PREFACE

Plant life cycle is initiated with the onset of seed germination. Young plants undergo a juvenile growth phase and then enter a long vegetative phase depending upon the species. Transition from vegetative phase to reproductive phase is usually abrupt but critical for the survival of the species. A plethora of genes act in concert to control the switch from one phase to another, including floral transition, which helps the plant achieve competency to flower and set seed. Thus, these genes are important candidates which could serve as tools for modifying the flowering time, floral architecture and seed set in cereal crops and other agronomically important plant species.

Our group at South Campus participated in rice genome sequencing as a part of the International Rice Genome Sequencing Project (IRGSP) between the years 2000 to 2005. Immediately thereafter, a major programme was launched to globally analyse the genes involved in transition to flowering and panicle development leading to seed maturation. To achieve this objective, whole genome microarray was carried out for generating expression profiles of tissues representing various stages of reproductive development. A rather large percentage (>80%) of genes in rice were differentially expressed during one or the other stages of reproductive development. Focus in our group has been on the members of the gene families encoding for proteins harbouring homeodomain, bZIP domain and F-box. Some of the members of these gene families are also induced when subjected to various abiotic stresses. A few genes have been prioritized, largely based on their microarray based expression profile, for functional characterization in the model dicot system *Arabidopsis* and rice. These include three homeodomain protein genes and one encoding F-box protein.

The homeodomain family represents an important group of transcription factors present in most of the eukaryotes. Plant homeobox genes were first reported in maize and subsequently discovered in *Arabidopsis*, tomato, rice and other plants. This family is characterized by a conserved homeodomain, which binds to the DNA to regulate gene expression. However, many new domains have been identified which are present along with this homeodomain and thus contribute to diversity of
these transcription factors. Till date, many subclasses have been identified, which differ from each other in both structure and function. This group of proteins performs a plethora of functions in plants ranging from their role in plant development, light signalling, adaptation to abiotic stress and adverse environmental conditions.

Among the plant homeodomain proteins characterized in this study, OsHOX14 belongs to HD-ZIP I subfamily since it harbours a leucine zipper domain in addition to homeodomain. OsHOX14 expression is relatively low in vegetative tissues but considerably high in early stages of panicle development and attenuates after fertilization and during seed maturation. Second homeodomain gene, OsBLH, analysed in this study has been assigned to BELL subfamily and its Arabidopsis homolog, ATH1, has been claimed to enhance the activity of FLC, a major floral repressor in Arabidopsis. OsBLH preferentially expresses in shoot apical meristem (SAM) and its expression declines gradually on transition to flowering, panicle development and seed set. These two genes, OsHOX14 and OsBLH, were thus characterized and analysed with the view to unravel if they have any role to perform during reproductive development by raising transgenics in Arabidopsis and/or rice. It appears from the analysis of Arabidopsis transgenics overexpressing these two homeodomain genes that OsHOX14 may regulate organ size and OsBLH could be involved in regulating transition to flowering.

Another HD-ZIP I family member, OsHOX22, has also been functionally characterized in the present study not with respect to its role in development but abiotic stress response. When checked for its expression, it was found to be drastically up-regulated under abiotic stress conditions, including drought, cold and salt stress and thus was chosen for further analysis. The Arabidopsis plants overexpressing this gene did not show any phenotypic variation but displayed a hypersensitive response to ABA and abiotic stress treatments when compared to WT; strikingly, the T-DNA insertion line of its homolog in Arabidopsis, conferred tolerance to abiotic stress.

F-box proteins also represent a large multigene family, which form an important component of protein degradation machinery in plant and animal systems. A large number of F-box genes have been identified till date, which perform a variety of functions in light and hormone signalling, and plant development. In the
present work, OsFBLD10, a rice F-box protein gene was characterized, which too had a high expression in SAM and its transcript levels decreased considerably immediately on initiation of panicle development. The rice transgenics where this gene was silenced displayed an early flowering phenotype, thus suggesting that it could be kind of a negative regulator of floral transition and may be involved in vegetative SAM maintenance.

Thus, the present study shows that homeodomain and F-box proteins are important components of developmental pathways and stress signalling cascades in plants. The results obtained in the present study are presented in detail and discussed appropriately for each gene separately. Since major focus was on homeodomain protein genes, Review of Literature only deals with “Homeodomain Class of Transcription Factors”. Some essential background about the characteristics and role of F-box proteins has also been provided by way of “Introduction” in ‘Results and Discussion’ section pertaining to OsFBLD10 gene. ‘Materials and Methods’ have been combined for all sections in the form of a separate Chapter. Summary and Conclusions mark the end of this thesis and highlight the salient findings of the work carried out during the past six years. In fact, work was initiated with a few more genes, simultaneously, but the data presented pertain to only four genes where some reasonable progress has been made. It was more of an exploratory work to begin with, based on the microarray profiles generated for various stages of reproductive development and abiotic stress response. In between, the progress on raising rice transgenics was also thwarted due to some infections in the greenhouse, thus hampering the overall progress. Thus, the work is in no way complete with respect to the elucidation of the precise functions of these genes. Despite the adversities, at least some useful leads have become available, which are entirely new to the literature, and will help to make vertical progress now and achieve the ultimate goal, which appears to be reachable in the foreseeable future.