

Comprehensive Two-dimensional Gas Chromatograph Quadruple Mass Spectrometer for Plant Metabolite Analysis

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Sample Preparation Introduction Applications of plant metabolomics - Identification of metabolic engineering targets Oryza sativa Echinochloa utilis Panicum miliaceum - Understanding of stress response subsp. japonica (Japanese (millet) barnyard millet) (rice) - Genetically modified food certification - Human nutrition 30 mg of Samples Characteristics of plant metabolite analysis ◄ Stir, then centrifuge 900 µL of Extraction Solution Several thousands of target compounds such as organic Add 400 µL Milli-Q water acids, amino acids, sugars etc. Different concentration levels for each compound 400 µL of Supernatant Solution Ultra-high separation efficiency and wider dynamic range required Residue ◄ Add 100 µL of BSTFA Heat at 800C for 60 min GC×GC-OMS (TMS derivatization) GCXGC-OMS Experimental **Analysis Conditions** System Configuration of GCxGC-QMS GCxGC Column: 1st DB-5 30 m x 0.25 mm I.D., df = 1.0 μm



GC-MS: GCMS-QP2010 Ultra (Shimadzu Corp.) GC*GC modulator: ZX1-GCxGC modulator (Zoex Corp.)





(Pearl millet) ▲ Add 1 mL water / methanol / chloroform (1 / 2.5 / 1) Add internal standard (10 μL of 0.1 mg/mL TA, 005 mg/mL HDA, and C24) Stir, then centrifuge; separation into two phase Dryness under nitrogen gas flow at 35°C

Setaria italica

2nd BPX-50 2.5 m x 0.1 mm I.D., df = 0.1 µm Injection: split (1:50)

injection.	spiit (1.50)
Injection volume:	1 μL
Injection temp.:	280°C
Column temp.:	100°C (4min)→2°C /min→320°C (10 min)
Carrier gas:	He (Constant = 150 kPa)
Modulation time:	6 sec

MS

Interface temp.: 280°C lon-source temp.: 200°C Ionization mode: El MS mode: scan (*m/z* 50-500) Event time: 0.03 sec 20,000 u/sec



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Results Scan Interval and Chromatographic Peak Shape



Analysis Results of oryza sativa subsp. japonica



Although this component was not be separated by 1st column, it was separated by GCxGC.



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Similarity Index	Number of Chromatographic Peaks				
	А	В	С	D	
> 800	50	19	80	7	
700 - 799	609	368	649	377	
600 - 699	1329	1377	1101	1704	
500 - 599	158	186	128	245	
< 499	1	0	3	0	
Total	2147	1950	1961	2333	
>600 (%)	92.6	90.4	93.3	89.4	

Summary

- A fast scanning quadruple mass spectrometer (QMS) was shown to have a sufficient scan speed to fully characterize the ultra narrow peaks generated by the GC X GC system.
- Using this system, cereal samples (oryza sativa subsp. japonica (rice), echinochloa utilis (Japanese barnyard millet), panicum miliaceum (millet), and setaria italica (pearl millet)) were analyzed.
- The number of detected chromatographic peaks ranged from 1950 to 2333.
- These results demonstrated the GCxGC-QMS can be effectively used to detect several thousand plant metabolites in a wide concentration range.



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