New Aspects on Atrazine Biodegradation

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ABSTRACT

The world practice of using agrochemicals for long periods, in an indiscriminated and abusive way, has been a concern of the authorities involved in public health and sustainability of the natural resources, as a consequence of environmental contamination. Agrochemicals refer to a broad range of insecticides, fungicides and herbicides, and among them stands out atrazine, a herbicide intensively used in sugarcane, corn and sorghum cultures, among others. Researches have demonstrated that atrazine has toxic effects in algae, aquatic plants, aquatic insects, fishes and mammals. Due to the toxicity and persistence of atrazine in the environment, the search of microbial strains capable of degrading it is fundamental to the development of bioremediation processes, as corrective tools to solve the current problems of the irrational use of agrochemicals. This review relates the main microbial aspects and research on atrazine degradation by isolated microbial species and microbial consortia, as well as approaches on the development of techniques for microbial removal of atrazine in natural environments.

Key words: atrazine, biodegradation, bacteria, fungi, microbial consortium

INTRODUCTION

Atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-s-triazine] is a selective herbicide belonging to the family of the s-triazines, which contains in its chemical structure an aromatic hexameric and symmetrical ring constituted by three carbon and three nitrogen atoms in alternate positions (Fig. 1). Atrazine is worldwide used, often in combination with other herbicides (Chan & Chu, 2005), to control broadleaf and grassy weeds in agriculture, especially in corn, sorghum and sugar cane crops and in conifer reforestation planting (Ribeiro *et al*., 2005). Atrazine kills susceptible plants by binding to the quinone-binding protein in photosystem II, thus, inhibiting the photosynthetic electron transport.

Atrazine is a pollutant of environmental concern due to its low biodegradability and its high potential to contaminate the surface waters and groundwater (Chan & Chu, 2005). Although it is a banned or regulated substance in several countries, 100 ng l^{-1} to 1μg l^{-1} concentrations have been reported in surface waters (Parra *et al*., 2004).

Once in aquatic environment, atrazine may alter the structure and function of the communities. Standard toxicity tests performed on five microalgal species of different taxonomic families revealed differential sensitivity to atrazine exposure. Species listed in order of increasing sensitivity were: *Isochrysis galbana*, *Dunaliella*

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tertiolecta,   Phaeodactylum   tricornutum,
Pseudokirchneriella   subcapitata   and
Synechococcus sp. (Weiner *et al.*, 2004).
Comparing the acute toxicity of 40 herbicides
exerting nine different modes of action on the

green alga *Raphidocelis subcapitata,* Ma *et al.*
(2006) found that photosynthesis was the most
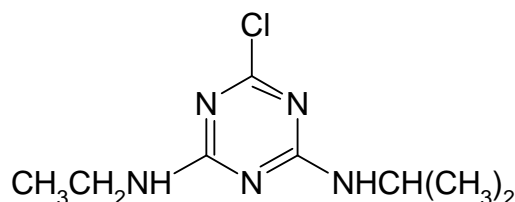sensitive process, and atrazine was among the
most toxic herbicides tested.

Figure 1 - Chemical structure of atrazine.

Triazinic compounds such as atrazine, simazine,
propazine, as well their metabolites, mainly 2-
hydroxyatrazine,   diaminochlorotriazine,
deethylatrazine and deisopropylatrazine, were
shown to induce mammary gland tumors in
Sprague-Dawley (SD) female rats (Stevens *et al.*,
1994). Atrazine has also been suggested to be a
potential disruptor of normal sexual development
in male frogs (Hayes *et al.*, 2002; Murphy *et al.*,
2006) as well as to alter some aspects of the
immune response (Christin *et al.*, 2004). In 2007,
the United States Environmental Protection
Agency (USEPA) began reviewing several
epidemiological cancer studies concerning atrazine
and its possible association with carcinogenic
effects in humans.

