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Global understanding of metabolite changes in Arabidopsis suspension cells using ^{1}H-NMR spectroscopy

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Objectives

To develop methodology for comprehensive understanding of metabolic changes in Arabidopsis suspension cells during sucrose starvation using ^{1}H-NMR spectroscopy.

Materials and Methods

1. Plant materials : Suspension cultured cells of Arabidopsis
2. Methods: sucrose starvation, ^{1}H-NMR spectroscopy, principle component regression (PCR) analysis

Results and Discussion

We have developed a rapid, powerful, and simple tool for comprehensive understanding of sucrose starvation using ^{1}H-NMR spectroscopy. Total sugar content decreased rapidly after 3 h of deprivation whereas total free amino acid content increased. Phenylalanine and asparagine that are markers of protein and amino acid degradation under stress condition accumulated continuously until 72 h of starvation. These results were consistent with the results of sugar-starved maize root tips using HPLC. Recently, gene expression profiling during sucrose starvation from Arabidopsis was reported. Therefore, systematic approach of expression profiling and metabolic profile enabled us to understand the relationship between starvation and senescence. Also the analysis of metabolome using ^{1}H-NMR spectroscopy could be applied to study other physiological mechanisms.

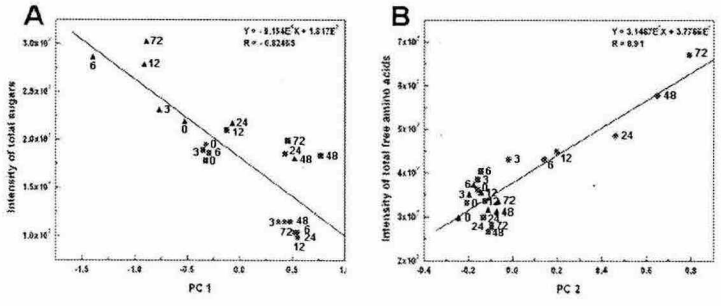

Fig. 1. PCR plots from ^{1}H-NMR spectral data during sucrose starvation. Symbols and numbers represent 0% (●), 3% (■), and 6% (▲) sucrose treatment and time of sucrose starvation. A: total sugar content; B: total free amino acid content.

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