

Biodiversity of the atrazine chlorohydrolase (*atzA*) gene in soil microbial communities as a function of triazine treatment history

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s-Triazines are the most widely used pesticides globally and are moderately persistent and mobile in soils. They are the most commonly detected pesticides in surface and ground water as well as in precipitation. *s*-Triazines are carcinogenic and believed to act as endocrinedisruptors. Due to their widespread use and frequent detection in the environment, there is ongoing concern regarding their impact on human and ecosystem health. The catabolic genes *atzABC* and *trzD* in the degradative pathway of atrazine, a widely used chloro-*s*-triazine, are highly conserved (99 to 100% sequence identity for *atzA*) in all known atrazine-degrading bacteria (approximately six bacterial cultures). While *atzA* has been detected in soils with a high capacity to degrade atrazine it is not known if indigenous soil bacteria responsible for mediating atrazine biodegradation possess these genes or closely related homologs. The purpose of this study was to develop a PCR method based on primers derived from *atzA* of *Pseudomonas* ADP that could be used to monitor the frequency of *atzA* in agricultural soils with the long term goal of investigating the diversity of *atzA* PCR products with denaturing gradient gel electrophoresis (DGGE). Genomic DNA was extracted and purified from agricultural soil with a long-term atrazine exposure history and high capacity to degrade atrazine. A PCR method was developed that could amplify *atzA* homologs from soils but it suffered from a high detection limit based on experiments with *atzA*-amended soils. Our preliminary results suggest that the frequency of *atzA* in the soils we examined is low and atrazine degradation is mediate by an alternate pathway or by homologs of *atzA* that were not detectable by our PCR assay. However, optimization of the method to lower the detection limit must be made before further gene diversity studies can proceed.