**ABSTRACT**

Rice is a dietary staple for a large part of the world’s human population which is grown under varying water regimes ranging from flooded to rainfed upland condition. The predominantly rice-growing areas in Asia are often threatened by severe abiotic stresses, the most common being drought which affects the yield potential of rice across all agro-climatic regions of the globe. Interestingly, some of the rice varieties of Northeast India are found to be drought tolerant e.g. Banglami. Comparative biochemical and physiological analyses of the variety with a high-yielding variety Luit confirmed this. Keeping all these points in view, high throughput RNA-Seq of the variety Banglami in presence and absence of drought was performed as an attempt to study the differential gene expression in Banglami. The RNA isolated by Trizol reagent (Invitrogen) was used for preparation of paired-end libraries using Illumina TruSeq RNA Library Preparation Kit. Libraries were sequenced using 2 X 150 PE chemistry on NextSeq. The reads were aligned against the indica reference assembly (ASM465v1). The expression analysis of the genes revealed 25,272 and 24,408 numbers of expressed genes in well watered control and drought stressed sample, respectively. Further analysis revealed 391 numbers of genes showing differential expression among which 86 were up-regulated and 305 were down-regulated. Among the differential expressed genes a number of genes were found to be very important for development of drought stress tolerant behaviour. Further, downstream analysis like Gene Ontology enrichment analysis, KEGG pathway analysis and QTL mapping were also performed which revealed important informations regarding the differentially expressed genes under drought stress condition in particular and the whole transcriptome of the Banglami variety of rice in general. The present study identified altered gene expression in rice induced by drought stress and provided a comprehensive map of drought responsive genes and pathways. Thus the results of the present investigation can serve as valuable genetic resource for gene expression, genomics and functional genomics studies in general and drought stress research in rice in particular.