

PREFACE

Understanding the responses of plants to their environment in terms of adaptability and performance is of paramount importance for selecting and/or developing cultivars that can withstand the unwanted environmental changes. Apart from the interest in factors important for ecological and evolutionary distribution, much of the present day interest in agri-biotechnology is on selecting stress resistant quality cultivars. Modern agriculture is affected by environmental factors such as water-logging, drought, temperature, light, and salt stress. Sustainable agriculture in harsh environment requires an understanding of the ways that plant antioxidants and genes respond to abiotic stresses. In recent years, biochemical and transcriptional analysis of plants under abiotic stress brought to light some of the complex mechanisms of stress tolerance. Understanding of mechanisms that operate in signal perception, transduction and downstream regulation as well as cellular pathways that are involved in abiotic stress responses provide valuable information of plant's tolerance to such stresses.

Drought tolerance is a complex trait, expression of which depends on the action and interaction of different morphological, physiological and biochemical characters. The level of drought stress correlates with the degree of changes in these characters which provides the scope for identifying drought tolerant cultivars and the study of tolerance mechanism at molecular level thereof. Under drought, plants accumulate various compatible solutes and antioxidants for maintaining water homeostasis. For the biosynthesis of these solutes and compounds, numbers of genes and genetic pathways get activated. Hence, a detail knowledge of physiological and biochemical changes under drought provides the scope of correlation with transcriptional analysis, and considerably broadens the possibility of understanding the lying mechanism of tolerance.

Identification and characterization of genes expressed differentially under drought stress has gained much attention in crop plants research. Dramatic improvements in DNA sequencing technology have paved the way for the use of large-scale single-pass cDNA sequencing which has given rise to large EST collections to address many

biological questions. It facilitates to study the genetic mutation, conservation, repeat markers, phylogeny as well as functional and comparative genomics, finally to answer questions of tolerance to drought by some genotypes. The answers itself provide us the scope for identifying tolerant cultivar and understanding their lying mechanism of tolerance. Moreover, recognition of genes and genetic pathways that involved in response to drought enhances the possibility of promoting crop improvement through direct genetic modification.

Being a woody perennial with a life span of more than 60 years, tea plant experiences several abiotic stresses. Amidst all, drought is an important recurrent constraint to world tea cultivation including India. For the identification, selection and/or production of drought tolerant cultivars, there is an urgent need of comprehensive physiobiochemical and molecular analyses of drought stress responses of this important cash crop. Hence, the present work as embodied in this thesis entitled 'Generation and Characterization of Expressed Sequence Tags of Tea (*Camellia sinensis* (L.) O. Kuntze)' was initiated in the year 2007 with broad objectives of physiobiochemical and transcriptional analyses in tea under drought stress keeping in mind the following specific objectives.

- 1) Physiological and biochemical analyses of drought stress responses.
- 2) Construction of cDNA libraries.
- 3) Sequencing of Expressed Sequence Tags and *in silico* analysis

The status of this work with respect to physiobiochemical and transcriptional analyses of tea and their results and inferences drawn thereof is presented in seven major chapters in the thesis. Besides, there are also supplementary details given as appendix at the end.