

Integrated Analysis of Coffee Aroma by using a Headspace GC-HRMS - Developing an Integrated Analysis Technique using Data Acquired by GC/EI and GC/Soft Ionization -

Product: Mass spectrometer (MS)

[Introduction]

Electron ionization (EI) is a hard ionization method that is commonly used with gas chromatography mass spectrometry (GC-MS). The mass spectral fragmentation patterns produced by EI are used for library database searches to identify compounds. Conversely, soft ionization methods like field ionization (FI) tend to produce clear molecular ions with minimal fragmentation. When high-resolution MS is used with these ionization techniques, the accurate masses for the fragment ions produced by EI and the molecular ions produced by soft ionization provide an additional dimension of information for the analytes. Combining the exact mass information with the results of conventional library search can enhance the accuracy of identification compared to the use of library search alone. In this work, we introduce the msFineAnalysis software and use it to automatically combine data acquired by GC/EI and GC/soft ionization for the qualitative analysis of coffee headspace.

[Experimental]

A commercial coffee was prepared as follows:

- 1) One gram of coffee beans was loaded into a 22 mL vial, 15 mL of boiling water was added, and the vial was sealed.
- 2) After the sample was cooled to room temperature, 10 mL of the supernatant was loaded into another vial, and 2 µL of an internal reference (p-Bromofluorobenzene) solution was added to the sample.
- 3) Finally, 2 mL of the above solution was transferred to the vial for the headspace sampler and sealed in a vial that was then used as a sample.

Table 1 shows the measurement conditions used for the headspace/GC-TOFMS system.

Table 1. Measurement Conditions

[Conditions of headspace sampler]	
System	MS-62070STRAP (JEOL)
Mode	Trap mode
Extract	3 times
Heating condition	60°C, 15 min

[GC-TOFMS Conditions]	
System	JMS-T200GC (JEOL)
Ionization mode	EI+: 70 eV, 300 µA FI+: -10 kV, 8mA (Carbotec 5 µm)
GC column	ZB-WAX, 30 m x 0.18 mm, 0.18 mm
Oven temp.	40°C (3 min) → 30°C/min → 250°C (10 min)
Inlet temperature	250°C
Inlet mode	Split 30:1

[Results and Discussion]

Figure 1 shows the operational flow chart for the integrated analysis steps used for the JEOL msFineAnalysis software (chart on the right). First, the data is acquired by using both EI and soft ionization (SI), and all peaks and associated mass spectra are detected in the chromatograms. Afterwards, the mass spectra produced by these ionization methods are linked using their retention times, and these linked mass spectra are recorded as single components. Next, the EI mass spectrum is used for the library database search (1), and the SI mass spectrum is used to identify the analyte molecular ion (2). Afterwards, the molecular ion is used for exact mass analysis to determine possible elemental compositions, and these candidate formulas are then filtered by using the EI library search results (3). Next, the molecular ion is subjected to isotopic pattern analysis to help further limit the candidate formulas (4). Each candidate formula is then used as a search constraint for the exact mass analysis of the EI fragment ions (5). If the molecular ion formula candidate is incorrect, the EI fragment ions will not result in many (if any) compositional formulas, thus indicating that the molecular ion formula is not a good candidate for that particular analyte. These results are then output as an integrated qualitative report (6).

