Constructed wetlands for the treatment of cyanotoxins: Initial results

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Background

Increased pressure towards the use of surface waters for crop irrigation is a consequence of water scarcity. In this waters, Cyanobacteria Harmful Blooms (CyanoHB) are occurring more frequently and intensively as a consequence of climate change. The lack of regulation are pushing countries to irrigate their crops using polluted water despite the serious risks for ecosystem and human health.

Constructed wetlands are a promising and cost-effective technology to remediate cyanotoxins pollution.

Objective

Study CWs and its mechanisms as a bioremediation technology to recycle cyanoHB-polluted water for crop irrigation **(fig. 1)**.

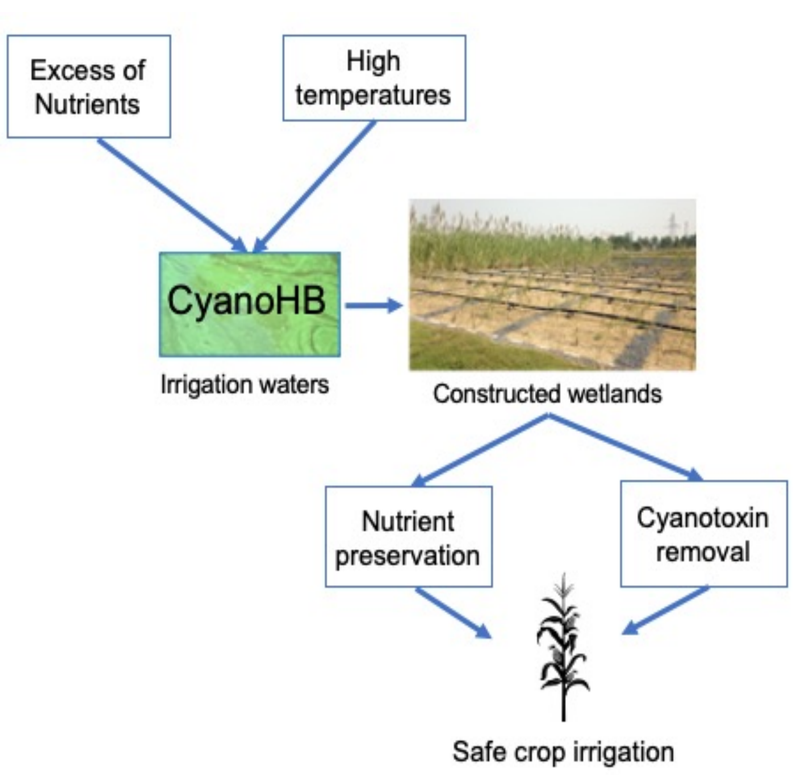


Fig. 1: *diagram of the project overview*

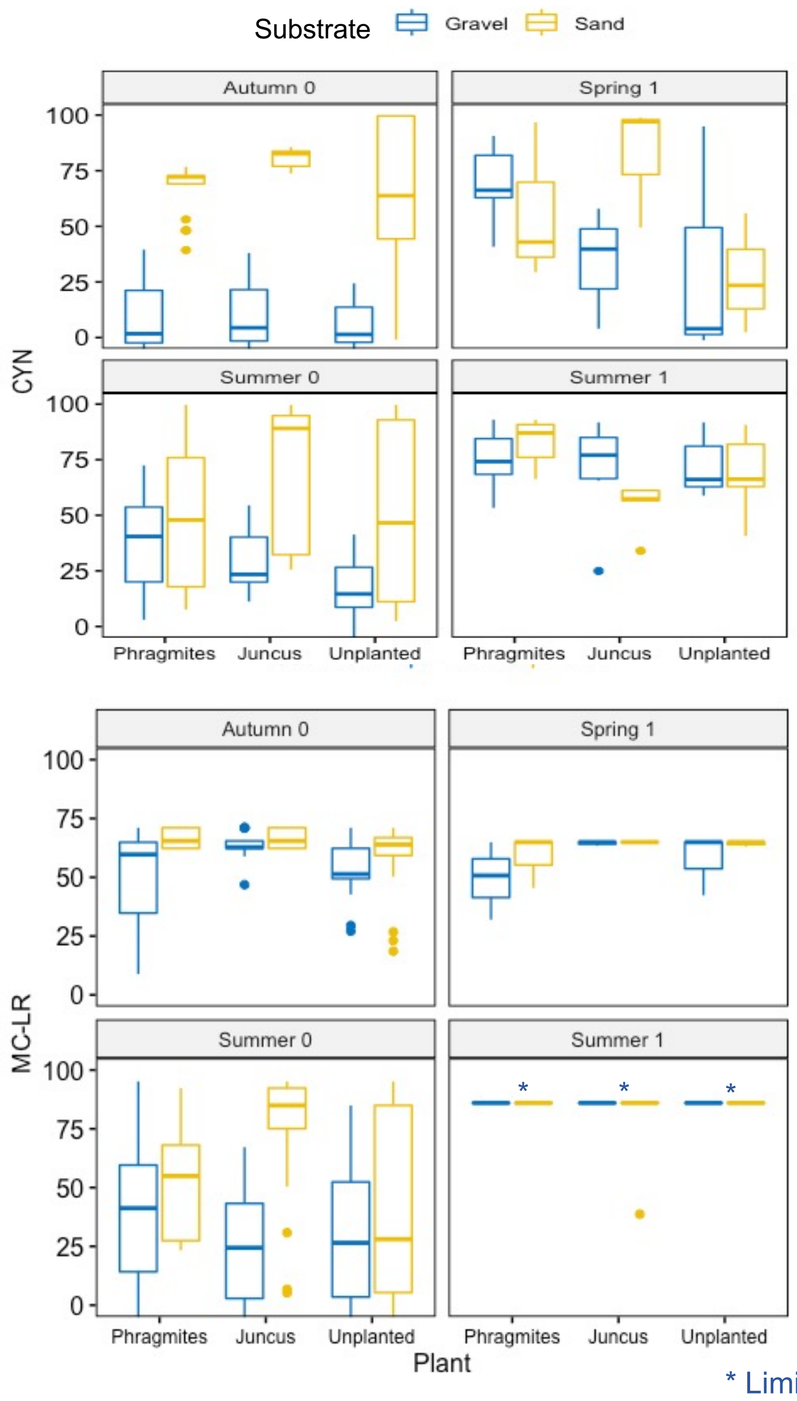
Materials & Methods

Currently, 18 mesocosms vertical flow CW (12L each) are running. To mimic cyanoHB in our systems, we added 10 µg L^{-1} Microcystin-LR and cylindrospermopsin. Sampling campaigns and quantification of cyanotoxins by HPLC-MS/MS together, end-point water measurements (pH, TOC, TN...) are being performed.

Also, 16S qPCR and Amplicon sequencing of the bacterial community are used to characterise the degrading biofilm formed within the systems.

Results & Discussion

The system is continuously running for one year. Stabilization of the systems and improvement of the removal rates is shown, mainly for CYN which it is usually harder to oxidise **(fig. 2)**.



* Limit of detection

Fig. 2: *graph showing MC-LR and CYN removal percentage results after one year of system operation showing the effect of three different variables: substrate, plant and season.*

Statistical analysis showed significant influence of the three main variables (season, plant and substrate) on the toxins degradation.

It was also found a significant variable interaction substrate - season in both toxins and a three variable interaction in MC-LR.

Next steps

1. Finding novel cyanotoxin transformation products by High Resolution LC-MS/MS & Isotope labelling (metabolomics).
2. Microbial community structure analysis of the first 16S Amplicon sequencing data using QIIME2.
3. Studying kinetics of cyanotoxin degradation & bacterial community dynamics.

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