

# National Symposium on Blending Conventional and Modern Plant Pathology for Sustainable Agriculture December 4-6 , 2012

## Souvenir cum Abstracts

Venue:

Indian Institute of Horticultural Research  
Hesaraghatta Lake Post, Bangalore-560 089

### Organizers



### Sponsors



Department of  
Biotechnology  
Government of India



Department of  
Science and Technology  
Government of India



Department of  
Horticulture  
Government of Karnataka



NABARD  
COMMITTED TO RURAL PROSPERITY

## Lead Presentation

### **L1- Exploiting proteomics approach to unravel red rot resistance mechanism in sugarcane**

R. Viswanathan\*, V. Ganesh Kumar, P. R. Rahul, A. Ramesh Sundar and P. Malathi  
Division of Crop Protection, Sugarcane Breeding Institute, ICAR, Coimbatore 641007  
Email: rasaviswanathan@yahoo.co.in

The red rot of sugarcane caused by the fungus *Colletotrichum falcatum* is one of the major constraints in India and other South Asian countries. Voluminous amount of studies have been carried out for the past several decades, to understand sugarcane-red rot interaction. These studies revealed the differential expression/ accumulation of several pathogenesis related proteins (like chitinases, glucanases, thaumatin like proteins) and secondary metabolites among red rot resistant and susceptible sugarcane varieties. However, key molecular components responsible for these assorted responses are still not clear. In the present study, a proteomics approach involving two-dimensional gel electrophoresis (2-DGE) was used to understand the changes/ differences in the stalk proteome of red rot resistant and susceptible sugarcane cultivars viz., Co 93009 and CoC 671, respectively during interaction with *C. falcatum*. The proteomic analysis revealed the up-regulation of about 106 proteins and down-regulation of about 30 proteins, in response to pathogen inoculation. These differentially expressed protein spots were then characterized by MS analysis. The major portion of the up-regulated proteins belonged to the signal transduction and transcription/transcription factors categories. Metabolism and cell growth/ development categories represented majority of down-regulated proteins. Among the differentially regulated proteins, quantitative difference in expression was noticed between resistant and susceptible cultivars. The important proteins identified include calcium dependent protein kinase, ACC synthase, cytokinin oxidase and R2R3-MYB transcription factor. The cell death response possibly mediated by calcium signaling seems to be the major resistance mechanism operating against *C. falcatum* in the resistant variety. In conclusion, tight regulation characteristic of resistance response against biotrophic pathogens was observed in the resistant variety, whereas, in the susceptible variety the response was more general and passive. The present study is the first such effort in elucidating key components responsible for sugarcane resistance to red rot. The results clearly demonstrated the suitability of proteomic techniques in deciphering components involved in host pathogen interaction. Further, large genome size, polyploidy and aneuploidy in cultivated sugarcane make proteomic approach more appropriate to understand host resistance against *C. falcatum*.