Tetrabromobisphenol-A (TBBPA) Biotransformation in Vegetated and Non-Vegetated Salt Marsh Sediments

Beth Ravit, Max M. Häggblom, and Joan G. Ehrenfeld
Rutgers University, New Brunswick, NJ

Beth Ravit
Graduate Program Environmental Science
Rutgers University, Cook College
New Brunswick, NJ 08901
Phone 201-774-1614
Fax 201-767-6931
Email bravit@eden.rutgers.edu

ABSTRACT

Anthropogenic impacts and differences in the belowground biomass of vegetation may potentially select for sediment microbial communities with different biogeochemical functional capabilities. This study compared the ability of *Spartina alterniflora, Phragmites australis*, and unvegetated sediments to biotransform the organic contaminant tetrabromobisphenol A (TBBPA) to bisphenol-A (BPA). Samples were obtained from both contaminated and non-contaminated field systems and from plants growing in the Rutgers University greenhouse. Anaerobic microcosms were incubated in the dark at 28^0 C for 125 days. The rate of TBBPA debromination was significantly higher in *Spartina* sediments compared to the *Phragmites* and non-vegetated treatments. Microbial community structure was compared using phospholipid fatty acid (PLFA) analysis. Small, but significant differences appear to be related to the influence of the vegetation interacting with site-specific factors.

Phragmites australis *Spartina alterniflora*

Fig. 1. Belowground biomass of field sampled plants. *Spartina* fine root volume is much greater than *Phragmites*, while *Phragmites* rhizome volume is much greater than *Spartina.*

BACKGROUND

- Microbiota and macrophyte species are affected by the presence of contaminants, which may select for a particular microbial community composition (3).
- Plant species differ in rhizosphere carbon transport
- Microbial community composition and function responds to changes in the plant community (2).
- Naturally occurring phenolic compounds are released by plant roots
- Morphology and biomass of *Phragmites* and *Spartina* root systems differ substantially (1)
- Microbial community structure can be inferred from the presence of phospholipid fatty acids (PLFAs) (4)

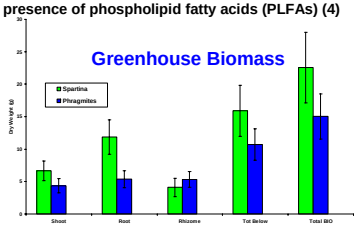

Fig. 2. Plant biomass in g dry weight for shoots, fine roots, rhizomes, total belowground, and total plant. *Spartina* fine roots were significantly greater than *Phragmites*.

MATERIALS AND METHODS

FIELD SAMPLES

- Transects were set up within monospecific populations of each plant species
- Three replicate cores were extracted from each plot
- Cores were divided into 10 cm subsections and frozen at –20^o C for PLFA analysis
- Sediment blocks were excavated to determine belowground biomass

ANAEROBIC MICROCOSMS

- Anaerobic microcosms were established using 50 g fresh sediment and 50 ml methanogenic media
- Microcosms were incubated with TBBPA (225-275 µM)
- Loss of TBBPA and formation of BPA were determined by HPLC analysis.
- Fatty acids were extracted from samples, and the lipid fraction was obtained through separation on a silicic acid column, and methylated following MIDI protocols.
- Identification of individual fatty acids was determined based on GC retention time using the MIDI Sherlock Microbial Identification System.

GREENHOUSE SAMPLES

- *Phragmites* rhizomes and *Spartina* shoots were incubated in the Rutgers University greenhouse
- Rhizosphere sediment samples were transferred to anaerobic microcosms as above.

Field Belowground Biomass

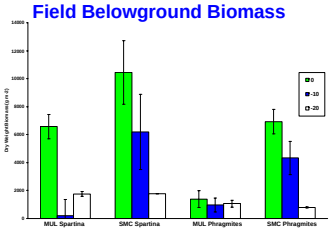

Fig. 3. Plant biomass in g dry weight for field samples from Saw Mill Creek and Mullica. *Spartina* belowground biomass was greater than that of *Phragmites*, and biomass was greater for both species in the contaminated SMC system than in the MUL plants.

RESULTS

BPA Formation

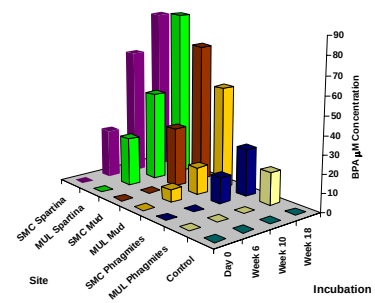

Fig. 4. Formation of BPA from field samples over an 18 week incubation period. Rate and extent of *Spartina* biotransformation was greater than that of both *Phragmites* and non-vegetated treatments.

