



Review

Do genetically modified plants affect adversely on soil microbial communities?

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ABSTRACT

With the increase in the number of commercial applications and larger cultivation areas of genetically modified (GM) plants, their biosafety for soil microorganisms has become a controversial issue. The effects on the diversity and abundance of soil microorganisms are important components of evaluation of the biosafety risks of GM plants. So far, no definite conclusions have been drawn about whether GM plants can negatively affect soil microorganisms. In this review, we discuss the advances that have been made in recent years in the research into the effects of GM plants on soil microbial communities. It has been argued that foreign gene products that are released from the residue of GM plants into soil by root exudation may affect soil microbial communities. Moreover, foreign genes may change the genetic and functional properties of soil microorganisms via horizontal transfer. The advantages and disadvantages of various detection technologies—from classical culture-dependent methods to modern molecular protocols—are reviewed here. To accurately and comprehensively evaluate the effects of GM plants on microorganisms, we discuss the factors that should be considered in the assessment of risks of GM plants for soil microorganisms (e.g., foreign proteins, marker genes, plant varieties, and environmental factors), as well as the problems and prospects related to biosafety assessment platforms for GM plants.

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Abbreviations: AMV, alfalfa mosaic virus; ARDRA, amplified ribosomal DNA restriction analysis; ARISA, automated ribosomal intergenic spacer analysis; Bt, *Bacillus thuringiensis*; CaMV, cauliflower mosaic virus; CFUs, colony-forming units; CLPP, community-level physiological profile; DGGE, denaturing gradient gel electrophoresis; FISH, fluorescence in situ hybridization; GM, genetically modified; GFP, green fluorescent protein; NGS, next generation sequencing; PRSV, papaya ringspot virus; PLFAs, phospholipid fatty acids; RT-PCR, real-time PCR; RFLP, restriction fragment length polymorphism; RISA, ribosomal intergenic spacer analysis; T-RFLP, terminal restriction fragment length polymorphism.

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1. Introduction

Microorganisms, an important component of soil, play a major role in ecosystem processes such as substance transformation and energy exchange. Moreover, the abundance and diversity of microbial communities are important indicators of dynamic changes in soil ecosystems (Powell et al., 2015; van der Heijden et al., 2008a, 2008b, 2008c). Soil microorganisms are the link between soil and plants, integrating these two systems. In the soil, because the rhizosphere is a special ecological environment, the abundance and diversity of soil microorganisms in the rhizosphere are far higher than those in non-rhizosphere soils (Filion, 2008). Plant–microorganism interactions in the rhizosphere soil are a major factor in the regulation of plant growth and development. Variations in root exudate composition and abundance may alter soil microbial biodiversity and activity as well as have different effects on harmful or beneficial microbes (Icoz and Stotzky, 2008).

The foreign genes in genetically modified (GM) plants express new traits that can increase the commercial value of their specific functions and applications (Halford and Shewry, 2000; Wolfenbarger and Phifer, 2000). The success of GM plants highlights the progress that researchers have made in transforming nature; however, with the increased numbers of commercial applications and larger cultivation areas, the environmental safety of GM plants has been receiving increasing attention (Andow and Zwahlen, 2006). Since the commercialization of GM plants, many scientists have assessed their ecological risks (Icoz and Stotzky, 2008; Kos et al., 2009; Liu, 2010; Velkov et al., 2005; Velkov et al., 2005). Studies have shown that the physiological and metabolic changes in GM plants and the release of their foreign expression products (e.g., Bt protein) into the soil ecosystem might impact soil microbial diversity (Hannula et al., 2014; Liu et al., 2005; Sanahuja et al., 2011; Sanchis, 2010).

The effects on the diversity and abundance of soil microbial communities are important factors in the evaluation of the biosafety risks of GM plants (Kolseth et al., 2015; Turrini et al., 2015; Wolfenbarger and Phifer, 2000). On the basis of related previous reviews, in this paper, we focus on the recent advances in the understanding of the effects of GM plants on soil microbial communities and in the applied researches and detection technologies in related to analysis those effects. Factors to be considered in the assessment of risks of GM plants for soil microorganisms are proposed, and the problems and prospects of a biosafety assessment platform for GM plants are discussed.

2. Mechanisms underlying the effects of GM plants on soil microorganisms

GM plant residues in soils are present in two forms—foreign genes and their products—that may influence soil microbial communities through the following two pathways.

2.1. Effects of foreign gene products on soil microorganisms

In a farmland ecosystem, the roots of GM plants inevitably interact with microbes in the soil. Foreign and native proteins (e.g., new proteins produced after induction of changes in a catabolic pathway) released from GM plants into the soil via root exudation may have effects on soil microbial communities (Giovannetti et al., 2005). Due to the activities of GM proteins and promoters, foreign genes in GM plants can directly influence soil microbial communities, for example, by changing certain functional microorganism groups or soil biodiversity. The expression of insecticidal crystal proteins in plants is a representative case of accumulation and persistence of GM products in the soil. Studies have shown that after entering soils, Bt protein rapidly binds to soil clay and humic acid. Bound Bt protein retains its insecticidal activity for 234 days and is not easily broken down by soil microorganisms (Zwahlen et al., 2003). This activity of Bt toxin is retained and sometimes enhanced by adsorption and binding to clay (Tapp and Stotzky, 1995). Small amounts of Bt toxin, which are similar to the commercial microbial Bt formulations, produced in GM plants may persist in soil for several weeks or months (Strain and Lydy, 2015). Persistent low levels of Bt toxin may affect some non-target organisms and repeated use of Bt-producing plants may cause toxin accumulation (Palm et al., 1996).

2.2. Effects of horizontal gene transfer (HGT) on soil microorganisms

Foreign genes can be integrated into the genomes of soil microorganisms via horizontal transfer, resulting in changes in the genetic and functional properties of soil microorganisms. The likelihood of gene transfer from transgenic plants to microorganisms is dependent on the transgene copy number and on the presence of homologous sequences for recombination (Demaneche et al., 2011). Soil contains an active gene bank comprising extracellular DNA, from which some microorganisms can obtain necessary foreign DNA under conditions of environmental stress. After entering the soil gene bank, foreign DNA may become a part of the gene transfer chain, for example via transformation,

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