

Microcystin-LR degradation by enriched bacteria isolated from different units of Drinking Water Treatment Plant

Kumar P. ⁽¹⁾, Brar S.K. ⁽¹⁾, Maximiliano C. ⁽²⁾, Galvez R. ⁽³⁾, Karmanshahi-pour A. ⁽⁴⁾

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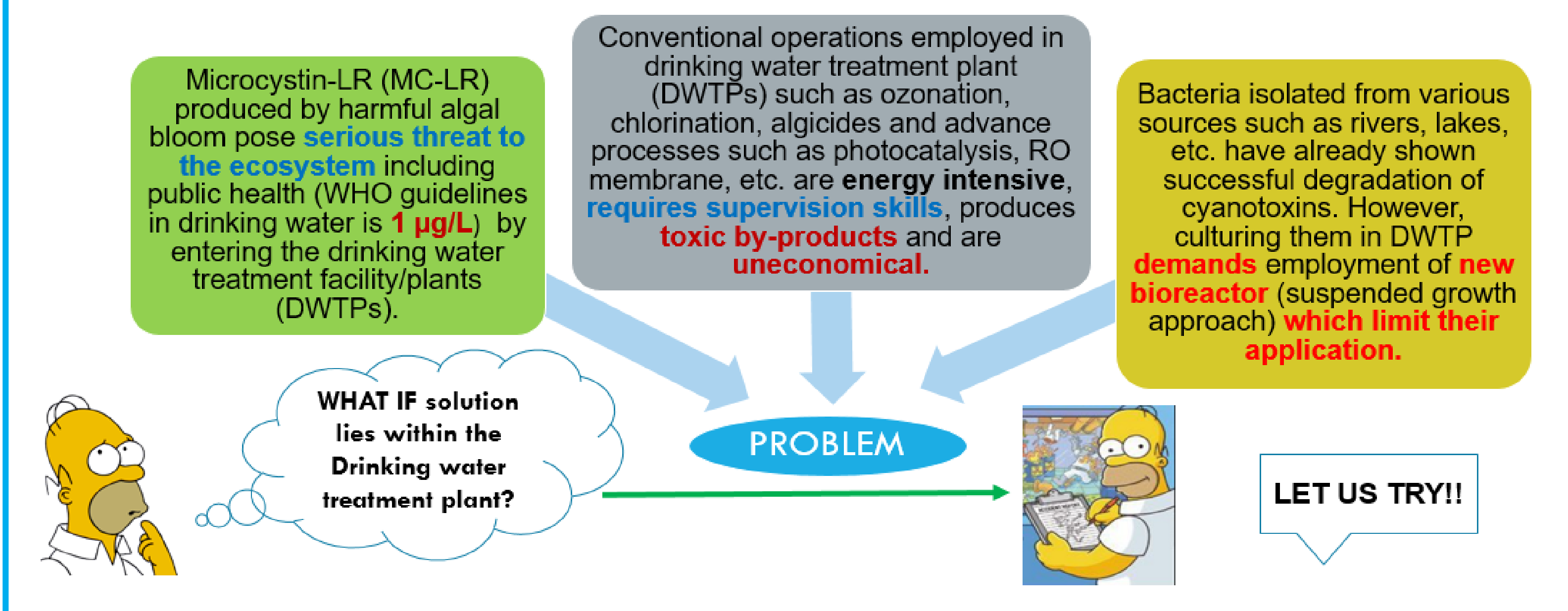
(1) INRS-ETE, Université du Québec, (2) IIMyC-CONICET, Funes 3350, Mar del Plata 7600, Argentina, (3) Department of Civil Engineering, Laval University, (4) Biorefining and Remediation Laboratory, Department of Process Engineering and Applied Science, Dalhousie University



INTRODUCTION

- The occurrence of cyanobacterial harmful algal bloom (CHABs) producing cyanotoxins affect fresh and marine systems as well as public health. Among all the cyanotoxins, microcystin variant MC-LR is the most toxic (due to their cyclic and persistent nature) and commonly found cyanotoxin in the aquatic ecosystem.
- When these cyanotoxin reaches the DWTPs, conventional treatment operations become inefficient in cyanotoxin removal (especially dissolved MCs) and produce toxic byproducts which are often difficult to characterize [1].
- The biological approach has not only shown promise in fully degrading cyanotoxins but it is also known to produce less toxic end products (up to 160-fold less) [2].
- Many studies involving degradation of MC-LR by isolating indigenous bacterial species have been explored including some in-situ bacterial species as well [3,4]. Here, the ability of different bacterial communities present in different operational units of the DWTP (i.e. influent water to the DWTP, sedimentation unit and the filtration unit) have been explored to develop a potentially sustainable solution for this global drinking water issue.

