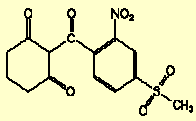
Isolation and characterization of mesotrione-degrading bacteria from a French agricultural soil

Isabelle Batisson[1], Olivier Crouzet[1], Pascale Besse-Hoggan[2], Martine Sancelme[2], Jean-François Mangot[1], Clarisse Mallet[1], Jacques Bohatier[1]

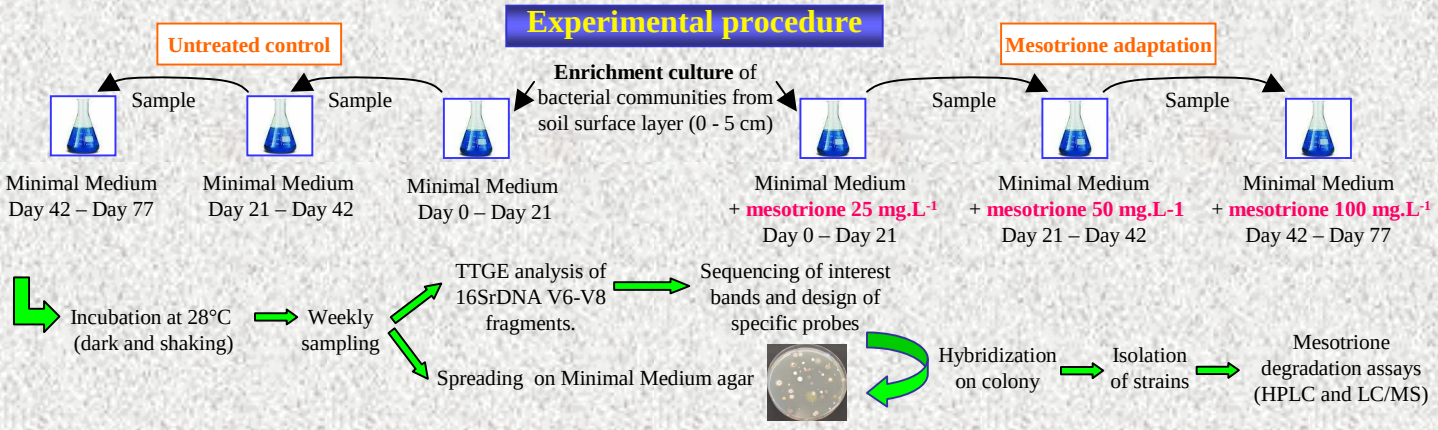
1: Université Blaise Pascal-Clermont II, Laboratoire Microorganismes : Génome et Environnement (LMGE), UMR CNRS 6023, France.
2: Université Blaise Pascal-Clermont II, Laboratoire de Synthèse Et Etude de Systèmes à Intérêt Biologique, UMR CNRS 6504, France.

Introduction and objectives

Mesotrione is a new triketone herbicide used on maize cultures to substitute atrazine banned in 2003 in France. To date, two mesotrione biotransformation products [4-methylsulfonyl-2-nitrobenzoic acid (MNBA) and 2-amino-4-methylsulfonylbenzoic acid (AMBA)] have been described. However, because of its recent use, little information is available about the fate and impact of mesotrione and its biodegradation products in the environment. This study aimed to isolate mesotrione-degrading bacterial strains that could thus help in elucidating its metabolic pathway and in predicting its impact on structure, diversity and function of soil microbial communities.

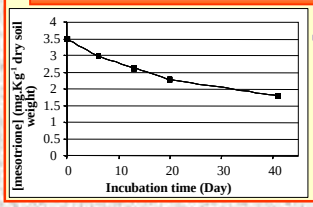


Experimental procedure



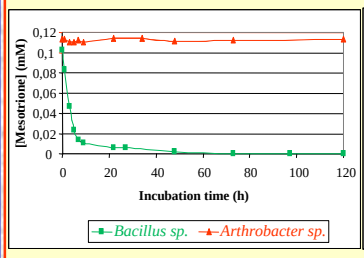
Results

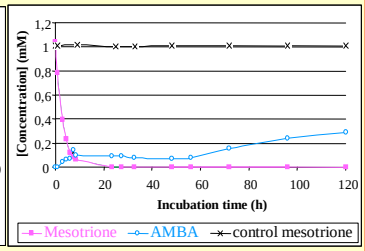
Mesotrione degradation by natural soil microflora



⇨ Soil was sprayed with 10 times the agronomic rate of mesotrione (4.5 mg.Kg^{-1} dry weight). A progressive decrease in mesotrione along the 40-day incubation time was observed, resulting in the biotransformation of almost 50% of the compound by natural microbial communities. This evidenced the capacity of this soil to biotransform mesotrione.

Bacterial isolate capacity to degrade mesotrione

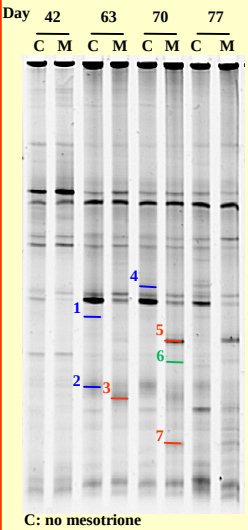




⇨ *Arthrobacter* sp. strain did not degrade 0.1 mM mesotrione. By contrast, the *Bacillus* sp. isolate completely degraded 0.1 mM mesotrione.

⇨ *Bacillus* sp. isolate completely degraded 1 mM mesotrione within 24 h of incubation. The AMBA metabolite appeared after 3 h, accumulated in the medium and increase up to a maximum of 0.3 mM.

Analyses of bacterial genetic diversity (TTGE)



C: no mesotrione

M : mesotrione 100 mg.L^{-1}

⇨ During enrichment cultures, differences in soil bacterial communities between control (C) and treated microcosms (M) were mainly observed for the highest mesotrione concentration (100 mg.L^{-1}). Ubiquitous band (band 6), bands only found in mesotrione-treated flasks (bands 3, 5, 7) and bands only visible in control flasks (bands 1, 2, 4) were apparent.

⇨ V6-V8 16SrDNA bands were sequenced and BLAST affiliated:
1: Uncultured *bacterium* clone L3B_344
2: *Acidovorax facilis*
3: *Acidovorax sp.* NO-1
4: Unidentified *bacterium* wb1_A01
5: Uncultured *Verrucomicrobia bacterium*
6: *Bacillus sp.*
7: *Arthrobacter sp.*

⇨ Two strains adapted to mesotrione (*Bacillus sp.* and *Arthrobacter sp.*) were isolated from MM agar medium by the colony hybridization method and tested for their ability to degrade mesotrione in pure culture.

Conclusions/Perspectives

Enrichment cultures coupled to fingerprint molecular approaches emphasize the impact of mesotrione on soil bacterial communities (sensitivity/adaptation). One adapted bacterial strain, assigned to *Bacillus sp.*, was shown to efficiently and completely degrade mesotrione in pure culture with accumulation of AMBA metabolite in the medium. Several other biodegradation products were also produced during mesotrione degradation by *Bacillus sp.* and they are now under characterization in the laboratory for help in understanding biodegradation pathway. Use of this strain in bioremediation could also be of great importance to environment.