Although atrazine has toxic effects on life, its
metabolites,   including   deethylatrazine   and
deisopropylatrazine, are currently assumed to be
less toxic than their parent (Kross *et al.*, 1992;
EPA 2002). However, especially in agricultural
soils, deethylatrazine and deisopropylatrazine,
which retain the chlorine atom, are considered
phytotoxic (Honout *et al.*, 1998).

Biodegradation of atrazine

Atrazine is considered persistent due to its
moderate water solubility (33 mg l^{-1} at 20°C) and
low soil sorption partition coefficient (K_d = 3.7 l
kg^{-1}). Although the halogen, methylthioether, and
N-alkyl substituents on the s-triazine ring of this
group of herbicides hinder the microbial
metabolism (Wackett *et al.*, 2002), some reports
have demonstrated the ability of some soil
microorganisms to degrade atrazine partially or
totally directing it to carbon dioxide and ammonia

formation (Mandelbaun *et al.*, 1995; Rosseaux *et al.*, 2003; Sing *et al.*, 2004a).

The biodegradation of atrazine in soil is space
variable, being slower in subsurface zones than in
surface soil. Under vadose zone and subsurface
aquifer conditions, low temperatures and the lack
of degrading organisms are likely to be primary
factors limiting its biodegradation (Radosevich *et al.*, 1996).

The research on atrazine-degrading microorganisms
has   been   directed   to   the   isolation   and
characterization of natural occurrence lineages in
environments contaminated with this pesticide.
According to Rhine *et al.* (2003), the repeated
exposure to atrazine can increase biodegradation,
which may be also enhanced as a result of limited
N availability. Fang *et al.* (2001) observed that the
number of atrazine degrading bacteria did not alter
significantly   prior   to   atrazine   exposure,   but
significantly   reduced   the   acclimation   period
preceding the onset of mineralization. Silva *et al.*
(2004) demonstrated the occurrence of fast
atrazine mineralization after an acclimatization
period of approximately 28 days.

Atrazine degradation by bacteria

Among bacteria, there are reports on atrazine
degradation   by   individual   strains   such   as
Pseudomonas sp. (Mandelbaum *et al.*, 1995; Katz
et al., 2001), *Rodococcus rhodochrous* (Jones *et al.*, 1998), *Acinetobacter* spp. (Singh *et al.*,
2004a), *Aerobacterium* sp., *Microbacterium* sp.,
Bacillus sp., *Micrococcus* sp., *Deinococcus* sp. and
Delftia acidovorans (Vargha *et al.*, 2005), as well
as by species consortia including *Agrobacterium
tumefaciens,   Caulobacter   crescentus,*

Pseudomonas putida, Sphingomonas yaniokuyae, Nocardia sp*., Rhizobium* sp*., Flavobacterium oryzihabitans* and *Variovorax paradoxus* (Smith *et al.*, 2005). *Pseudomonas* sp. ADP, isolated from soil contaminated with atrazine, was shown to mineralize completely the triazinic ring (Mandelbaum *et al.*, 1995). Sing *et al.* (2004a) isolated a bacterium member of *Acinetobacter* genus capable of degrading atrazine as a carbon source at concentration as high as 250 ppm. In granular activated carbon column filters inoculated with *R. rhodochrous*, atrazine degradation achieved 72.6% after 39 days (Jones *et al.*, 1998). The strain *D. acidovorans* D24 mineralized atrazine as a sole source of carbon and nitrogen (Vargha *et al.*, 2005).

The atrazine degrading bacteria generally initiate the degradation through a hydrolytic dechlorination, catalysed by the enzyme atrazine chlorohydrolase (AtzA), encoded by the *atzA* gene, followed by two hydrolytic deamination reactions catalysed by hydroxy-atrazine ethylamino-hydrolase (AtzB) and N-isopropyl-ammelide isopropyl-amino-hydrolase (AtzC), encoded by the genes *atzB* (*trzB*) e *atzC* (*trzC*), respectively (De Souza *et. al.,* 1996; De Souza *et. al.,* 1998a; Sadowsky *et al.,* 1998), which convert atrazine sequentially to cyanuric acid that is then completely mineralized to CO_2 and NH_3 by other three hydrolases. In some bacterial strains the biodegradation of atrazine initiate through N-dealkylation of the lateral ethyl and isopropyl chains to deethylatrazine and deisopropylatrazine (Kaufman and Blake, 1970) (Fig. 2).

