



## Bacterial community structure in atrazine treated reforested farmland in Wuying China



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### ABSTRACT

The Grain for Green (GFG) Project in China is currently the largest environmental rehabilitation project aimed at turning low-yielding farm land to forests and pastures. Such conversion of land use type also promotes remediation of the polluted environment. Soil microbes reflect soil function and are therefore considered an essential component of ecosystem restoration. To evaluate the environmental effects of converting atrazine polluted farmland to secondary forest, we determined soil chemical properties, soil bacterial communities and their responses to three types of land use (primary forest, PF; secondary forest, SF; farm land, FL) in Wuying, China. Our results showed that soil organic matter significantly decreases in the order PF > SF > FL. Bacterial 16S rRNA gene 454 pyrosequencing revealed that the soil bacterial diversity level remained unchanged. However between FL and the two forested sites, we observed an increase of Actinobacteria,  $\beta$ -proteobacteria and Firmicutes; and a decrease of Acidobacteria and Verrucomicrobia, while in SF the bacterial community structure was similar to PF. We conclude that reforestation permits bacterial community, resetting from FL back to a state that resembles natural conditions. In addition, 20 years of natural attenuation degraded soil atrazine residues in SF but traces remained in the soil. Reforestation generally resulted in favorable ecological impacts on soil quality and the bacterial community compared with active farm fields.

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### 1. Introduction

In 1999, the Chinese government launched the Grain for Green (GFG) Project, a state campaign to restore ecological balance by returning low-yielding farmland to forests and pastures. With a budget of approximately 40 billion US dollars and a targeted area of 146 700 km<sup>2</sup>, GFG is one of the largest environmental rehabilitation projects in the world, and has drawn much attention both in China and internationally (Uchida et al., 2005; Qiu et al., 2011).

Microbes perform most of the biogeochemical functions in soil and are therefore considered an essential component of ecosystem restoration (Harris et al., 2009). On the other hand, the structure of the soil microbial community is significantly influenced by many factors, such as ground vegetation (Carney and Matson, 2006), land use (Jangid et al., 2008), soil properties (Fierer and Jackson, 2006; Rajaniemi and Allison, 2009; Bach et al., 2010), etc., Agricultural

practices, such as the use of fertilizers and pesticides, greatly alter soil characteristics (Matson et al., 1997). Atrazine, 2-chloro-4-ethylamino-6-isopropylamino-s-triazine, is widely used in China to control broad-leafed weeds, and it may cause pollution of the environment due to its high mobility and persistence in soil and water (Wang et al., 2010). Furthermore, atrazine is harmful to many organisms and to human health (dos Santos and Martinez, 2014). Residues of atrazine and its metabolites have been detected in the soil, surface water and groundwater of agricultural areas years after application (Zaya et al., 2011). Thus, despite reestablishment of forests, atrazine may persist in formerly farmed soils for a long time. Few attempts have been made to assess the residual concentrations and effects of atrazine in a conserved secondary forest, especially the influence of atrazine residues on the soil microbial community.

Studies of the effects of the GFG Project on microbial ecology have not been exhaustive. Soil microbial diversity and community composition are important indicators of soil health, which is influenced by factors such as pH, nutrients, organic matter and the application of chemical additives (Smith et al., 2000; Kennedy and

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