Spatial Distribution of Enhanced Atrazine Degradation across Northeastern Colorado Cropping Systems

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Reports of enhanced atrazine degradation and reduced residual weed control have increased in recent years, sparking interest in identifying factors contributing to enhanced atrazine degradation. The objectives of this study were to (i) assess the spatial distribution of enhanced atrazine degradation in 45 commercial farm fields in northeastern Colorado (Kit Carson, Larimer, Logan, Morgan, Phillips, and Yuma counties) where selected cultural management practices and soil bio-chemo-physical properties were quantified; (ii) utilize Classification and Regression Tree (CART) Analysis to identify cultural management practices and (or) soil bio-chemo-physical attributes that are associated with enhanced atrazine degradation; and (iii) translate our CART Analysis into a model that predicts relative atrazine degradation rate (rapid, moderate, or slow) as a function of known management practices and (or) soil properties. Enhanced atrazine degradation was widespread within a 300-km radius across northeastern Colorado, with approximately 44% of the fields demonstrating rapid atrazine degradation activity (laboratory-based dissipation time half-life [DT_{50}] < 3 d). The most rapid degradation rates occurred in fields that received the most frequent atrazine applications. Classification and Regression Tree Analysis resulted in a prediction model that correctly classified soils with rapid atrazine DT_{50} 80% of the time and soils with slow degradation (DT_{50} > 8 d) 62.5% of the time. Significant factors were recent atrazine use history, soil pH, and organic matter content. The presence/absence of *atzC* polymerase chain reaction (PCR) product was not a significant predictor variable for atrazine DT_{50}. In conclusion, enhanced atrazine degradation is widespread in northeastern Colorado. If producers know their atrazine use history, soil pH, and OM content, they should be able to identify fields exhibiting enhanced atrazine degradation using our CART Model.

ATRAZINE [2-chloro-4-(ethylamino)-6-(isopropylamino)-s-triazine] is a widely used soil-applied herbicide for controlling many broadleaf weeds in corn (*Zea mays* L.), grain sorghum (*Sorghum bicolor* L.), and sugarcane (*Saccharum officinarum* L.). This herbicide is the basis for many weed management programs in these crops and farmers depend on atrazine to provide season-long residual control. However, enhanced atrazine degradation in soil from fields that have a history of atrazine use has been reported (Houot et al., 2000; Zablotowicz et al., 2006; Krutz et al., 2007, 2008a; Shaner and Henry, 2007; Bridges et al., 2008). Consequences of rapid atrazine degradation have also been noted. For example, farmers and extension agents in Colorado and Mississippi have reported a loss of residual weed control following atrazine application in corn (Shaner and Henry, 2007; Krutz et al., 2007, 2008a; Bridges et al., 2008).

Enhanced atrazine degradation is due to the selection of soil microorganisms that can utilize atrazine as a N and/or C source. A wide range of atrazine-degrading bacteria have been isolated from soils across the world and the enzymes and their corresponding genes have been elucidated and studied (Krutz et al., 2010). The widespread distribution of *atzABC* genes has been used to monitor for the presence of atrazine-degrading microbes in the soil via polymerase chain reaction (PCR) analysis of DNA extracted from the soil (Shapir et al., 2000; Martin-Laurent et al., 2003; Krutz et al., 2008b). Shapir et al. (2000) determined the copies of the *atzA* gene g^{-1} soil using a magnetic capture hybridization method in combination with nested PCR to detect very low copy numbers of the gene. They could detect *atzA* in most of the soils they tested, but the initial number was correlated with the atrazine use history of the field. In atrazine-enriched soils, they could also detect *atzB* and *atzC*. Krutz et al. (2008b) could amplify *atzBC* genes from atrazine-adapted soils from Mississippi and Colorado but could not produce a positive response in whole soil DNA analysis from nonadapted soils from either state. Martin-Laurent et al. (2003), using a quantitative competitive PCR assay, found that *atzC* transitorily increased in

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