Pseudomonas sp. ADP is the best-characterized bacterial strain capable to degrading the herbicide atrazine. The atrazine catabolic pathway in this bacterium contains six enzymatic steps encoded by *atzABC* and the *atzDEF* genes. The *atzABC* genes have been shown to be widespread and plasmid borne in a number of bacteria isolates (de Souza *et al.*, 1998a; de Souza *et al.,* 1998b; Rousseaux *et al.,* 2001; Topp *et al.*, 2000; Wackett *et al.,* 2002). In *Pseudomonas* sp. ADP, the *atzABCDE* genes are harbored on the catabolic plasmid pADP-1 (Martinez *et al.,* 2001).

In *Pseudomonas* sp. ADP, the *atzDEF* operon encodes cyanuric acid amidohydrolase (AtzD), biuret amidohydrolase (AtzE), and allophanate hydrolase (AtzF), involved in cleavage of the cyanuric acid to carbon dioxide and ammonia, which is assimilated as a nitrogen source (de Souza *et al.,* 1998a). García-González *et al.* (2003) have demonstrated that atrazine catabolism is induced under nitrogen-limited growth in a manner reminiscent of general nitrogen control in *Pseudomonas* sp. ADP.

The *atzABC* genes are constitutively expressed and are not regulated either by induction of atrazine or by repression of other N sources in this strain (Martínez *et al.,* 2001; Devers *et al.*, 2004). The *atzDEF* genes are divergently transcribed from AtzR, predicted to encode a transcriptional LysR-type regulator. A putative LTTR binding site can in fact be found upstream of *atzD* gene, thereby suggesting that transcription of the *atzDEF* operon may be regulated and the protein encoded by the *orf99* (AtzR) play a role in this regulation. The *atzDEF* operon resides in a contiguous cluster adjacent to the *orf99*, a potencial LysR-type transcriptional regulator (Martínez *et al.,* 2001).

In order to analyze the regulation of the expression of *atzDEF* genes, *atzD-lacZ* and *atzR-lacZ* transcriptions fusions were obtained, and the β-galactosidase assay was performed by García-González *et al.* (2005). Expression of the cyanuric acid degradation *atzDEF* operon is specifically induced by cyanuric acid. The AtzR regulator activates the expression of *atzDEF* operon in the presence of cyanuric acid and represses its own synthesis. The expression of the *atzR* gene was also induced by nitrogen limitation and repressed by AtzR. Nitrogen regulation of *atzD-lacZ* and *atzR-lacZ* expression was dependent on the alternative sigma factor σ^N and NtrC (activator of σ^N promoters), hence suggesting that the cyanuric acid degradation operon may be subject to general nitrogen control. However, *atzDEF* transcription appears to be driven by the major sigma factor σ^{70}, while *atzR* is transcribed from a σ^N dependent promoter. In fact, the *atzR-lacZ* was almost abolished in an *rpoN* (σ^N) mutant. Expression of *atzR* from a heterologous promoter revealed that although NtrC regulation of *atzD-lacZ* requires the AtzR protein, it is not the indirect result of NtrC-activated AtzR synthesis. AtzR activity is in turn modulated by the presence of cyanuric acid and by a nitrogen limitation signal transduced by the Ntr system. The mechanism for NtrC mediated activation of *atzDEF* expression has been not yet identified (García-González *et al.*, 2005). The effect of nitrogen on the herbicide degradation pathway is strongly relevant to the use of this strain in bioremediation, since many agricultural

fields are rich in nitrogen owing to routine fertilization.

