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Metagenomic Assessment of the Effects of Genetically Modified Crops on Microbial Ecology and Physicochemical Properties of Soil

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Abstract : Genetically modified crops are already phenomenally successful and are grown worldwide in more than eighteen countries on more than 67 million hectares. Nigeria, in October 2018, approved Bacillus thuringiensis (Bt) cotton and maize; therefore, the need to carry out environmental risk assessment studies. A total of 15 4L octagonal ceramic pots were filled with 4kg of soil and placed on the bench in 2 rows of 10 pots each and the 3rd row of 5 pots, 1st-row pots were used to plant GM cotton seeds, while the 2nd-row pots were used for non-GM cotton seeds and the 3rd row of 5 pots served as control, all in the screen house. Soil samples for metagenomic DNA extraction were collected at random and at the monthly interval after planting at a distance of 2mm from the plant's root and at a depth of 10cm using a sterile spatula. Soil samples for physicochemical analysis were collected before planting and after harvesting the GM and non-GM crops as well as from the control soil. The DNA was extracted, quantified and sequenced; Sample 1A (DNA from GM cotton Soil at 1st interval) gave the lowest sequence read with 0.853M while sample 2B (DNA from GM cotton Soil at 2nd interval) gave the highest with 5.785M, others gave between 1.8M and 4.7M. The samples treatment were grouped into four, Group 1 (GM cotton soil from 1 to 3 intervals) had between 800,000 and 5,700,000 strains of microbes (SOM), Group 2 (non GM cotton soil from 1 to 3 intervals) had between 1,400,600 and 4,200,000 SOM, Group 3 (control soil) had between 900,000 and 3,600,000 SOM and Group 4 (initial soil) had between 3,700,000 and 4,000,000 SOM. The microbes observed were predominantly bacteria (including archaea), fungi, dark matter alongside protists and phages. The predominant bacterial groups were the Terrabacteria (Bacillus funiculus, Bacillus sp.), the Proteobacteria (Microvirga massiliensis, sphingomonas sp.) and the Archaea (Nitrososphaera sp.), while the fungi were Aspergillus fischeri and Fusarium falciforme. The comparative analysis between groups was done using JACCARD PERMANOVA beta diversity analysis at P-value not more than 0.76 and there was no significant pair found. The pH for initial, GM cotton, non-GM cotton and control soil were 6.28, 6.26, 7.25, 8.26 and the percentage moisture was 0.63, 0.78, 0.89 and 0.82, respectively, while the percentage Nitrogen was observed to be 17.79, 1.14, 1.10 and 0.56 respectively. Other parameters include, varying concentrations of Potassium (0.46, 1,284.47, 1,785.48, 1,252.83 mg/kg) and Phosphorus (18.76, 17.76, 16.87, 15.23 mg/kg) were recorded for the four treatments respectively. The soil consisted mainly of silt (32.09 to 34.66%) and clay (58.89 to 60.23%), reflecting the soil texture as silty – clay. The results were then tested with ANOVA at less than 0.05 P-value and no pair was found to be significant as well. The results suggest that the GM crops have no significant effect on microbial ecology and physicochemical properties of the soil and, in turn, no direct or indirect effects on human health.