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Bioinformatics Analysis of Rice Defense Response for Blast Infection

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ABSTRACT: *Magnaporthe oryzae* causes the devastating blast disease of rice and effects entire crop production in all the rice growing regions of the world. To explore rice- *M. oryzae* interaction we used microarray data GEO18361 and identified differentially expressed genes at 2nd day i.e. 48 hours post inoculation of blast fungus using R and bioconductor packages. Majority of the identified genes at this time interval showed up regulation. In total 1107 differentially expressed genes were identified, out of which 111 were down regulated. Gene ontology annotation of these genes suggests that up regulated genes are involved in defence response mechanisms and represent GO terms as diterpenoid metabolic process, lipid metabolic process, diterpene phytoalexin metabolic process, phytoalexin metabolic process, cellular nitrogen compound metabolic process, terpenoid metabolic process, isoprenoid metabolic process whereas down regulated genes are involved in processes like DNA recombination, response to stimulus, DNA metabolic process, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process and primary metabolic process. Thus we can conclude that rice activates biochemical processes by over expressing genes to combat blast infection.

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