

Multi-channel Attached Algae Flow-ways: Design Optimization for Enhanced Biomass Productivity and Quality

Sungwhan Kim¹, Jihoon Yang¹, Tyler Phillips Eckles¹, Ryan W. Davis^{1, *}

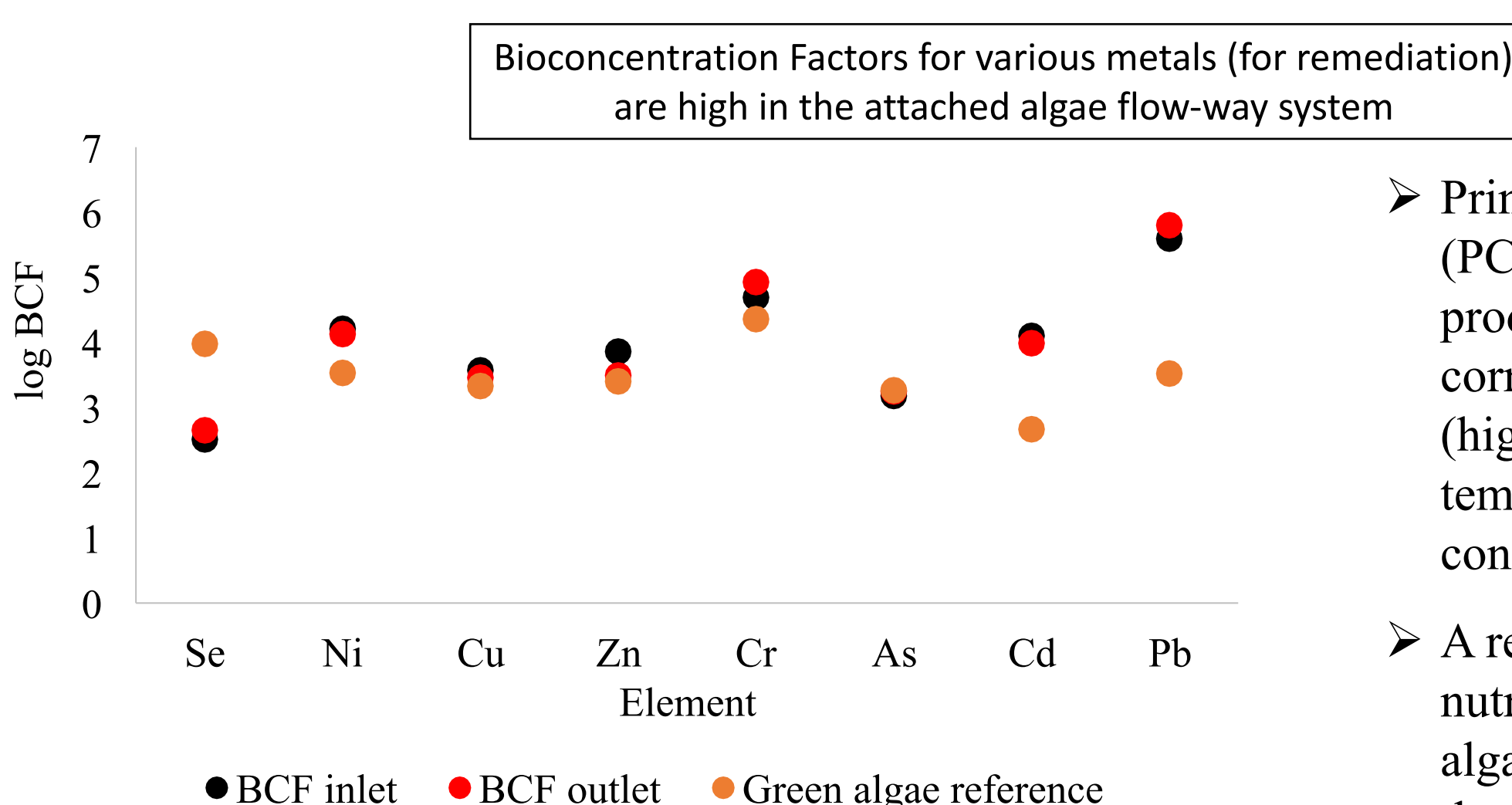
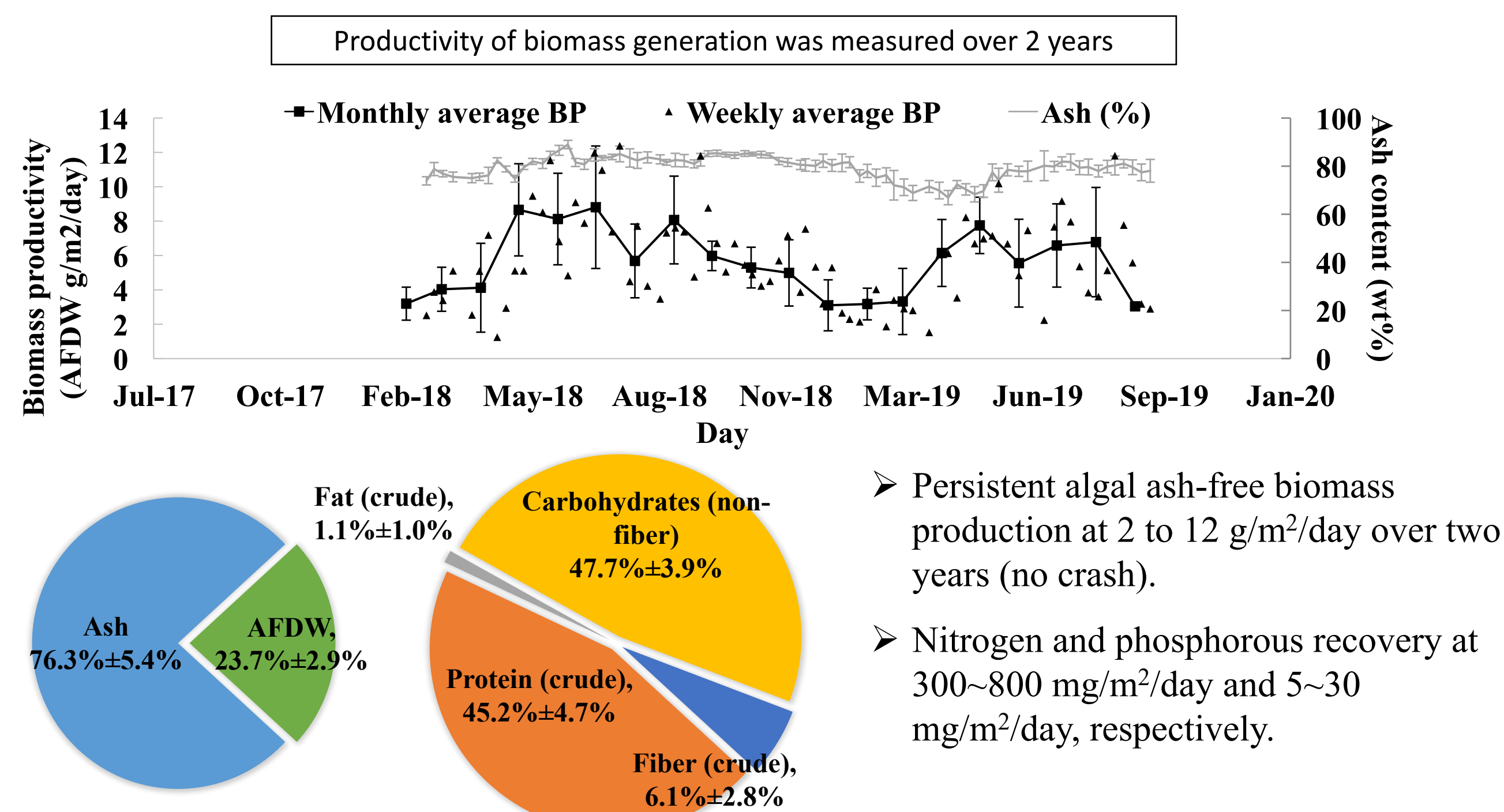
