GENETIC DIVERSITY OF BANANA (*Musa* spp.) AND ITS RELATION TO PLANT PARASITIC NEMATODES IN TANZANIA.

Doreen M Mgonja[1,3], Gladness E Temu[1], Sylvester L Lyantagaye[1], Joseph C Ndunguru[3] Nessie D Luambano[2]

[1]University of Dar es Salaam, College of Natural and Applied Sciences, Molecular biology and Biotechnology Department, P.O. Box 35179 Dar es Salaam, Tanzania. [2]Sugarcane Research Institute, P.O. Box 30031, Kibaha, Tanzania.

[3]Mikocheni Agricultural Research Institute, Sam Nujoma Road, Box 6226, Dar es Salaam, Tanzania,

Introduction

Bananas (*Musa* spp.) are one of the most economically important crops in Tanzania. Banana production in Tanzania is largely constrained by pest and diseases mainly plant parasitic nematodes, particularly the burrowing and root lesion nematodes (FAOSTAT, 2013; Coyne , 2009). Control of nematodes through resistant varieties has been difficult due to limited information on genetic and genomic resources that may be important in supporting the development of farmers preferred varieties. In addition, names and accurate identities o f banana are not clearly known hence, limiting sustainable farming. Characterization of crops based on DNA markers is the measures for correct and quick identification of similar or closely-related cultivars. This study was conducted to assess genetic diversity of 159-banana varieties [using simple sequence repeat (SSR) markers] and their association to plant parasitic nematodes.

Materials and methods

Plant materials

A total of 159 banana varieties used in this study were collected from major banana growing areas of Tanzania (Figure 2)

Genomic DNA extraction

Genomic DNA isolation was done from the collected banana leaves using modified CTAB method.

SSR-PCR amplification

A total of 20-polymorphic banana SSR primers were used to amplify DNA isolated from banana leaf samples. The band profiles were scored and recorded. The data were analysed on NTSYS software pc 2.0 and the Poymorphic information content (PIC) values were calculated and recorded

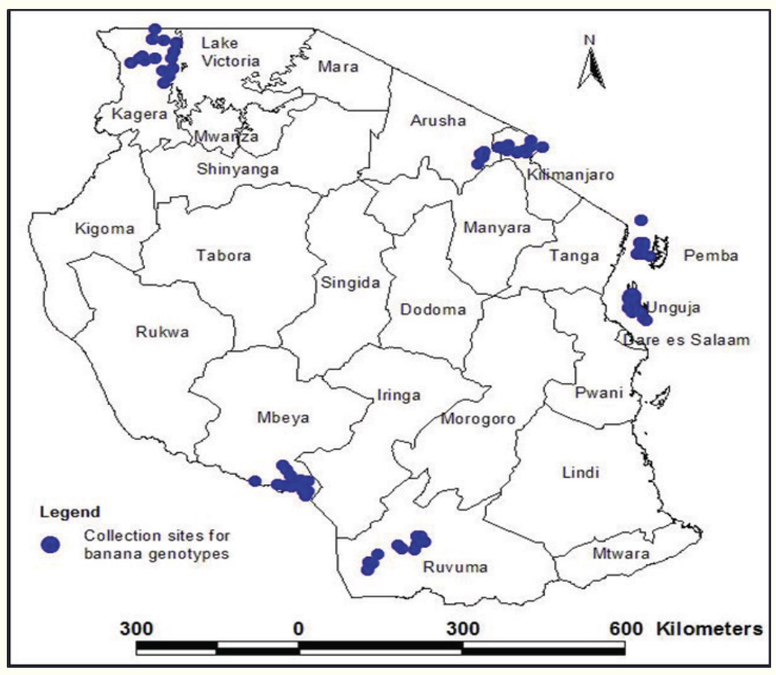

Figure 2.Map of Tanzania showing banana growing regions

Results and discussion

Genetic diversity based on PIC values

Twenty SSR primer pairs were polymorphic and generated a total of 63 distinct reproducible bands. The number of polymorphic bands detected with each primer pair ranged from 2 to 4 with an average of 3.15 per primer pair. The polymorphic information content values of each primer pair ranged from 0.50 to 0.75 with an average of 0.60.

