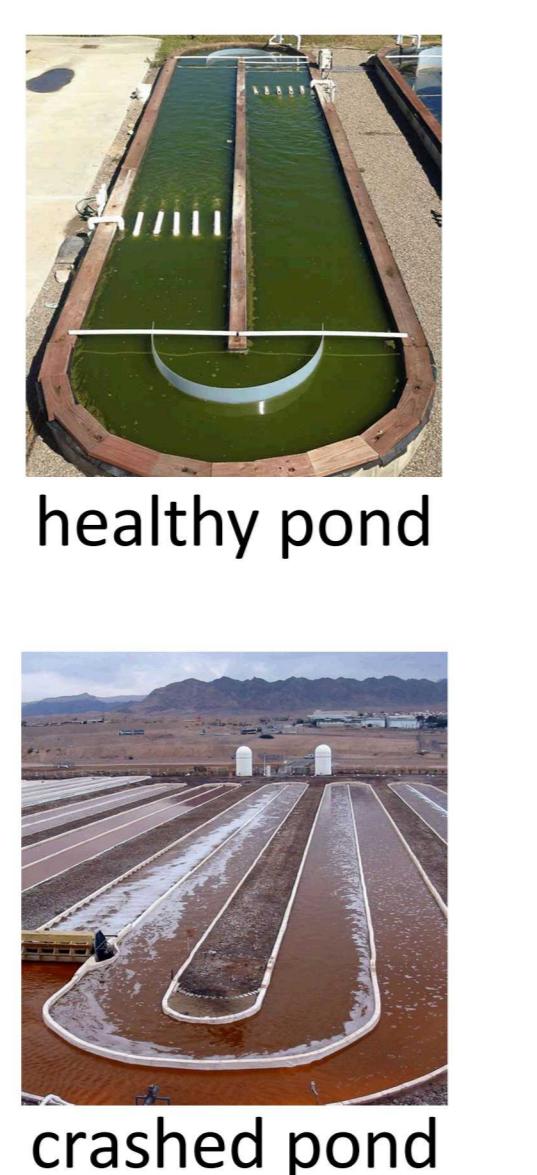


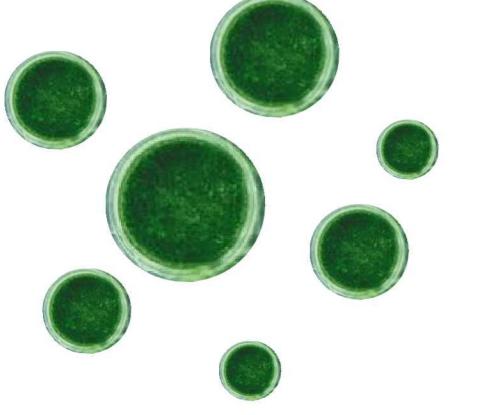
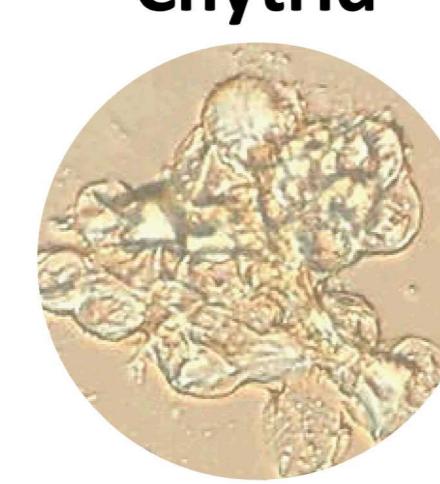
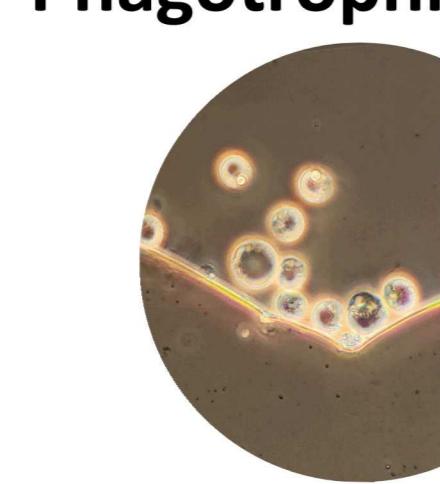
Background

