The 12th International Symposium on Plant Virus Epidemiology

12th IPVE Symposium

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28 January -1 February 2013

ARUSHA, TANZANIA

Evolution, Ecology & Control of Plant Viruses

Program and Book of Abstracts

About ICPVE

The International Committee for Plant Virus Epidemiology (ICPVE) is a subject committee of the International Society for Plant Pathology (ISPP). The ISPP was founded in 1968 in the United Kingdom, for worldwide development of plant pathology. The ISPP sponsors International Congress of Plant Pathology, and International Meetings of its Subject Committees. ICPVE, since formation in 1979, has conducted eleven international symposia in different parts of the world. This 12th IPVE Symposium in Arusha, Tanzania, is the first to be held in the Africa.

The Previous IPVE Symposia were held in:

1. UK, Oxford, 28 - 31 July 1981
2. Australia, Corowa, 25 - 27 August 1983
3. USA, Orlando, 6 - 8 August 1986
4. France, Montpellier, 1 - 5 September 1989
5. Italy, Valenzano (Bari), 27-31 July 1992
6. Israel, Jerusalem, 23 - 28 April 1995
7. Spain, Aguadulce (Almeria), 11 - 16 April 1999
8. Germany, Ascherleben, 12 - 17 May 2002
9. Peru, Lima (CIP), 4 - 7 April 2005
10. India, Hyderabad (ICRISAT), 15 - 19 October 2007
11. USA, Ithaca (Cornell University), 20 - 24 June 2010

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12th International Symposium on Plant Virus Epidemiology

Evolution, Ecology and Control of Plant Viruses

28 January - 1 February 2013

The Ngurdoto Mountain Lodge

Arusha, Tanzania

Symposium organized by

International Committee on Plant Virus Epidemiology and

International Institute of Tropical Agriculture

IITA

Research to Nourish Africa

in partnership with

Mikocheni Agricultural Research Institute (MARI), Tanzania

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Program & Book of Abstracts

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Overview of the Program

27 January 2013: Sunday

1600 hrs onwards: Participants arrival and registration

28 January 2013: Monday

0815-0900	Registration and conference kit distribution
0900-1000	Inauguration
1030-1200	Session - 1. Changing phase of plant virus epidemiology
1200-1330	Lunch break
1330-1500	Session - 2. Climate change and Modeling (I)
1500-1530	Refreshment break
1530-1700	Session - 2. Climate change and Modeling (II)
1700-1830	Poster session - 1
1830 onwards	Welcome cocktail and dinner

29 January 2013: Tuesday

0815-1000	Session - 3. Virus vectors and virus-vector interactions (I)
1000-1020	Refreshment break
1020-1220	Session - 3. Virus vectors and virus-vector interactions (II)
1220-1330	Lunch break
1330-1510	Session - 4. IPM (CRSP, special session)
1510-1730	Refreshment break and Poster session - II
1730-1900	Session - 5. ICPVE business meeting
1900 onwards	Executive Dinner

30 January 2013: Wednesday: Excursion

31 January 2013: Thursday: Concurrent sessions

	Conference hall - 1	Conference hall - 2
0815-1000	Session - 6: Diagnostics and surveillance (I)	Session - 7: Epidemiology and ecology (I)
1000-1020	Refreshment break	
1020-1205	Session - 6: Diagnostics and surveillance (II)	Session - 7: Epidemiology and ecology (II)
1205-1330	Lunch break	
1330-1500	Session - 8: Disease control (II)	Session - 9: Virus evolution (II)
1500-1530	Refreshment break	
1530-1615	Session - 8: Disease control (II)	Session - 9: Virus evolution (II)
1615-1800	Poster Session - III	
1900 onwards	Dinner	

1 February 2013: Friday

0815-1000	Session - X: Plant virology in sub-Saharan Africa
1000-1030	Refreshment break
1050-1230	Session - X: Plant virology in sub-Saharan Africa
1230 onwards	Lunch break and departures