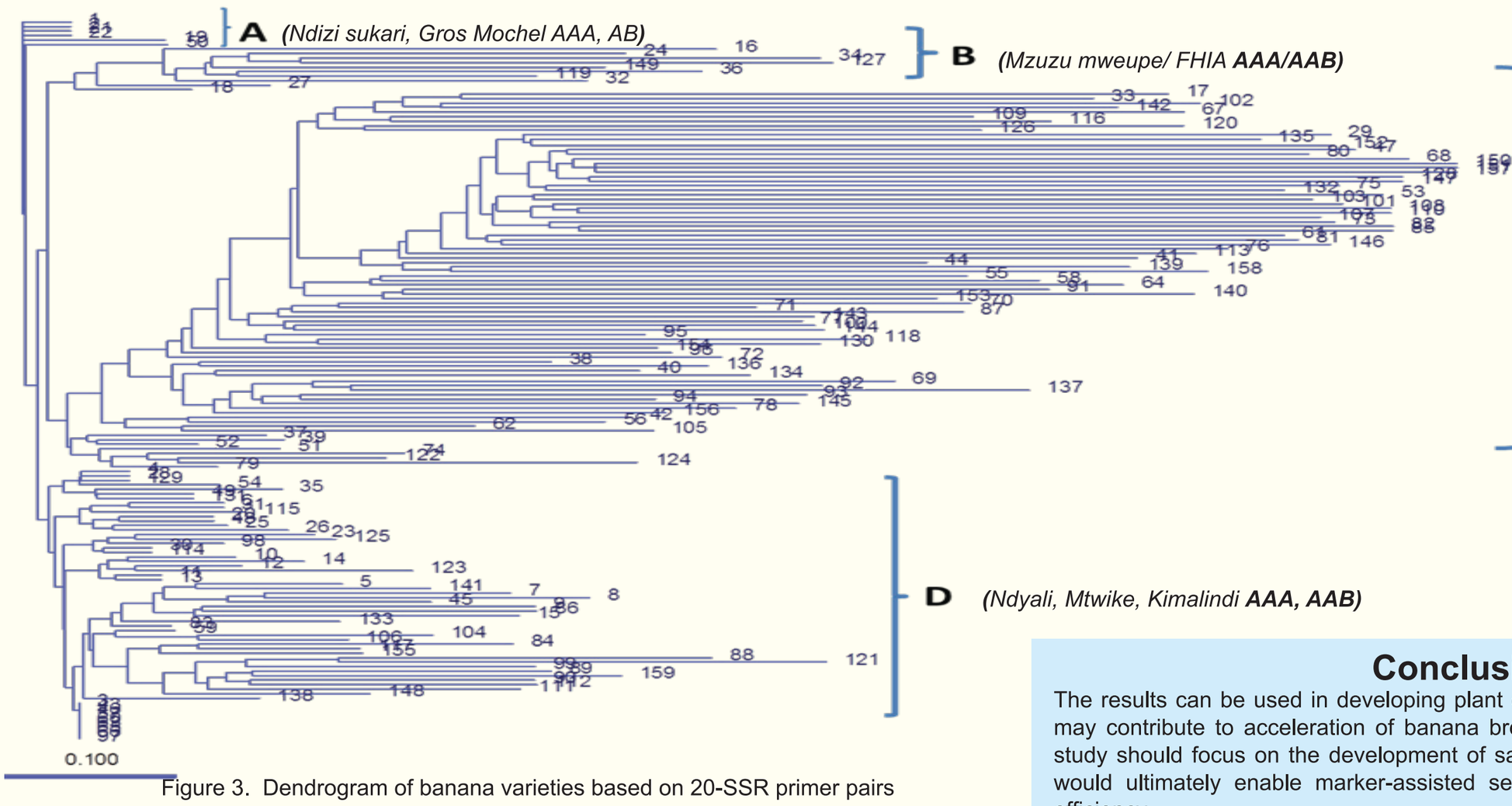

Figure 3. Dendrogram of banana varieties based on 20-SSR primer pairs

The UPGMA cluster analysis separated the 159-banana cultivars into four major groups (Figure 3) . **Cluster A** is composed of fewest genotypes (1, 19, 21, 22 and 50) - All from Kagera except genotype no. 1 from Pemba. **Cluster B** contains 10 genotypes: 3-Kagera 3-Mbeya; 2-Ruvuma; 1- Zanzibar and 1-Pemba. **Cluster C:** The largest- with 87 genotypes. **Cluster D:** 57 genotypes. The results revealed a high genetic diversity among the 159-bananacultivars.

Figure 1. Banana field showing toppling due to nematodes damage and roots damaged by nematodes

Table 2. Banana genotypes related to nematode species associated with different genotypes from different regions and altitudes of Tanzania.

Highest mean nematode count/100 mls							Lowest mean nematode count/100 mls				
Altitude zone	Nematode spp.	Genotype	Region	Altitude level (masl)	Mean nematode count/100 mls	Cluster	Genotype	Region	Altitude level (masl)	Mean nematode count/100 mls	Cluster
1	*R. similis*	MzuMwWZ	Zanzibar	42	617	D	MtwNZ	Zanzibar	17	17	C
	P. goodeyi	GurZRMb	Mbeya	477	5317	D	MtwMP	Pemba	34.7472	33	C
	P. coffeae	KijCZ	Zanzibar	46	700	C	PukWZ	Zanzibar	7	17	C
2	*R. similis*	TokKMb	Mbeya	581	223	C	HarRMb	Mbeya	565	17	B
	P. goodeyi	TokKMb	Mbeya	581	650	C	HarRMb	Mbeya	565	17	B
	P. coffeae	MshNR	Ruvuma	1080	717	C	KiskNR	Ruvuma	955	13	C
3	*R. similis*	TokRMb	Mbeya	1250	3783	C	JamAA	Arusha	1255	17	D
	P. goodeyi	MwamMR	Mbeya	1358	3183	C	BokSR	Ruvuma	1014	17	C
	P. coffeae	BukSRR	Ruvuma	1077	533	D	BokSR	Ruvuma	1014	17	C
4	*R. similis*	NshaKK	Kagera	1603	1567	C	KanKK	Kagera	1603	17	C
	P. goodeyi	MkojMKi	Kilimanjaro	1527	1500	C	MzuMR	Ruvuma	1557	10	D
