Identifying the Microbial Mechanisms responsible for Accelerated Degradation

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Introduction
• Following the repeated application of some pesticides to soil, their rate of dissipation has been shown to increase
• This phenomenon is termed accelerated degradation (AD) and microorganisms are often implicated
• AD has implications for the fate of pesticides in the environment

Aims
1. To determine if AD can occur at agriculturally relevant levels in pesticide naive soils
2. To explore the microbial mechanisms that may be responsible for the phenomena;
   2a. Increase in microbial activity
   2b. Changes in the structure of the bacterial community
   2c. Capacity for atrazine degradation

Methods
• Atrazine was selected as the model compound as its degradation by microorganisms is well established (Shaner et al., 2007)
• Dissipation of atrazine has been tracked over three atrazine applications of 6 mg kg⁻¹ in two soils using HPLC-UV
• One of the soils was set aside & the other under traditional agricultural practice. Both soils had similar properties & were naive to atrazine & its homologs
• ATP was used as an approximate measure of microbial activity (Nannipieri et al., 1990)
• Bacterial community structure was analysed in great depth, by applying 454 pyrosequencing of the variable 3-5 regions of the bacterial 16S rRNA gene
• The capacity for atrazine degradation was assessed by using amplified known atrazine degrading genes using the polymerase chain reaction (PCR)

1. Atrazine dissipation increased in naive soils at agriculturally relevant levels

• The rate of atrazine dissipation increased significantly from the first to the third application (t-test, p<0.05; DT50 17.3 to 1 days) (figure 1).

2a. The increase in atrazine dissipation is not due to an increase in total microbial activity

• Soil sub-samples over three atrazine applications did not have significantly different ATP levels (t-test, p>0.3).
• Indicating microbial activity across the experiment was fairly consistent, and is not responsible for the increased dissipation of atrazine (fig. 1).

2b. Several bacterial taxa have responded positively to atrazine applications

• Members of the Betaproteobacteria, Chloracidobacteria, MC47, SOGA31 and Xanthomonadaceae are found in significantly higher relative abundance in atrazine treated soils, compared to controls.

Conclusions
1. Accelerated degradation of atrazine has been demonstrated to occur at agriculturally relevant levels in naive soils
2a. ATP levels indicate microbial activity was constant throughout the experiment
2b. Several groups of bacteria were found at significantly higher abundance in the presence of atrazine
2c. Both soils have the genes known to confer the capacity to degrade atrazine
• In combination this study suggests that the bacterial communities in these soils, have responded to atrazine by proliferation of specific degraders (figure 3) that have the capacity to resist or degrade atrazine (table 1).

Future work
• Monitor the abundance of the atrazine degrading genes over repeated atrazine applications
• Identity which bacterial taxa contain the atrazine degrading genes & whether this changes between applications
• Determine the presence of the atrazine metabolites

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