Pseudomonas sp. ADP is able to degrade atrazine as a sole nitrogen source and can also grow using phenol as the carbon source. Genes encoding phenol degradation are located on its chromosome.

A multicomponent phenol hydroxylase converts phenol to catechol, which is further metabolized via *ortho* pathway using catechol 1,2-dioxygenase (Neumann *et al.*, 2004). The strain was stimulated to degrade high concentrations of phenol (1,000 mg l^{-1}) and atrazine (150 mg l^{-1}) simultaneously.
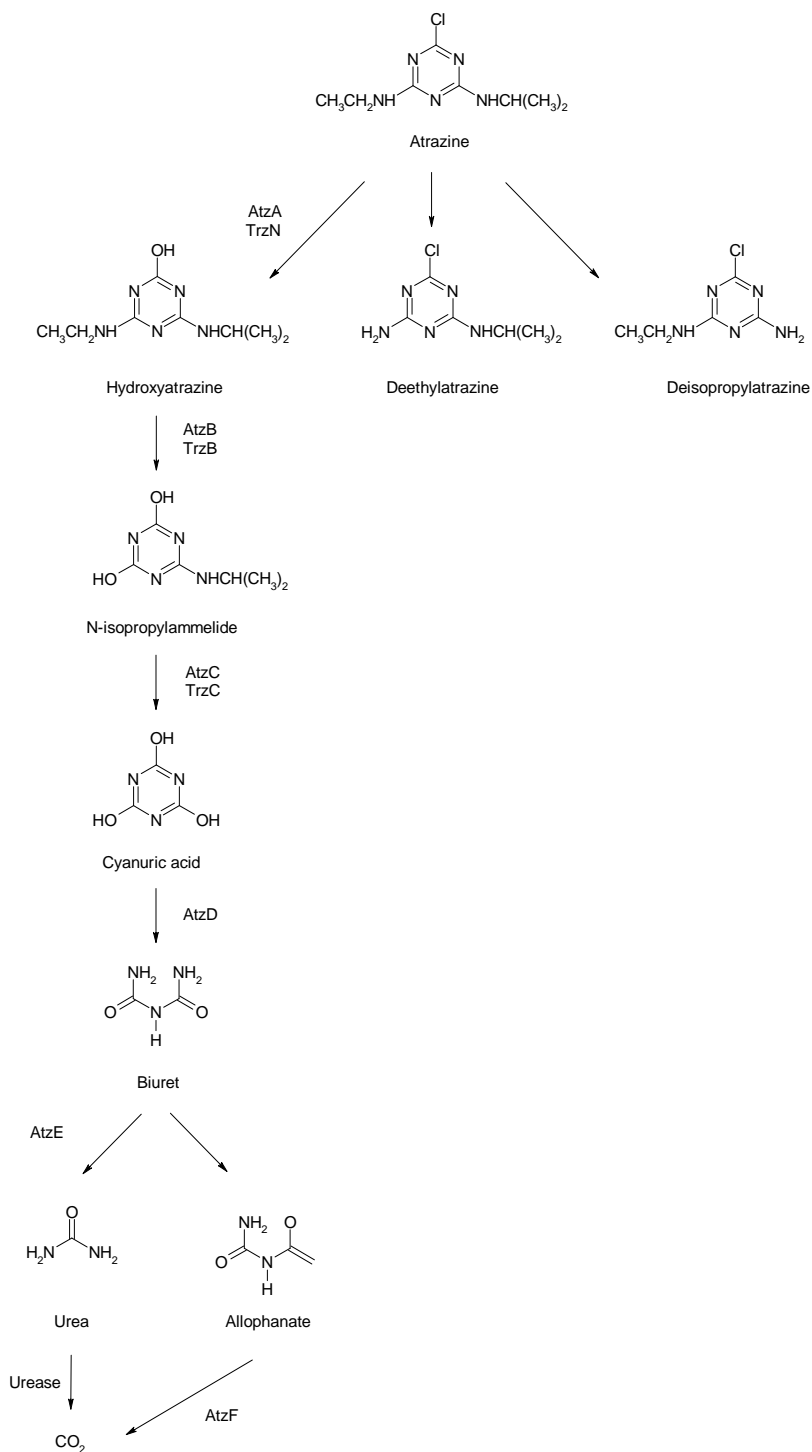

