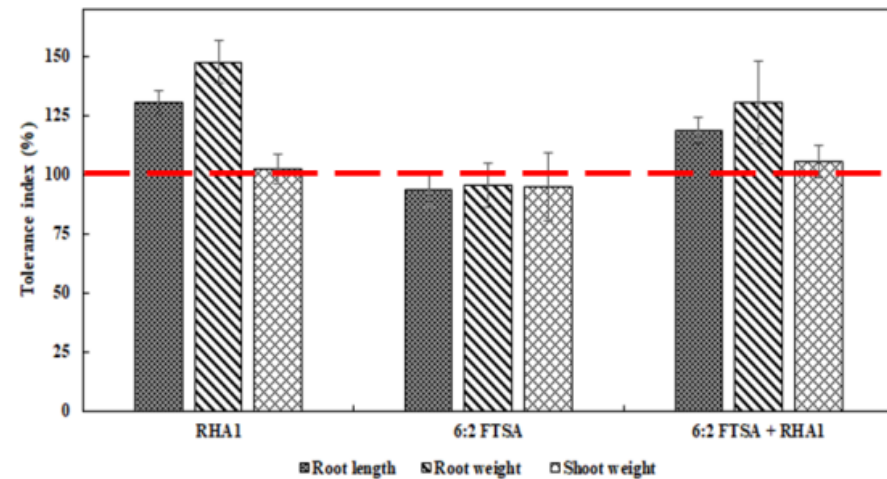
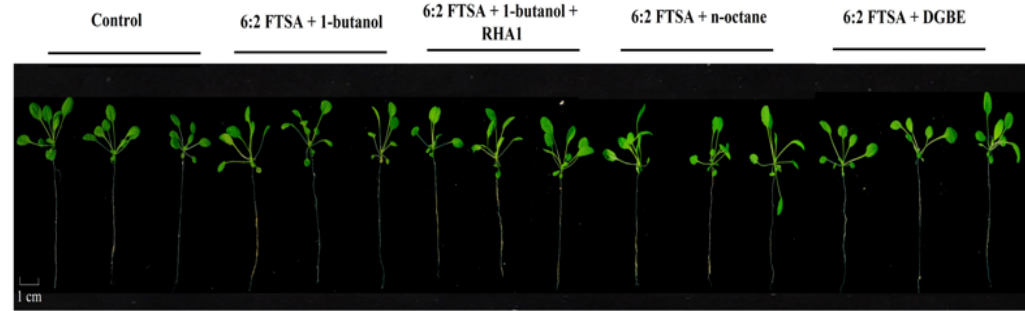
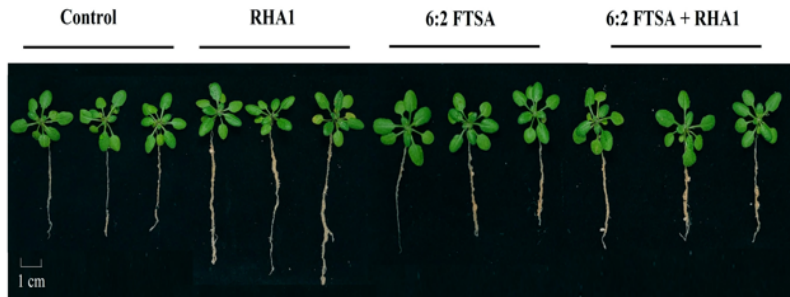
Soil DNA
fractionation

