

CHAPTER 48

PLANT MOLECULAR BIOLOGY

Doctoral Theses

391. AGARWAL (Pinky)
Transcriptome Analysis During Seed Development in Indica Rice and Characterization of Seed-Preferential Genes/Promoters in Transgenic Systems.
Supervisor : Prof. Akhilesh K. Tyagi
Th 16436

Abstract

One common features of the meals of about 50% population around the world is the consumption of the careal crop rice. It is estimated that India needs to produce 122 million tonnes of rice by 2020 to fulfill its requirements. Thus efforts are being made to improve the yield of this crop. Studies the entire process of seeds development in this crop plant. The seed development stages have been classified into five stages, depending on the significant changes occurring in the seed. The classes are S1 (0-2 DAP), S2 (304 DAP), S3 (5-10 DAP), S4 (11-20 DAP) an S5 (21-29 DAP). A microarray has been performed on all the above stages.

Contents

1. Literature review on seed development. 2. Materials and methods. 3. Results. 4. Discussion. 5. Summary and conclusions. Bibliography.

392. AMANJOT SINGH
Rice (*Oryza sativa* L.) Hsp100 gene Family : Genetic Complexity and Regulation.
Supervisors : Prof. Anil Grover and Prof. Indranil Dasgupta
Th 16440

Abstract

The study reaffirms that OsClpB proteins are important component in the heat shock response. So far, only the

OsClpB-Cyt has been analyzed in details in this context. It is important that wet experiments are also done with other two isoforms of OsClpB protein in near future. The expression profilings of all ClpBs need to be studied under heat as well as different other abiotic stresses which can potentially affect the protein quality. It should be interesting to look for the proteins with which ClpBs interact. It should be worthwhile to analyze how ClpB protein refold the deantued proteins in various compartment of the cell namely cytoplasm, mitochondria and chloroplast.

Contents

1. Introduction. 2. Review of literature. 3. Material and methods. 4. Results and discussion. 5. Summary and conclusions. Bibliography.

393. CHAUHAN (Harsh)
Development of Doubled Haploid Technology for Transgenics and Molecular Characterization of Heat Tolerance in Wheat.
 Supervisor : Prof. Paramjit Khurana
Th 16435

Abstract

Describes the cloning and characterization of the wheat chloroplastic small HSP26 and cloning of its promoter by directional genome walking. Both the gene and the promoter were characterized through transgenic approach using Arabidopsis thaliana as a model system. Detailed transcription analysis was undertaken through subtractive cDNA hybridization. Some of the genes representing different developmental stages were analyzed in detail through real time quantitative PCR. Establishes the use of DH for utility in genetic transformation efforts and shows the stable integration of the introduced gene, HVA1, for abiotic stress tolerance in wheat.

Contents

1. Transcriptome analysis of high temperature stress in wheat and characterization of genes of interest. 2. The chloroplastic small heat shock protein (sHSP26) is necessary for tolerance to heat stress and taken part in seed maturation to germination. 4. Summary and conclusions. Bibliography.

394. MUKHERJEE (Shubhankar)
Identification and Systematic Analyses of Genes Encoding SET Domain and Polycomb Repressive Complex 2 (PRC2) Proteins in Rice and their Expression Profiling.
 Supervisor : Prof. Jitendra P. Khurana
Th 16439

Abstract

Deals with the identification of SET-domain coding and PRC2 complex genes in rice, their expression analyses across a large number of tissues related to vegetative and reproductive growth in rice, and functional characterization of few genes among these groups to deduce their role in the development of rice plant. The identification and proper classification of SET-domain containing and PRC2 complex proteins were achieved in rice, and light was shed upon the relationship between the SET-domain proteins conserved among plant and other kingdoms of life. Expression analyses of these genes (SET-domain coding and PRC2 complex) provided us the preliminary clues regarding the tissue-specific expression of particular genes and their expression co-relatedness among small subsets of tissues.

Contents

1. Review of previous work. 2. Material and methods. 3. Results and discussion. 4. Summary and conclusions.

395. SHARMA (Pooja)
Molecular Characterization and Functional Validation of Cryptochrome Genes in Brassica and Rice (Oryza Sativa ssp. Indica)
 Supervisor : Prof. Jitendra P. Khurana
Th 16434

Abstract

Provides functional evidence for the role of BnCRY1 in regulating photomorphogenic responses, such as hypocotyl growth inhibition and anthocyanin accumulation; the over-expression of BnCRY1 makes a plant over-sensitive to blue light imparting a semi-dwarf phenotype of B. juncea plants. The characterization of BnCRY2 also revealed its redundant role (vis-a-vis BnCRY1) in regulating plant height, and also in controlling radial expansion of the stem and cotyledon size.

1. Review of literature on structural organization, signaling and functional significance of blue light receptors : Cryptochromes.
2. Materials and methods. 3. Results and discussions.
4. Summary and conclusions. Bibliography.

396. SHARMA (Rita) Nee RITA ARORA
Transcriptome Profiling During Panicle Development in Indica Rice and Functional Characterization of Candidate Genes and Promoters in Transgenic Rice and Arabidopsis.
 Supervisors : Dr. Sanjay Kapoor and Prof. Akhilesh K. Tyagi
Th 16437

Abstract

Efforts to delineate the key genes involved in rice reproductive organ development. A large number of genes have been characterized in Arabidopsis for involvement in different aspects of flower development unfolding the floral regulatory pathways. Two high-throughput techniques, microarrays and LongSAGE, were employed for genome-wide transcript profiling during temporal stages of panicle development. To evaluate the panicle-specific promoters, five genes, exhibiting stage-specific high-level expression during panicle development, were selected and promoter-reporter constructs were generated by using 5' regulatory regions of these genes.

Contents

1. Review of literature on molecular basis of flower development: A comparative account between Arabidopsis and rice.
2. Materials and methods. 3. Results. 4. Discussion.
5. Summary and conclusions. Bibliography.

397. SOLANKE (Amol Kumar U.)
Sequencing of Part of Tomato Chromosome 5 and Study of Stress-Regulated Genes in Tomato.
 Supervisor : Dr. Arun K. Sharma
Th 16438

Abstract

Deals with the sequencing of a part of chromosome 5 and the study of stress regulated genes from tomato. For tomato genome sequencing project, physical mapping was carried out for BACs

of short arm of chromosome 5. Twelve BAC clones associated with 5 nucleation points have been sequenced and submitted to GenBank and SGN database. To speed-up the sequencing project, new CAPs markers have been designed from gene-rich BAC end sequences using introgression lines, so that these BAC clones could be used directly for sequencing. OSISAPI, a rich gene characterized for stress tolerance in tobacco, had been expressed in tomato and molecular characterization of transgenic plants was carried out. Further, complete Stress Associated Protein (SAP) gene family has been identified, clones and characterized from tomato. To understand global changes during cold stress in tomato, subtractive cDNA libraries were prepared from the cold-treated tomato seedlings and genes were functionally annotated.

Contents

1. Review of literature.
2. Materials and methods.
3. Results.
4. Discussion.
5. Summary and conclusions. Bibliography.