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Analysis of promoter sequences from next generation transcriptome sequencing data of wheat near isogenic lines challenged with leafrust pathogen

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Promoters are non-coding regions in genomic that contain information crucial to the activation or repression of downstream genes. They are located upstream of the transcription start site (TSS) of a gene. The promoter region consists of certain short conserved DNA sequences known as cis-elements or motifs. The promoters are recognized by RNA polymerase, which then initiates transcription of the relevant gene under its control. Promoters control the expression of genes in response to one or more transcription factors. Prediction of promoters is of utmost importance in order to understand the regulation and expression patterns of genes, where confidence and accurate estimation is of fundamental requirement. With increasing numbers of plant genome sequences becoming available, it has become important to develop robust computational methods for detecting plant promoters. In the present study, four transcriptomes were sequenced using the Next Generation Sequencing technique SOLiD (Sequencing by Oligonucleotide Ligation and Detection). The CLC Genomics Workbench was used to assemble and analyze the transcriptomes. Preliminary examination of the sequences using softwares available at the website of SoftBerry revealed several promoters/ regulatory sequences. Softwares like TSSP-TCM, PlantProm DB, plant promoter database (ppdb) and GLAM2 were used to confirm promoters/ regulatory sequences/ motifs. The studies were focused on analysis of the promoters and check the expression levels of different promoters under different conditions of pathogenesis. We could obtain approximately 600 promoters and analysis of the expression profile revealed expression to be as high as 9133 times in infected conditions as compared to mock inoculated plants.

Biography

Sneha has completed her MSc in Bioinformatics in 2012 and Dharmendra Singh has submitted his Thesis for PhD in 2011 in the Department of Biotechnology, BIT Mesra, Ranchi. Dr Kunal Mukhopadhyay is a professor in the Department of Biotechnology, BIT Mesra, Ranchi since 2003 and specializes in plant molecular biology. The major focus of the research group is molecular biological studies of biotic stresses, particularly leafrust disease in wheat.

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Isolation of thermophile producing helicase for nucleic acid- based detection for fast diagnosis

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Helicase-producing thermophilic microorganisms were successfully isolated from hot springs in the from Ulu Legong Hot spring, Kedah, Malaysia and were identified up to genus level. The light and scanning microscopy technique were used to identify the morphology of the isolate. Chromosomal DNA from the organism was isolated and used to amplify 16S rRNA and UvrD gene fragments. The gene was amplified by a set of universal primers (F_UNI16S and R_UNI16S). The phylogenetic tree, homological analysis, and detailed comparison of the sequences showed that 16SrRNA gene sequence of the isolate had closest similarities with Anoxybacillus sp. Isolates gave PCR fragments of 2149bp which represent the UvrD gene and 1500bp which represent the 16S rRNA respectively of Anoxybacillus. Thermophile producing helicase (UvrD) was successfully isolated for Nucleic Acid- Based Detection for Fast Diagnosis.

Biography

Sreenivasan Sasidharan has completed PhD in Biotechnology from University Science, Malaysia. He is the lecturer in USM. He has published more than 100 papers in reputed journals .This project funded by Universiti Sains Malaysia research grant RUC (1001/ PSKBP/86300110).

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