

Application Data Sheet

GCMS

Gas Chromatograph Mass Spectrometer

Analysis of Amino Acids Contained in Green Tea

Amino acids contained in green tea were treated with EZ:faastTM (Phenomenex, Inc.), which enables easy pretreatment, and then analyzed by GC-MS.

Experiment

Pretreatment

Green tea was treated with EZ:faast. Norvaline was added as an internal standard.

A GCMS-QP2010 Ultra (with high-power oven) was used for the measurements. The analysis conditions, shown in Table 1, were in conformity with the "Amino Acid Analysis Methods" in the "GC/MS Metabolic Components Database."

Table 1: Analysis Conditions (GC/MS Metabolic Components Database: Amino Acid Analysis Methods)

GC-MS : GCMS-QP2010 Ultra (with high-power oven)

Column : ZB-AAA (length: 10 m, 0.25 mm I.D.) (Phenomenex, Inc.)

[GC]

Injection quantity : 1 µL Interface temperature: 280°C Vaporization chamber temperature: 280°C Ion source temperature: 200°C Column oven temperature: $110^{\circ}\text{C} \rightarrow (30 \text{ °C/min}) \rightarrow 320^{\circ}\text{C}$ Solvent elution time : 0.4 min Control mode : Constant pressure (15 kPa) Data sampling time : 0.5 min to 7 min

Injection mode : Split Measurement mode: Scan

Split ratio : 15 : m/z 45-450 (3,333u/sec) Mass range Carrier gas : Helium

Event time : 0.15 sec

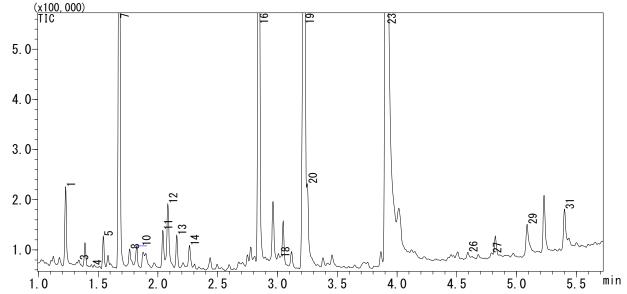
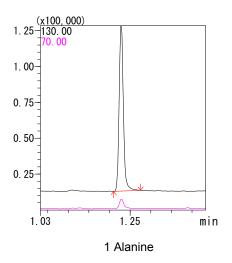


Fig. 1: Total Ion Current Chromatogram (TIC) for Amino Acid Derivatives in Green Tea The numbers for each component follow the serial numbers in the "GC/MS Metabolic Components Database."

1 Alanine 8 Leucine 14 Asparagine 23 Glutamine 3 Glycine 10 Isoleucine 16 Aspartic acid 26 Lysine 4 alpha-aminobutyric acid 11 Threonine 18 4-Hydroxyproline 27 Histidine 5 Valine 12 Serine 19 Glutamic acid 29 Tyrosine 7 Norvaline (I.S.) 13 Proline 20 Phenylalanine 31 Tryptophan

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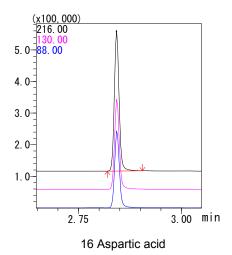


Fig. 2: Examples of Mass Chromatograms for Amino Acid Derivatives

Summary

Pretreatment using the EZ:faast kit, following by analysis using the GCMS-QP2010 Ultra, which is equipped with a high-speed scanning function, enabled rapid analysis of amino acids. With this combination, it took only 15 minutes per sample from pretreatment to analysis.

(Reference: Shimadzu Application News No. M246 Analysis of Amino Acids Using Fast-GC/MS and Metabolite Database)

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