Figure 2 - Atrazine degradation pathways in bacteria

Whereas atrazine did not show any significant toxic effects on the cell, phenol reduced growth and activated or induced typical membrane-adaptive responses known for the genus *Pseudomonas,* just to name a few, changes in the fatty acid composition of membrane lipids and isomerization of *cis*-unsaturated fatty acids to trans-unsaturated fatty acids (Heipieper *et al.,* 1992; von Wallbrunn *et al.,* 2003). This showed that *Pseudomonas* sp. ADP could be usefully employed in the study on the regulatory interactions among the catabolic genes and stress response mechanisms during the simultaneous degradation of toxic phenolic compounds and a xenobiotic N source such as atrazine.

The ability to degrade atrazine by using the products of *atzABCDEF* is not an exclusivity of the *Pseudomonas* genus. Recently, a strain CDB21 was identified as a novel β-proteobacterium exhibiting 100% sequence identity with the uncultured bacterium HOCLCi25 (GenBank accession number AY328574). CDB21 also possesses the entire set of genes of atrazine degradation present in *Pseudomonas* (Iwasaki *et al.*, 2007). The nucleotide sequences of the *atzABCDEF* genes of strain CDB21 were 100% identical to those of *Pseudomonas* sp. ADP, which suggested a dispersal of the *atz* genes in the environment. According to this, studies revealed that *atzABC* genes were widespread, having been detected in Canada, U.S.A., France, Croatia and China, and were also highly conserved (>97% similarity) indicating their recent dispersion within soil microflora (de Souza, 1998a; Rosseaux *et al.*, 2001; Devers *et al.*, 2004).

Devers *et al.* (2005) demonstrated that the atrazine-degrading plasmid ADP1::Tn5 was transferred from *Agrobacterium tumefaciens* St96-4 to soil microflora at a frequency of 10^{-4} per donor cell. In two of the gram-negative transconjugants isolated, namely *Variovorax* sp. MD1 and MD2, the *atzA* and *atzB* genes had moved from pADP1::Tn5 to the chromosome. A recent study demonstrated for the first time the involvement of the insertion sequence *IS1071* in the transposition of catabolic genes (Devers *et al.,* 2007). These authors also suggested that *IS*-mediated transposition of the *atz* genes could also be indirectly involved. Indeed, such rearrangements led to diversification of the *atz* genetic supports and could contribute to increase the frequency of horizontal gene transfer (HGT) of the *atz* genes.

According to Ostrofsky *et al.* (2002), the gene *trzD*, present in *Pseudomonas* NRRLB-12228, was involved in s-triazinic ring cleavage, and was not dominant among atrazine degrading population in soil. The *Chelatobacter heintzii* Citl, that showed the capacity to mineralize up to 80% of atrazine in 14 days, possessed the atrazine degrading genes *atzABC* and *trzD* (Rousseaux *et al.*, 2003). According to Piutti *et al.* (2003), *Nocardioides* sp. SP12 utilized a different degradation pathway combining the genes *trzN*, which codified a chlorohydrolase, with *atzB* and *atzC*, leading to a product with the same characteristics as the cyanuric acid (Fig. 2). *Arthrobacter* sp. strain isolated from the rhizosphere of atrazine-resistant plant by Vaishampayan *et al.* (2007) utilized atrazine as the sole nitrogen source and harbours *atzBCD* and *trzN* on chromosomal DNA with high sequence similarity with *trzN* from *Nocardioides* sp. C190.