C^{12} DNA

C^{13} DNA

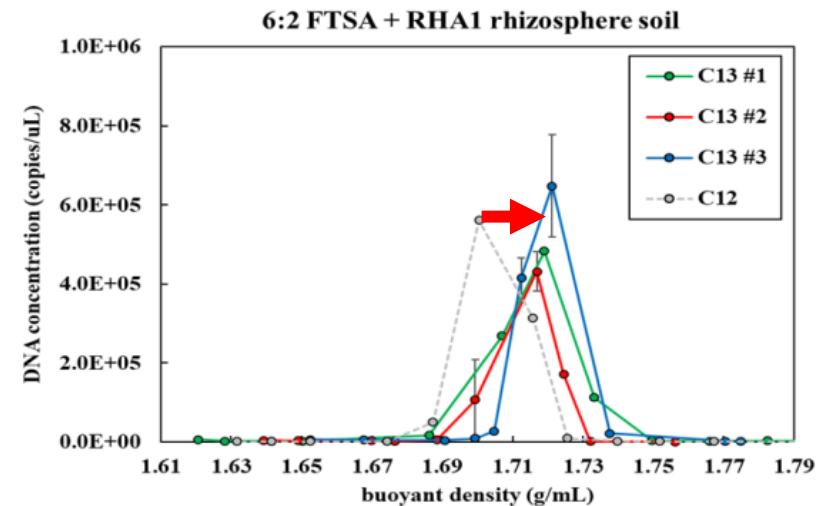
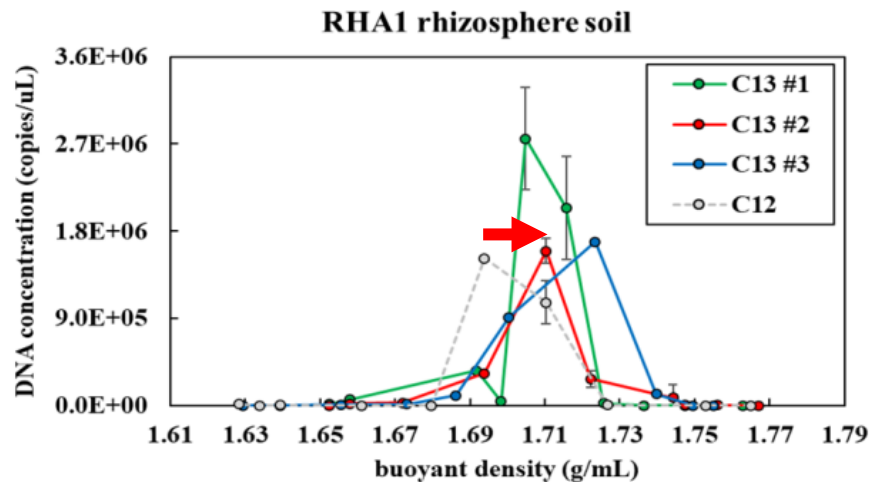
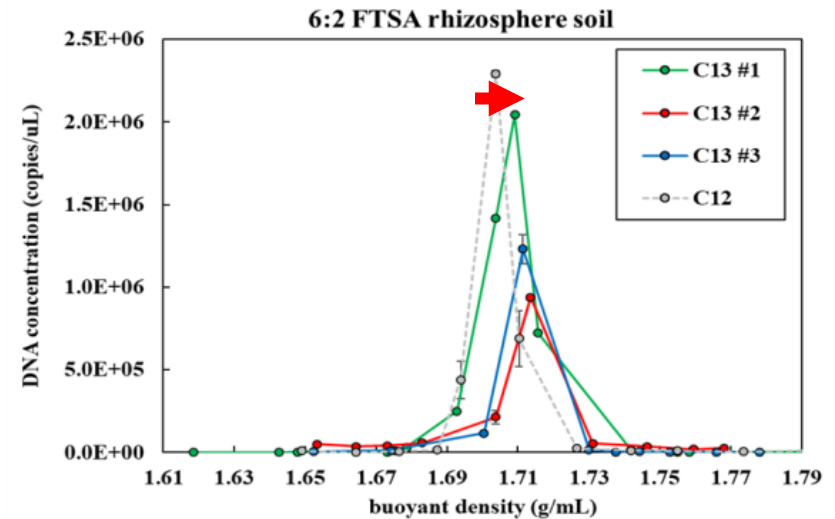
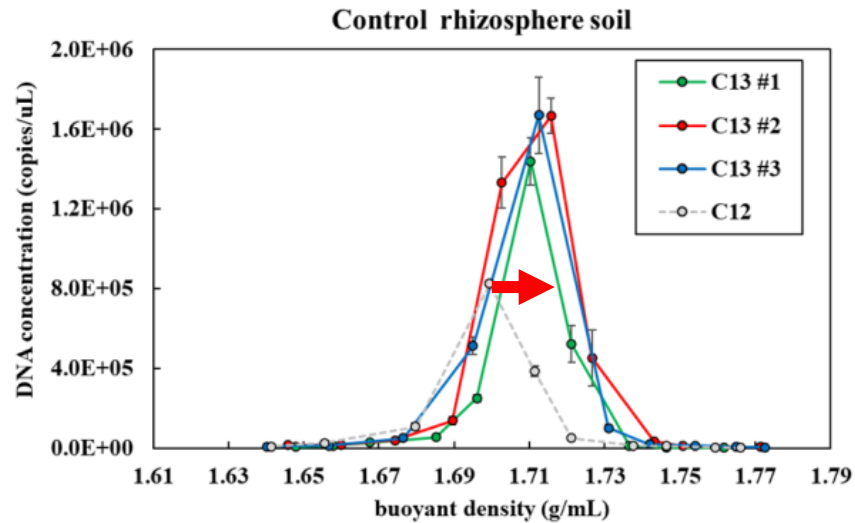