- Algal biofuel production cost can be reduced through elimination of pest-induced “pond crashes”^{1,2}
- Current methods to eliminate pests include regular additions of pesticides, incurring a consistent cost³
- The cultivation of microalgae with unique bacterial consortia results in the death of their rotifer predators,⁴ and potentially additional pests such as chytrids and phagotrophic algae
- Protective molecules produced in microalgae-bacterial consortia co-cultures can be identified with metabolomics tools



Crop

Pests

Biofuel Microalga	Rotifer	Chytrid	Phagotrophic Alga
			

- Hypothesis:** Select bacteria in our consortia produce small molecules that protect microalgae from predators and pathogens.
- Objective:** Identify protective small molecules produced by bacteria isolated from our unique consortia.

Experimental Design

Metabolomics

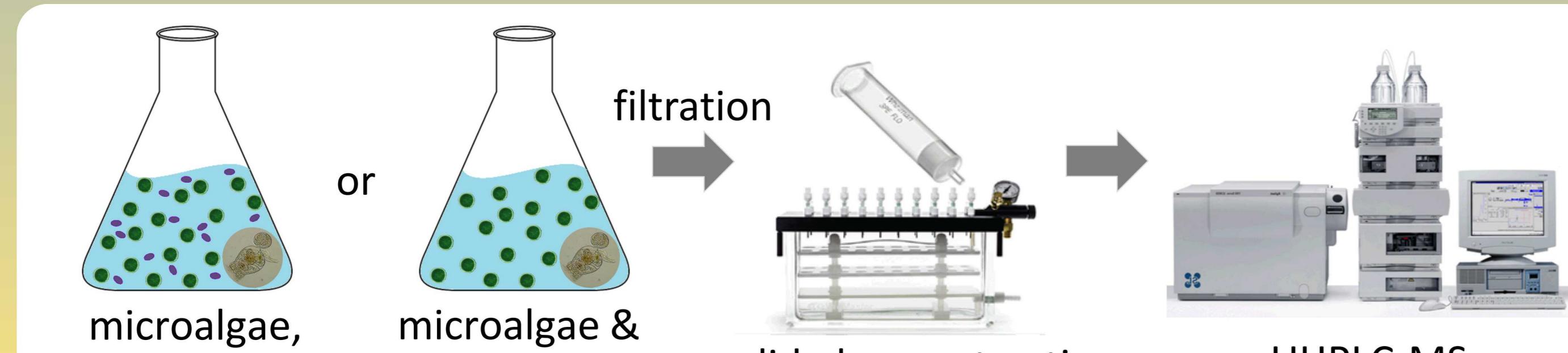


Figure 1: Workflow for identifying small molecules produced by protective bacteria in microalgae-bacterial co-cultures. Metabolites are extracted from filtered algal culture conditioned media and analyzed using spectroscopic methods (UHPLC-MS and ¹H NMR) prior to molecule identification.