Little is known about the biodegradability of atrazine under anoxic and methanogenic conditions in soils. In anaerobic systems, atrazine is more resistant to degradation, with the half-life values varying from 160 to 330 days (Gu *et. al.*, 2003). However, *Pseudomonas* sp. ADP was shown to mineralize more than 50% of 2.8 μM atrazine within 14 days under both aerobic and denitrifying conditions (Clausen *et al.*, 2002). The bacterium M91-3 was able to use atrazine as the sole carbon and nitrogen source under anoxic conditions leading to hydroxytriazine and triazinic ring cleavage between C-2 and N. These results suggested a possible application of this bacterium in a fixed bed reactor for anaerobic removal of atrazine and nitrate from water (Crawford *et al.*, 1998).

In a laboratory scale system for the treatment of Danube river water, the main atrazine metabolite was hydroxyatrazine (Vargha *et al.*, 2005). Atrazine utilizing strains isolated from sediment showed diverse atrazine metabolism leading to ammeline and ammelide products. Because dealkylated and dechlorinated metabolites are more easily degraded than atrazine and hydroxyatrazine, subsequent mineralization could be performed by an adapted microbial consortium.

Atrazine degradation by microbial consortia
The biotic degradation of atrazine can follow several metabolic pathways that involve stepwise transformations mediated by single species or microbial consortia. Although several atrazine-

degrading bacteria have been isolated and their individual catabolic pathways extensively studied, the cooperative metabolism of atrazine is yet poorly described.

In a microbial consortium, after the dechlorination of atrazine by *Nocardia* sp., the resulting hydroxyatrazine was afterwards degraded in two different ways. In one of them, *Nocardia* sp. converted hydroxyatrazine to N-ethylammelide via an unidentified gene product, whereas in the other, hydroxyatrazine generated by *Nocardia* sp. was hydrolyzed to N-isopropylammelide by *Rhyzobium* sp., which contained the gene *atzB*. All the members of the consortium contained *atzC*, responsible for the cleavage of the ring, besides the gene *trzD*. However, none of the microorganisms showed to carry *atzD*, *E* or *F* genes (Smith *et al.*, 2005).

Kolic *et al.* (2007) characterized a four-member atrazine-mineralizing community enriched from an agrochemical factory soil, which was capable of rapidly mineralizing atrazine (approx. 78% of atrazine was released as $^{14}CO_2$ within 6 days). The analysis of the genetic potential of individual community members reveled that two *Arthrobacter* strains, named ATZ1 (carrying *trzN* and *atzC* genes) and ATZ2 (carrying *trzN*, *atzB* and *atzC* genes) might be involved in the upper pathway producing cyanuric acid, and that other two members, *Ochrobactrum* sp. CA1 and *Pseudomonas* sp. CA2 (both carrying *trzD* gene), were responsible for cyanuric acid catabolism.

The physical and chemical associations of microbial community members in biofilms lead to interactions at the genetic level intra and inter-species. Some bacteria in contaminated environments are in fact submitted to genetic events, such as transformation, transduction and conjugation, thus acquiring improved abilities to degrade hazardous substrates (Stoodley *et al.*, 2002). Perumbakkan *et al.* (2006) demonstrated that it was possible to modify the microbial biofilms through natural transformation in order to improve their biodegradation capabilities. These authors transformed biofilm communities with the gene *atzA* that encoded atrazine chlorohydrolase. Both kinds of biofilms communities, pure and soil-derived cultures, were transformed with *atzA* gene cloned in the broad host plasmid pBBR1NCSS, and all of them displayed the ability to degrade atrazine. These results suggested that the natural transformation should be useful as a tool to enhance bioremediation process performed by biofilms.

