Interactions between pesticides and microorganisms: The case of biodegradation of synthetic β-triketone herbicides

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Introduction

Agricultural use of pesticides ensures a higher crop quality and production but it also one of the major sources of diffuse pollution in the environment. Microbial degradation is considered as an important dissipation process limiting the accumulation of pesticides in the environment. In this context, two bacterial strains able to degrade sulcotrione, a β-triketone herbicide, were isolated from an agricultural soil previously exposed to this herbicide.

Bacterial isolation procedure: one soil, two strategies

Characterization of Pseudomonas sp. 1OP, a sulcotrione-degrading bacteria (Strategy A)

Characterization of Bradyrhizobium sp. SR1, a sulcotrione and mesotrione degrading bacteria (Strategy B)

Degradation kinetics of (A) sulcotrione and (B) mesotrione by Bradyrhizobium sp. SR1 in resting cell experiments. Cumulative formation of metabolites during sulcotrione (CMBA) and mesotrione degradation is represented.

Study of sulcotrione metabolites

Microbial toxicity of sulcotrione and mesotrione metabolites

The toxicity of triketone molecules and their related metabolites was estimated by monitoring 4-hydroxyphenylpyruvate dioxygenase inhibition (HPPD). Toxicity due to HPPD inhibition was mainly linked to parent molecules, and not to the formed metabolites.

Genetic localization of sulcotrione degradation in Pseudomonas sp. 1OP

Plasmid profiles from Pseudomonas sp. 1OP obtained in MSM+sulcotrione or in absence of sulcotrione in a rich medium revealed the presence of a >12 kb plasmid. 1OP plasmid was eliminated by curing experiment carried out on rich medium and sulcotrione-degrading ability was lost without peptide selection pressure.

Conclusion: Two degrading strains exhibiting different genetic features

- Pseudomonas sp.1OP was the first bacterial strain described in the literature as capable of degrading sulcotrione to 2-chloro-4-methylbenzoic acid (CMBA). Its growth performances have shown that initial neutral pH conditions and 183 μM of sulcotrione seemed to be the best cultural environment for this strain. The isolate harboured a catabolic plasmid involved in sulcotrione biodegradation process.
- Bradyrhizobium sp. SR1 was able to biotransform two β-triketone herbicides, sulcotrione and mesotrione. The dissipation of sulcotrione and mesotrione led to the accumulation of different known metabolites: CMBA and MBMA/AMBA. A 14,000 Tn5 mutant library was constructed using a Tn5 mutagenesis approach conducted on Bradyrhizobium sp. SR1. Full sequencing of mutants are ongoing to identify possible degrading gene candidates.

Genetic localization of sulcotrione degradation in Bradyrhizobium sp. SR1

Plasmid profiles from (1) Bradyrhizobium sp. SR1. The size of the plasmid is indicated in kb (2) Sphingomonas sp. SH. used as molecular weight marker. SR1 plasmid was not eliminated by curing experiment carried out on rich medium and that sulcotrione-degrading ability was maintained without pesticide selection pressure.