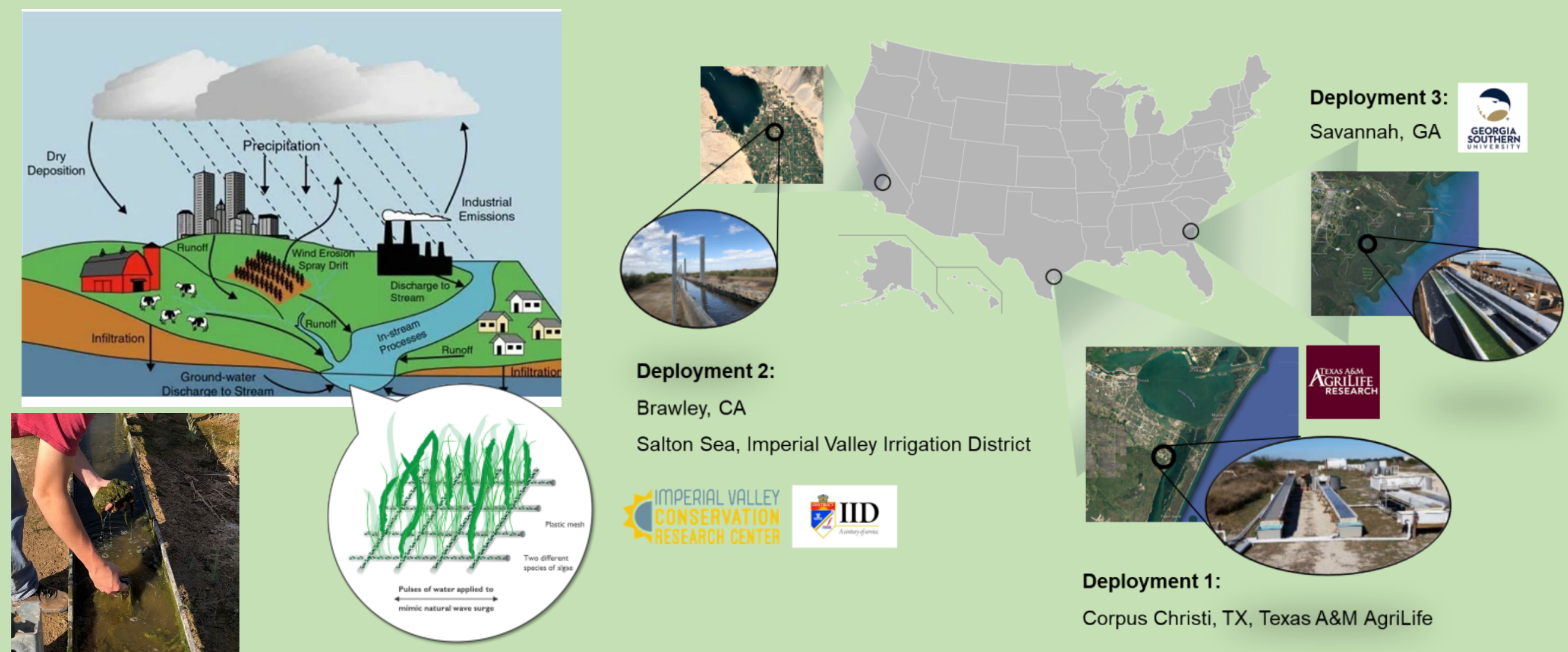
¹Sandia National Laboratories, 7011 East Ave., Livermore, CA 94550, United States