Atrazine degradation by fungi

The degradation of atrazine was also observed in fungi such as *Aspergillus fumigatus, Aspergillus ustus, Aspergillus flavipes, Rhizopus stolonifer, Fusarium moniliforme, Fusarium roseum, Fusarium oxysporum, Penicillium decumbens, Penicillium janthinellum, Penicillium rugulosum, Penicillium luteum, Trichoderma viride*. It proceeds through N-dealkylation of either alkylamino group; however, with qualitative and quantitative differences, leading to two main degradation products, deethylatrazine and deisopropylatrazine (Kaufman and Blake, 1970).

The potential of the white-rot fungi to perform *in situ* bioremediation has been ascribed to their ability to degrade a variety of xenobiotic chemicals via free radical mechanism mediated by extracellular peroxidases (Reddy, 1995). Degradation of atrazine by the white-rot fungus *Phanerochaete chrysosporium* was demonstrated by a 48% decrease of the initial herbicide concentration in the growth medium within the first 4 days of incubation. Results point out 25% mineralization of the ethyl group of the herbicide and the formation of hydroxylated and/or N-dealkylated metabolites; however, no mineralization of ring-14C-labeled atrazine was observed (Mougin *et al.*, 1994). In non-sterile soil samples amended with the same white-rot fungus in the presence of wood chips, atrazine was mineralized especially in summer, spring and fall (Entry *et al.*, 1996). *Pleurotus pulmonarius* is another lignocellulolytic fungus that has been found to degrade atrazine in liquid culture, producing mainly the N-dealkylated metabolites deethylatrazine, deisopropylatrazine and deethyl-deisopropylatrazine and the hydroxypropyl metabolite hydroxyisopropylatrazine (Masaphy *et al.*, 1993). In a solid medium based on a mixture of cotton and wheat straw, *P. pulmonarius* was not capable of mineralize the triazinic ring, being part of atrazine adsorbed to the straw, and another portion transformed into either chlorinated or dechlorinated atrazine metabolites, as the result of the activity of both the fungus inoculated and the natural bacterial population (Masaphy *et al.*, 1996a). Manganese concentrations up to 300 µM enhanced atrazine transformation by this fungus with accumulation of both N-dealkylated and

propylhydroxylated metabolites, probably due to an increase in non specific oxidative activities involved in the transformation of xenobiotic compounds (Masaphy et al., 1996b).

Strategies for microbial removal of atrazine

The technique of bioaugmentation, that is, addition of natural microbial strains or genetically engineered variants to decontaminate polluted soil, is a strategy often utilized when low biodegradation is detected in the contaminated site. Rousseaux et al. (2003) observed that the introduction of 10^4 UFC g^{-1} of *Chelatobacter heintzii* Cit1 in soil poorly mineralizing atrazine resulted in a 3-fold increase in such a capacity. Gupta & Baummer (1996) studied the effect of poultry litter, commonly applied to the soil as manure before the utilization of atrazine, on the biodegradation of atrazine and verified that the rate of atrazine removal in soil was two times faster than without the litter; nutrients (mainly nitrates and phosphates) present in litter did not play any role in the degradation of atrazine.

In a field-scale remediation study of a soil contaminated by an accidental spill of atrazine (up to 29,000 ppm), bioaugmentation was performed using a killed and stabilized whole-cell suspension of recombinant *E. coli* engineered to overproduce atrazine chlorohydrolase, AtzA. After eight weeks, atrazine levels declined by 52% in plots containing killed recombinant *E. coli* cells, whereas 77% biostimulation was detected in plots that received 300 ppm of phosphate (Strong et al., 2000). Cell-free crude extracts from *Pseudomonas* sp. ADP containing the enzymes that catalyzed atrazine degradation were entrapped in sol-gel glass; however, there was a significant loss of activity in comparison with the non-entrapped crude extract (Kauffmann & Mandelbaum, 1996). This strategy could be only a promising alternative for the bioremediation of atrazine, since the consequences of release of engineered live cells to the environment are already unknown.