Bacterial Extractions for Bioassay Screening

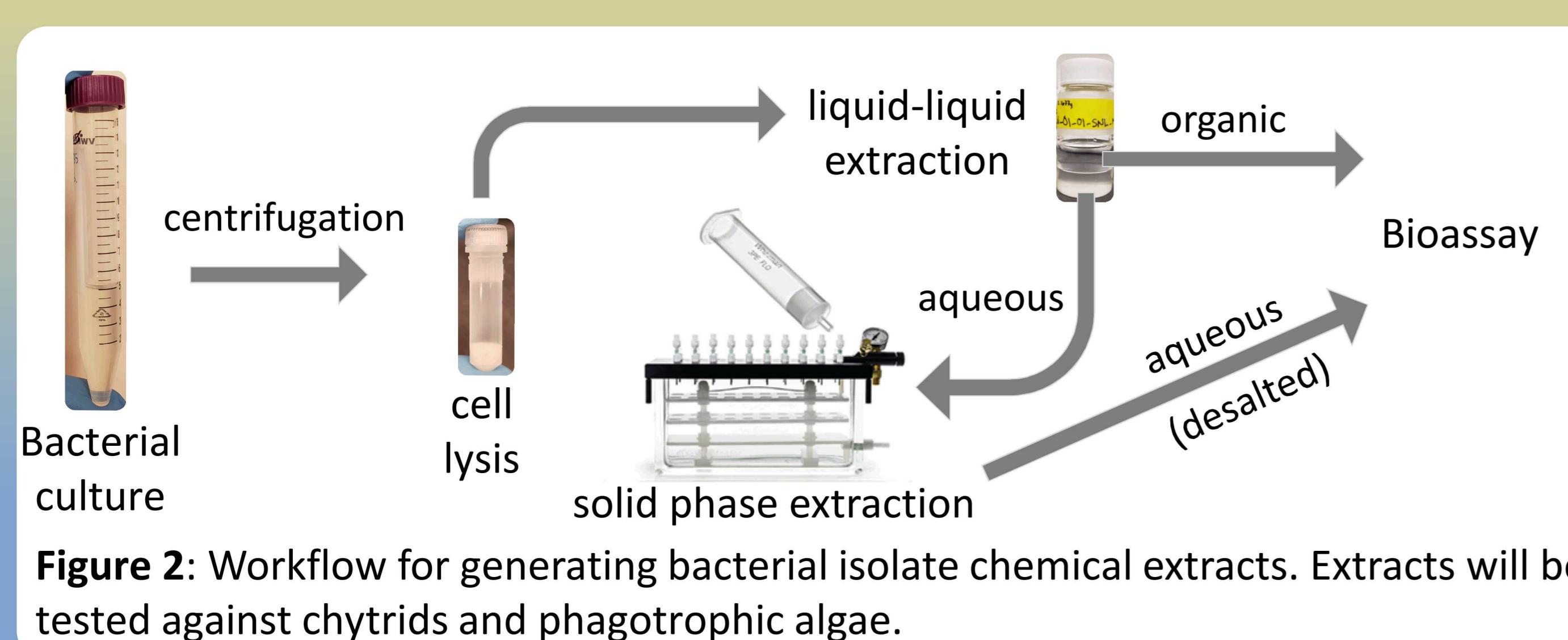


Figure 2: Workflow for generating bacterial isolate chemical extracts. Extracts will be tested against chytrids and phagotrophic algae.

Results

Exometabolome Extracts of Different Algae-bacterial Co-cultures Have Different Chemical Profiles

