Chapter 1:

Introduction
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Plants spend their whole life cycle being confined to the place where they have germinated or have been transplanted. When faced with environmental adversities, either they fight back or succumb to death. Fighting back and resilience against the environmental odds are not the characteristics of every plant, but a few which possess them. It depends on the ability of the plants to be equipped with intricate gene regulatory mechanisms. The cellular machinery in response to stress includes different second messengers (e.g., calcium (Ca\(^2+\)), cyclic nucleotides, phospholipids, sugars, amino acids), transcription factors (activators and repressors), transcriptional, post-transcriptional, translational and post-translational regulators; enzymes encoding compatible solutes, solute transporters, reactive oxygen species etc. The surviving plants integrate these several components of different mechanisms in an orderly manner to create an equilibrium between the internal and the external milieu which ultimately favors its growth and development.

Plants that successfully withstand stresses are constantly monitoring their external milieu and are transmitting that information inside the cells triggering a timely and appropriate cellular response. But the final execution of the cellular response happens in a stepwise manner. One of the important changes that happen immediately upon stress perception is the increase in the cytosolic [Ca\(^{2+}\)]. The occurrence of Ca\(^{2+}\) as a second messenger is ubiquitous and is involved in almost all the plant processes. Accumulating evidences indicate that Ca\(^{2+}\) mediated signaling is involved in the transduction of physical signals such as temperature, wind, touch, light, and gravity; oxidative signals such as those arising from pathogen attacks; and hormone signals such as ethylene, abscissic acid (ABA), gibberellins, and auxin. Specificities of different Ca\(^{2+}\) signaling pathways are impregnated in the specific “Ca\(^{2+}\) signatures”, which are patterns of information encoded by frequency and amplitude of [Ca\(^{2+}\)]. Moreover, the concept of nuclear Ca\(^{2+}\) signaling is getting on a firmer base day by day. Many Ca\(^{2+}\) regulated transcription factors have already been described in animals. Considering the importance of transcription factor as the master regulator of the cell and the crucial role of Ca\(^{2+}\) signaling during different stresses, engineering
plants with Ca\textsuperscript{2+} regulated transcription factors should be regarded as a very promising approach.

To genetically engineer plants towards stress tolerance with calcium regulated transcription factors, a detailed understanding of the signaling pathways they are involved in, is very much necessary. Moreover, the regulation of the particular signaling pathway differs from plant to plant. Hence the information and knowledge gathered for a particular species may not be directly applicable to another crop. In view of this, study of species specific transcription factor is very much warranted.

Calmodulin (CaM) binding transcriptional activator, popularly dubbed as “CAMTA”, is a group of transcription factors that are directly regulated by Ca\textsuperscript{2+}/CaM binding and have been implicated to be involved in different stress related signaling pathways. The present study was undertaken to clone and characterize this family of transcription factors from pokkali, a well-known salinity tolerant rice cultivar, to decipher its role and regulation under different abiotic stresses with particular reference to salinity stress. The present work was taken up with the following specific objectives.

i) \textit{In sillico} transcript analyses of Arabidopsis CAMTA genes to get hints regarding their involvement in abiotic stresses.

ii) Bioinformatics searches and analyses of CAMTA family members at different rice related databases.

iii) Cloning of CAMTA family members from a salt tolerant rice cultivar, pokkali.

iv) Transcript analyses of different CAMTA family members of rice under different stress conditions.

v) Detailed biochemical and functional analyses of one of the interesting CAMTA family members.

vi) To address the regulation of one of the CAMTA members at the post-transcriptional level.