Microbial
community analysis

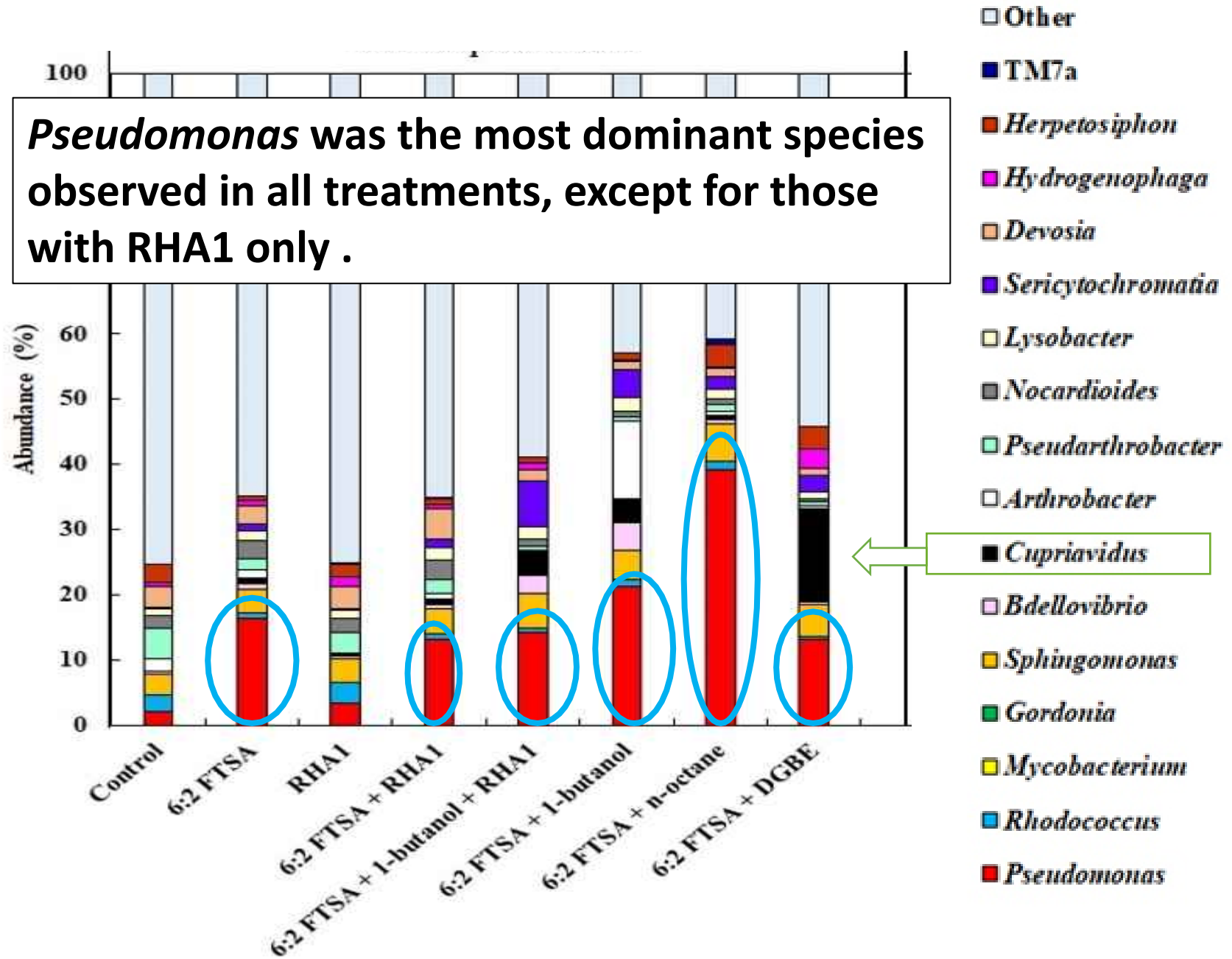


- 6:2 FTSA had no effects on plant growth
- RHA1 promoted plant growth
- Butanol and DGBE did not affect plant growth, but addition of octane promoted plant growth slightly.
- Approximately 15 % of spiked 6:2 FTSA was removed from the soil.

