## Protein fingerprint diversification of rice seeds after space environment

 $\label{lem:condition} \mbox{Lu Weihong, Sun Yeqing} *, ZhengQiandGuanShuanghong \\ \mbox{Department of Life science \& Engineering, Harbin Institute of Technology. China}$ 

(E-mail: lwh@hit.edu.cn yqsun@hit.edu.cn /phone: +86-451-86418326)

To study protein fingerprint diversification of rice seeds induced by space environment, we selected three series mutants induced in Chinese recoverable satellite in 1996 for 15 days, including (1) Series 971: 971ck, the control sample in ground. 971-5 and 971-4, samples after space derivation. (2) Series 972: 972ck, the control sample in ground. 972-4 and 972-1, samples after space derivation. (3) Series 974: 974ck, the control sample in ground. 974-5 and 974-8, samples after space derivation.

The proteins were extracted and separated to 4 groups: Albumin, Globulin, Prolamine and Glutelin from the seeds of ground control group and inducted by space environment group. Using RPLC method, Reference peak was selected in every group and its relative retention time was 1.000. The relative retention time of other peaks was the ratio. Calculate the contents due to the peak areas and draw a conclusion that some contents of protein were changed in the seeds of the mutant varieties. There are character peaks among different varieties as the fingerprint.

Comparative analysis the fingerprint of Albumin, Globulin and Prolamine, can find the different in varieties identify.

The protein express abundance and easy be detected in the seeds. So using RPLC method, the Protein Fingerprint can identify breed handily and steadily.

Keywords: rice seeds/ Space environment/ Protein Fingerprint