5.0 Summary

Resistance can be host-specific or non-host-specific. In case of host-specific resistance, specific pathogen recognition is governed by resistance genes. The specific interaction of R-gene of the host and **avr** gene of the pathogen results in changes in certain components of the plant signal transduction pathways, which ultimately leads to localized cell death at the site of infection and thus prevents further growth of the pathogen. In case of race specific resistance, a series of plant disease resistance genes have been cloned by transposon tagging or map-based cloning from several crops and model species such as *Arabidopsis thaliana*. With the help of molecular marker technology, it is possible to generate a genetic map of chickpea that holds promise for use in marker-assisted selection and positional cloning of agronomically important genes.

An essential tool for characterizing genomes is the availability of Bacterial artificial chromosomes (BAC) libraries with large genomic DNA inserts. Plant BAC libraries have been used for a number of structural genomic applications. Of the many uses, one of the very essential uses is to develop the resources for the positional cloning of genes.

Chickpea (*Cicer arietinum* L.) is a self-pollinated, diploid annual species. It is the third important grain legume crop worldwide after pea and common bean. It is cultivated mainly on Indian sub-continent, in West Asia, North Africa, Americas and Australia. The productivity of this crop could not be enormously increased by conventional breeding. Major constraints for increasing seed productivity are the fungal diseases fusarium wilt caused by *Fusarium oxysporum* and Ascochyta blight caused by the pathogen *Ascochyta rabei*. Fusarium wilt is soil borne disease and chemical control is expensive and impractical. Resistant cultivars are the most effective means of controlling the disease. This work describes developing a genetic linkage map of Chickpea, tagging the wilt resistance loci and construction of a large insert BAC library for identification and cloning of resistant genes for *Fusarium* wilt. The first step towards identification and isolation of R-genes is the availability of a genetic linkage map and tightly linked molecular landmarks. A genetic linkage map of chickpea in an intraspecific cross of WR-315 (a resistant cultivar) and C-104 (a late wilting cultivar) with 24 newly mapped molecular landmarks was developed. The development of linkage maps which facilitates tagging and analysis of genes requires the need of large numbers of polymorphic markers such as AFLP and STMS which has been widely
used in genetic mapping. In this study, low levels of polymorphism were detected with both AFLP and STMS markers. The most closely linked marker, STMS9 was identified at a distance of 0.2 cM from foc1 in linkage group 4 (LG 4) which corresponds to LG 2 of chickpea consensus map. Additionally, 2 more STMS markers STMS10 and STMS11 were identified at a distance of 1.0 and 3.0 cM respectively, flanking the foc1 loci. Newly identified 24 molecular landmarks, once integrated into the reference map of chickpea may also be useful to tag other phenotypic traits. The tightly linked markers would provide the molecular basis for marker assisted selection, introgression breeding for wilt resistant cultivars and finally to clone the candidate R-gene for foc-1 resistance.

As positional cloning is a promising method for isolating and studying genes, large insert genomic libraries, YACs and BACs are fundamental tools for identifying genes during positional cloning. A 10X genome coverage Chickpea BAC library was constructed having 42,240 BAC clones. The library was screened with the two closely linked markers STMS9 and STMS10 from the genetic linkage map. In total eighteen BAC clones were positive, amongst which four BAC clones were positive with both STMS9 and STMS10 and rest fourteen clones were positive with either STMS9 or STMS10.

Further, during parallel work done in the laboratory on transcript profiling during chickpea-Fusarium interaction, a gene coding for Leucine rich repeat (LRR) containing protein was identified. As most of the R genes cloned so far contain LRR domain, it was quite intriguing to clone and characterize this gene. Towards this we started with 3' and 5' RACE is in progress.

As a future plan these positive BAC clones with tightly linked molecular markers for Fusarium loci would be used to clone and characterize the R-gene for foc resistance and to obtain a full length CaLRR1 and to do the functional characterization.