Chapter 1

Figure 1.1 Contribution of Indian agriculture to global production of chickpea............. 4

Figure 1.2 The potential seed yield of about 5 t/ha has been reported in chickpea......... 8

Figure 1.3 Schematic representation of the life cycle of wilt causing soil borne fungi, depicting saprophytic and parasitic growth and successive phases of colonization and pathogenesis (Beckman and Roberts, 1995)........................................ 8

Figure 1.4 LG2 and LG5 from the integrated genetic map of chickpea generated by Millan et al., 2006 data from Winter et al. (2000), Huttel et al. (2002) and Pfaff & Kahl (2003)........................................................................................................ 21

Figure 1.5 The scheme of classical cDNA-AFLP................................................................ 26

Chapter 2

Figure 2.1 a) Chickpea seedlings hydroponically growing in growth chamber..............46

b) JG-62 seedling showing wilting symptoms after infection with FOC1 while Vijay seedlings are healthy after infection

c) Root morphology of JG-62 and Vijay after infection

d) Difference between infected roots of Vijay covered with fungal mycelial mass and non-infected roots without any fungal mycelia

Figure 2.2 Representative amplification profiles generated by RAPD primers.............47

Figure 2.3 Representative amplification pattern from three cDNA libraries, resistant control (RC), resistant infected (RI) and susceptible infected (SI), displayed by cDNA-AFLP visualized on 6% polyacrylamide gel by silver staining......... 48

Figure 2.4 TDFs identified after differential display were categorized into five classes and are schematically represented as the three circles representing the three libraries under study Green- Resistant infected; Red- Susceptible infected; Blue-Resistant control, and the area under the overlap denotes the different classes detailed in Table 2............................................................................................... 49

Figure 2.5 Reverse northern analysis of TDFs identified by cDNA-AFLP and cDNA-RAPD in chickpea roots............................................................................ 53

Figure 2.6 Induction of transcript accumulation in chickpea roots after challenge with FOC1 analyzed by Northern blot................................................................. 56

Chapter 3

Figure 3.1 RT-PCR amplification of the two 14-3-3 genes from Cicer arietinum root cDNA................................................................................................................. 71

Figure 3.2 Deduced amino acid sequence alignment of the two chickpea 14-3-3 isoforms with 14-3-3 protein sequences from Medicago (ABE79090), V. faba (BAB17822, P42653, P42654), P. sativum (CAB42546, CAB42547), V. angularis (BAB47119), L. esculentum (T07387, T07389, T07383, CAB65693), G. hirsutum (ABD63905), M. amurensis (AAC15418), P. canescens (AAD27823), retrieved using blastx from GenBank.......................... 73

Figure 3.3 The phylogenetic tree generated using deduced amino acid sequences of the two chickpea 14-3-3 gene isoforms (Ca1433-1 and Ca1433-2) and the protein
sequences retrieved from the GenBank database by each of the isoform using blastp………………………………………………………………………

Figure 3.4 A phylogenetic tree shows the topology of the chickpea (Ca1433-1 and Ca1433-2) and Arabidopsis (GRF) 14-3-3 families separated into four major groups, based on cDNA sequences………………………………………………………… 75

Figure 3.5 The Ca1433-1 and Ca1433-2 genes from C. arietinum were blasted using the CVit Blast tool to place them on the Medicago physical map………………… 76

Figure 3.6 Reverse transcription (RT)–PCR analysis of Ca1433-1 gene expression patterns in the incompatible and compatible chickpea-FOC1 interactions in a time course of 1-8 DAI (Days after Inoculation)…………………………………… 78

Figure 3.7 Reverse transcription (RT)–PCR analysis of Ca1433-2 gene expression patterns in the incompatible and compatible chickpea-FOC1 interactions in a time course of 1-8 DAI (Days after Inoculation)…………………………… 79

Figure 3.8 Phosphopeptide binding to plant 14-3-3…………………………………… 81

Figure 3.9 A 3D model for Ca1433-2 was built using deduced amino acid sequences which were loaded into the CPH-modeling server to generate the PDB file based on homology…………………………………………………………… 82

Figure 3.10 The information about Arabidopsis 14-3-3 gene structures………………………… 84

Chapter 4

Figure 4.1 Transposable elements classified as class I and class II types based on the presence and arrangement of genes…………………………………… 95

Figure 4.2 Reverse northern of TDFs similar to retroelements identified by cDNA-AFLP.. 101

Figure 4.3 The frequency of TCs from different crops annotated as transposable elements in the TIGR database is represented as percentages…………………………………… 104

Figure 4.4 Frequency of transposable element like ESTs in the TIGR database represented as percentages from Medicago truncatula and Glycine max………. 107

Figure 4.5 Frequency of transposable element like ESTs in the TIGR database represented as percentages from the roots of Medicago truncatula and Glycine max during different stress conditions………………………………………………………… 110

Figure 4.6 Number of ESTs in the TIGR database annotated as TEs from different plant parts of Medicago truncatula and Glycine max represented as percent……… 113

Chapter 5

Figure 5.1 Different genes that are induced during the host-pathogen interaction in the resistant and susceptible varieties…………………………………… 118

Figure 5.2 A time-space model of longitudinal and lateral host-parasite interactions…… 121