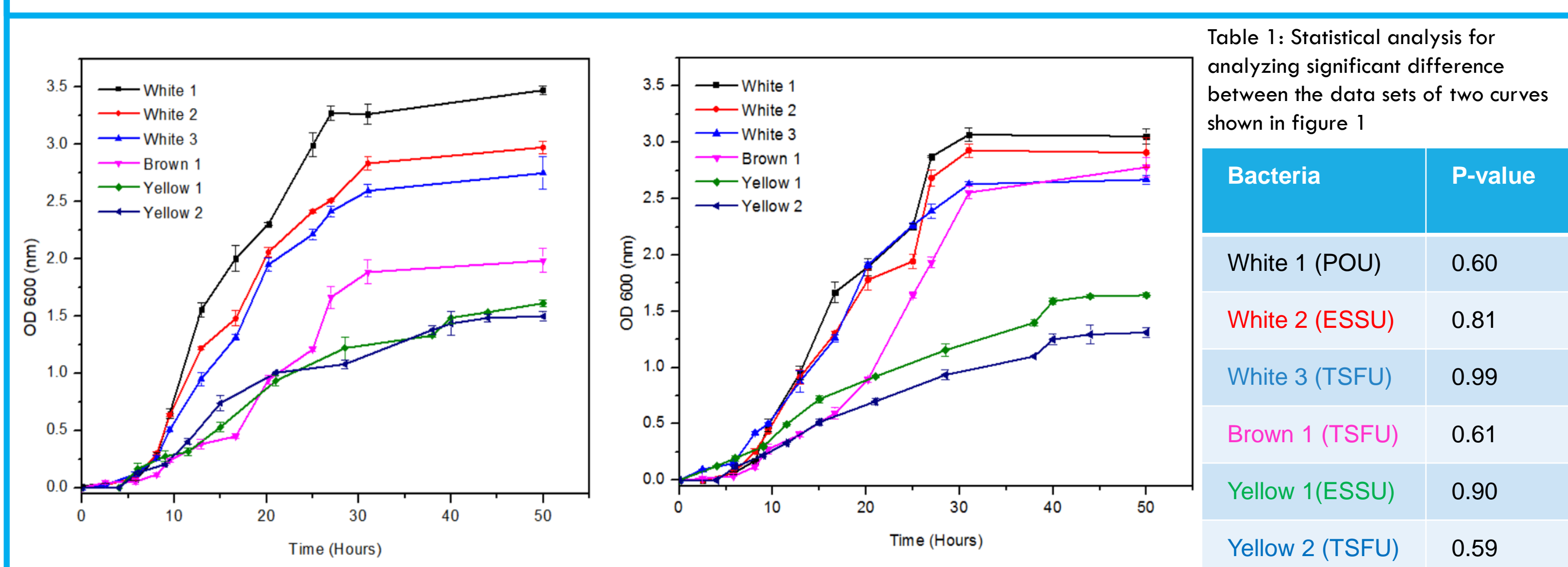
PROBLEM



OBJECTIVE/METHODOLOGY

OBJECTIVES	METHOD	INSTRUMENT USED
To isolate and study growth curve of the bacterial community from different units of the DWTPs (Ste-Foy, Canada)	Cells isolated based on dominance and color morphology	Basic molecular biology
To test their toxicity tolerance level in presence of microcystin-LR	Cell viability count in presence of 10 µg/L and 100 µg/L MC-LR	Statistical analysis (t-test/one-way ANOVA; p-value analysis)
Comparing degradation rate and overall removal efficiency of microcystin-LR before and after the acclimatization process	Equal cell concentration (6x10 ⁶ cells/mL) of bacterial community isolated from different units of DWTPs were spiked in flask with mineral salt media (60 mL) containing 200 µg/L	High performance liquid chromatography (HPLC)
Identification of the formed by-products and their toxicity level	Relative abundance of the by-products based on their m/z value during mass spectra analysis	Mass spectrometry (MS), Bio-indicator organism (<i>Rhizobium Melitoli</i>)