Bioaugmentation with *Pseudomonas* sp. ADP together with citrate or succinate biostimulation markedly increased atrazine mineralization in a soil that had an indigenous potential for atrazine biodegradation (e.g., addition of 11.6 mg of citrate per g of soil increased mineralization of 337.4 µg of atrazine per g of soil from < 2 to 79.9% in 13 days) (Silva et al., 2004). Cellulose substantially stimulated atrazine side-chain dealkylation by soil microflora in comparison with other carbon-

containing substrates, being the rate and extent of mineralization of the ethylamino side chain significantly accelerated by a decrease in the C/N ratio of the amendment. Glucose release or a transient production of glucose as an end-product of cellulose depolymerization might induce the catabolic repression of dealkylation enzyme systems and be responsible for a decrease in the atrazine side-chain mineralization (Yassir et al., 1998). The biodegradation of atrazine by an anaerobic mixed culture was higher in co-metabolic process than in the absence of external carbon source or carbon and nitrogen source (first-order degradation rates of 5.5×10^{-4}, 2.5×10^{-5} and 1.67×10^{-5} day^{-1} respectively), being maximum atrazine degradation observed in a medium composed of 300 mg l^{-1} of dextrose and 5 mg l^{-1} of atrazine.

As most atrazine-degrading bacteria use this herbicide as a nitrogen source, the presence of preferential nitrogen sources in the environment is detrimental to atrazine degradation. Nitrogen amendments were in fact shown to decrease atrazine degradation rates by *Pseudomonas* sp. ADP (Clausen et al., 2002; García González et al., 2003). In fungi, nitrogen suppressed mineralization of atrazine but stimulated the primary growth, thereby suggesting that N could alter the microbial processes and C uptake and thus influence the rates of herbicide degradation (Entry et al., 1993).

In rhizosphere soil, an increased degradation of xenobiotic compounds may result from co-metabolic processes enhanced by organic substances originating from roots exudates with an overall increase in microbial activity (Fang et al., 2001). Atrazine was degraded faster in contaminated soil planted with Pennisetum (*Pennisetum clandestinum*) than in unplanted soil, corresponding to nearly 45 and 22% respectively within 80 days (Singh et al., 2004b). Contrarily, it was not so for atrazine degradation in grass rhizosphere (Fang et al., 2001).

Final remarks

This review highlights the main microbial aspects of atrazine degradation, focusing its catabolism by indigenous and engineered microorganisms as well as the effects resulting from biostimulation and bioaugmentation. An overview of these aspects reveals that the complete mineralization of atrazine is possible as a result of the microbial activity. Since a deep knowledge of the microbial

activity and its implementation in the engineering area are the basis for the expansion of the use of bioremediation systems, the remediation of natural environments contaminated with this herbicide is expected to be accomplished in the near future.

RESUMO

A prática mundial do uso de agroquímicos por períodos extensos, de maneira indiscriminada e abusiva, tem mobilizado as autoridades envolvidas em saúde pública e sustentabilidade de fontes naturais, como uma conseqüência da contaminação ambiental. Agroquímicos referem-se a uma ampla variedade de inseticidas, fungicidas e herbicidas, entre estes a atrazina, um herbicida intensivamente usado em culturas de cana-de-açúcar, milho, sorgo, entre outros. Pesquisadores têm demonstrado que a atrazina tem efeitos tóxicos em algas, plantas aquáticas, insetos aquáticos, peixes e mamíferos. Devido à toxicidade e à persistência da atrazina no ambiente, a busca de linhagens microbianas capazes de degradá-la é fundamental para o desenvolvimento de processos de biorremediação, com uma ferramenta corretiva para solucionar problemas decorridos do uso irracional de agroquímicos. Esta revisão relata os principais aspectos microbianos e pesquisas da degradação da atrazina por espécies microbianas isoladas e consórcio microbiano, bem como avanços no desenvolvimento de técnicas para remoção microbiana da atrazina no ambiente natural.

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