



Category: Bioinformatics

In silico identification and characterization of differential expressed genes (DEGs) associated with grain and panicle number in rice

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Abstract

Grain number is an important trait for yield in rice. Several genes have been identified controlling grain and panicle number, which has direct or indirect effect on yield. Some genes play a key role for panicle formation and number of panicles per plant. The number of panicles per plant is directly regulating the grain number per plant. In present study, *in silico* approach was adopted for identifying differentially expressed genes associated with grain number and panicle number. Further, pathway enrichment analysis of these genes performed. The microarray data, GSE51616, downloaded from the GEO database originally submitted by Wang et al. (2014). Young leaves in vegetative stage (35-days old) and developing panicles (0.1cm) from field-grown OX-Ghd7HJ19 transgenic and wild-type plants with two biological replicates were used to isolate RNA for chip analysis. Background correction and normalization of raw microarray data was carried out using the Robust Multichip Averaging (RMA) method of affy packages of R (v. 3.1.3). The linear regression model package, limma was utilized to classify chips into two groups. The Bayes method (Benjamini and Hochberg) was used to correct for multiple testing. Adjusted P-value < 0.01 and |logFC| > 2 was used as a cut-off to identify differentially expressed genes. We identified 393 differentially expressed genes, which mainly belongs to either Phosphatidylethanolamine-binding protein family or DUF3778 domain family. Proteins of these two families regulate formation of high grain number as well as panicle number. These genes like *Ghd7*, *Ehd1*, *Dep1*, Os10g0463400, Os03g0752800, Os03g0215400, Os06g0157700 and Os06g0157500 function to integrate the dynamic environmental inputs with phase transition, architecture regulation, and stress response to maximize the reproductive success of the rice plant. Thus, these genes can act as potential target protein for increasing grain and panicle number in rice plant, which will lead to increase in yield of rice grain.

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