RESULTS AND DISCUSSION

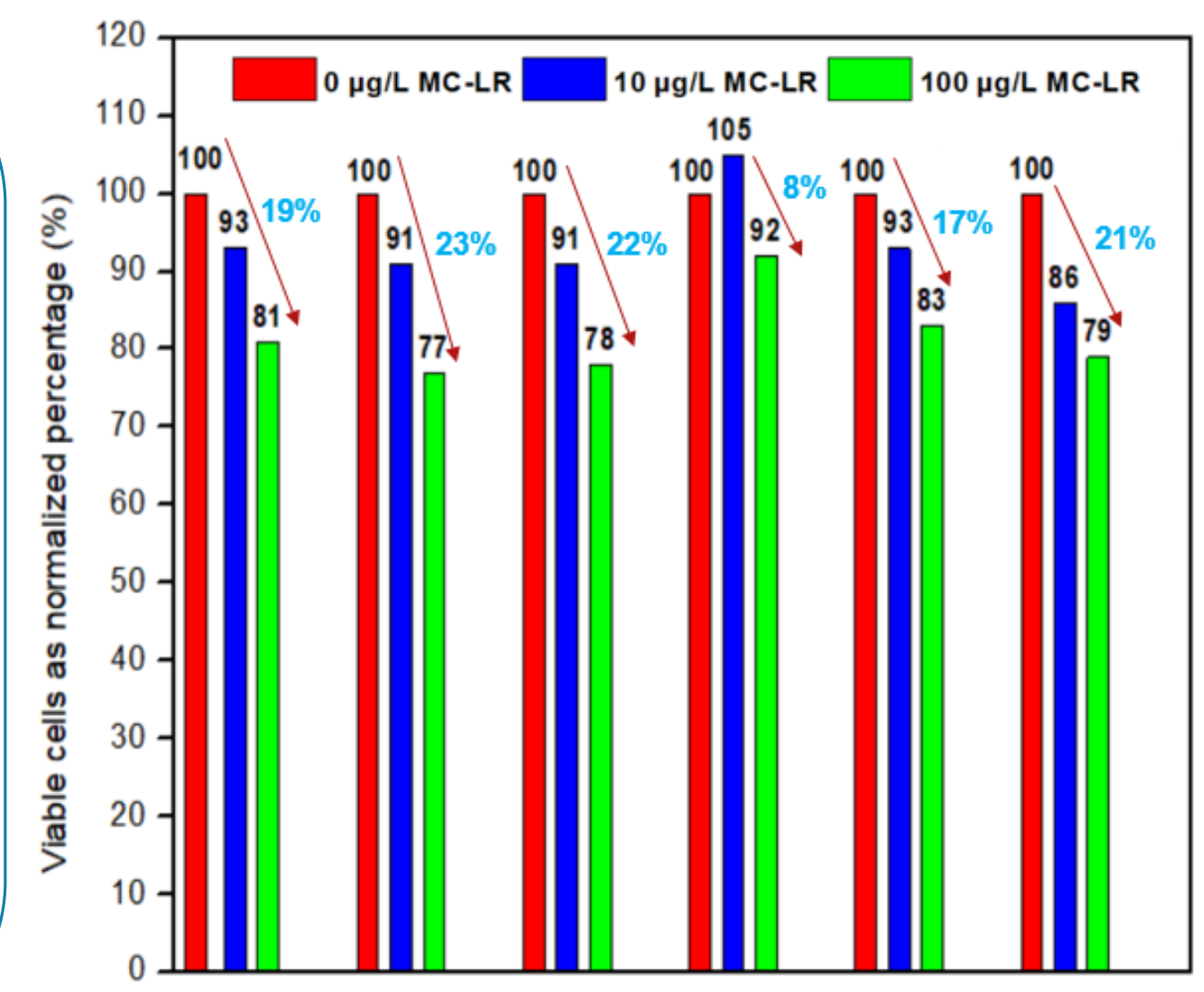


Formulated hypothesis for growth curve:

Null Hypothesis (H₀): No significant difference between the two sets of observation
Alternate Hypothesis (H₁): Significant difference between two data sets.

No significant difference (p-value > 0.05) was observed between the growth rate of all six bacteria when spiked with **10 µg/L and 100 µg/L MC-LR** (based on p-values).

Bacterial population decreased only by **19%, 23%, 22%, 8%, 17%, 21%** when tested with **100 µg/L MC-LR** for White 1, White 2, White 3, Brown 1, Yellow 1 and Yellow 2 bacteria respectively as compared to zero MC-LR case.



