

FATTY ACID ANALYSIS OF TOTAL LIPIDS FROM LEAVES OF RICE T-DNA INSERTIONAL LINES

In-Soon Kang, Hyun-Ju Kim, Byoung Yong Moon

Department of Biotechnology, Inje University, Gimhae 621-749, Korea

In order to screen some fatty acid mutants from the rice T-DNA tagging lines, we carried out the analysis of total lipids in the leaves of 458 rice individuals arbitrarily chosen from T-DNA insertional mutants that had been generated by Dr. G. Ahn of the Postech university. Rice leaves were harvested in July 2000, before flowering when the plant growth was most active. For the isolation of total lipids, the leaves were macerated in liquid nitrogen and further analyzed according to the procedure of Bligh and Dyer(1959). The resultant fatty acid methyl esters (FAMES) were provided to the GC analysis together with pentadecanoic acid as standard. Based on the chromatograms produced from each mutant individuals we identified several other retention times different from those of the wild-type plants. When the retention times of the individual fatty acid peaks were compared among different T-DNA insertional mutants, it was found that they could be classified into several different types of fatty acid compositions. Each group was arbitrarily named as type 1 to type XIII. When the mole percentages of the C₁₈ enoic fatty acids ($\Sigma 18:1+18:2+18:3$) were compared, 5.5% of the mutant individuals showed much lower degree of fatty acid unsaturation than the wild-type plants, in contrast to the other plants that showed a rather comparable value. We screened the mutant which showed the markedly reduced level of C₁₈ fatty acid unsaturation. The implications are dicussed in relation to the function of membrane lipids in plants.