29 January 2013: Tuesday: Poster Session II

PP-036 **Viruses of sweetpotato in Israel and their control**

Gad Loebenstein, *Jacob Cohen and Victor Gaba*
Department of Plant Pathology and Weed research, Agricultural Research Organization, Bet Dagan, Israel

PP-037 **On the effect of acid rains on pink hydrangea**

Vahida Šeremet
Tuzla, Akifa Šeremeta 14, Bosna and Herzegovina

PP-038 **Characterization of elite sweet potato genotypes for sweet potato virus disease (SPVD) resistance and high dry matter content in Tanzania**

Catherine Gwandu, ***Fred Tairo,*** *Emmarold Mneney and Alois Kullaya*
Mikocheni Agricultural Research Institute (MARI), P.O Box 6226, Dar es Salaam, Tanzania

PP-039 **Genetic resistance and gene action of maize germplasm to *Maize streak virus***

M. T. Salaudeen[1,2], *A. Menkir[1], G. I. Atiri[3] and P. Lava Kumar[1#]*
[1]International Institute of Tropical Agriculture (IITA), Oyo Road, PMB 5320, Ibadan; [2]Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria

PP-040 **Molecular characterization of integrated DNA molecules associated with cassava mosaic disease in East Africa**

H. Gabriel[1], *P. Sseruwagi[1], F. Tairo[1], H. Vanderschuren[3], M. E. C. Rey[2] and J. Ndunguru[1]*
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PP-041 **The mode of transmission of *Rice yellow mottle virus***

M. E. Abo[1], *A. A. SY[2], M. D. Alegbejo[3], A. S. Afolabi[6], A. Onasanya[5], F. E. Nwilene[5] and Y. Sere[4]*
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PP-042 **Aphids infesting potato in Kenya**

Hassan K. Were, *Florence M. Olubayo[c], Brian Fenton[d], John K. Karinga[b], J. Aura[c] and Lesley Torrance[d]*
[a]Masinde Muliro University of Science and Technology, P.O. Box 190-50100 Kakamega, Kenya; [2]KARI-Tigoni Research Centre, P.O. Box 338-00217, Limuru, Kenya [3]University of Nairobi, P.O. Box 29053 Nairobi, Kenya; [4]The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, UK

PP-043 **Cassava production enhancement in semi-arid and arid regions in Kenya**

K. Monjero[1], *J. Irungu[1] and D. Miano[1]*
[1]Kenya Agricultural Research Institute - Biotechnology centre, P.O. Box 14733-00800, Nairobi-Kenya

PP-044 **Mechanisms underlying resistance to groundnut rosette virus complex and its vector(s) in Uganda**

G. Otim[1], *M. S. Ochwo[1], B. Akello[2], M. Biruma[2], D. K. Okello[2] and I. O. Mugisa[1]*
[1]Makerere University, School of Agriculture, Crop Production Department; Kampala, Uganda; [2]National Semi-Arid Resources Research Institute, Serere, Uganda

PP-045 **Evaluation of diverse oilseed *Brassica* germplasm from Australia, China and India to identify *Turnip mosaic virus* resistance phenotypes**

Eviness P. Nyalugwe[1], *Martin J. Barbetti[1] and Roger A. C. Jones[1, 2]*
[1]School of Plant Biology, Faculty of Natural and Agricultural Sciences, University of Western Australia, Crawley, WA 6009, Australia; [2]Department of Agriculture and

PP-039: Genetic resistance and gene action of maize germplasm to *Maize streak virus*

