Prelude
Silk is known for its elegance, beauty and glamour and therefore popularly known as the queen of textiles. The science of silk production through mulberry (*Morus* spp.) cultivation and silkworm rearing is called mulberry-sericulture. The domesticated silkworm, *Bombyx mori* L. is a monophagous insect and its larvae feed solely on mulberry leaves to produce natural silk. In India about 90% of the silk production is contributed by the mulberry sector and the rest by Tasar (Tropical and Oak), Muga and Eri. Mulberry is a perennial, tree crop belonging to the family Moraceae, and is naturally distributed in the temperate and subtropical parts of northern hemisphere. About 50 countries in the world are reported to be engaged in sericulture of which 14 are in Asia. The total area under mulberry cultivation in India is about 1,85,000 hectares covering 19 states (Anonymous 2008). The past assessment depicts that more than 60% of the total cost of cocoon production spent towards mulberry cultivation (Das and Krishnaswami 1965). The major portion of the area under mulberry cultivation in India is in rain-fed or moisture deficit condition. Drought and limited water resources are the two major constraints to realize the potential yield of mulberry. In this context, mitigating drought affects by crop improvement and sustaining productivity with less water consumption are the major focuses in mulberry breeding programme. The complexity of the adaptation of the plants to water stress involves several diverse adaptive mechanisms. This has been one of the major reason for slow growth in crop improvement for moisture stress. Since the regulation of these traits is multigenic, a comprehensive approach is needed to improve crop productivity under water-limited situations. Under moisture deficit conditions, the nutritive value of the mulberry leaf decreases and thus becomes unsuitable for rearing highly productive silkworm races like bivoltine and bivoltine x multivoltine hybrids. Non-availability of drought tolerant mulberry lines for cultivation has seriously hampered desired level of productivity in the water deficit regions and thus affected the targeted silk production in the country. Therefore, development of improved variety is inevitable for cultivation in moisture deficit condition. Even though, the drought management practices offer alternative options to improve the realizable yield, it is increasingly understood that genetic improvement of crops for water stress tolerance is more rewarding. As breeding for drought tolerance *per se* is difficult, the key to enhancing productivity under water limited conditions lies in the mitigation of drought through trait improvement of cultivars. To achieve this, water use efficiency (WUE) and water mining capacity of the plant by root system need to be genetically improved. The conventional breeding methods based on morphological characters are found to be less efficient as they lack resolving power and
often mislead due to environmental influences (Wang and Patterson 1994). This problem can be addressed efficiently by biotechnological approaches, like marker assisted selection (MAS) based on the development of molecular linkage maps of crop species.

Molecular markers based genome characterization overcomes the problems that are associated with phenotype-based identification and also allow early selection of the target traits at seedling stage. Molecular marker technology has greatly contributed in identification of DNA markers associated with the traits and ultimately its effective utilization in marker assisted breeding for crop improvement and created the possibility of formulating new breeding strategies to develop varieties with specific traits. Phenotype is a result of genes x environment interaction and hence cannot be considered as stable indicators for the trait of interest. In quantitative trait loci (QTL) analysis, phenotypic markers are assessed along with the genotypic markers. These traits are termed as polygenic or quantitative because they result from a combined action of several genes (Tanksley et al. 1989). QTLs are genetic markers that are strongly associated with highly desirable characteristics of agronomic importance. QTL mapping and associated studies are becoming widespread approaches to dissect the genetic determination of many economically important traits in plant breeding. Numerous molecular marker linkage maps have been recently constructed in different tree crop species, thereby facilitating the localization of genes controlling important traits (Lu et al. 1998).

There are two component traits responsible for developing lines for moisture stress tolerance. One of them is WUE, which is represent a given level of biomass or grain yield per unit of water used by the crop and the second one is by improving the rooting characters. With increasing concern about the availability of water resources in both irrigated and rain-fed sericulture, there is renewed interest in trying to develop an understanding of how WUE in mulberry can be improved. The difficulty in identifying a physiological parameter as a reliable indicator of yield in dry conditions has suggested that yield performance over a range of environments should be used as the main indicator for drought tolerance (Voltas et al. 2005). Furthermore, only the WUE is not sufficient for improvement in yield so the rooting characters needs to be taken into consideration for overall improvement of yield under stress condition.

In this background, the study was envisaged to develop trait specific (WUE and root) mapping populations by identification of parental lines from diverse germplasm resources for construction of parent specific genetic linkage maps using polymerase chain reaction (PCR) based DNA markers. The main aim of the study was to locate the genomic regions (QTLs) controlling traits associated with WUE and rooting in mulberry. Besides, it was also planned to introgress high
WUE and high rooting traits in the same genetic background for selection of recombinants of mulberry with improved tolerance to moisture stress.

**The structure of the thesis is as follows:**
The study has been described in four distinct chapters with specific objectives. They are as follows:

**Chapter 1**
**Identification of parental lines for the development of mapping population for WUE and root traits**
The study involved screening of mulberry germplasm consisting of about 300 accessions in the field gene bank of Central Sericultural Research and Training Institute (CSRTI), Mysore to assess the genetic variability for moisture stress tolerance component traits and other growth parameters for identification of suitable parental combination for the development WUE and root trait specific mapping population. Further, it was aimed to identify polymorphic DNA markers among the selected parental lines for genome mapping and also to estimate diversity and interrelationships. A separate experiment was also undertaken for identification of divergent parental line for the development of mapping population for photosynthetic efficiency.

**Chapter 2**
**Development of mapping population for WUE trait, construction of linkage map and QTL analysis**
Under this chapter, trait specific mapping populations for WUE were developed using contrasting parental lines in mulberry identified under Chapter-1. The selected mapping population was used for phenotyping for WUE and related traits as well as genotyping using molecular markers for construction of parent specific linkage maps. The linkage map was used for identification of QTLs governing important traits related to WUE in mulberry.

**Chapter 3**
**Development of mapping population for root trait, construction of linkage map and QTL analysis**
The research work under this Chapter involved the development of mapping population for root trait using two pairs of contrasting lines of mulberry identified under the Chapter-1. The main purpose of the study was to develop parent specific genetic linkage maps using DNA markers. Further,
phenotyping of F1 segregating population was used map the genetic loci controlling mulberry growth/productivity and rooting.

Chapter 4
Introgression of WUE and root traits in mulberry and identification of improved lines
The main aim of the study under this chapter was the development of introgressed lines (ILs) by crossing the parental genotypes with high WUE and high rooting ability and to identify superior recombinants with improved performance for moisture stress by accurate phenotyping. The introgressed lines could be used for validation of identified QTLs for WUE and root traits in mulberry.

Each chapter is provided with a brief account of the importance of the study along with specific objectives under the section ‘Introduction’. Relevant research work already undertaken in the area is briefly discussed in ‘Review of literature’. The research materials and methodologies used in the study are described under the section ‘Materials and Methods’. The experimental outcomes and inferences along with conclusions are presented in the ‘Results’ and ‘Discussion’ section of each chapter respectively. The important contents of all the chapters have been summarized under ‘Summary and conclusions’.