

CHAPTER 17

GENETICS

Doctoral Theses

158. ANGRISH (Varsha)
Genetic and Functional Validation of a Putative ORF, Coding for Ketol-Acid Reductoisomerase (KARI) from Vibrio cholerae Strain 0139
Supervisor : Prof. Sheela Srivastava
Th 15294

Abstract

Isolates and characterizes the putative KARI ORF from Vibrio cholerae 0139 and inactivating the same as part of the anti- cholera strategy and protein for developing a control against the enzyme but truly against the pathogen V. cholerae also identify and characterize a novel drug target V. cholerae, and propose it as an attractive anti-cholera strategy for therapy.

Contents

1. Introduction. 2. Materials and methods 3. Results 4. Discussion
5. Summary and conclusions

159. DATTA (Sudipta)
Analysis of CaMV 35S Promoter and Testing Synthetic Promoters for Homology based Gene Silencing
Supervisor : Dr. Pradeep Kumar Burma
Th 15295

Abstract

Develops a synthetic promoter by bringing together the modifications which were earlier tested individually. As the developed synthetic promoters did not function at par with 35S, it was decided to identify the cis-elements of the subdomains B3 and B4. This was done by testing the role of CRWE in transgenic lines as well as by Linker Scanning Mutagenesis of subdomain B4. The main reason for developing the synthetic promoters is to avoid TGS. Tests the influence of silencing loci (271-known

to inactivate 35S promoter) on the synthetic 35S truncated (domain A) promoter, developed by placing known cis-elements of domain A in a variant DNA stretch.

Contents

1. Introduction. 2. Analysis of CaMV35S promoter and synthetic promoters 3. Analyzing the effect of silencing loci on the modified domain A promoters. & Bibliography.

160. MALHOTRA (Mandira)
Genetic Analysis and Manipulation of IAA Biosynthesis in Rhizospheric Isolates : Azospirillum brasilense SM and Pseudomonas fluorescens Psd.
 Supervisor : Prof. Sheela Srivastava
 Th 15296

Abstract

Elucidates the molecular mechanism of IAA biosynthesis by two natural rhizospheric isolates, Azospirillum brasilense SM and Pseudomonas Fluorescens Psd. Deciphers the genetic basis of IAA biosynthesis by rhizospheric bacterial isolates and analyzing the effect of manipulation of such a characteristic.

Contents

1. Introduction. 2. Materials and methods 3. Results 4. Discussion 5. Summary & conclusions

161. PANDEY (ROOPALI)
Transgenic Tomatoes for Improved Fruit Characteristics Through Genetic Manipulation of Polyamine Biosynthesis.
 Supervisor : Dr. M. V. Rajam
 Th 15468

Abstract

The commonly cultivated tomato provides a major focus for improvement of crop quality through genetic engineering. Identification of ripening related cDNAs has enabled the modification of specific aspects of ripening by manipulating gene expression of ripening genes. Recent study by the over-expression of polyamine biosynthetic gene S-adenosylmethionine decarboxylase (SAMDC) was found to be useful in delaying ripening as well as fruits with improved characteristics.

Biosynthetic pathways for polyamines (PAs) and ethylene in plants share S-adenosylmethionine (SAM) as a key intermediate. Accumulation of PAs in the developed transgenics (both LeADC and LeODC) showed significant delay in on-vine ripening (about 10-15 days) and extended shelf life of 10-15 days as compared to controls. The transgenic fruits showed increased cold tolerance as compared to wild-type fruits.

Contents

1. Introduction. 2. Review of literature. 3. Materials and methods. 4. Results and discussion. 5. Summary and conclusions. 6. References and appendix.

162. RAMCHIARY NIRALA
Molecular Mapping of Yield Components and Seed Glucosinolate Traits in Brassica Juncea.
 Supervisor : Prof. Akshay K. Pradhan
 Th 15297

Abstract

Maps quantitative trait loci for agronomic and yield related traits and aliphatic glucosinolates in order to facilitate the marker-assisted introgression of favourable alleles from east European to Indian type Brassica juncea. Dissects the yield-related traits into their component loci (QTL) and genes involved in glucosinolates biosynthesis to develop a suitable breeding strategy for the genetic improvement of B. juncea.

Contents

1. General introduction. 2. Construction of high-density molecular map 3. QTL mapping of agronomic and yield component traits 4. Genetic analysis and tagging of seed glucosinolate traits 5. Implications of QTL mapping in B. juncea breeding. Summary and conclusion.

163. SOHAN LAL
Genetic Susceptibility to Parkinson's Disease : Insights from Candidate Genes from Multiple Pathways.
 Supervisor : Prof. B.K. Thelma
 Th 15467

Abstract

Investigates the role of 50 SNPs from 25 candidate genes involved in the synthesis and metabolism of dopamine, metabolism of xenobiotic compounds, genes from the oxidative stress and inflammatory pathways and neurotrophic factors in the development of PD, using a case control based association analysis. To avoid the limitation of non-replication of results across different association studies, investigations were first carried out in a South Indian cohort and then replicated in a much larger North Indian sample set. Of all these genes tested, we observed a significant allelic/genotypic association of only NAD[P]H: quinone oxidoreductase 1 (NQO1) SNP rs1800566 ($p < 0.05$) in both South and North Indian sample sets. In addition, four dopamine β -hydroxylase (DBH) haplotypes were associated with PD in the South Indians and three of these were replicated in a larger sample set from North India. Of these, two haplotypes, C-A-G-C ($p = 0.000001$, OR = 0.49; 95%CI = 0.37-0.65) and C-A-G-T ($p = 0.000005$, OR = 1.76; 95%CI = 1.38-2.25) showed a highly significant association with the North Indian cohort, which remained significant even after Bonferroni correction for multiple comparisons was applied (critical $p = 0.001$ for 50 tests). These observations suggest that NQO1 and DBH genes are important candidates conferring susceptibility for developing idiopathic PD in Indians and this is the first study from India.

Contents

1. Review of literature and introduction. 2. Materials and methods. 3. Candidate gene polymorphisms and their contribution to sporadic PD. 4. Genotype-phenotype correlations in PD. 5. LRRK2 gene mutations and PD. 6. Appendix and references.

164. TIWARI (Arun Kumar)
Role of Oxidative Stress Pathway Gene Polymorphisms in two Complex Phenotypes: Chronic Renal Insufficiency and Tardive Dyskinesia.
 Supervisor : Prof. B. K. Thelma
 Th 15466

Abstract

Investigates the contribution of polymorphisms in genes from the oxidative stress pathway to the development/ progression of two complex phenotypes, namely, chronic renal insufficiency

(CRI) in type 2 diabetes mellitus patients and tardive dyskinesia in chronic schizophrenia patients. Superoxide overproduction has been proposed as a single unifying mechanism leading to insulin resistance, β -cell dysfunction, impaired glucose tolerance and ultimately to type 2 DM and diabetes associated macro and microvascular complications. Analysing the functional polymorphisms in genes involved in the detoxification of these free radicals or other downstream pathways, demonstrated the role of polymorphism(s) in SOD2 (MnSOD), UCP1, UCP2, eNOS, GSTP1 and GFPT2 genes in chronic renal insufficiency among type 2 DM patients. A notable finding common to all observations made in this study was the excess of the wild type/functionally efficient allele.

Contents

1. Review of literature and introduction (OS &CRI). 2. Materials and methods (OS &CRI). 3. Results (OS &CRI). 4. Discussion (OS &CRI). 5. Oxidative stress and tardive dyskinesia. 6. CYP1A2 and tardive dyskinesia. 7. Annexure and references.