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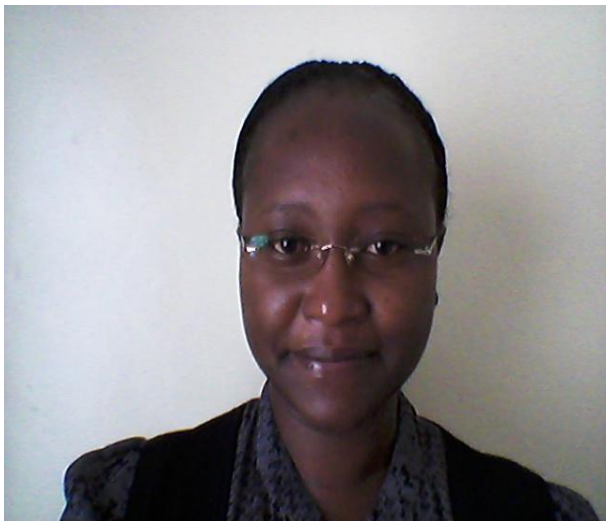

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Research Interests

Crop protection (nematodes) and risk assessment of the effect of genetically modified crops on nematodes.

Publications in Journals:

1. Maina, S., **Karuri, H.** and Ngend'o, R. **2020**. Nematode metabolic footprints, ecological and functional indices in tropical maize-beans agro-ecosystems under different farming practices. *Acta Oecologica* 108: 103622
2. Maina, H., **Karuri, H.**, Rotich, F. and Nyabuga, F., **2020**. Impact of low-cost management techniques on population dynamics of plant-parasitic nematodes in sweet potato. *Crop Protection* 137:105311.
3. Maina S., **Karuri H.**, and Ng'endo RN., (**2019**). Nematode soil food webs in maize agro-ecosystems and their implication on plant-parasitic nematodes. *Phytoparasitica*. https://doi.org/10.1007/s12600-019-00769-4
4. Namu, J., Alakonya, A., **Karuri, H.**, Nyaga, J., Masanga, J. Njeri, Editah. (**2019**). Response of Selected Kenyan Rice Cultivars to Infection by Root Knot Nematode (*Meloidogyne incognita*). *J. Crop Sci. Biotech*. 2019 (March) 22 (1) : 47 ~ 54
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9. **Karuri, H.W.**, Amata, R., Amugune, C.N. and Waturu, C.N. **2013**. Reproduction of root knot nematode (*Meloidogyne icognita*) on Bt cotton expressing Cry1Ac and Cry2Ab2 protein. Journal of Applied Biosciences 69:5487-5495.
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11. **Karuri, H.W.**, Amata, R., Amugune, C.N. and Waturu, C.N. **2013**. Nematode diversity in soil from a field trial with decomposing Bt cotton expressing Cry1Ac and Cry2Ab2 protein. Spanish Journal of Agricutural Research, 11:968-979.
12. **Karuri, H.W.**, Amata, R., Amugune, C.N. and Waturu, C.N. **2013**. Effect of transgenic cotton expressing Cry1Ac and Cry2Ab2 protein on entomopathogenic nematodes, *Steinernema karii* and *Heterorhabditis bacteriophora*. African Journal of Agricultural Research, 8:4280-4284.
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17. **Karuri, H.W.**, E.M. Ateka, R. Amata, A.B. Nyende and A.W.T. Muigai, **2009**. Characterization of Kenyan sweet potato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8: 2169-2175.

Presentation of Papers at Academic and professional Conferences:

1.**Karuri, H.W**., Amata, R., Amugune, C.N. and Waturu, C.N. 2013. Free living nematodes in cotton agroecosystems of Kenya. The first interdisciplinary international conference of Eldoret University and Anambra State University held on 3rd-5th September, 2013 at University of Eldoret, Kenya.

2. Ngubia, J.N., Ateka, E.M., Kihurani, A.W., Amata, R., Ndolo, P. and **Karuri, H.W**. 2012. Field resistance of sweet potato genotypes to sweet potato virus disease. The 13th KARI Biennial scientific conference held on 22-26th October 2012 in Nairobi, Kenya.

3. **Karuri, H.W**., Amata, R., Amugune, C.N. and Waturu, C.N. 2010. Nematode communities associated with cotton (*Gossypium hirsutum L*.) in Kenya. The 12th KARI Biennial scientific conference held on 8- 12th November 2010 in Nairobi, Kenya.

