信息速递

近期发表论文

Global Transcriptome and Co-Expression Network Analysis Reveal Contrasting Response of Japonica and Indica Rice Cultivar to γ Radiation

发布日期：2019-09-05　　浏览次数：29

Zhang X, Huang N, Mo L, Lv M, Gao Y, Wang J, Liu C, Yin S, Zhou J, Xiao N, Pan C, Xu Y, Dong G, Yang Z, Li A, Huang J, Wang Y, Yao Y

Abstract

Japonica and indica are two important subspecies in cultivated Asian rice. Irradiation is a classical approach to induce mutations and create novel germplasm. However, little is known about the differential response between japonica and indica rice after γ radiation. Here, we utilized the RNA sequencing and Weighted Gene Co-expression Network Analysis (WGCNA) to compare the transcriptome differences between japonica Nipponbare (NPB) and indica Yangdao6 (YD6) in response to irradiation. Japonica subspecies are more sensitive to irradiation than the indica subspecies. Indica showed a higher seedling survival rate than japonica. Irradiation caused more extensive DNA damage in shoots than in roots, and the severity was higher in NPB than in YD6. GO and KEGG pathway analyses indicate that the core genes related to DNA repair and replication and cell proliferation are similarly regulated between the varieties, however the universal stress responsive genes show contrasting differential response patterns in japonica and indica. WGCNA identifies 37 co-expressing gene modules and ten candidate hub genes for each module. This provides novel evidence indicating that certain peripheral pathways may dominate the molecular networks in irradiation survival and suggests more potential target genes in breeding for universal stress tolerance in rice.

Key words: gamma irradiation; gene network; morphology; rice (Oryza sativa L.); transcriptomic analysis

https://www.ncbi.nlm.nih.gov/pubmed/31491955