A constructed floating wetland microbiome for per- and poly-fluoroalkyl substance (PFAS) bioremediation

Larissa M. F. Oppermann[1,2], John Awad[3], Falko Mathes[1], Adrienne Gregg[3], Ka Yu Cheng[1], Sasha N. Jenkins[2], Anna H. Kaksonen[1]

[1]CSIRO Environment, Waterford, Western Australia, Australia
[2]UWA School of Agriculture and Environment, The University of Western Australia, Perth, WA 6009, Australia
[3]CSIRO Environment, Urrbrae, South Australia, Australia

PFAS have received widespread attention due to their recalcitrance, harmful human and environmental health impacts, and extensive distribution in the environment. Current treatments for PFAS-contaminated sites are often hindered by high costs, environmentally disruptive techniques, and the recalcitrance of the C-F bond to degradation. Constructed floating wetlands (CFWs) offer a promising bioremediation strategy for PFAS-polluted surface water, as they can be retrofitted into waterbodies with minimal structural alterations and may then allow contaminant uptake and microbial transformations.

This study used near full-length 16S rRNA gene amplicon sequencing to investigate the microbiome of a field-scale CFW treating stormwater run-off from a PFAS contaminated site in South Australia. The study aimed to compare community composition and PFAS uptake efficiency between various plant species (*Juncus krausii, Eleocharis acuta* and *Scirpus validus*), as well as various plant growth support media (combinations of gravel, granular activated carbon, or almond biochar). Preliminary results indicated that regardless of variation in media type or plant species, the most significant differences in microbial community were seen between the environmental niches sampled ($p=0.001$). Rhizosphere communities varied by plant species, as well as by presence of carbon-based sorbents in the media ($p=0.04$). Results also suggested that taxa from *Pseudomonas*, *Cupriavidus* and *Delftia*, were present in both the rhizosphere and root biofilm samples albeit at low abundances (0.0019% to 3.4%). These genera have been previously linked to PFAS biotransformation as they possess dehalogenase genes, however further research would clarify the microbial contributions to PFAS degradation and phytoremediation within CFWs.