Abstracts

INTERACTION OF *FUSARIUM OXYSPORUM* f. sp. *VASINFECTUM* AND THE FUNGAL FEEDING NEMATODE *APHELENCHUS AVENAE* ON BT COTTON

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

The fungal feeding nematode *Aphelenchus avenae* (APH) feeds on different species of fungi including *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) that causes wilt in cotton. The objective of this study was to assess the interactions of FOV and APH on Bt cotton and its isogenic

counterpart (isoline) under greenhouse conditions. The treatments consisted of three levels, where Bt cotton, isoline and HART 89M were inoculated with: (i) APH alone; (ii) FOV alone and (iii) APH+FOV. Vascular discoloration, plant height, number of nodes, number of bolls, fresh shoot and root weight were recorded 180 days after planting (dap). Foliar symptoms were recorded throughout the growing season, and ELISA was used to determine the presence of Bt protein in soil and roots at180 dap. Whereas no Bt protein was detected in roots and soil of HART 89M and isoline, it was found in Bt cotton. The isoline was more susceptible to FOV and APH + FOV than Bt cotton and HART 89M. FOV and APH + FOV caused a reduction in plant height, number of nodes, number of bolls, fresh shoot and root weight but the decrease was greater in the FOV treatment. There was also a higher reduction of growth parameters in the FOV treatment than in APH. The number of nematodes in the APH + FOV treatment of Bt cotton and isoline were not significantly different. The isoline was more susceptible than HART 89M to FOV.

Key words: Trophic interactions, Bt cotton, *Aphelenchus*, *Fusarium oxysporum*

NEMATODE DIVERSITY IN SOIL FROM A FIELD TRIAL WITH DECOMPOSING BT COTTON EXPRESSING Cry1Ac AND Cry2Ab2 PROTEIN

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

The quality of decomposing plant materials may affect the soil community structure. The aim of the study was to determine the impact of decomposing Bt cotton and its isoline on soil nematode diversity. Bt cotton (06Z604D), isoline (99M03) and HART 89M (local non-Bt cotton cultivar) were planted for two seasons in a completely randomized block design in a confined field trial at Mwea, Kenya. After harvest the plant material was incorporated into soil and the nematode diversity was determined. The presence of Bt protein was evaluated using ELISA and insect bioassays. Abundance of bacteria feeding nematodes was significantly ($p < 0.05$) high but to a smaller extent in the Bt cotton plots (53.7% and 52% in the first and second season respectively) than in isoline (42.8% and 45% in the first and second season respectively). Insect bioassays detected Bt protein in the Bt cotton plots during the entire decomposition period in both seasons. There were no significant differences in nematode trophic groups composition between isoline and HART 89M. The effect of Cry2Ab2 and Cry1Ac protein in decomposing Bt cotton litter on soil nematodes was minimal. The study provides a basis for future studies on the impact of genetically engineered plants on soil nematodes in Kenyan agroecosystems.

Key words: *Bacillus thuringiensis;* biosafety; *Helicoverpa armigera;* nematodes.

REPRODUCTION OF ROOT KNOT NEMATODE (*MELOIDOGYNE INCOGNITA*) ON BT COTTON EXPRESSING Cry1Ac AND Cry2Ab2 PROTEIN

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

Objective: The sedentary endoparasite Meloidogyne incognita is an important plant parasitic nematode that infects cotton causing significant yield losses. The objective of this study was to evaluate reproduction of *M. incognita* in Bt cotton (06Z604D), isoline (99M03) and HART 89M (local non-Bt cotton cultivar) under greenhouse conditions.

Methods and results: Plant height, number of squares/bolls, fresh shoot and root weight were determined before root knot nematode (RKN) screening at 90 and 180 days after planting (DAP). Galling severity, egg mass index, number of juveniles and the presence of Bt protein in roots and soil were also determined. The ELISA detected Bt protein in soil and roots of Bt cotton but not in HART 89M and isoline plant tissues and soil. Reaction of Bt cotton and isoline to M. incognita was different with the transgenic cotton being more susceptible to RKN. HART 89M was more resistant to RKN infection compared with the isoline.