M. T. Salaudeen[1,2*], A. Menkir[1], G. I. Atiri[2] and P. Lava Kumar[1#]

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Maize streak virus (MSV, genus *Mastrevirus*, family *Geminiviridae*) transmitted by leafhoppers (*Cicadulina* spp.) can cause severe yield losses in susceptible maize (*Zea mays* L.) varieties. MSV is endemic in all the maize producing regions in sub-Saharan Africa (SSA). Use of maize lines and hybrids with appreciable levels of MSV tolerance remains the most effective and reliable control option. Knowledge of resistance background and mode of gene action is critical for breeding MSV-tolerant varieties. Two hundred and fifty maize inbred lines and their F_1 hybrids derived from the cross with MSV–tolerant inbred Tzi3 were arranged in alpha lattice design with two replications under screenhouse and field conditions, respectively. At 2 to 3 leaf stage seedlings were inoculated using viruliferous leafhoppers (*Cicadulina triangula*). Disease severity (scale 1 – 5; 1 means <10 % of leaf area covered with streak symptoms; 5 implies >75 % of leaf area covered with streaks) and yield components were recorded. Resistance classes were based on Area Under the Disease Progress Curve (AUPDC) determined by plotting the data on disease severity over time. Twenty seven (10.8%), 49 (19.6%) and 53 (21.2%) lines were highly resistant, resistant and moderately resistant, respectively. Amongst the hybrids, 28 were highly resistant, whereas 45 (18%) each were resistant and moderately resistant. The highest grain (6 t/ha) and cob yield (5.6 t/ha) were recorded in the highly resistant (Plot 1445 × Tzi3) and resistant hybrids (Plot 1452 × Tzi3), respectively. Cob weight per plant (257.9 g), grain weight per plant (173.6 g), and kernel number per plant (578) were highest in the moderately resistant hybrids (Plot 1381 × Tzi3). Resistance was polygenically inherited and under the influence of both dominant and recessive genes. Simple recurrent selection would facilitate maize breeding for MSV resistance in SSA.

Genetic resistance and gene action of maize germplasm to *Maize streak virus*

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Introduction

•*Maize streak virus* (MSV, genus *Mastrevirus*, family *Geminiviridae*) is an endemic threat to maize (*Zea mays* L.) in Africa. (Fig. 1). The virus is transmitted by leafhoppers (*Cicadulina* spp.). Use of MSV resistant maize lines and hybrids remains the most effective option for farmers. Knowledge of resistance background and mode of gene action is critical for breeding streak-resistant varieties.

Objective

•To identify MSV-resistant maize lines and determine mode of gene action for MSV resistance in F_1 maize hybrids.

Fig 1. Severe MSV infection in susceptible maize. Unproductive MSV-infected maize (arrow).

Materials and Methods

•Maize inbred lines (N=250) and their F_1 hybrids derived from the cross with resistant TZi_3 were evaluated against MSV under screenhouse and field conditions, respectively. The field trial was conducted at the IITA, Ibadan, Nigeria. Each hybrid was evaluated in one row of 5 m length; spacing was 0.75 m x 0.25 m.

Inoculations and symptoms severity assessment

•At 2 to 3 leaf stage seedlings were challenged with the virus using viruliferous leafhoppers *Cicadulina triangula*. Percentage of infected plants was taken. Disease severity was recorded using a scale of 1 – 5 (Fig. 2).. Detection of MSV in the leaves of inoculated plants was by enzyme-linked Immunosorbent assay (ELISA). Yield parameters were also recorded in the field trial.

