

NATIONAL SYMPOSIUM

Understanding host-pathogen interaction through science of omics

ICAR- Indian Institute of Spices Research, Kozhikode, Kerala
March 16-17, 2015

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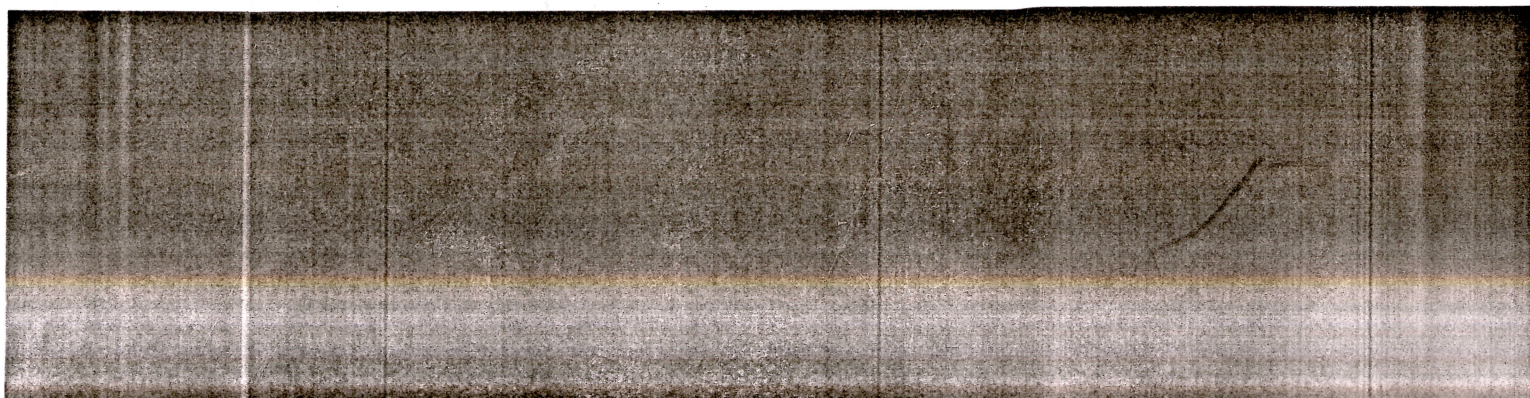


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Indian Phytopathological Society
New Delhi

ISBN! - 978 - 81 - 86872 - 49 - 9



ence enzymes; l cysteine-rich R and Crinkler *zstans* genome. of the genome. been predicted *tans* as well as es for effective gement will be

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to study path- gen genomes is enesis which in *chliobolus* spp. losses to cereal *P. triticina*) and a rust is region tion happening mber of patho- with transcrip- and detection of rapidly as dev- ated pathogens le. The compar- netabolism and ls to adapt to a mechanisms of s. The diversity iversity among me species. The

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gene products, particularly those associated with unique genomic regions, are candidates for pathogenic lifestyle differences. Therefore, key component is understanding determinants of virulence.

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Host-pathogen interaction in sugarcane - red rot pathogen: role of 3-deoxyanthocyanidin biosynthesis pathway enzymes

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Among the various biotic and abiotic stresses faced by sugarcane, red rot caused by the fungus *Colletotrichum falcatum* is the major constraint, leading to severe yield losses. Sugarcane produces reddish pigment during the host pathogen interaction which probably contains 3-deoxyanthocyanidin phytoalexins synthesized *de nova*. To understand the phytoalexins role in red rot resistance, detailed studies were conducted through HPLC assays and genomic approach, with a set of sugarcane varieties varying in red rot resistance. Our results clearly established that resistant varieties accumulated greater levels of phytoalexins as compared to the susceptible ones during pathogenesis. Induction of 3-deoxyanthocyanidin compounds *viz.*, apigeninidin, luteolinidin and cyanidin along with uncharacterized compounds of varying concentrations related to category of disease reaction on resistant (R) and susceptible (S) types was found. The differential accumulation of phytoalexin compounds against the pathogen colonization in compatible and incompatible interaction evidenced their active role in disease resistance by restricting pathogen progression in the latter. Subsequently studies were carried out to assess expression of transcripts involved in flavonoid biosynthesis pathway through RT-PCR revealed differential transcript expression of chalcone synthase, chalcone reductase, flavanoid 3'5' hydroxylase, dihydrofolate reductase and 4-coumarate Coenzyme A ligase among resistant and susceptible varieties after pathogen inoculation. However, phenylalanine ammonia lyase, coumarate-4hydroxylase, isoflavone reductase and chalcone isomerase transcripts were found to be constitutively expressed in both varieties. The results signify specific regulation of transcripts in resistant varieties as compared to the susceptible, as active phytoalexin induction and accumulation during pathogen intrusion which leads to restricting pathogen invasion in resistant plants.

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