Problem Statement

- Sustainable production of biomass as a feedstock for biofuel is needed.
- The conventional suspended cultivation method suffers from low biomass concentrations (0.1~1% of solid).
- Wasted nutrients in the agricultural runoff should be removed, otherwise can cause harmful algal blooms.
- Low biomass quality: high ash and low lipid contents.

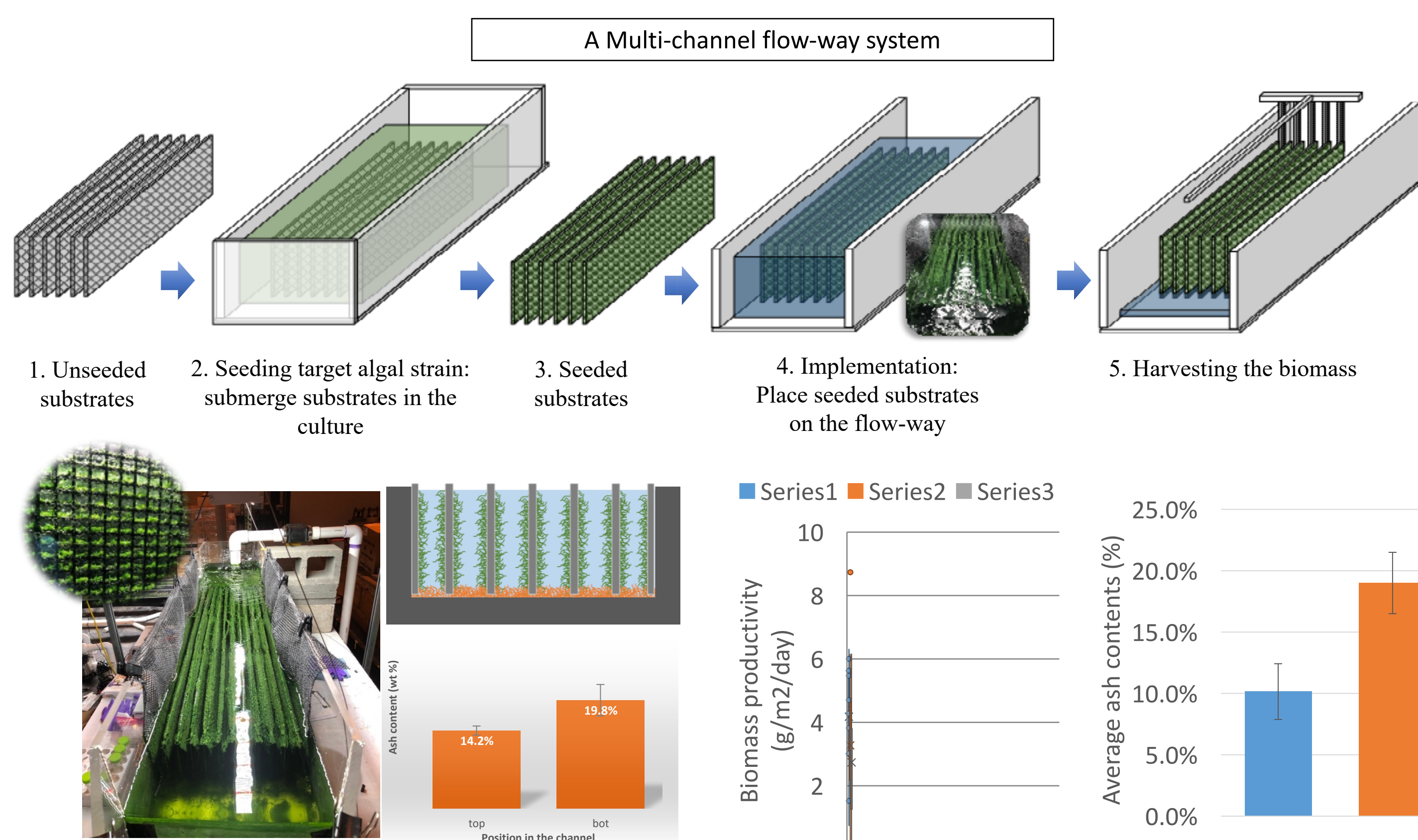
Objectives

- Improve footprint biomass productivity through optimization of design and operation of the attached algae flow-way
- Improve quality of biomass through the understanding of algae-associated microbial community dynamics and domination of key algal strains

