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Title of the thesis: Identification of novel long non-coding RNA (nc RNA) transcripts in nitrogen efficient Rice (*Oryza sativa* L.) genotypes

ABSTRACT

In the recent time, the biophysical constraint experiencing by farmers has become a matter of concern in rice cultivation. Nutrients were considered as the second most limiting factor after water. Nitrogen (N) is the most important macronutrient for plant growth. To identify long non-coding RNA (lncRNA) in N efficient rice genotypes is the aim of this research work. For this purpose in the first objective of the thesis exploration of the physiological, biochemical and molecular aspects of NUE under low N stress had been performed. Field trial was done over two years to screen a group of 113rice genotypes. Statistical analysis based on PCA found to be useful to find out contributing traits for nitrogen use efficiency. Initial field data were analyzed based on relative biomass and relative grain yield and the genotypes were classified into four quadrates. From this, 8 representative genotypes from each quadrat were taken for further study. Enzyme activities involved in N metabolism, root morphology, N concentration and uptake under low N were studied. N uptake kinetics study was done for further confirmation Based on the results; further grouping was done according to most contributing factors i.e. NUE at low N stress. With this grouping, two genotypes (RASI-Efficient and Responsive and RP Bio226 Inefficient and Non-responsive) were selected to study N responsive candidate long non-coding RNA (lncRNA). Then after analyzing public domain transcriptomics data, I have identified 138 nitrogen responsive lncRNAs. Lnc1 (high affinity nitrate transporter), lnc10 (zinc finger BED domain-containing RICESLEEPER 4-like), lnc16 (transcription factor ILI6 isoform X4), lnc29 (B3 domain-containing Os03g0184500), lnc30 (early nodulin-93), lnc31 (glutamic acid rich) were identified as novel lncRNAs differentially expressed in contrasting genotypes for N- use efficiency