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# Characterization of intriguing fungal pathogen *Fusarium sacchari* causing wilt in sugarcane

**R. Viswanathan*, M. Poongothai, P. Malathi, A. Ramesh Sundar, M. Scindiya, M.L. Chhabra# and C.G. Balaji**

Plant Pathology Section, ICAR-Sugarcane Breeding Institute, Coimbatore 641007
#ICAR-Sugarcane Breeding Institute Regional Centre, Karnal 132001

**E-mail:**
rasaviswanathan@yahoo.co.in

Sugarcane wilt caused by Fusarium sacchari was reported one hundred years ago from India and continues to cause significant losses to cane production and productivity in the country. However, research work on this important pathogen was limited especially on characterization of the fungus and its variability. The causal organism was found to vary with time and investigator and the disease could not be reproduced at ease under artificial conditions in the field. During the last 10 years, we made detailed disease surveys in most of the major sugarcane growing regions in the country and collected more than 300 Fusarium isolates infecting the crop. We have established variation in Fusarium isolates associated with sugarcane wilt, based on cultural, morphological, pathogenic and molecular characterization of the isolates. As the phenotype of the pathogen depends on varying environmental conditions, reliability and repeatability of the identity as seen earlier is doubtful. Molecular tools based on DNA analyses are being currently used as an alternative to cultural and morphological characters to characterize the variants of fungal species. Additionally the use of molecular tools for characterization would save time and are more reliable compared to phenotypic characters which vary with time and conditions. Hence further molecular studies were conducted with 50 isolates of the 117 isolates, characterized initially. In all the four different molecular tools viz., sequencing of internally transcribed region (ITS), randomly amplified polymorphic DNA (RAPD), inter-generic sequences-restricted fragment length polymorphism (IGS-RFLP) and inter simple sequence repeats (ISSR) used for characterization, morphologically distinct isolates formed separate clusters and isolates of F. sacchari grouped together in a cluster. Within this cluster, due to intraspecific variation F. sacchari,isolates were further grouped into many subclusters. In all the three different molecular tools used viz., RAPD, IGS-RFLP and ISSR, the chain-forming species separated in a cluster. rDNA ITS sequencing did not separate the F. verticillioidesisolates rather it grouped them together with other isolates. However, rDNA ITS sequencing helped in confident prediction of species other than F. sacchari in a separate group. Species other than F. verticillioidesviz., F. proliferatum, F. subglutinansand F. napiformeclustered away from F. sacchari.Critical application of the conventional techniques combined with molecular tools clearly established that F. sacchari as the causal agent of wilt in sugarcane. Other Fusariumsp isolated from wilt infected sugarcane stalks were found to be either secondary invaders or non-pathogenic in nature. However, it was found that Fusarium sp associated with pokkahboeng also causes stalk infections and produces wilt in certain varieties. Further studies in this area would bring complete characterization of the Fusaria associated with pokkahbeong and wilt in sugarcane. Also epidemiology of these sugarcane diseases will be clearly revealed, especially on survival of F. sacchari and its possible manifestation as foliar as well as stalk disease.