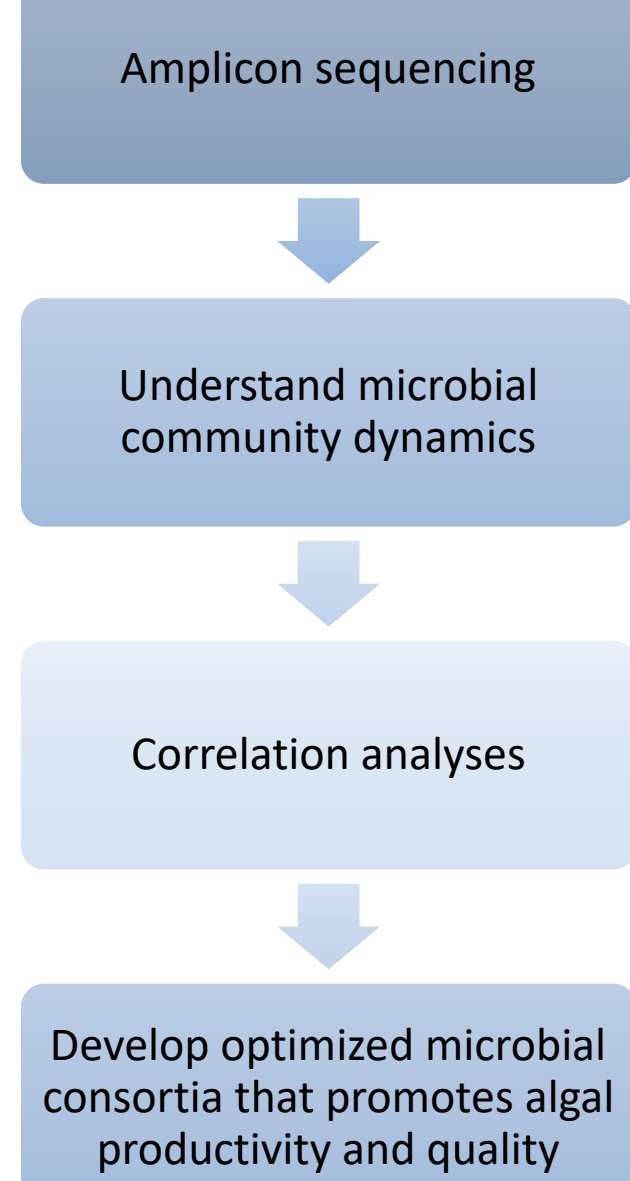


- Bioconcentration factor (BCF): $BCF = \frac{C_{algae}}{C_{water}}$
- $\log BCF < 3$: non accumulative, $3 < \log BCF < 3.7$: accumulative, $3.7 < \log BCF$: very accumulative.
- Green algae reference: *Cladophora Prolifera* (L. Losada, 2020)

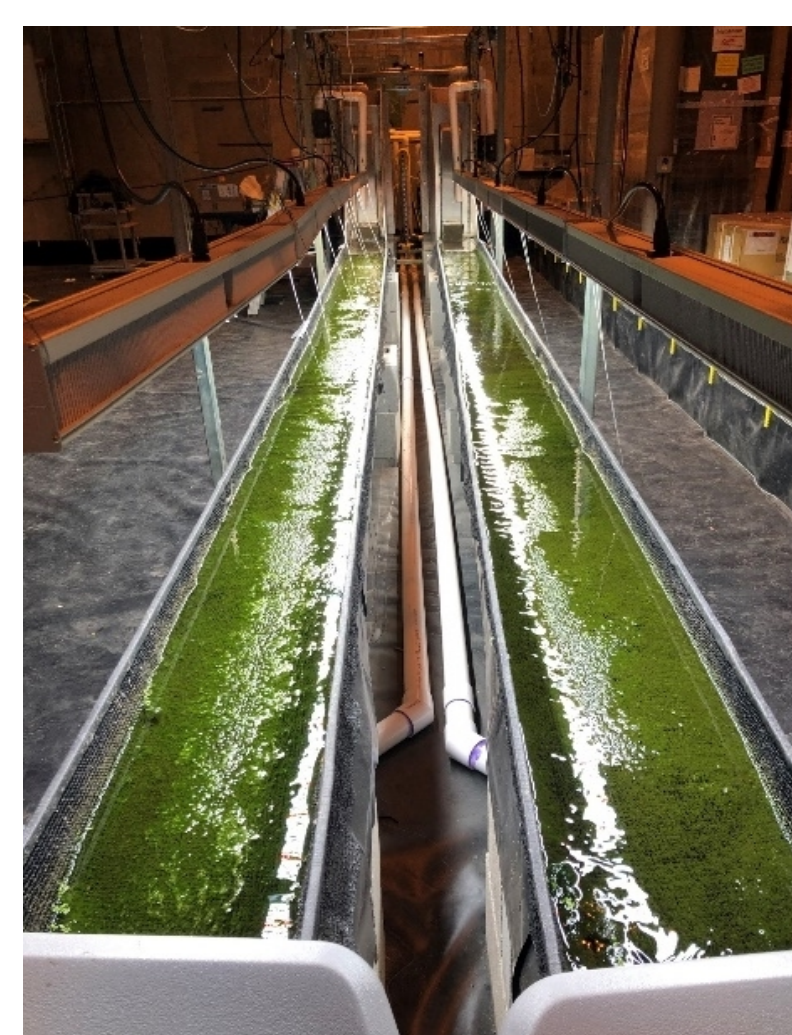
- Principal Component Analysis (PCA) shows that biomass productivity has a stronger positive correlation with weather conditions (high solar irradiation and warm temperature) than with concentrations of key nutrients
- A relatively weaker correlation with nutrient concentration offers the algae flow-way independence from the changes in nutrient availability
- Bioaccumulation of metal contaminants enables the algae flow-way a unique benefit to local ecosystem remediation.



