

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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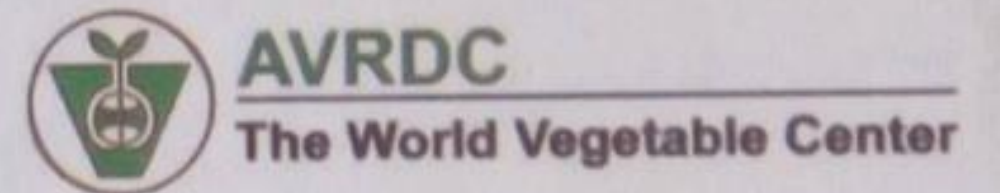
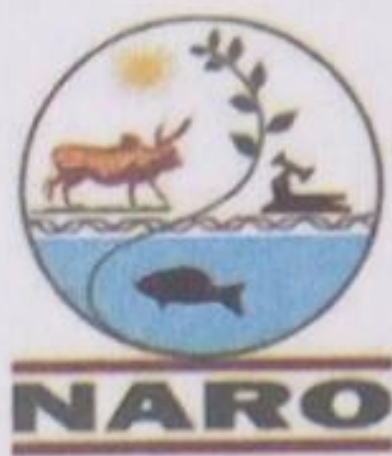
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PP137: QTLs to *Maize streak virus* tolerance in maize

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Maize streak disease (MSD) caused by the *Maize streak virus* (MSV; genus *Mastrevirus*) transmitted by leafhoppers, is an economically important disease of maize endemic in Sub-Saharan Africa. This disease is controlled using maize tolerant varieties - genotypes upon infection produce mild streak symptoms and no significant negative effect on yield. A mapping population of 250 F2 lines derived from a cross between a drought tolerant inbred maize and MSV tolerant line (No.1368) were artificially inoculated with viruliferous *Cicadulina triangular* one week post planting. Severity of MSV on the inoculated maize plants were scored on a scale of 1 to 5, 1 for highly resistant and 5 for highly susceptible. Quantitative Trait Loci (QTLs) conferring tolerance to MSV was mapped using 269 SNP markers. A linkage map comprising 11 linkage groups was constructed using Haldane mapping function at LOD 3.0. Composite interval mapping method was used to estimate the dominance and additive effect of the QTL. One QTL of major effect was identified on chromosome 3 at an LOD 3.6 explaining above 60% of phenotypic variance. Frequency distribution of MSD severity was bimodal signifying the presence of a major gene in the MSV tolerant parent. The identification of major QTL, upon validation, opens the avenue for marker-assisted breeding to introgress genes conferring MSV tolerance into other elite varieties.