National Symposium on Pathogenomics for Diagnosis and Management of Plant Diseases

24-25, October 2013

Abstract of papers

Organised by

Indian Phytopathological Society (South Zone)

&

Central Tuber Crops Research Institute (ICAR)

Venue: Central Tuber Crops Research Institute (ICAR)

Thiruvananthapuram 695 017, Kerala

ıalyzing the changes in the motifs and domains of ally distinct isolates of BBrMV.

ʼmorphic DNA analysis among the various *urica* causing powdery mildew diseases in

m and J. Rajalakshmi
ımil Nadu Agricultural University, Coimbatore- 625 104

leaves showing symptoms of powdery mildew dis-rmer's fields in different chilli growing areas of Ta-l pathogens were isolated from the infected leaves. l as *Leveillula taurica* based on morphological and ulence of all the fungal isolates was determined *in* n on detached chilli leaf assay. The measurement of aves revealed differences in the virulence between riability among isolates of *L.taurica* that differed by means of random amplified polymorphic DNA primers. Analysis of the genetic coefficient matrix RAPD profile showed that minimum and maximum ; the *L.taurica* were in the range of 12 to 100% re-using unweighted pair–group method with arithmetic ;eparated the isolates into three clusters (I, II and III) ʼersity among the isolates of *L.taurica* from chilli. ;e isolates namely Lv 4, Lv 10 and Lv 6 and Cluster Lv 2 and the cluster I have Lv1, Lv 3 ,Lv 5 and Lv 9

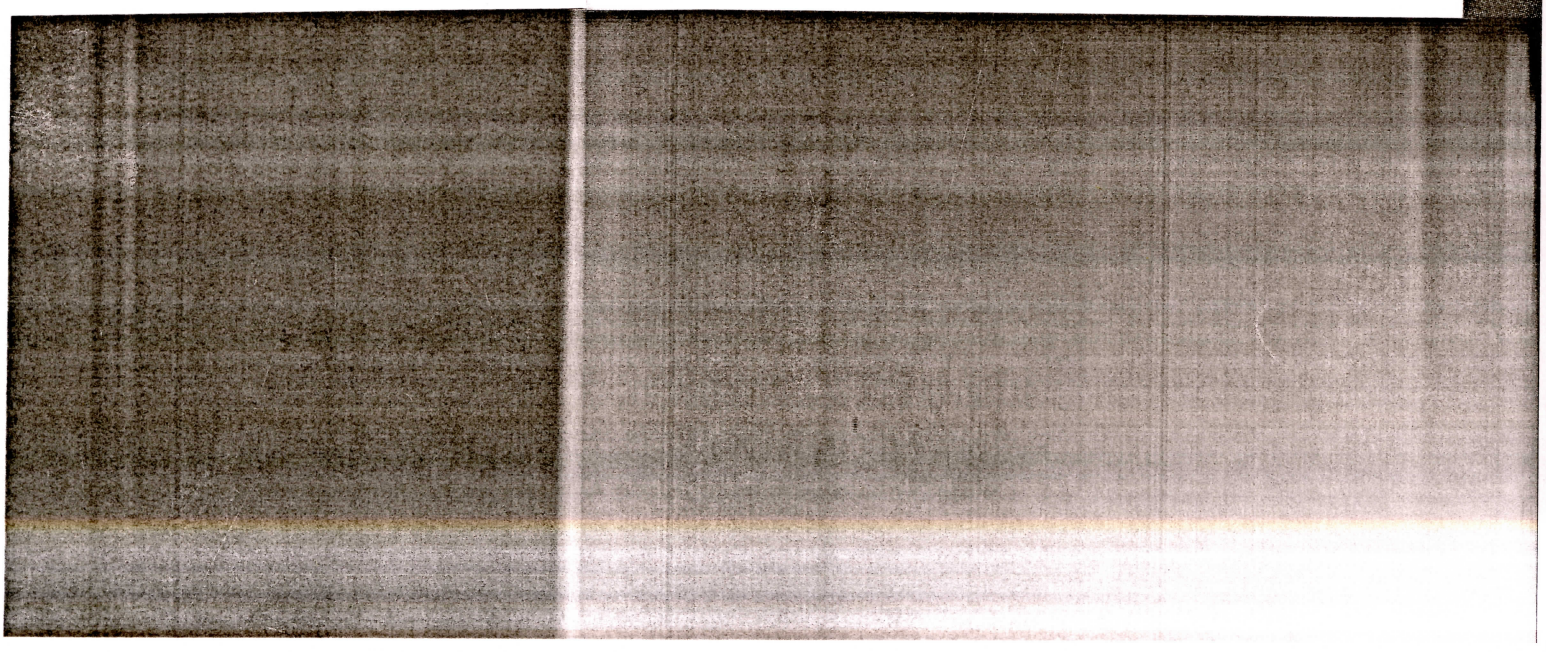
PG-P3

Recombination and negative selection pressure in the P1 gene of Indian *Sugarcane streak mosaic virus*

