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Radiation Fields, Effects and Risks in Human Space Missions (4)

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PROTEOMIC AND EPIGENETIC ANALYSIS OF RICE AFTER SEED SPACEFLIGHT AND
GROUND-BASE ION RADIATIONS

Abstract

Highly ionizing radiation (HZE) in space is considered as main factor causing biological effects to plant seeds. In previous work, we compared the proteomic profiles of rice plants growing after seed spaceflights to ground controls by two-dimensional difference gel electrophoresis (2-D DIGE) with mass spectrometry and found that the protein expression profiles were changed after seed space environment exposures. Differentially expressed proteins participated in most of the biological processes of rice including metabolic process, regulation of biological process, response to stimulus, cellular process and reproduction. To further investigate the radiation effects of space and compare proteomic effects between low-dose and high-dose ion radiation, we carried out ground-base carbon particle HZE radiation experiments with different cumulative doses to rice seeds. Results showed that proteins participating in most of the rice biological processes were also mainly involved in low-or high-dose radiation responses. Quantitative clustering analysis revealed that more proteins were regulated by high-dose radiation (2000mGy, 71.9%) than low-dose radiation (200mGy, 28.1%) treatments while the former tended to induce widely decrease expressions. Proteins responded to low-dose radiations preferred to change their expressions at the minimum dosage (2mGy, 77.3%). Protein nucleoside diphosphate kinase 1 (NDPK1) showed highly sensitivity to spaceflights and ion radiations, indicating its potential to be used as space radiation biomarker. We also found that spaceflight and ground-base radiations might induce epigenetic changes on rice plants, especially the DNA methylation changes. Early results suggested that there were correlations between DNA methylation polymorphic and genomic mutation rates. In addition, the 5-methylcytosine located in coding gene's promoter and exon regions could regulate gene expressions thus influence protein expressions. So whether there is correlation between genome DNA methylation changes and protein expression profile alterations caused by space radiation is worth for further investigation. Therefore we are using the same radiation rice samples, applying methylation sensitive amplification polymorphism (MSAP) for scanning genome DNA methylation changes; at the same time detecting gene expression levels of the space radiation sensitive gene-NDPK1 and performing cytosine methylation sequencing in the promoter and exon regions of the gene. By comparing the epigenetic changing with proteomic changing profiles

from the holistic “-omics” and specific sensitive gene aspects, the present work might provide new insights for further understanding of radiation mechanisms of space environment.