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Review

# Current research scenario for microcystins biodegradation – A review on fundamental knowledge, application prospects and challenges

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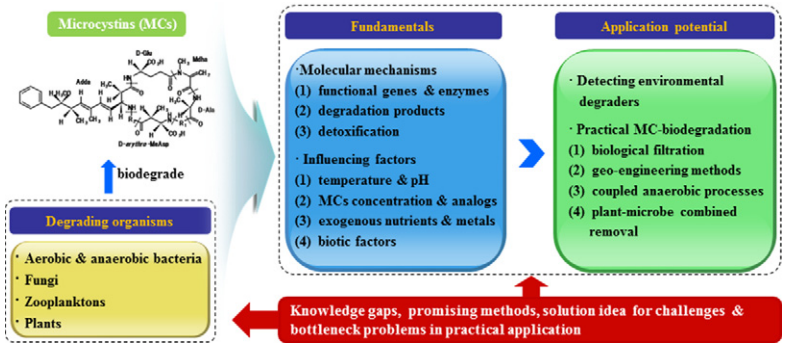
## HIGHLIGHTS

- The review recounts current research advances for microcystins biodegradation.
- Microcystins degradation by diverse organisms and involved mechanisms are reviewed.
- Microcystins biodegradation efficacies affected by multiple factors are summarized.
- The ideas to solve bottleneck problems in application of biodegradation are discussed.
- Data gaps and future direction in microcystins biodegradation research are proposed.

## GRAPHICAL ABSTRACT

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## ABSTRACT

Microcystins (MCs) are common cyanotoxins produced by harmful cyanobacterial blooms (HCBs) and severely threaten human and ecosystems health. Biodegradation is an efficient and sustainable biological strategy for MCs removal. Many novel findings in fundamental knowledge and application potential of MC-biodegradation have been documented. Little effort has devoted to summarize and comment recent research progress on MC-biodegradation, and discuss the research problems and gaps. This review deals with current research scenario in aerobic and anaerobic biodegradation for MCs. Diverse organisms capable of degrading MCs are encapsulated. Enzymatic mechanisms and influence factors regulating aerobic and anaerobic MC-biodegradation are summarized and discussed, which are essential for assessing and reducing MC-risks during HCBs episodes. Also, we propose some ideas to solve the challenges and bottleneck problems in practical application of MC-biodegradation, and discuss research gaps and promising research methods which deserve special attention. This review may provide new insights on future direction of MC-biodegradation research, in order to further broaden its application prospects for bioremediation.



*Abbreviation:* AVB, aquatic vegetable bed; DWS, drinking water sludge; EPS, extracellular polymeric substances; GAC, granular activated carbon; GEMs, genetically-engineered microorganisms; HE, heterologous expression; MCs, microcystins; MC-LA, microcystin-LA; MC-LF, microcystin-LF; MC-LW, microcystin-LW; MC-LY, microcystin-LY; MC-LR, microcystin-LR; MC-RR, microcystin-RR; MC-YR, microcystin-YR; MLS, modified local sand/soil; MLS-FCT, MLS flocculation-capping technology; MRT, macrophyte-based restoration technology; PBs, periphyton biofilms; PPs, protein phosphatases; qPCR, quantitative PCR; SIP, stable isotope probing; SMs, submerged macrophytes; tGSH, total glutathione; VS, volatile solid; WTFs, water treatment facilities; WTP, water treatment plant.

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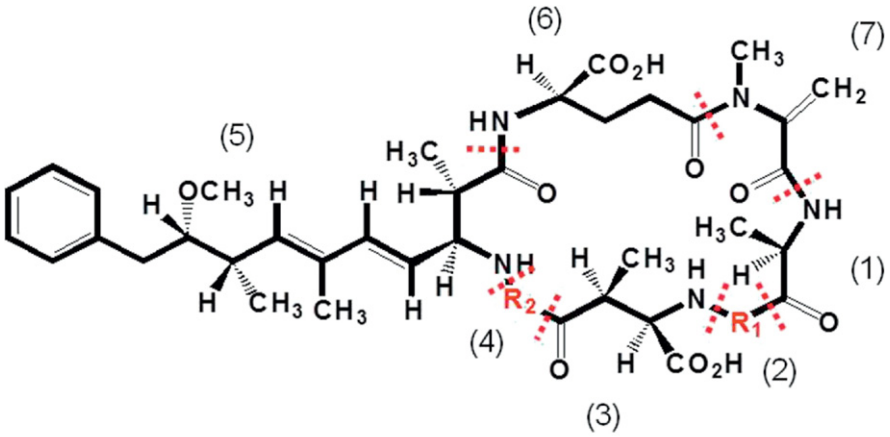
**Contents**



## 1. Introduction

Harmful cyanobacterial blooms (HCBs) frequently occur in eutrophic freshwater ecosystems worldwide (Paerl et al., 2011). The production of toxic metabolites (i.e., cyanotoxins) during HCBs that threaten human and ecosystem health is a major concern (Codd, 1995). Microcystins (MCs) are the most widespread cyanotoxins, and can be synthesized intracellularly by several cyanobacterial genera including *Microcystis*, *Anabaena*, *Planktothrix* and *Nostoc* (Botes et al., 1982; Christiansen et al., 2003; Yan et al., 2004b; Jungblut and Neilan, 2006). Intracellular MCs are released into water bodies via cell lysis caused by natural senescence and/or physical stress (Ross et al., 2006).

As a group of cyclic heptapeptides, MCs share a general structure of cyclo-(D-Ala$^{(1)}$-$R_1^{(2)}$-D-isoMeAsp$^{(3)}$-$R_2^{(4)}$-Adda$^{(5)}$-D-isoGlu$^{(6)}$-Mdha$^{(7)}$-), where $R_1$ and $R_2$ represent a pair of highly variable L-amino acids (Fig. 1). Over 100 structural analogs of MCs have been identified mostly due to the substitution of variable L-amino acids in $R_1$ and $R_2$ sites (Puddick et al., 2014). Among MCs analogs, microcystin-LR (MC-LR) is




| MCs analogs | Variable L-amino acids | |
|---|---|---|
| | $R_1$ | $R_2$ |
| MC-LR | Leu (L) | Arg (R) |
| MC-RR | Arg (R) | Arg (R) |
| MC-YR | Tyr (Y) | Arg (R) |
| MC-LF | Leu (L) | Phe (F) |
| MC-LW | Leu (L) | Trp (W) |
| MC-LA | Leu (L) | Ala (A) |
| MC-LY | Leu (L) | Tyr (Y) |

**Fig. 1.** General chemical structure of MCs with two variable L-amino acids at sites $R_1^{(2)}$ and $R_2^{(4)}$. (1) D-Ala: D-Alanine; (3) D-iso-MeAsp: D-*erythro*-β-methyl-aspartic acid; (6) D-iso-Glu: D-Glutamic acid; (7) Mdha: *N*-methyl-dehydroalanine (Sivonen and Jones, 1999).