

论文

空间诱变水稻多蘖矮突变体不同分蘖期蛋白质组研究

王巍¹, 魏力军¹, 王俊敏², 徐建龙³, 孙野青^{1,4}

- 1. 哈尔滨工业大学生命科学与工程系, 黑龙江哈尔滨 150001;
- 2. 浙江省农业科学院作物与核技术应用研究所, 浙江杭州 310021;
- 3. 中国农业科学院作物科学研究所, 北京 100081;
- 4. 大连海事大学环境系统生物学研究所, 辽宁大连 116026

摘要:

JB-1返回式卫星搭载水稻(*Oryza sativa* L.)丙95-503干种子,地面种植后筛选出多蘖矮杆突变体R955。利用荧光差异显示双向电泳(2-D DIGE)对突变体播种后第14天(未发生分蘖)、第21天(分蘖起始)、第55天(最高分蘖期)3个营养生长期叶片总蛋白进行分离及定量分析(未搭载植株为对照),检测到在各发育时期共有97个蛋白点发生差异表达,经串联质谱鉴定后得到59个独特的蛋白。功能分析发现能量代谢、光合作用、蛋白代谢、氮元素同化、氨基酸代谢以及胁迫应答等过程均参与了突变体的分蘖发育。对差异蛋白在不同时期相对表达量的K-均值聚类分析显示不同功能蛋白表现不同表达模式。两因素差分析(Two-way ANOVA)筛选出S-类核糖核酸酶可能与水稻分蘖性状直接关联。

关键词: 水稻 多蘖矮 空间诱变 蛋白质组 S-类核糖核酸酶

COMPARATIVE PROTEOMIC ANALYSIS OF A HIGH-TILLERING DWARF MUTANT INDUCED BY SPACEFLIGHT AT DIFFERENT TILLERING STAGES

WANG Wei¹, WEI Li-jun¹, WANG Jun-min², XU Jian-long³, SUN Ye-qing^{1,4}

- 1. Department of Life Science and Engineering, Harbin Institute of Technology, Harbin, Heilongjiang 150001;
- 2. Institute of Crop and Nuclear Technology Utilization, Zhejiang Academy of Agricultural Sciences, Hangzhou, Zhejiang 310021;
- 3. Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081;
- 4. Institute of Environmental Systems Biology, Dalian Maritime University, Dalian, Liaoning 116026

Abstract:

To investigate changes of proteins during rice tiller development, a comparative proteomic analysis between a high-tillering dwarf mutant R955 induced by spaceflight and its ground control was performed at three developmental stages during the vegetative growth, i. e. at days 14 (no tiller appearance), 21 (initial tillering) and 55 (maximum tillering) after sowing. Analysis of the protein spots on two-dimensional fluorescence difference gel electrophoresis 2-D DIGE images revealed 97 proteins that were differentially expressed at the three stages. Among them, 59 unique proteins were successfully identified by mass spectrometry. Through functional and quantitative analysis of proteomic data, it was found that biological processes including energy pathway, photosynthesis, protein metabolism, nitrogen assimilation, amino acid metabolism and stimulus response were mainly involved in tiller development in mutant plant. K-means clustering revealed that proteins regulated at different stages tended to be involved in different biological processes. Two-way analysis of variance (Two-way ANOVA) showed that S-like was directly correlated RNase with the high-tillering ability.

Keywords: rice tillering dwarf space mutation proteome S-like RNase

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通讯作者: 孙野青(1959-),女,黑龙江哈尔滨人,博士,教授,研究方向为环境系统生物学。Tel:0411-84725675;E-mail: yqsun@hit.edu.cn

作者简介: 王 巍(1981-),女,辽宁抚顺人,博士生,研究方向为空间生物学。Tel:0411-84723633-831;E-

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