Conclusion and application of findings: The study has demonstrated that Bt cotton (06Z604D) is susceptible to *M. incognita*. The results indicate the importance of integrating nematode management practices such as the use of organic amendments and nematicides with other cultural practices in future Kenyan Bt cotton agroecosystems.

Keywords: *Bacillus thuringiensis*, Biosafety, root knot nematode, cotton

EFFECT OF BT COTTON EXPRESSING Cry1Ac AND Cry2Ab2 PROTEIN ON SOIL NEMATODE COMMUNITY ASSEMBLAGES IN MWEA, KENYA

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

Objective: The nematode community structure in soil cultivated with Bt cotton (containing Cry1Ac and Cry2Ab2 protein), isoline (non Bt cotton) and HART 89M (non Bt cotton) was evaluated in a field trial at Ndomba in the Central Province of Kenya.

Methods and results: The experiment was laid out in a completely randomized block design. Soil was collected for two seasons at 0, 30, 60, 90, 120, 150 and 180 days after planting (DAP). Presence of Bt protein in roots and soil was determined using ELISA and insect bioassays. Nematodes were extracted from soil using centrifugal-floatation method and identified to genus level using a compound microscope. ELISA analysis of soil samples indicated that Bt protein was present at 150 and 180 days after planting. Bacteriovorous nematodes were present in significantly ($P<0.05$) higher numbers in the Bt cotton (46.9%) than in isoline (42.1%) plots.

Conclusion and application of findings: Cry1Ac and Cry2Ab2 protein in Bt cotton (06Z604D) does not have a direct effect on nematode diversity. The results provide important biosafety data that will be useful in pre- and post release monitoring of potential negative impacts of Bt cotton cultivation in Kenya.

Keywords: Risk assessment, Renyi diversity, Bt cotton

EFFECT OF TRANSGENIC COTTON EXPRESSING Cry1Ac and Cry2Ab2 PROTEIN ON INFECTIVITY OF THE ENTOMOPATHOGENIC NEMATODES, *STEINERNEMA KARII* AND *HETERORHABDITIS BACTERIOPHORA*

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

Entomopathogenic nematodes are used in biological control of pests. The cry proteins from insect resistant cotton may affect their infectivity. The effect of *Bacillus thuringiensis* (Bt) cotton (06Z604D) on infectivity of *Heterorhabditis bacteriophora* and *Steinernema karii* was investigated in the green house. The nematodes were introduced into pots containing Bt cotton (06Z604D), isoline (99M03) and Hart 89M (local non Bt cotton cultivar). After 6 months, the nematodes were recovered from soil and their infectivity towards *Galleria mellonella* larvae was determined. The presence of Bt protein in roots and soil was determined at the end of the growing season by qualitative enzyme-linked immunosorbent assay (ELISA). Bt protein was present in the roots and soil of Bt cotton. No Bt protein was detected in HART 89M and isoline roots and soil. There was a significant species*time* treatment interaction and the nematodes collected from all the treatments caused >50% mortality.

Key words: *Bacillus thuringiensis,* entomopathogenic nematodes, virulence

OCCURRENCE AND DISTRIBUTION OF SOIL NEMATODES IN COTTON (*GOSSYPIUM HIRSUTUM* L.) PRODUCTION AREAS OF KENYA

Karuri, H.W., Amata, R., Amugune, N. and Waturu, C.

