

環境因子對稻米之泛素基因家族成員表現的影響

張淑芝 孫智雯*

國立臺灣師範大學生命科學系

(收稿日期：2006.10.11，接受日期：2006.10.19)

摘 要

泛素是一種廣泛存在真核生物體內的高度保守性蛋白質，可參與調控各種生物功能，包括耗能性蛋白質降解作用、核酸修復、細胞週期循環，維持染色體結構、逆境反應、細胞間交互作用、各類細胞信息傳遞、內噬作用、病毒感染、致癌基因的調節、計畫性細胞凋亡、及植物生理反應的調節。而細胞內的泛素是從兩群基因家族成員所轉錄轉譯而成，這些成員包括聚合泛素基因及泛素延伸基因。為了瞭解稻米泛素基因家族成員的表現，是否會受到不同環境因素所影響，我們經由序列收集及比對分析，共找到了 10 個泛素基因家族成員，分別是 3 個聚合泛素基因及 7 個泛素延伸基因。再藉由反轉錄聚合酶連鎖反應的定量方法，來比較稻米的泛素基因群在不同環境因子下的表現差異。結果顯示熱處理促使 *osUBQ2* 和 *osUBQ9* 基因表現量增加；*osUBQ3*、*osUBQ4* 以及 *osUBQ5* 基因傾向在幼苗組織中表現；而 *osUBQ7* 基因在營養器官中具有組織特定性表現。

關鍵詞：泛素、聚合泛素基因、泛素延伸基因、基因表現、反轉錄聚合酶連鎖反應、稻米

*通訊作者：孫智雯 (Chih-Wen Sun)；FAX：886-2-29312904；E-mail：cwsun@ntnu.edu.tw

Effects of Environmental Factors on Expression of Ubiquitin Gene Family in Rice

Shu-Chih Chang, Chih-Wen Sun*

Department of Life Sciences, National Taiwan Normal University
Taipei, Taiwan

(Received: 11 October 2006, accepted: 19 October 2006)

ABSTRACT

Ubiquitin, a highly conserved protein in eukaryotic organisms, is generally participated in ATP-dependent proteolysis, DNA repair, cell cycle control, maintenance of chromatin structure, stress response, cell-cell interaction, signal transduction, endocytosis, viral infection, regulation of oncogenes, and regulation of plant physiological responses. Cellular ubiquitins are encoded by two types of ubiquitin gene families, polyubiquitin gene and ubiquitin extension gene. In order to understand whether the expression of rice (*Oryza sativa* L.) ubiquitin genes are regulated by different environmental factors, we first collect sequences of ubiquitin genes from several rice-related genome databases, and compare them in detail to avoid redundant gene sequences. We found 10 ubiquitin genes in rice genome, including 3 polyubiquitin genes and 7 ubiquitin extension genes. Furthermore, quantification of gene expression by RT-PCR technique indicated that these genes expressed differentially under different treatments. The heat-shock treatments increased the expression levels of *osUBQ2* and *osUBQ9* genes; the *osUBQ3*, *osUBQ4*, and *osUBQ5* genes preferentially expressed in young seedlings; whereas *osUBQ7* gene were specifically expressed in roots.

Key words: ubiquitin, polyubiquitin gene, ubiquitin extension gene, gene expression, reverse transcription-polymerase chain reaction (RT-PCR), *Oryza sativa*