

Abstract

This study was conducted with the aim of determining the impact of genetically modified (GM) cotton on the diversity of below ground fauna. The entomopathogenic nematode, *Steinernema kariii* infectivity to the larvae of the wax moth was also used to determine the effect of *Bacillus thuringiensis*-cotton protein endotoxin on below ground biodiversity. Soils from the confined field trial area had a diverse fauna that included Hemiptera, Hymenoptera, Coleoptera, spiders, wireworms and chaffer grubs. Cotton containing Bt series, non Bt cotton and kenaf were grown in pots under confined conditions and uprooted at flowering stage. Soils from the rhizosphere (soils that adhered to the roots) were tested for the presence of Bt endotoxin using the Quick Stix Comb strip method and were found to be positive for the endotoxin even within non Bt treatments. Those soils were then inoculated with *S. kariii* and fifth instar larvae of the wax moth, *Galleria mellonella* in the laboratory. Cadavers of *Galleria* larvae were recovered from the soils over a period of 10 days and dissected to confirm the cause of mortality. Data was transformed using $\text{SQRX} + 1$, subjected to Analysis Of Variance (ANOVA) and means separated using LSD. Results from the study showed that there were no significant differences between treatments. *Galleria* larva mortality due to *S. kariii* infections were 64%, 63%, 61% and 50% for HART89M, sterilized soil, Bt cotton and Isoline treatments respectively. A number of false positives were recorded during the experiment for the Bt toxin implying that further refinement of the Quick Stix comb strip technique is required.