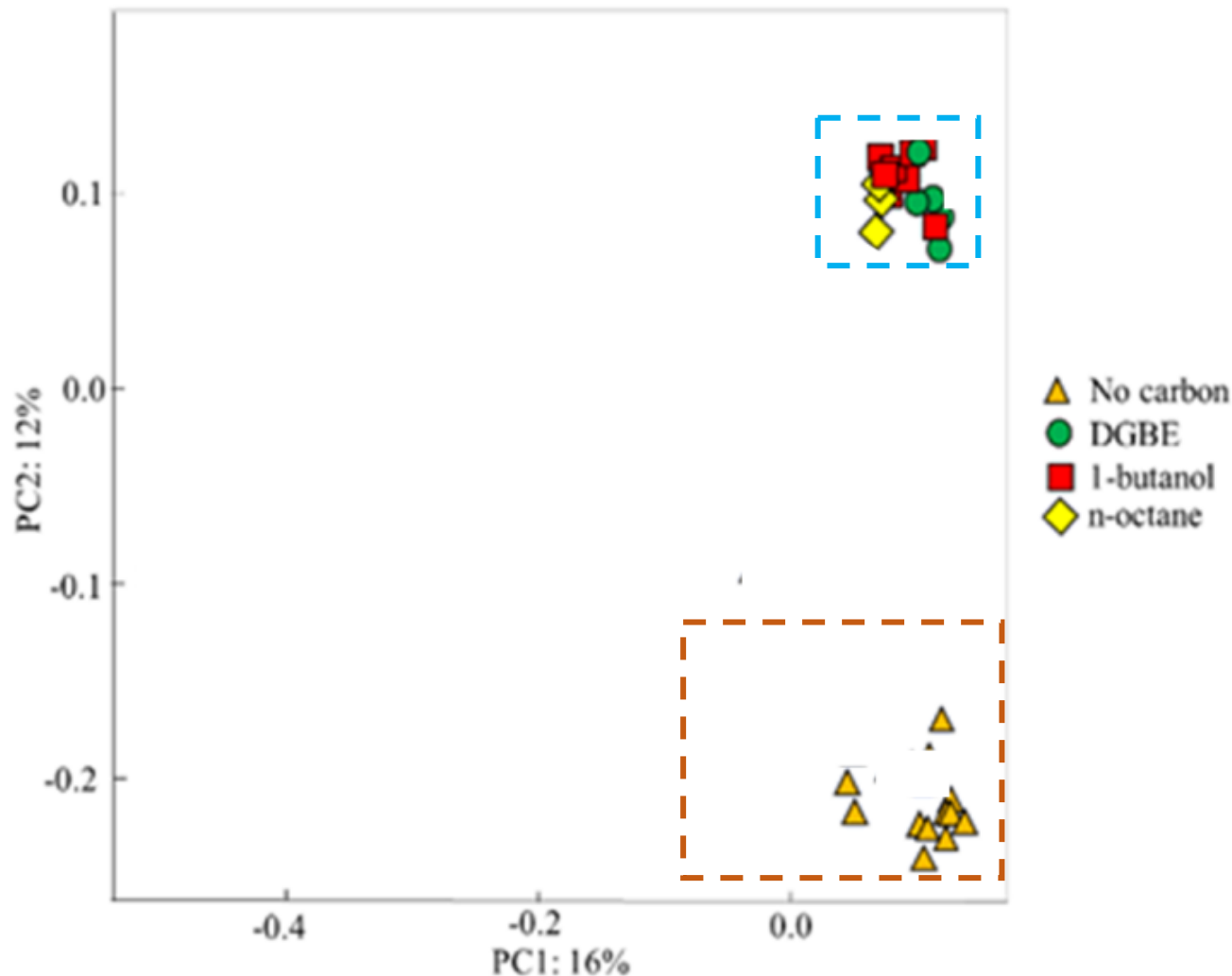
Peaks of the ^{13}C -DNA shifted toward right



Microbial communities assimilated ^{13}C -labeled root exudate



Shifts of rhizosphere microbiomes that assimilated ^{13}C -labeled root exudate: Effects of C Sources



Take Home Messages

- Amendment of 6:2 FTSA-degrading culture, strain RHA1, can promote plant growth.
- ^{13}C stable isotope probing suggested that *Pseudomonas* was the most predominant active rhizosphere bacteria while the spiked RHA1 was less competitive in rhizosphere zone compared to bulk soil.
- Carbon sources, such as 1-butanol, octane, and DGBE, are an important driver caused the composition of shifting in the microbial community, in spike of the presence of root exudates.

Thank You

