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A transcriptomic study on cold stress in two Indian rice varieties using RNA-Seq analysis

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Abstract

Cold weather negatively affects the growth of seedling, which ultimately decrees the production of crops. Studies were done in the context of cold stress related to rice (Oryza Sativa) production, which is an important staple crop taken as food by half of the human population worldwide. It's always been a challenge to tackle out the problems related to such stress conditions. Rice is a model organism for monocots, finding out the molecular markers can help improve different crop varieties against cold stress. Advancement in High throughput techniques such as RNA-Seq, gives us an opportunity to revisit all the aspects of previous studies and improve them in more depth. Here we chose rice at seedling stage of both cold tolerant and susceptible genotype for our transcriptome level study under normal temperature, cold stress, and recovery condition. In our experiment, Genome wide expression profile of both the genotypes at all three different conditions was studied. We detected a total of 3217 and 485 common regulated differentially expressed genes (DEGs) during cold stress and recovery condition respectively. Followed by their gene ontology (GO) enrichment analysis for different functions they involved. By combining co-expression study and cluster analysis, we suggested few of the genes which may be highly responsible for cold stress and not reported before. These results expand the opportunities to explore cold stress and their recovery for crop plants with more detail in future.