RESULTS AND DISCUSSION

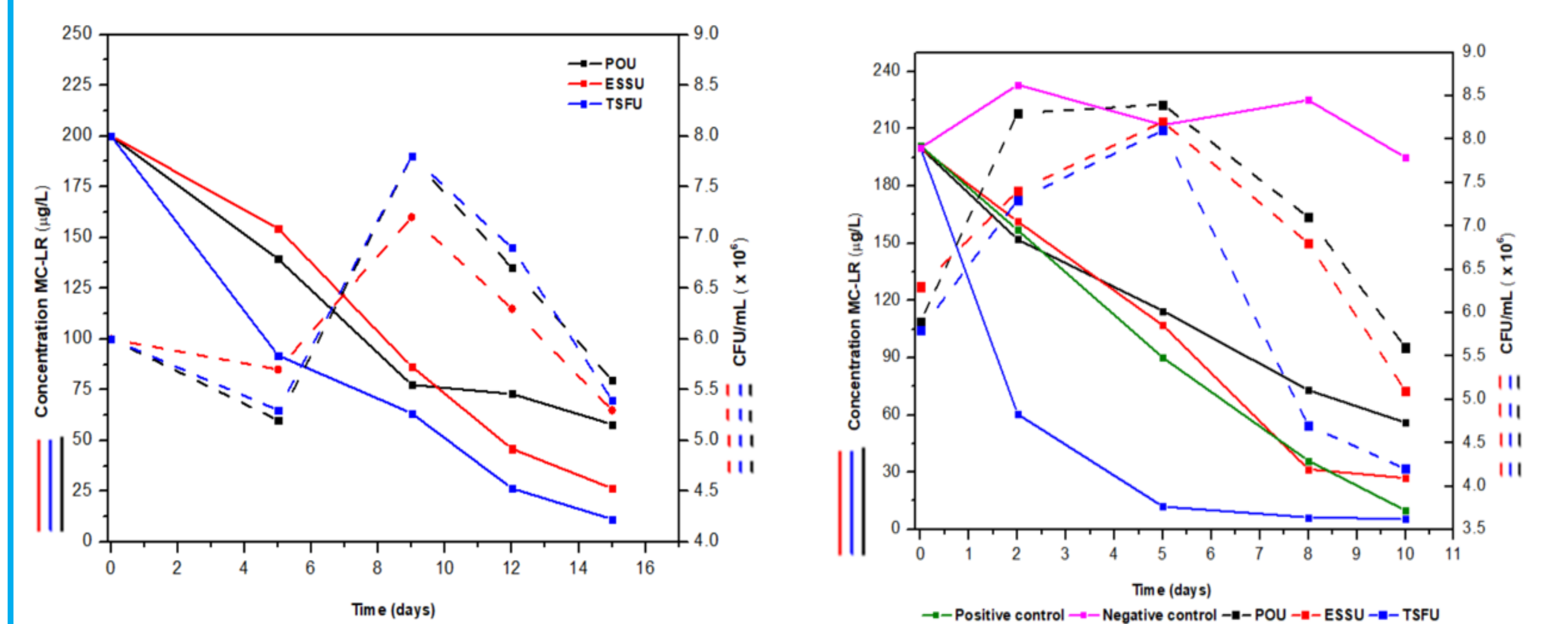


Figure 2: Draw-down curve for acclimatization phase (left) and post acclimatization (right) phase

- **Acclimatization phase:** Bacterial cell concentration isolated from ESSU, POU, TSFU decreased to 5.2x10⁶, 5.7x10⁶ and 5.3x10⁶ CFU/mL respectively at the end of 5 days but increased to 7.8 x10⁶, 7.2 x10⁶, 7.8 x10⁶ CFU/mL respectively after 9 days.
- **Post-acclimatization phase:** Bacterial cell concentration isolated from ESSU, POU, TSFU increased to 8.4x10⁶, 8.2x10⁶ and 8.1x10⁶ CFU/mL respectively at the end of 5 days gave sign of positively getting acclimatize to the MC-LR environment.
- Mass spectra revealed several accompanied ions at m/z 155.99, 213.14, 268.24, 332.93, 553.29, 571.27, 599.34 and 862.48. By-product with m/z of 862.5 forms due to hydrolysis of mother ion (m/z 995) followed by the further loss of Adda portion and amino groups (**microcystinase enzyme encoded by *mlrA* gene is responsible**) [5].
- These hydrolyzed linear by-products formation is also linked to the **reduced toxicity levels (up to 160-fold)**.