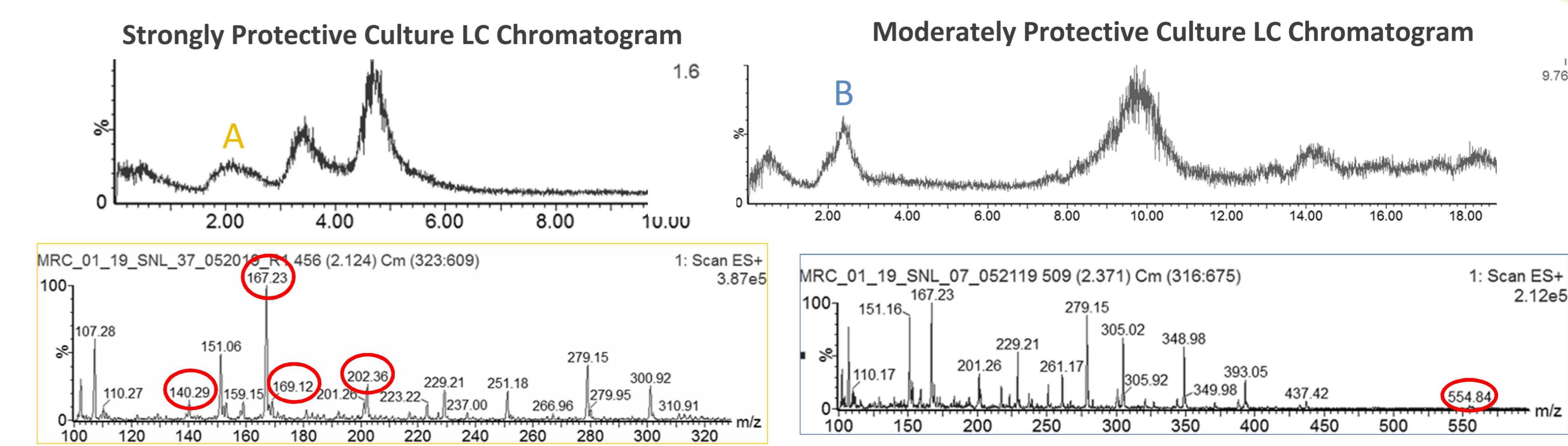
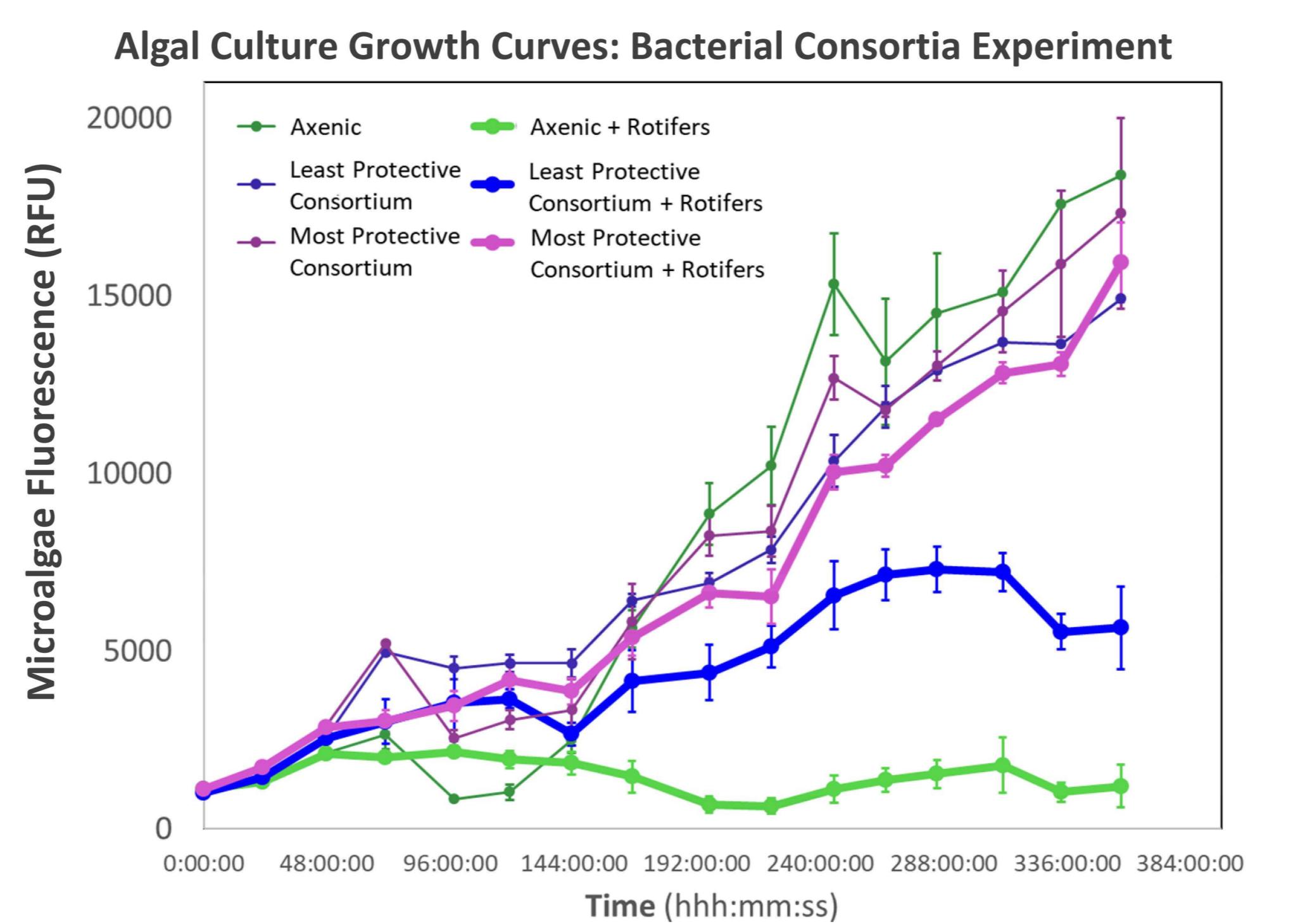