K. Bagyalakshmi, B. Parameswari, C. Chinnaraja, R. Viswanathan

Plant Pathology Section, Division of Crop Protection,
Sugarcane Breeding Institute (ICAR), Coimbatore
E mail: rasaviswanathan@yahoo.co.in

Sugarcane streak mosaic virus (SCSMV), a member of the genus *Poacevirus*, of this family, an important viral pathogen affects the sugarcane production in India. The genome has a single open reading frame that is translated in to a large polypeptide and consequently cleaved into functional proteins. This virus causes mosaic of sugarcane along with the *Sugarcane mosaic virus* (SCMV) which is a serious disease causing varietal degeneration reported from India in 1999 and later has been reported from geographically different Asian countries. The coding region for P1 peptidase is located at the very beginning of the viral genome of the family *Potyviridae*. P1 was thought of as serine peptidase with RNA-binding activity and with possible influence in cell-to-cell viral spreading. In order to unveil its mechanism of evolution we initiated the study by characterizing 10 P1 gene of Indian isolates and the sequences were compared with previously reported SCSMV isolates from different countries. Comparison of all of the sequenced virus isolates revealed a high level of diversity in the P1 gene (83–98% nt sequence identity; 87–100% aa sequence identity), and the Indian isolates were found to be the most divergent (up to 9% variation at the amino acid level). Phylogenetic analysis revealed clustering of 17 SCSMV isolates into two groups. Group I included isolates from India (except SCSMV-TPT) and Pakistan, and group II consisted of isolates from Japan, Indonesia, Thailand and SCSMV-TPT. The results obtained from phylogenetic study were further supported with the SNPs (single nucleotide polymorphism), INDELs (insertion and deletion) and evolutionary distance analysis. A significant proportion of recombination sites were found at the N terminal region of P1 gene of Indian isolates. Analysis of selection pressure indicated that the P1



gene of Indian SCSMV isolates is under strong negative selection. It is likely that recombination, along with strong negative selection, enhances the speed of elimination of lethal mutations in the P1 gene of Indian SCSMV isolates.

PG-P4

Assessing the incidence of grain discolouration and seed mycoflora load in rice varieties

C. Jeyalakshmi, R. Renuka and C. Rettinassababady

Department of Plant Pathology,
Pandit Jawaharlal Nehru College of Agriculture & Research Institute,
Karaikal – 609 603, U.T. of Puducherry
E-mail: csjayal@yahoo.co.in

Experiments were conducted to assess the grain discolouration (%) and seed mycoflora load in the popularly grown rice varieties of the Cauvery delta region of U.T. of Puducherry. Ten representative panicles of ADT 39, ADT 43 ADT 46, CR 1009, KKLR1, Samba Mahsuri and White ponni collected randomly at harvest from Pandit Jawaharlal Nehru College of Agriculture and Research Institute farm during February 2013 and per cent grain discolouration was assessed as per IRRI, (1998). Seed mycoflora assay was carried out and observations on fungal growth were recorded and frequency occurrence of mycoflora was calculated. The results revealed that the variety White Ponni was statistically different from other varieties by recording the maximum grain discoloration of 40 per cent. The variety CR 1009 recorded the lowest incidence (13.00%). Eight mycoflora *viz., Aspergillus niger, A. flavus, Curvularia lunata, Fusarium moniliforme, Helminthosporium oryzae, Microdochium oryzae, Penicillium* sp. and *Rhizopus* sp were found to be associated with the grain discoloration. Of which, C. *lunata* and *H. oryzae* were present in all test varieties. The presence of the aflatoxicosis fungi *Aspergillus* sp. was noticed in all test varieties except ADT 39, however it harboured *Rhizopus* sp. The study on the distribution of mycoflora in the grain discolouration revealed that *Penicillium* sp. is the most frequently isolated fungus with 30.57 per cent distribution followed by *C. lunata* (18.85%), *H. oryzae* (17.14%) and *F. moniliforme* (10.00%). The *A. niger* and *A. flavus* were less frequently distributed