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Soil microbial biomass and root growth in Bt and non-Bt cotton

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The introduction of transgenic Bacillus thuringiensis (Bt) cotton (Gossypium hirsutum L.) has had a substantial impact on pest management in the cotton industry. While there has been substantial research done on the impact of Bt on the above-ground parts of the cotton plant, less is known about the effect of Bt genes on below ground growth of cotton and soil microbial biomass. The aim of this research was to test the hypothesis that Bt [Sicot 80 BRF (Bollgard II Roundup Ready Flex®)] and non-Bt [Sicot 80 RRF (Roundup Ready Flex®)] transgenic cotton varieties differ in root growth and root turnover, carbon indices and microbial biomass. A field experiment was conducted in Narrabri, north-western NSW. The experimental layout was a randomised block design and used minirhizotron and core break and root washing methods to measure cotton root growth and turnover during the 2008/09 season. Root growth in the surface 0-0.1 m of the soil was measured using the core break and root washing methods, and that in the 0.1 to 1 m depth was measured with a minirhizotron and an I-CAP image capture system. These measurements were used to calculate root length per unit area, root carbon added to the soil through intra-seasonal root death, carbon in roots remaining at the end of the season and root carbon potentially added to the soil. Microbial biomass was also measured using the ninhydrin reactive N method. Root length densities and length per unit area of non-Bt cotton were greater than Bt cotton. There were no differences in root turnover between Bt and non-Bt cotton at 0-1 m soil depth, indicating that soil organic carbon stocks may not be affected by cotton variety. Cotton variety did not have an effect on soil microbial biomass. The results indicate that while there are differences in root morphology between Bt and non-Bt cotton, these do not change the carbon turnover dynamics in the soil.