Characterization of soil bacteria capable of degrading selected organic pesticides applied in horticultural farms in Kenya

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A thesis submitted in partial fulfillment for the degree of Master of Science in Biotechnology in the Jomo Kenyatta University of Agriculture and Technology

2011

ABSTRACT

Pesticide use has been one of the major factors in improving productivity in agricultural enterprises. Pesticide residues in food and drinking water when ingested affect human health while ecosystems are also affected through loss of biodiversity. The aim of the research was to survey pesticide usage in farms under horticultural production, isolate bacterial strains, evaluate their biodegradation potential of selected pesticides, characterize the bacteria isolates morphologically, biochemically and molecularly. A survey in four horticultural regions of central and rift-valley Kenya showed that out of the twenty two (22) formulations of organophosphorus pesticides used by farmers diazinon had the highest proportion of application at 45.9%., followed by dimekill at 18.9% and least in application was brigade at 5.5%. Linuron was mostly applied with an 18.1% proportion of application followed by isoproturon at 13.2% and the least in proportion of application was Neprapamide at 2.7%. Through enrichment cultures total of thirty one (31) isolates were obtained from diazinon and linuron contaminated soils of which thirteen (13) isolates had the ability to degrade linuron while eighteen (18) isolates could degrade diazinon. Degradation of the pesticides was monitored by High pressure liquid chromatography (HPLC). Bacterial isolates had significant levels ($P<0.05$) of the pesticides degradation. Isolate DJk-4A was the best diazinon degrader at 95.8% degradation followed by isolate DKi-6A at 93.66% while isolate DLoG-8A was the third best degrader at 92.75%. Isolates LJk-5C had the highest level of linuron degradation at 99.36% followed by LWa-2A at 98.94% and the third best degrader was isolate LWa-2C at 95.54%. Identification of various degradation intermediate metabolites was aided by GC-MS analysis. Diversity of the isolates was assessed through DNA sequencing and BLAST search. Phylogenetic analysis of the 16S rRNA gene sequences showed diazinon degraders clustered into six genera namely; *Paracoccus*,

staphylococcus, Pseudomonas, Enterobacter, Klebsiella and *Proteus.* Isolates DJk-4A clustered with *Pseudomonas sp* with a 97% sequence similarity to Pseudomonas *pituda.* Isolate DKi-6B clustered with *Staphylococcus sp* with a sequence similarity of 99% to *Stapylococcus xylosus* while isolate DLoG-8A had a 98-% sequence similarity to *Paracoccus sp.* Linuron degrading isolates clustered into eight genera namely; *Myroides, Lysinibacillus, Arthrobacter, Stenotrophomonas, Burkholderia, Xanthomonas, Pseudomonas* and *Enterobacter*. Isolate LWa-2A was positioned among *Arthrobacter sp* with a 97% identity to *Arthrobacter globiformis.* Isolate LWa-2C clustered with *Burkholderia sp* with a 99% sequence identity with *Burkholderia cepacia.* Isolate LJk-5C clustered with *pseudomonas sp* with a sequence similarity of 98% to *pseudomonas migulae.*

The study showed that isolates from the genera *Pseudomonas, Staphylococcus, Paracoccus, Arthrobacter and Burkholderia* could be used to remediate diazinon and linuron contaminated soils under horticultural production. Further studies should be done to identify and characterize proteins involved in the biodegradation activities of these pesticides.