	P. coffeae	KatMR	Ruvuma	1557	66	C	MkojMKi	Kilimanjaro	1527	0	C

The results shows that the highest mean count of nematodes were from genotype GurZRMb - altitude zone 1, followed by TokRMb– Altitude zone 3 (Table 2.) which are commonly cultivated genotypes. However, some of the introduced genotypes such as FHIA 23 were moderately affected by *R. similis* and *P. goodeyi*. This supports the possibility of the PPN to adapt and spread into different environments regardless of their original environments. The results shows that *P. goodeyi* and *R. similis* are highly distributed in all zones, although zone 2 had the lowest count o these nematode populations. In addition, *P. goodeyi* were highly abundant in altitude zone 1, the low land and humid climate while the previous report showed that *P. goodeyi* are confined in high cool altitudes. This indicates that these nematodes are spreading and able to adapt to new environmental conditions.

Conclusion

The results can be used in developing plant disease management strategies and may contribute to acceleration of banana breeding programs worldwide. Further study should focus on the development of saturated genetic linkage maps which would ultimately enable marker-assisted selection and improve crop selection efficiency

Acknowledgements

This work is sponsored by Sugarcane Research Institute (SRI) Kibaha through PEARL banana nematode project coordinated by Dr. Nessie Luambano

Reference

1. Food and Agricultural Organisation of the United Nations (FAOSTAT) 2013.
2. Coyne D. 2009 Pre-Empting Plant-Parasitic Nematode Losses on Banana in Africa: Which Species Do We Target? *Proc. IS on Banana Crop Protection Sustainable Productivity & Improved Livelihoods*.