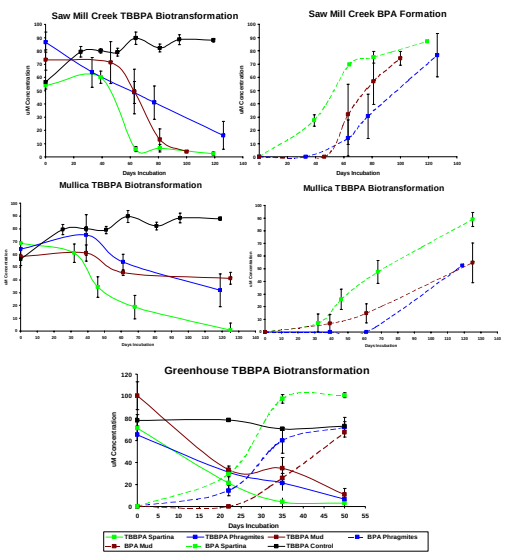

Fig. 5. Anaerobic biotransformation of TBBPA to the end product BPA over a period of up to 125 days incubation. Loss of TBBPA and formation of BPA occurred at a faster rate in the *Spartina* microcosms than in *Phragmites* or non-vegetated mud treatments.

Principal Components Analysis

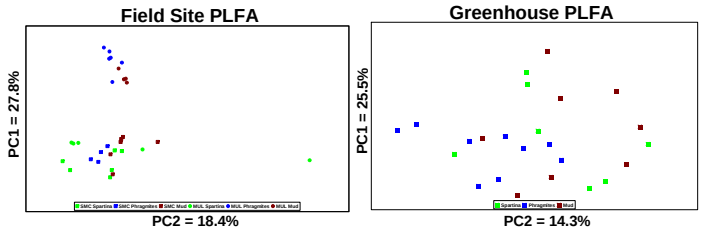

Fig. 6. Principal Components Analysis of PLFA from field and greenhouse samples. The MUL site shows a separation between *Spartina* and the *Phragmites* and non-vegetated samples. There is no such separation in the SMC samples. The greenhouse appears to have a *Phragmites* cluster, but no cluster for the *Spartina* or mud treatments.

CONCLUSIONS

- *Spartina alterniflora* belowground biomass was significantly greater than *Phragmites australis* belowground biomass under field conditions
- Formation of *Spartina* fine roots was significantly greater than *Phragmites* fine root formation under greenhouse conditions
- Sediments associated with *Spartina alterniflora* from all sites dehalogenated TBBPA at a faster rate than sediments associated with *Phragmites australis* or non-vegetated mud
- The contaminated site microbial communities produced BPA at a faster rate than the non-contaminated site microbial communities
- PCA revealed significant differences in microbial fatty acids in the non-contaminated Mullica samples. These differences were not found in sediment microbial populations from the contaminated Saw Mill Creek site
- The *Phragmites* greenhouse sediments appear to form a PCA cluster, but no cluster was apparent in the *Spartina* or non-vegetated treatments
- A correlation between PLFA sediment profiles and the ability of a microbial community to biotransform TBBPA was not observed in this study

REFERENCES

1. Armstrong, J., Armstrong, W., Becket, P.M., Halder, J.E., Lythe, S., Holt, R., Sinclair, A. 1996. Pathways of aeration and the mechanisms and beneficial effects of humidity- and Venturi-induced convections in *Phragmites australis* (Cav.) Trin. Ex. Steud. Aquatic Botany 54:177-197.
2. Grayston, S.J., Wang, C.D., Campbell, Edwards, A.C. 1998. Selective influence of plant species on microbial diversity in the rhizosphere. Soil Biol. Biochem 30:369-378.
3. Karthikeyan, S., Wolfaardt, G.M., Korber, D.R., Caldwell, D.E. 1999. Functional and Structural Responses of a Degradative Microbial Community to Substrates with Varying Degrees of Complexity in Chemical Structure. Microb. Ecol. 38:215-224.
4. King, J.D., White, D.C., Taylor, C.W. 1977. Use of lipid composition and metabolism to examine structure and activity of estuarine detrital microflora. Appl. Environ. Microbiol. 33:1177-1183.

ACKNOWLEDGMENTS

- We gratefully acknowledge the Meadowlands Environmental Research Institute (MERI), the Educational Foundation of America, NSF Grant EAR-0120616 and NJWRRI for providing funding.
- We thank Oscar Abelleira, Michael Ovadia, Tish Robertson, Mike Bartels, James Voordeckers, Dr. Jean-Christophe Clement, and Dr. Elisha Tel-Or for assistance in the field and laboratory.
- We thank Ed Konsevick and Joe Sarnoski from New Jersey Meadowlands Commission (NJMC) for providing boat transportation to the Hackensack Meadowlands site, Dr. Faith Bellinger and Jonathan Harris for greenhouse assistance.