

densely packed structure has high density and low floatation index as well as higher hardness value than loosely packed structure. High positive correlation ($r=0.667$) between vitreousness and 27-kDa gamma zein content justifies hypothesis of 27- kDa gamma zein role in kernel vitreousness. Unraveling of the missing information on improved protein quality and modified

kernel texture in QPM may accelerate development of Quality Protein Maize in countries where it can impact human nutrition.

Nirupma Singh

ICAR-Indian Institute of Maize Research
Pusa Campus, New Delhi 110 012
e-mail: nirupmasingh@rediffmail.com

Whole genome and transcriptome analysis of *Colletotrichum falcatum* to decipher specific adaptation as an intriguing stalk pathogen

Red-rot of sugarcane, caused by fungal pathogen *Colletotrichum falcatum*, is a major challenge in sugarcane cultivation. Although tropical region of India remained free from the rot for many decades in the past century; from 1970s, the disease has caused extensive losses to cane cultivation in Tamil Nadu, Andhra Pradesh, Gujarat and Odisha. Onslaught of red-rot continues in both subtropical and tropical states, excepting Maharashtra and Karnataka. Affected canes are unfit for milling owing to inversion of sucrose into reducing sugars. Emergence of new variants of the pathogen

genome / transcriptome was required to understand pathogen biology and its molecular signatures governing virulence / host adaptation

C. falcatum pathotype CF06 (isolated from sugarcane cv CoC 671; MTCC accession number 12142) was sequenced using HiSeq 2000 platform (Genotypic solutions, Bengaluru) and assembled into contigs and scaffolds based on the pair-end library using Velvet assembler and contig extension/ scaffolding done by SSPACE.

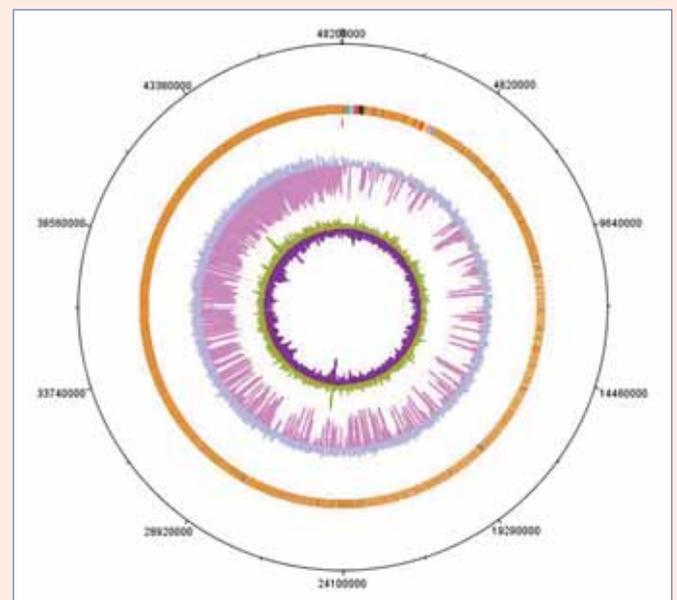
Genome of *C. falcatum* is 48.2 MB with predicted 12,270 genes at 150x coverage (Bio Project ID-272959, Accession number - PRJNA272959). This sequenced genome of *C. falcatum* is found comparable in size to the recently reported *Colletotrichum* spp. The arsenal of *C. falcatum* genes involved in hemibiotrophic lifestyle is found similar



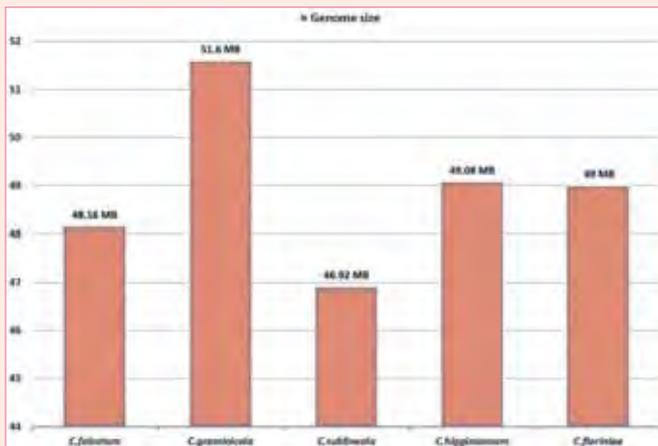
Severe devastation on sugarcane-crop in the recent red-rot epidemics in the east coast region of the country

causes frequent breakdown of varieties in the field. Overall, pathogen exhibited enormous variation in virulence, which was not clearly understood. Although about 11 pathotypes of the pathogen have been identified through differential host interaction, but the pathogenicity mechanism could not be properly established.

