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Review of Biodegradation of Carbofuran: Microbial Degradation and Enzymatic Mechanisms

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ABSTRACT

Carbofuran, a highly toxic systematic carbamate pesticide, is widely used in agriculture but poses severe environmental and health risks due to its persistence and mobility in soil and water. Conventional chemical and physical remediation methods are costly and generate secondary pollutants, making microbial degradation an eco-friendly alternative. This review had found the articles (28 articles selected from Scopus database) that discovered various bacterial and fungal species, including *Sphingomonas*, *Pseudomonas*, *Enterobacter*, and *Rhodococcus*. All these bacterial have demonstrated carbofuran-degrading capabilities through enzymatic hydrolysis (e.g., CehA hydrolase) and oxidative pathways (e.g., CfdC monooxygenase). Despite improvement in research finding, a systematic understanding of microbial degradation efficiency, genetic regulation, and field applicability remains underexplored and require a lot of future research.

Keywords: Carbofuran; Carbamate pesticide; Microbial degradation; Bacterial; Enzyme biodegradation.

1. INTRODUCTION

Carbofuran is a highly toxic systematic carbamate pesticide. It is widely used in agriculture to control insect pests, nematodes, and mites (Fenoll et al., 2011). Despite its effectiveness as pesticide, carbofuran can cause environmental and health risks due to its lifespan in soil and water, high toxicity to non-target organisms, and likely to contaminate food chains (Kumar et al., 2018). Given its widespread use and environmental hazards, the degradation of carbofuran has become a serious research focus, with microbial offering excellent strategies.

Microbial degradation is a key mechanism for carbofuran removal in the environment. Various bacterial and fungal species, including *Sphingomonas, Pseudomonas, Methylobacterium*, and *Aspergillus*, have been reported to metabolize carbofuran into less toxic compounds (Gupta, 1994; Kim et al., 2015; Zhang et al., 2018). These microorganisms offered hydrolytic, catalytic and oxidative pathways to break down the carbofuran. Carbofuran degradation by microbe has been linked to specific catabolic genes, such as *cehA* and *mcd*, encoding carbofuran hydrolase and methylcarbamate hydrolase, respectively (Tomasek & Karns, 1989; Chaudhry & Ali, 1988; Hong et al., 2007). Understanding the microbial pathways particularly in enzymatic mechanisms play a pivotal role in carbofuran degradation for developing bioremediation techniques to lessen carbofuran contamination.
Enzyme such hydrolases, oxidoreductases, and ligninolytic enzymes contributing to the

breakdown Carbofuran and has been extensively studied for its ability to catalyze the hydrolysis of the carbamate linkage, yielding non-toxic metabolites (Yang et al., 2019). Additionally, oxidative enzymes such as monooxygenases and laccases have been implicated in the transformation of carbofuran into phenolic derivatives (Bano & Musarrat, 2003). Advances in enzyme engineering like enzyme immobilization techniques could enhanced the potential for large-scale pesticide degradation (Liu, 2020).

This review was made to discover current knowledge on microbial and enzymatic degradation of carbofuran, emphasizing the biochemical pathways and enzyme involvement. By elucidating all these data, this review work might to contribute to the development of efficient and eco-friendly strategies for carbofuran remediation.

2. METHODOLOGY

This review refers to the PRISMA review protocol. The articles were searched in Scopus database search engine (years 2014 and above) .The string search as following: TITLE-ABS-KEY (carbofuran biodegradation) AND PUBYEAR > 2014 AND PUBYEAR < 2026 AND (LIMIT-TO (DOCTYPE , "article")) AND (LIMIT-TO (EXACTKEYWORD , "Carbofuran")) AND (LIMIT-TO (LANGUAGE , "English"). During this process,58 articles were discovered and only 15 articles were selected for the screening process that hit the criteria of “Carbofuran microbial degradation” and undergone review processed.

3. RESULT AND DISCUSSION

Table 1. Microbe and enzyme involve in carbofuran degradation.

No	Enzyme / Gene (Alias)	Host Organism	Genetic Context (plasmid/chromosome; cluster)	Citation
1	CehA (carbamate hydrolase)	*Sphingobium* sp. CFD-1	Mobile elements around cehA; conserved among CF degraders	Jiang et al. (2020)
2	CehA + cfdC ($FMNH_2$/$FADH_2$ monooxygenase)	*Sphingomonas* sp. CDS-1	cfd genes conserved vs. *Novosphingobium* KN65.2	Yan et al. (2018)
3	cfd cluster (cfdC/E/F) + cehA (comparative genomics)	*Sphingobium* spp. CFD-1/CFD-2; *Novosphingobium* KN65.2	cehA and cfd cluster on two plasmids; flanked by IS6100	Jiang et al. (2022)
4	IpcH (novel hydrolase)	*Rhodococcus* sp. D-6	Chromosomal; low identity (<27%) to known carbamate hydrolases	Zhu et al. (2024)

5	Extracellular transformation; metabolome shifts	*Chryseobacterium* sp. BSC2-3	Genes for IAA biosynthesis reported	Park et al. (2022)
6	EPS-linked catabolism & metabolites	*Cupriavidus* sp. ISTL7	n/a	Gupta et al. (2019)
7	Multi-enzyme system (Mcd; RamA)	*Enterobacter* sp. Z1	Multi-gene response (genomics/proteomics/qPCR)	Zhang et al. (2020)
8	Pathway prediction & substrate rules	*Novosphingobium* sp. KN65.2	Rieske dioxygenases & flavin monooxygenases emphasized	Schittich et al. (2024)
9	Substrate specificity (generalist vs specialist)	*Novosphingobium* sp. KN65.2 vs *P. fluorescens* P17	n/a	Schittich et al. (2022)

The biodegradation of carbofuran through microbial and enzymatic pathways presents a promising solution for mitigating their toxicity in environment. Microbial degradation, facilitated by diverse bacterial and fungal species, play significant role for bioremediation. Studies as shown in Table 1 have identified key microorganisms, such as *Sphingomonas* and *Pseudomonas*, capable of metabolizing carbofuran into less toxic intermediates. These findings align with earlier research as mentioned above that highlighting the role of carbofuran hydrolase (*cehA*) and methylcarbamate hydrolase (*mcd*) genes in beginning the process of degradation. Future studies should explore more on the discovering of microbial consortia to enhance degradation under several environmental situations.

Again, this review found that enzymatic mechanisms offer good approach for carbofuran breakdown, with hydrolases playing pivotal roles. Carbofuran hydrolase, for instance, catalyses the hydrolysis of the carbamate bond, yielding non-toxic compounds (Yang et al., 2019). Similarly, oxidative enzymes such as monooxygenases and laccases contribute to the transformation of carbofuran into phenolic derivatives (Bano & Musarrat, 2003). Despite this discovery, the practical application of free enzymes is limited by their instability and high production costs. Recent developments in enzyme immobilization and protein engineering present opportunities to overcome these limitations (Liu et al., 2020). For instance, immobilized enzymes exhibit enhanced stability and reusability, making them suitable for large-scale remediation. Further research should focus on improving the catalytic efficiency and scalability of these enzymatic systems.

4. CONCLUSION

In conclusion, while microbial and enzymatic degradation pathways offer effective means for carbofuran remediation, their success depends on addressing key challenges such as environmental variability, enzyme stability, and another factor such the production of intermediate toxicity. Future research should prioritize the development of robust, scalable, and

eco-friendly biodegradation systems to ensure sustainable environmental management.

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