Figure 3: Left) Algal culture growth curves for bacterial consortia experiment. Above left) Liquid chromatography mass spectrometry (LC-MS) chromatogram for an algal-bacterial (**strongly protective**) culture conditioned media extract. The mass spectrum for peak A (gold outline) shows m/z signals for distinct metabolites (red circles). Above Right) LC-MS chromatogram for an algal-bacterial (**Moderately protective**) culture conditioned media extract. The mass spectrum for peak B (blue outline) shows an m/z signal for a distinct metabolite (red circle).

Descriptive Statistics Indicate that Strata-X is the Best Extraction Method for Profiling Algal Culture Exometabolomes

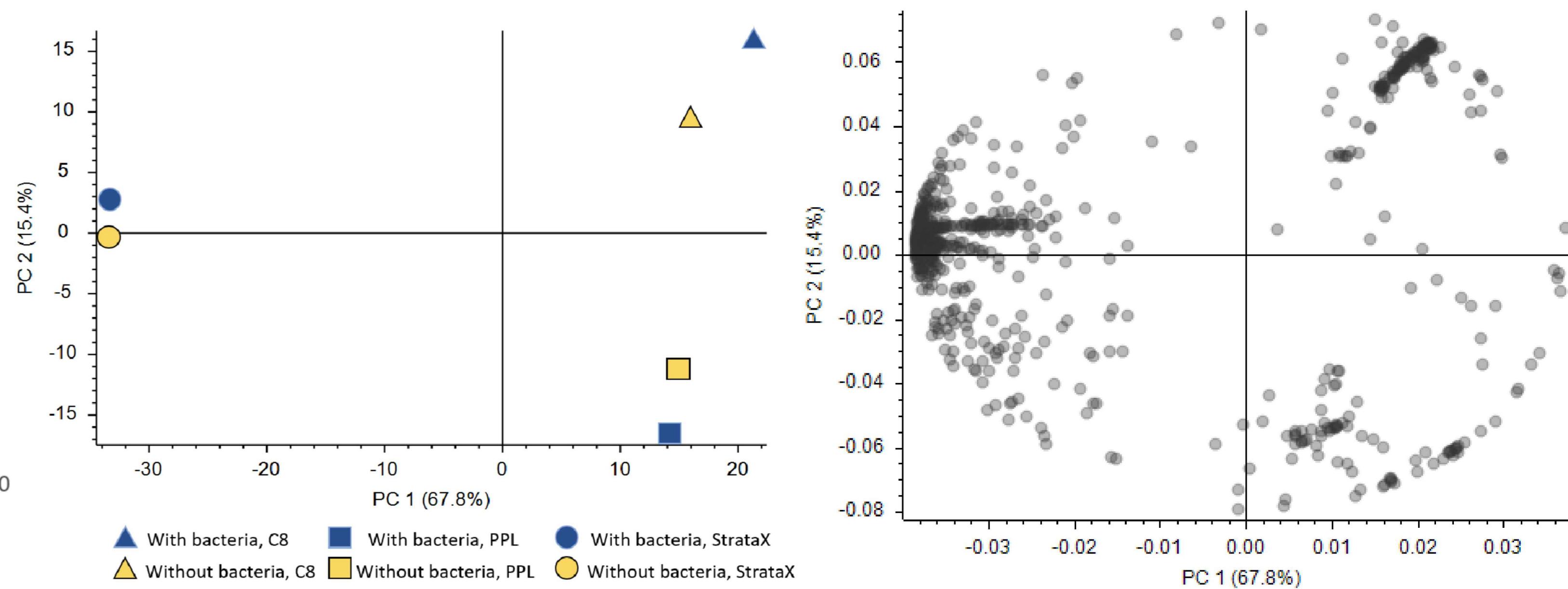
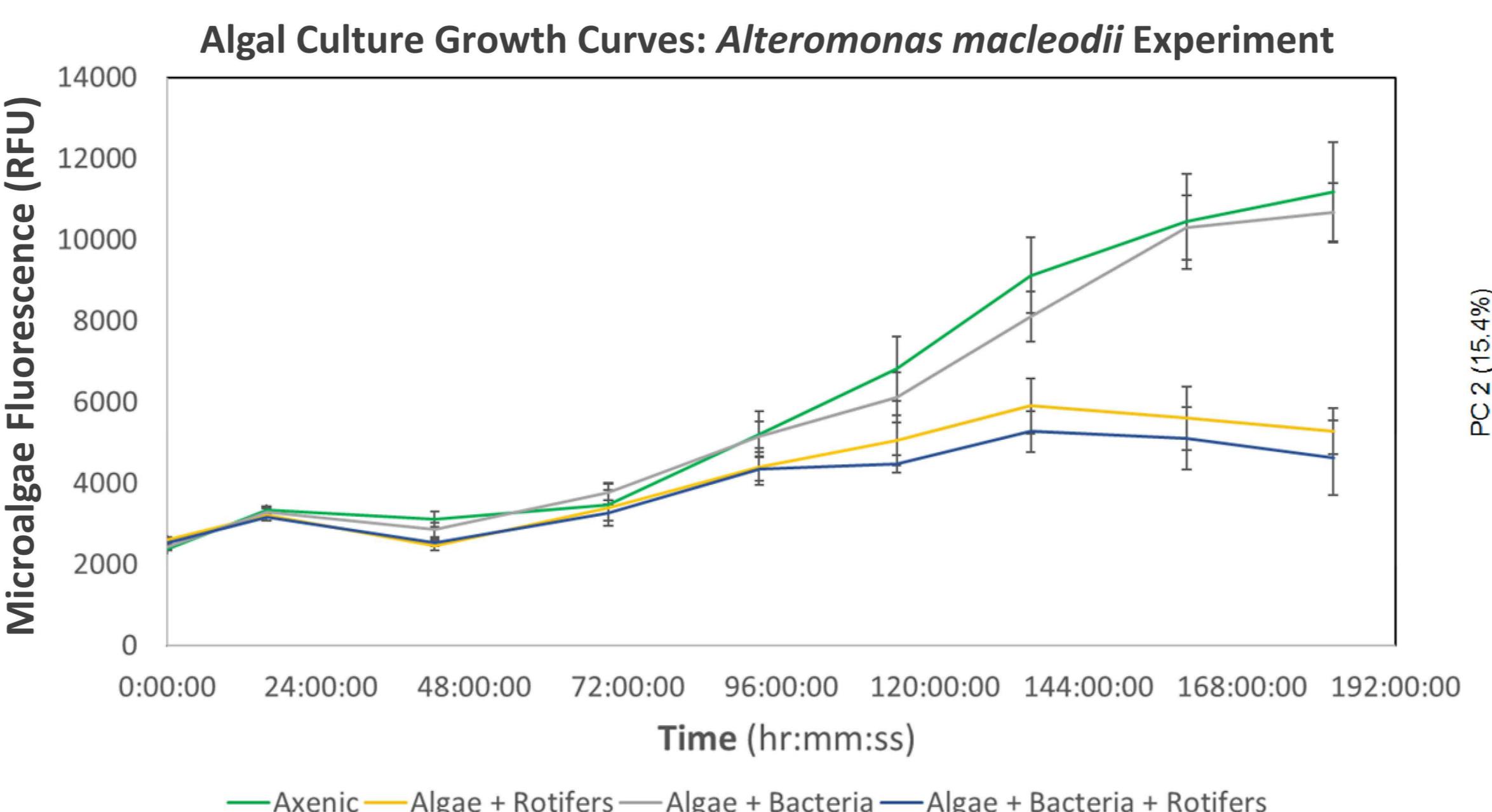
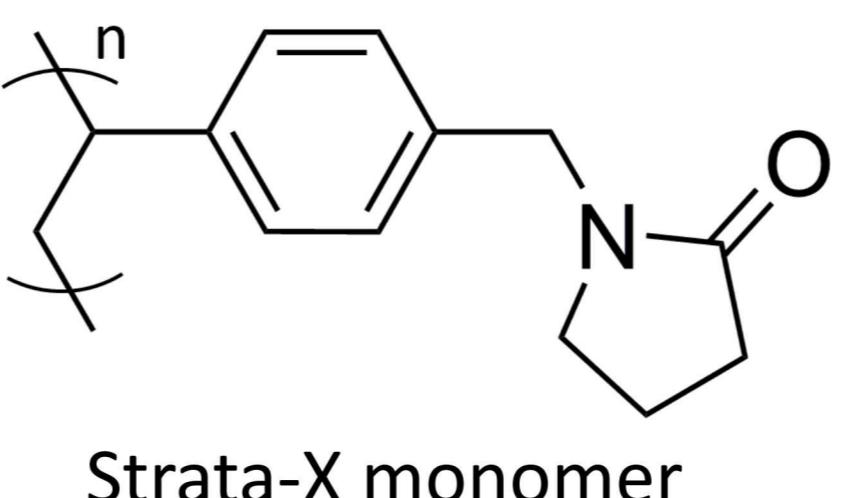