Lately, a few genes such as chitin synthase and those involved in melanin biosynthesis involved in pathogenicity were characterized. But the complete information on



Colletotrichum falcatum genome: The genome map constructed using ARTEMIS software - first circle denotes the size of genome (48.16 MB); second orange yellow frame consists of full length scaffolds; pink and blue colour circles denote presence of GC content and purple and green colour circles denote AT content.



Genome size of *C. falcatum* and other *Colletotrichum* spp.

to *C. graminicola* and *C. sublineola*, infecting related hosts maize and sorghum, respectively. The *falcatum* genome has revealed presence of plant cell-wall degrading enzymes (PCW), candidate secretory effectors (CSEPs), transposable elements, primary and secondary metabolites, membrane transporters, signaling molecules, CAZy, mating proteins, involved in the development, and sclerotic management proteins. Analysis of such genes revealed that *C. falcatum* has adopted a hemibiotrophic lifestyle with the expansion of secondary metabolites, membrane transporters and with the crucial role of plant cell-wall degrading proteins in establishing infection strategy with uniqueness.

Further, sequencing of expressed transcripts of the fungal pathogen using Illumina Hi-Seq technology generated a total of 53,410,513 reads (50 bp read length), specific to *C. falcatum*. The sequences were assembled into 24,732 transcripts, representing 23,136 predicted coding regions. GO analyses suggested prevalence of genes associated with cellular components like cell envelope, and

extracellular, macromolecules and membrane enclosed organelles and among the transcripts, genes associated in majority with molecular functions like antioxidant, binding, catalytic activities, electron carrier, enzyme regulator and transcription regulator. Genes associated with biological processes were categorized into anatomical structure formation, growth, pigmentation, establishment of localization and response to stimulus. KEGG pathway analysis suggested prevalence of genes encoding carbohydrates, lipids, glycans, cofactors, vitamins, terpenoids, polyketides kinases, proteases, glycoside hydrolases, cutinases, cytochrome P450 and transcription factors in transcriptome.

The transcriptome analysis has identified several putative pathogenicity determinants, candidate effectors and transition specific metabolites. Interestingly, large number of transcripts encoding biotrophy-necrotrophy transition and membrane transporters were identified, and gene enrichment analysis revealed that numbers of transporters encoded by *C. falcatum* are significantly more compared to other *Colletotrichum* species.

Exploration of genome and transcriptome has paved a way in understanding biology of red- rot pathogen, and this has identified several unique putative genes/functions required for its pathogenesis in sugarcane. This work lays the foundation for facilitating future research towards understanding this intriguing host-pathogen interaction.

R. Viswanathan, C. Naveen Prasanth, P. Malathi and A. Ramesh Sundar
ICAR-Sugarcane Breeding Institute
Coimbatore (Tamil Nadu) 641 007
e-mail: r.viswanathan@icar.gov.in

Transcriptional changes in immunoglobulin isotypes of rohu in response to *Argulus siamensis* infection

A challenge experiment with an ectoparasite *Argulus siamensis* was conducted to evaluate changes in adaptive immune response in skin, head-kidney and mucus of infected rohu (*Labeo rohita*) by quantitation of expression of Ig heavy chains by real-time PCR. IgM level reached its peak 30 d post-infection in head -kidney tissue, while IgM transcripts were below detectable range in skin and mucus. IgZ and IgD levels up-regulated significantly post-infection in all the three tissue samples. Early up-regulation of IgD was observed in skin and mucus, compared to head-kidney. This study has shown that

parasitic invasion can trigger varied expressions of immunoglobulin type to provide systemic as well as local protection in the host. Appearance of high level of expression of IgZ and IgD in skin and mucus, in particular, would pave the way for vaccine development against *A. siamensis*, which feeds on tissues.

ICAR-Central Institute of Freshwater Aquaculture
Kausalyaganga
Bhubaneswar (Odisha) 751 002
e-mail: director.cifa@icar.gov.in