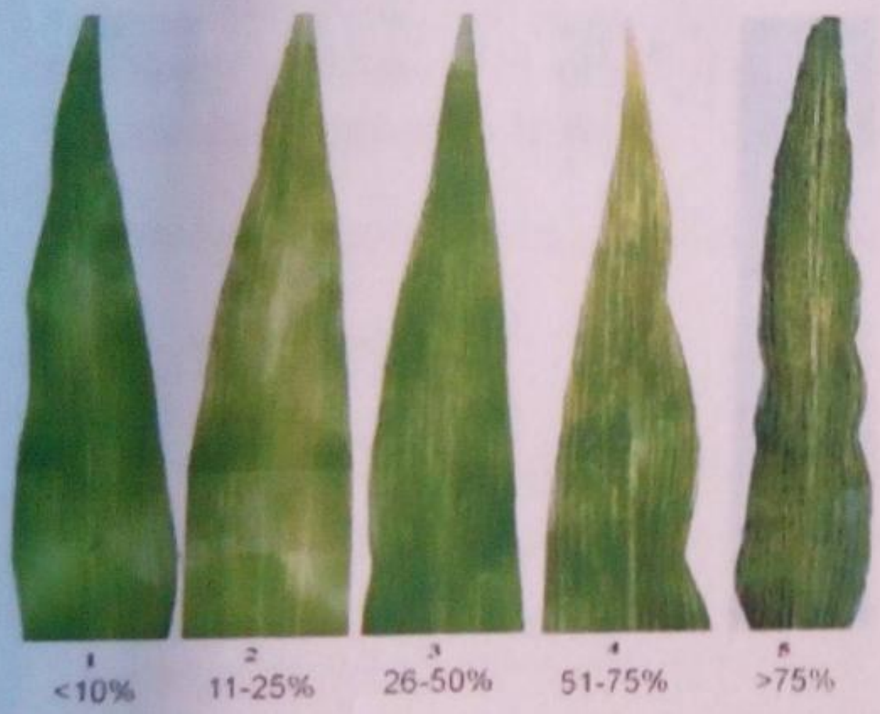

Fig. 2. Percentage of leaves covered with streaks after inoculation with Maize streak virus which were used as the scale for measuring symptom severity

Statistical analyses

•Symptom severity scores were analysed by Area Under Disease Progress Curve (AUDPC), for resistance class determination (Shaner and Finney, 1977), and Gaussian test (UNIVARIATE MODES PLOT) for genetics of inheritance.

$$AUDPC = \sum_{i=1}^{n} [(Yi + 1 + Yi)/2] [Xi + 1 - Xi]$$

where:
Yi = streak severity at the ith observation
Xi = time (weeks) at the ith observation
n = total number of observations

The remaining traits were subjected to analysis of variance (ANOVA) using the General Linear Model (PROC GLM) of SAS.

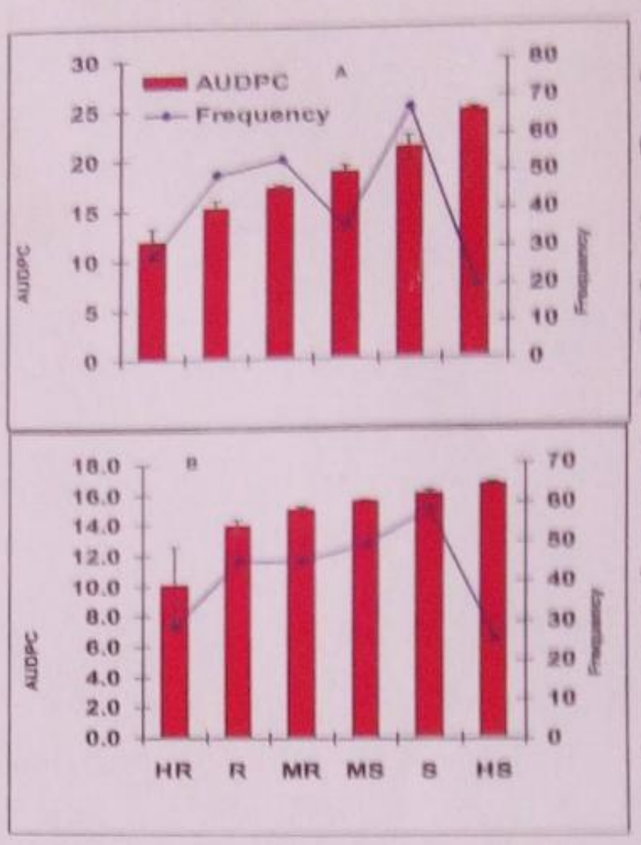

Fig.3. Area Under the Disease Progress Curve (AUDPC) and frequency of resistance classes from maize inbred lines (A) and F_1 hybrids (B) inoculated with Maize streak virus