Figure 4: Left) Algal culture growth curves for *Alteromonas macleodii* experiment. This bacterium was selected to determine whether it could protect algae from rotifers like the bacterial consortia. Middle) Principal component analysis of reversed phase C18 LC-MS data acquired for algae + rotifers (gold) and algae + bacteria + rotifers (blue) conditioned media extracts. Three different solid phase extraction methods are represented by triangles (C8), squares (PPL), or circles (Strata-X). Right) Loadings plot where each point represents a molecular mass with a corresponding retention time. These points are responsible for the separation and grouping of treatment groups.

Conclusions

- Exometabolome extracts of algal cultures grown with moderately and very protective bacterial consortia have different chemical profiles
- Extracted molecules appear to be polar organic metabolites
- Metabolite concentrations are very low
- Strata-X is the best solid phase extraction method for extracting metabolites from algal culture conditioned media



Future Work

- Determine chemical features in MS metabolomics spectra unique to microalgae-bacterial consortia co-cultures that did not crash in the presence of rotifers
- Bioassay-guided fractionation/isolation, spectroscopic characterization, and structure elucidation of protective molecules
- Acquisition of full biological profiles for protective metabolites
- Development of a bioassay and testing the bioactivity of bacterial isolate metabolites against chytrids and phagotrophic alga *P. malhamensis*

References and Acknowledgements

1. Sun A et al. (2011) Energy, 36, 5169-5179.
2. Hamilton CE and Rossmeissl N. (2014) Department of Energy.
3. Smith VH and Crew T. (2014) Algal Research, 4, 23-34.
4. Fisher CL et al. (2019) 40, 101500.

I would like to thank Emily, Anne Marie, Bhawan, and Sam for their advice, Dr. David Gaul for his assistance with LC-MS, and my undergraduate Hailey for her help with method development. This work was supported by LDRD funding from a collaboration with Sandia National Laboratories. SAND No. SAND2020