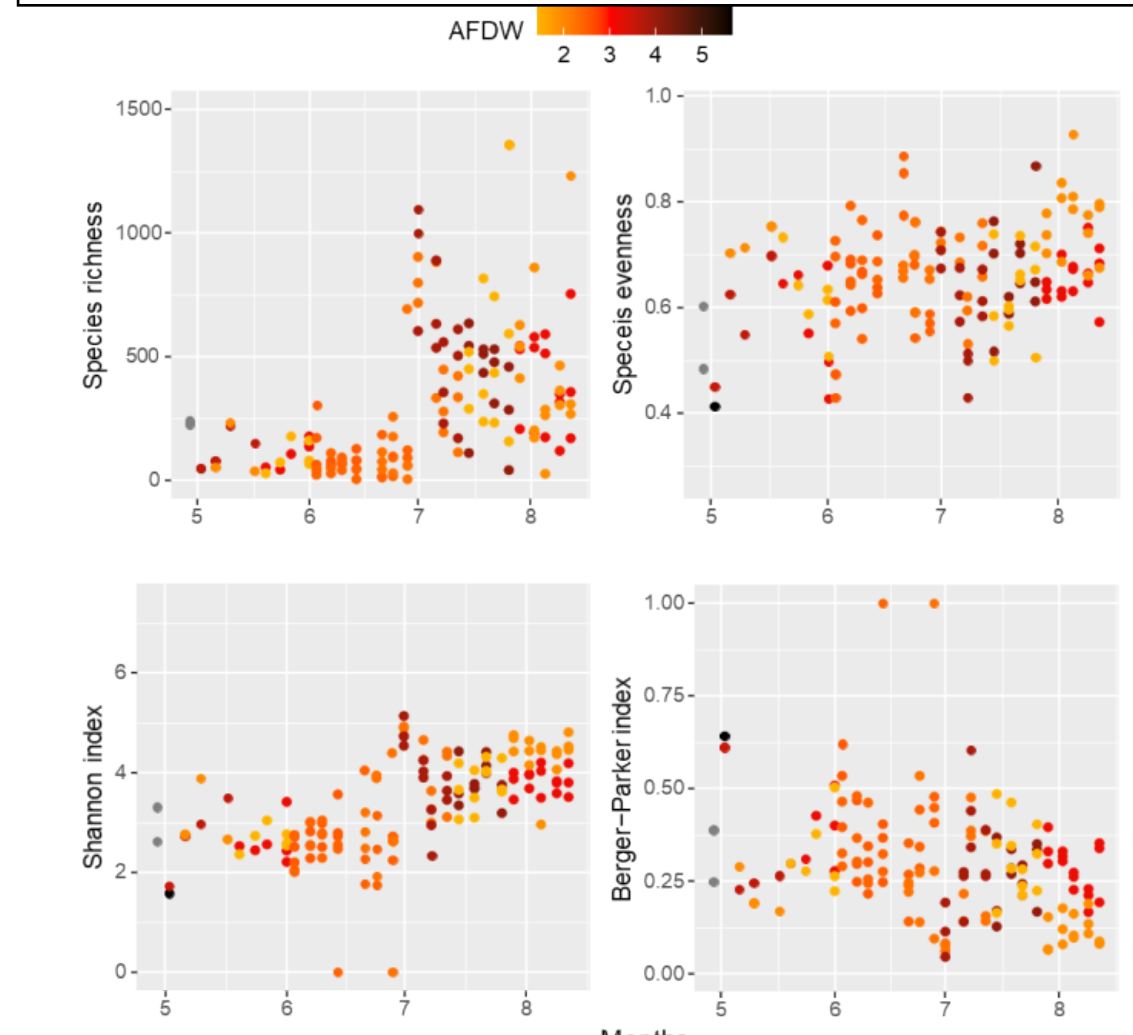
Strategy



Photographs of indoor pilot system

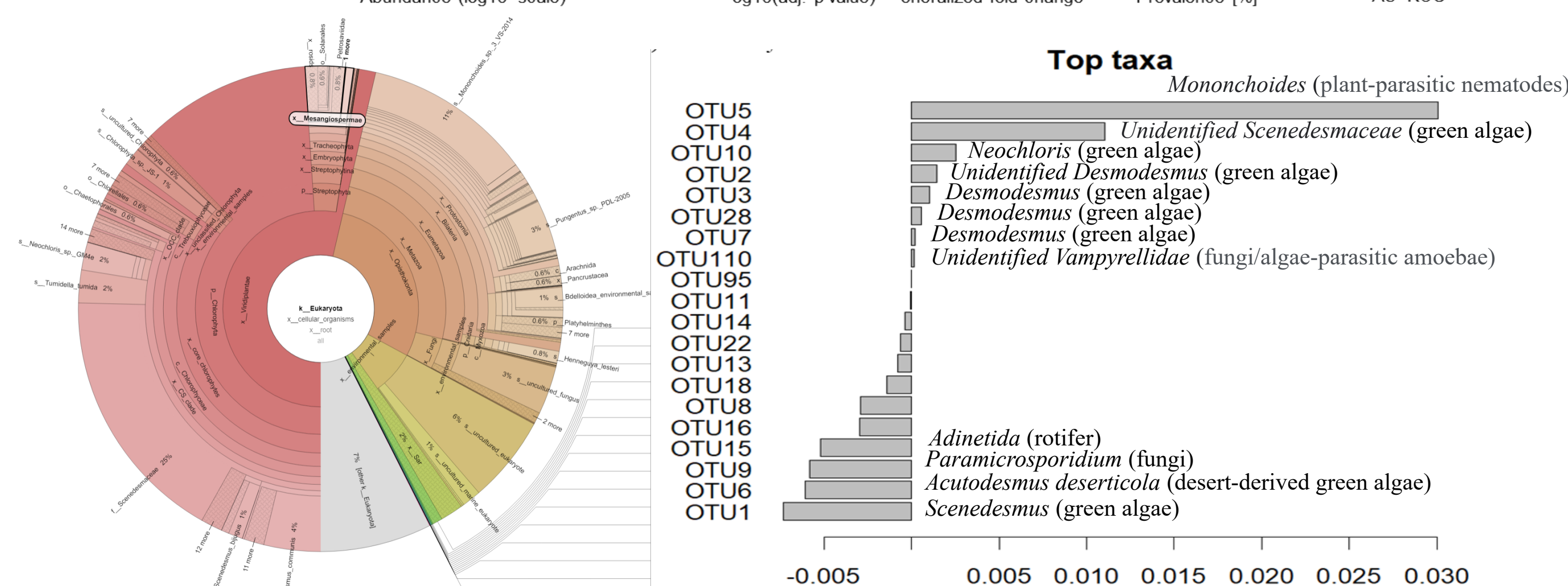
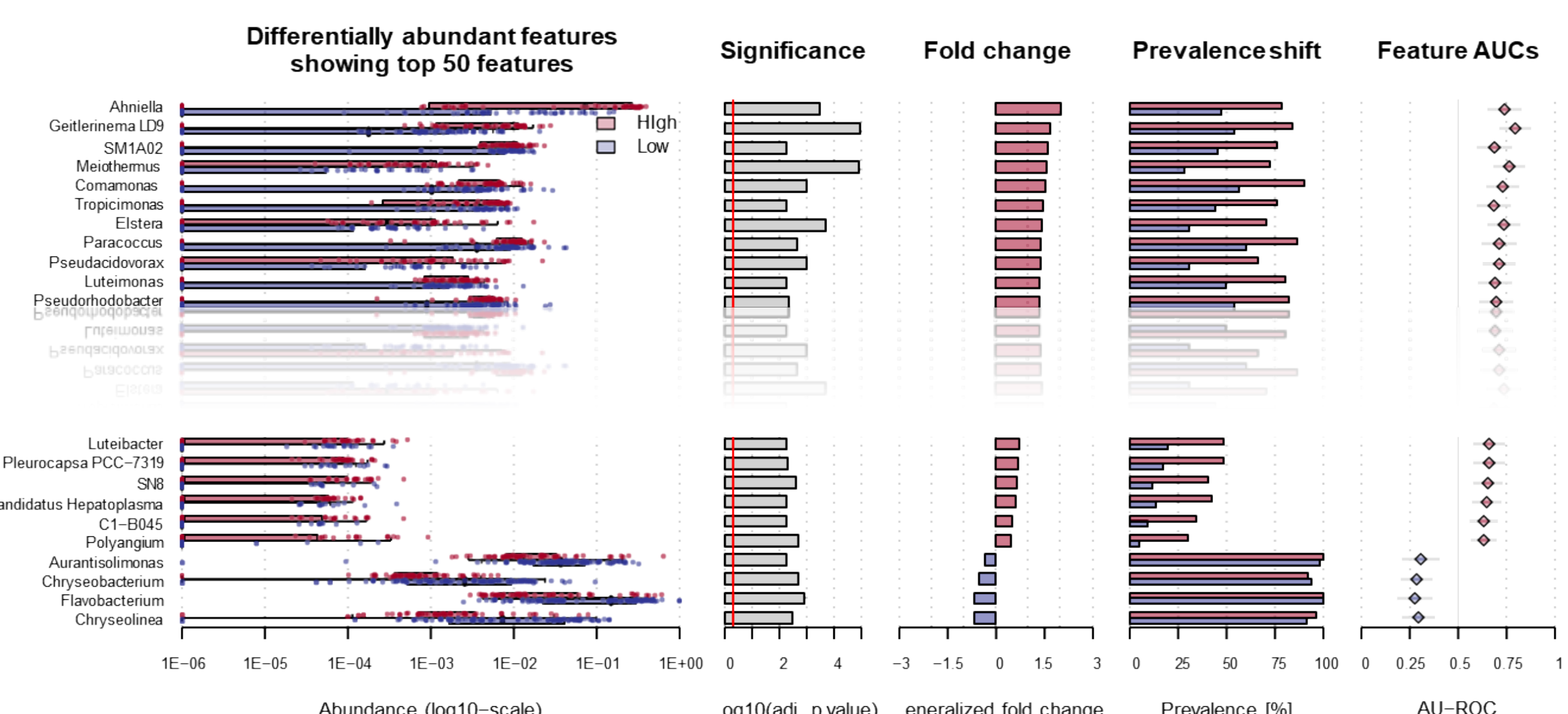


Diversity of microbial communities in the system



- Diversity of bacterial community increased over time along with their richness and evenness.
- No significant effect of biomass productivity and position of flow-way on diversity changes.

Microbial communities of 16s (bacterial) and 18s (eukaryotes) and their correlation with biomass productivity



- Relative abundance of microbiome between two group (high (>3 g/m²/day) and low ash-free biomass productivity) was assessed.
- Abundances of top 50 features across two different groups (high vs. low) have shown significantly different.
- Cross-validation accuracy is high with AUC = 0.837 (AUC>0.6 is typically considered accurate)
- Relative abundances of 27 bacterial genera collectively associated with ash-free biomass productivity of the flow-way with 17 of them positively associated and 10 of them negatively associated.