Chapter 1
Introduction
Development, growth, and survival of eukaryotic organisms necessitate precise and coordinated regulation of thousands of genes. Majority of the protein coding genes in eukaryotes are regulated at the transcriptional level by promoters. The nucleotide sequences present in cis and upstream to the coding sequences, called promoters are critical in specifying the pattern of gene regulation. Promoters are modular structures and consist of short stretches of nucleotide sequences (6-10 bases) each defining a specific expression pattern. The combination of such elements imparts unique transcriptional gene regulation of cognate genes. Promoter sequences help in accurate transcription initiation by recruiting the RNA polymerase II for transcription initiation complex at core promoter sequence. These sequences not only control the spatial and temporal pattern of gene expression but also determine level of transcription. Study of promoters is not only helps in understanding gene regulation but is also relevant for genetic engineering.

Identification of tissue, developmental stage and environmental stimuli specific plant promoters has emerged as one of the frontier areas of plant molecular biological studies. The functional genomic approach like T-DNA based promoter trapping has become the popular choice for identification of novel plant promoters over the conventional approaches which require information about the cDNA or mRNA of the gene.

The trichomes present over aerial plant parts have been shown to retard herbivory and also serve as small factories for synthesizing biomolecules in plant systems. Besides this, study on trichomes has also helped in understanding the basic mechanism of cellular development, differentiation, and cell fate determination. Therefore, it is worthwhile to identify a promoter sequence that is able to drive gene expression specifically in the trichomes. Despite the availability of huge proteome (Wienkoop et al. 2004) and transcriptome (Kryvych et al. 2008) data on trichomes from a total of 14 plant species only a few promoter sequences are available till date, thus identification and isolation of trichome specific promoter would thus be very useful to engineer plants producing important metabolites in trichomes. Thus, trichome specific promoter sequence was chosen as the subject of investigation for the present study using promoter trap approach.
The objectives of the study were as follows:

i) Screening and characterization of T-DNA tagged mutant promoter trap population for trichome specific expression

ii) In-silico analysis of the sequence obtained

iii) Evaluation of the efficacy of the putative promoter

iv) Characterization of the $SHN2$ gene