Table 2: Degradation rate and removal efficiency of MC-LR by bacterial community isolated from three different units of DWTP

Treatment Unit	Degradation rate (before acc.) acc.= Acclimatization	Removal efficiency (before acc.)	Degradation rate (after acc.)	Removal efficiency (after acc.)	Increase in degradation rate
Pre-ozonation Raw water (POU)	9.46 µg/L/day	71.1 ± 7.37 %	14.46 µg/L/day	72.1 ± 6.4 %	52.8 %
Sedimentation unit (ESSU)	11.56 µg/L/day	86.7 ± 3.19 %	17.32 µg/L/day	86.2 ± 7.3 %	49.8 %
Filtration unit (TSFU)	12.58 µg/L/day	94.35 ± 10.63 %	19.45 µg/L/day	97.2 ± 8.7 %	54.6 %

FUTURE SCOPE

In-situ bacterial biofilm can find application in future for cyanotoxin removal within DWTPs!!

- Highest removal efficiency of MC-LR (97%) is possible with enriched bacterial community present in filtration unit of DWTPs.
- Also, the toxicity analysis as observed by bioindicator organism (*Rhizobium Melitoli*) showed significant amount of living bacteria present (based on absorbance value due to change in color) for final degraded samples as compared to standard microcystin-LR (300 µg/L).
- In future, suitable biofilm formation over filtration media (sand, anthracite) can serve the purpose of total cyanotoxin biodegradation. In this way, no additional treatment unit will be required.

Change in color of MTT dye (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide: **Yellow to Blue** ppt) indicating cell viability in degraded MC-LR samples when tested for toxicity.

CONCLUSION

- Indigenous bacterial community isolated from different units of DWTPs (water sample from pre-ozonation unit (POU), effluent-sludge mixture from sedimentation unit (ESSU) and top-sand layer water sample from filtration unit (TSFU)) showing potential in degrading MC-LR.
- **Maximum degradation** of MC-LR was reported for **enriched bacterial community** isolated from TSFU achieving 97.2 ± 8.7% followed by 86.2 ± 7.3 % and 72.1 ± 6.4 % for enriched bacterial culture isolated from ESSU and POU, respectively.
- The ultimate degradation efficiency achieved was almost similar to non-enriched bacterial degradation but the **biodegradation rate increased** by 52.8% (9.46 µg/L/day to 14.46 µg/L/day), 49.8% (11.56 µg/L/day to 17.32 µg/L/day) and 54.6% (12.58 µg/L/day to 19.45 µg/L/day) for POU, ESSU and TSFU **enriched bacterial community** respectively.
- Mass spectra analysis depicts linearization involving hydrolysis of MC-LR structure (which is linked to reduced toxicity level) confirming *mlrA* gene presence from previous studies.

REFERENCES:

- Chen P, Zhu LY, Fang SH, Wang CY, Shan GQ (2012) Photocatalytic Degradation Efficiency and Mechanism of Microcystin-RR by Mesoporous Bi₂WO₆ under Near Ultraviolet Light. *Environ Sci Technol* 46: 2345–2351.
- Somdee, T., Thunders, M., Ruck, J., Lys, I., Allison, M., & Page, R. (2013). Degradation of [Dha7]MC-LR by a Microcystin Degrading Bacterium Isolated from Lake Rotoiti, New Zealand. *ISRN Microbiology*, 2013, 1-8.
- Neilan, B., Yang, F., Zhou, Y., Yin, L., Zhu, G., Liang, G., & Pu, Y. (2014). Microcystin-Degrading Activity of an Indigenous Bacterial Strain *Stenotrophomonas acidaminiphila* MC-LTH2 Isolated from Lake Taihu. *PLoS One*, 9(1), e86216
- Chen, J., Hu, L. B., Zhou, W., Yan, S. H., Yang, J. D., Xue, Y. F., & Shi, Z. Q. (2010). Degradation of Microcystin-LR and RR by a *Stenotrophomonas* sp. Strain EMS Isolated from Lake Taihu, China. *Int J Mol Sci*, 11(3), 896-911.
- Edwards, C., Graham, D., Fowler, N., and Lawton, L. A. (2008) Biodegradation of microcystins and nodularin in freshwaters. *Chemosphere* 73, 1315–1321.