A baseline survey was conducted to determine the occurrence and distribution of soil nematodes associated with cotton in major growing areas in Kenya. Such baseline data on soil nematode abundance, diversity and ecosystem function in cotton ecosystems are valuable in providing a basis for comparison with organisms from transgenic cotton fields. Transgenic cotton plants expressing Cry1Ac and Cry2Ab proteins, from the soil bacterium *Bacillus thuringiensis* (Bt), provide effective control of lepidopteran pests. However, the potential effects of these proteins on soil nematofauna are unknown in Kenya. Soil samples were collected from nine locations of western (Odiado, Angorom and Ochundo locations), coast (Baharini, Mpeketoni and Witu locations) and central (Kajiji, Tebere and Nyangati locations) Province. Nematodes were extracted and recovered from soil samples using the Whitehead and Hemming tray method and identified under a light microscope according to their morphological characters. They were classified according to their feeding habits. Twenty seven genera of plant parasites, bacteriovores, fungivores, predators and omnivores were identified. Bacterial, fungal feeding and parasitic nematodes were the most abundant trophic groups across all Provinces. There were significant differences in the numbers of bacteriovores ($P \leq 0.01$) and plant parasites ($P \leq 0.05$) between the Provinces but no difference was observed in the numbers of fungal feeding nematodes. There was a significant difference in genus richness within locations in western and coast Provinces ($P \leq 0.001$). The combined maturity index ($\sum$MI) did not vary significantly within the locations. The Shannon index (H') showed variations within locations in western ($P \leq 0.001$) and coast Province ($P \leq 0.01$). Soil texture, P and K were correlated with abundance of some nematode genera. The bacteria feeders, *Acrobeles* and *Rhabditis* showed positive correlations to K ($r = 0.592$, $P \leq 0.05$ and $r = 0.128$, $P \leq 0.05$) and P ($r = 0.406$, $P \leq 0.05$, and $r = 0.252$, $P \leq 0.05$) while *Aphelenchus* was positively correlated to P ($r = 0.375$, $P \leq 0.05$). The plant parasitic genera *Meloidogyne* and *Pratylenchus* showed significant negative correlation to N ($r = -0.513$, $P \leq 0.05$ and $r = -0.226$, $P \leq 0.05$). It is clear from this baseline data that plant parasitic and

free living nematodes are widespread in cotton fields and any potential effects of Bt cotton on these nematodes may affect the nematode community structure and their ecosystem functions.

Key words: Cotton, soil nematodes, survey.

EVALUATING DIVERSITY AMONG KENYAN SWEET POTATO GENOTYPES USING MORPHOLOGICAL AND SSR MARKERS

Genetic diversity of 89 sweet potato genotypes was evaluated using morphological and molecular markers. Eighteen aerial and sixteen storage root characters were used in the morphological characterization. Analysis of variance showed that all the characters evaluated were significantly different ($P<0.01$) between the genotypes. The dendrogram obtained using phenotypic characters separated the genotypes into two major clusters with a Euclidean distance ranging from 0.0 to 6.98. Twenty three unique alleles, ranging from 3 to 6 per locus were detected using six simple sequence repeats (SSR) markers. Cluster analysis showed a Jaccard co- efficient ranging from 0.5 to 1.0 indicating high genetic diversity. Comparison between morphological and molecular data using the mantel test revealed a low correlation ($r = -0.05$) between the two data sets. Despite the poor correlation both techniques showed a high degree of variation among the genotypes suggesting great genetic diversity in Kenyan sweet potato genotypes that can be utilized in breeding programs.

Key Words: Genetic diversity; SSR markers; Morphological characters; Sweet potato; Cluster analysis

SURVEY OF SWEET POTATO VIRUSES IN WESTERN KENYA AND DETECTION OF *CUCUMBER MOSAIC VIRUS*

Sweet potato is an important food crop worldwide, but several pests and diseases limit its production. In eastern Africa, virus-induced diseases rank second to weevils in causing yield reduction. Symptomatic sweet potato cuttings (327) were collected from Nyanza and Western Provinces in western Kenya in 2009. The samples were tested for *Sweet potato feathery mottle virus* (SPFMV), *Sweet potato chlorotic stunt virus* (SPCSV), *Sweet potato mild mottle virus* (SPMMV), Sweet potato chlorotic fleck virus (SPCFV), *Sweet potato latent virus* (SPLV), Sweet potato caulimo-like virus (SPCa-LV), *Cucumber mosaic virus* (CMV), C-6, *Sweet potato virus G* (SPVG) and *Sweet potato mild speckling virus* (SPMSV) using nitrocellulose membrane enzyme-linked immunosorbent assay (NCM-ELISA). SPFMV, SPCSV, SPCFV, SPMMV and CMV were detected and 89% of the samples as a whole were found to be infected. SPFMV was detected in all infected samples followed by SPCSV (55%). Multiple infections were detected in the majority of the samples (80%) and the most common dual infection was with SPFMV and SPCSV (52%). The occurrence of CMV was low (5%) but was confirmed by RT-PCR with amplification of a 670 bp coat protein gene fragment from total RNA. This is the first record of CMV in sweet potato in Kenya.

Key words: Sweet potato, CMV, NCM-ELISA, RTPCR, diagnosis, survey.

Books Published

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