Analysis of Food Products Using the LC-2030C LT and the LCMS-2020

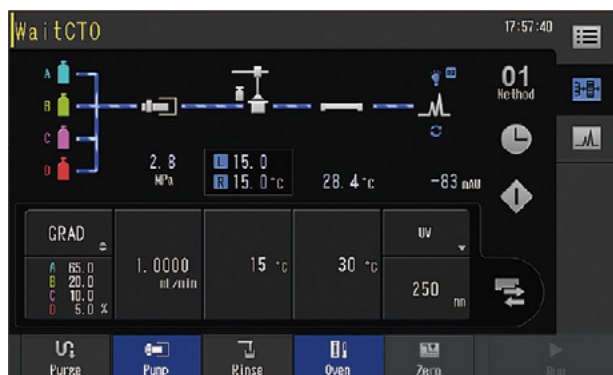## Improved Qualitative Performance Utlizing Mass Spectrometry

LC/MS is capable of separation by mass and the identification of components from MS spectral information. As a result, LC/MS has been widely used in the field of food analysis. Combining the i-Series (LC-2030C LT), which features a compact size and multi-specimen handling, with the LCMS-2020, which provides excellent qualitative capacities, enables accurate, high-quality quantitative and qualitative analysis of food products. This includes the analysis of a wide range of components, from effective components to toxic components, in foods.

With the i-Series, all operations from sample placement to starting analysis can be performed at the instrument, thereby keeping operations in the laboratory to a minimum. In addition, if a flow line selection valv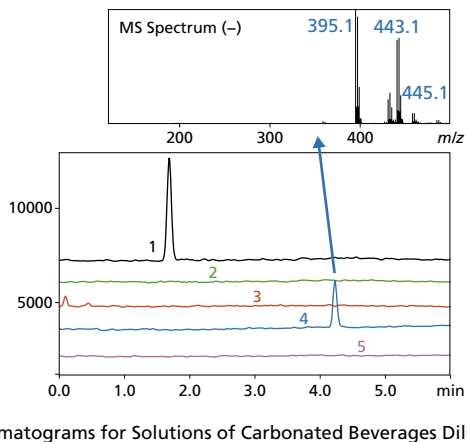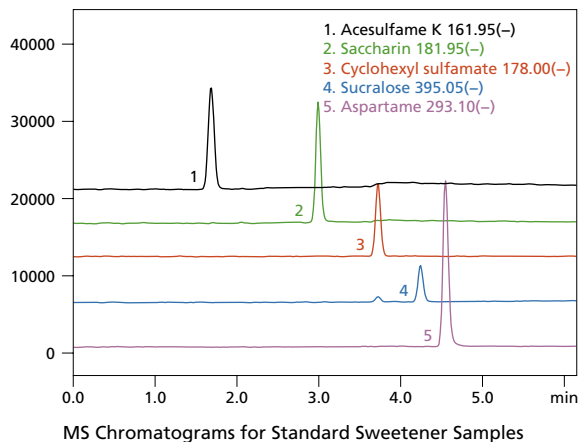e is installed between the i-Series and the LCMS-2020, the selection valve can be used to load components into the mass spectrometer only for the time band in which target components are eluted, even for food samples, which contain many impurities.

■ Analysis of Sweeteners Using the LCMS-2020

Low-calories sweeteners are now widely used in food products. Sweeteners exhibit distinct flavors different from sucrose and glucose, so flavors are adjusted by combining multiple sweeteners or other methods. This publication shows the results of an analysis of carbonated beverages and a mixed standard solution of synthetic sweeteners utilizing the i-Series and the LCMS-2020. Sucralose is known for its poor light absorption, which makes it a difficult component to detect using a UV detector. In contrast, the LCMS-2020 can easily analyze these sweeteners.

1. Acesulfame K 161.95(−)
2. Saccharin 181.95(−)
3. Cyclohexyl sulfamate 178.00(−)
4. Sucralose 395.05(−)
5. Aspartame 293.10(−)

MS Chromatograms for Standard Sweetener Samples

MS Spectrum (−)

Chromatograms for Solutions of Carbonated Beverages Diluted 400×

■ Quick Amino Acid Analysis via Detection by Mass

In amino acid analysis via HPLC, a long analysis time is required in order to separate the amino acids. When detecting by mass, however, the analysis time can be shortened while avoiding the impact of impurities.

1. 3-Aminoisobutyric acid
2. GABA
3. Citruline
4. (Cys)2
5. Cystathionine
6. Asp
7. Thr
8. Sar
9. Ala
10. β-Ala
11. α-aminoadipic acid
12. Gln
13. Ser
14. Glu
15. Pro
16. Val
17. Theanine
18. Met
19. Leu
20. Ile
21. Hydroxyproline
22. Tyr
23. Methionine Sulfone
24. Phe
25. Trp
26. Arg
27. Hydroxylysine
28. Orn
29. Lys
30. His
31. Carnosine
32. Anserine
33. Methylhistidine

MS Chromatogram for a Standard Sample of 39 Amino Acids

1.Ala 90.00(+)
2.Glu 147.00(+)

Positive   147.05   [M+H]⁺
149.95

Negative   [M+H]⁻
145.05   147.05   152.00

Chromatograms for Commercially Available Supplements
(Dissolved in Water and Diluted 50×)

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