HR = highly resistant; R = resistant ; MR = moderately resistant; MS = moderately susceptible; S = susceptible ; HS = highly susceptible

Table 1. Relative performance of maize hybrids infected with MSV

Parameter	Ls mean
Incidence (%)	38.9 – 67±10.2*
Plant height (cm)	141.9 – 194.9±10.7*
Cob yield (t/ha)	1.2 – 6.6±0.8**
Cob weight/plant (g)	91.4 – 257.9±20.3
Grain weight/plant (g)	57.6 – 173.6±15.9
Grain yield (t/ha)	1.1 – 6.0±0.7**
100 kernel weight (g)	22.5 – 36.2±52.4*
Kernel no./plant	152 – 578±54.3

* = *significant at p = 0.05*

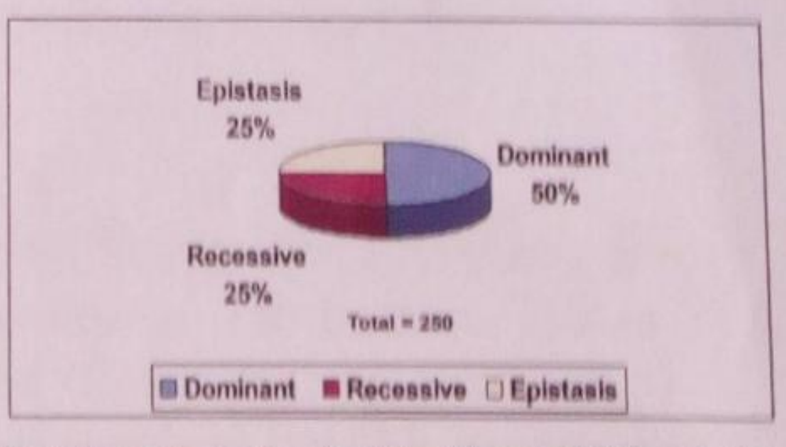

Fig.4.Percentage of maize inbred lines exhibiting various gene actions when crossed with streak resistant maize inbred Tzi_3

Results

•None of the genotypes was immune to infection but substantial differences for MSV resistance was found.

•One hundred percent infection occurred in the maize lines whereas values varied between 38.9 and 67% among the hybrids.

•Twenty seven (10.8%), 49 (19.6%), and 53 (21.2%) lines were highly resistant, resistant, and moderately resistant, respectively (Fig. 3A).

•Amongst the hybrids, 28 were highly resistant, whereas 45 (18%) each were resistant and moderately resistant (Fig. 3B).

•The hybrids differed significantly for the yield traits (Table 1). The highest grain (6t/ha) and cob (6.6t/ha) yields came from the highly resistant (Plot 1445 × TZi_3) and moderately resistant (Plot 1452 × TZi_3), respectively.

•Cob weight per plant (257.9 g), grain weight per plant (173.6 g), and kernel number per plant (578) were highest in the moderately resistant hybrid (Plot 1381 × TZi_3)

•Resistance to MSV was found to be polygenic. Fifty % of the lines crossed with streak resistant parent resulted in dominant gene action, whereas 25% each showed recessive and epistatic gene actions (Fig. 4)

•ELISA indicated higher virus titre in susceptible compared to the resistant genotypes

Conclusions

•Resistant maize lines are sources of MSV genes for breeding programmes.
•Visual symptom scoring was positively correlated with serological test.
•Simple recurrent selection and early selection of the evaluated genotypes is recommended.

References

Shaner, G. and Finney, R. E. (1977). The effect of nitrogen fertilization on the expression of slow-mildewing resistance in knox wheat. Phytopathol. 67:1051 – 1056