Cereal seeds are one of the most important sources of nutrition for the humankind. Rice grains, like other cereals seeds, consist of a monocotyledonous embryo, starchy endosperm, and a protein-rich aleurone layer that surrounds the endosperm. The embryo forms as a result of fertilization of egg cell by the sperm nucleus, whereas, endosperm is the product of the second sperm nucleus fusing with the polar nuclei. The endosperm forms the edible part of the grain, and hence is important both nutritionally and commercially. Many regulatory processes are involved in seed development and transcription factors play a major role (Agarwal et al, 2011). MADS box transcription factors are homeotic genes that are involved in plant growth and development. A detailed characterization of MADS gene family in rice revealed that some of members express in a seed-specific manner (Arora et al, 2007).

A preliminary work in our laboratory had shown that the overexpression of one of the MADS box TFs drastically alters plant architecture. Since seed development involves a complex interplay of various plant hormones for proper development of embryo and endosperm, any alteration in the hormonal signaling and reception pathways could cause drastic phenotypes. Henceforth, functional validation of this gene was thought to resolve a number of unanswered questions concerning the process of seed development.

In this project an effort was made towards studying and functionally characterizing the functioning of this seed-specific transcription factor (TF), MADS29, in rice. This involved, studying the expression of MADS29 using a combination of microarray, qPCR, western and immunolocalization analyses. The RNAi based knockdown phenotype was characterized to highlight its role in endosperm and embryo development. The over expression of this gene was also studied in transgenic plants and heterologous BY2 cell line systems. The protein-protein interactions of this TF were checked with other seed expressing MADS box TFs using bimolecular fluorescence assay to determine other important players during seed development. The domains important for MADS29 functioning were also delineated. The data generated in such studies will contribute to the pool of knowledge, which can be utilized for improving rice grain production in the future.

This thesis has been divided into six sections. The first section provides an introduction and review of literature relating to hormonal control of endosperm development followed by the materials and methods used during the course of this study. The results achieved have been reviewed in the third section, followed by a discussion and conclusions of the results and bibliography of the literature relevant to this work has been enlisted in the fifth section. Finally in the appendix the publications based on this work have been listed.