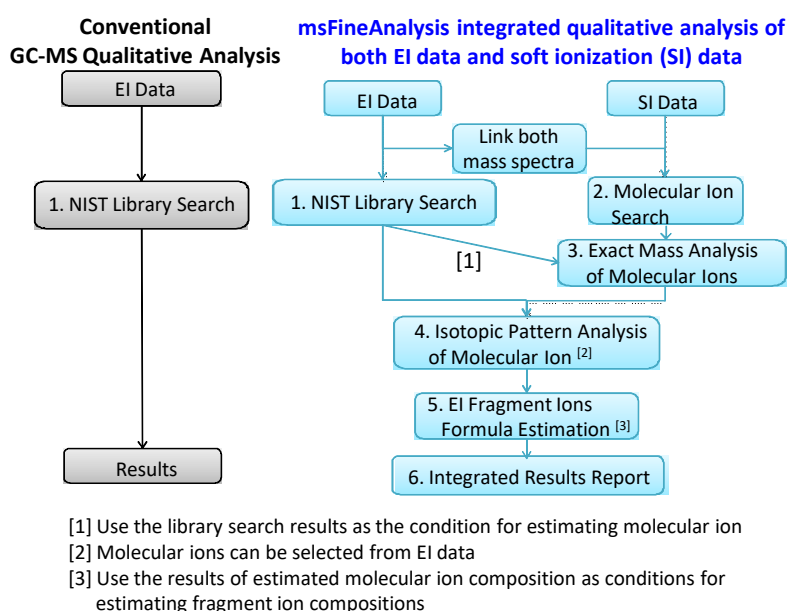


Figure 1. Qualitative Analysis Flow

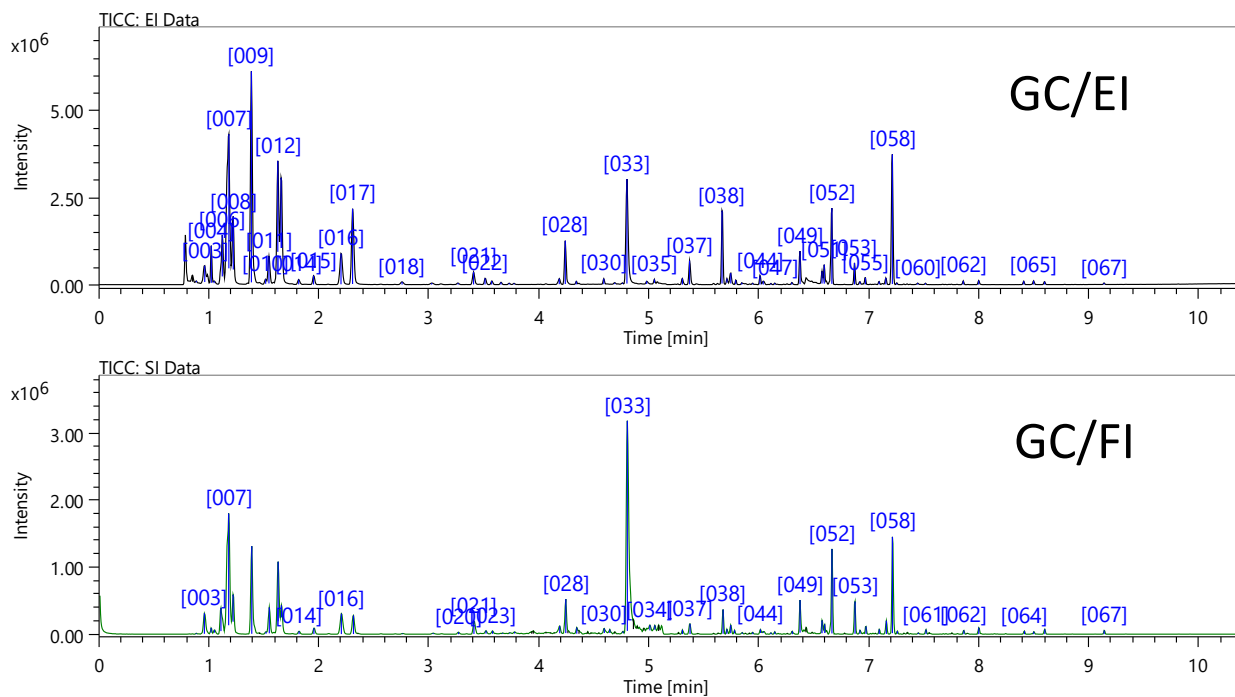


Figure 2. TIC chromatograms of coffee aroma acquired by a HS/GC/TOFMS

General		Total Result										Library Search Result					
ID	RT [min]	Height	Link	IM	m/z	Library Name	Similarity	Formula	Adduct/Loss	Calculated m/z	Error [mDa]	Isotope Matching	EI Fragment Coverage	BEST Similarity	Library Name	Formula	MW
040	5.75	296876	✓	108.06748	Isomer	-	C6 H8 N2	none	108.06820	-0.72	0.73	75	803	Pyrazine, ethyl-	C6 H8 N2	108	
041	5.79	122847	✓	74.03713	Isomer	-	C3 H6 O2	none	74.03623	0.90	0.96	100	831	2-Propanone, 1-hydroxy-	C3 H6 O2	74	
042	5.85	54829	✓	137.11745	-	-	C9 H15 N	none	137.11990	-2.45	N/A	80	695	Pyrazine, 2,3-dimethyl-	C6 H8 N2	108	
043	5.95	36170	✓	96.05688	Isomer	-	C6 H8 O	none	96.05697	-0.09	0.86	100	864	2-Cyclopenten-1-one, 2-methyl-	C6 H8 O	96	
044	6.01	258750	✓	190.16582	-	-	C9 H22 N2 O2	none	190.16758	-1.76	0.79	100	729	Benzene, 1,3-bis(1,1-dimethyl-)	C14 H22	190	
045	6.04	99089	✓	108.07868	Isomer	-	C7 H10 N	+H	108.08078	-2.09	N/A	100	872	Pyridine, 3-ethyl-	C7 H9 N	107	
046	6.11	32895	✓	122.08255	Isomer	-	C7 H10 N2	none	122.08385	-1.30	0.66	100	848	Pyrazine, 2-ethyl-3-methyl-	C7 H10 N2	122	
047	6.15	44410	✓	122.08286	Isomer	-	C7 H10 N2	none	122.08385	-0.99	0.85	71	728	Pyrazine, trimethyl-	C7 H10 N2	122	
048	6.30	57941	✓	136.09850	Isomer	-	C8 H12 N2	none	136.09950	-1.00	0.86	83	817	Pyrazine, 3-ethyl-2,5-dimethyl-	C8 H12 N2	136	
049	6.38	948575	✓	116.04593	-	-	C5 H8 O3	none	116.04680	-0.86	0.94	100	865	3-Furaldehyde	C5 H4 O2	96	
050	6.58	351542	✓	110.03586	Isomer	-	C6 H6 O2	none	110.03623	-0.37	0.94	100	881	Ethanone, 1-(2-furanyl)-	C6 H6 O2	110	
051	6.60	946071	✓	67.04309	Isomer	-	C4 H5 N	none	67.04165	1.44	0.95	100	928	Pyridole	C4 H5 N	67	
052	6.67	2174265	✓	140.04467	Isomer	-	C7 H8 O2	none	140.04680	-2.13	0.99	100	914	2-Furanmethanol, acetate	C7 H8 O3	140	
053	6.87	620192	✓	124.05018	-	-	C7 H8 O2	none	124.05188	-1.70	0.82	100	855	2-Furanacetaldehyde, 5-methyl-	C6 H6 O2	110	
054	6.92	75659	✓	154.05896	Isomer	-	C8 H10 O3	none	154.06245	-3.48	N/A	100	748	2-Furanmethanol, propanoate	C8 H10 O3	154	
055	6.97	190190	✓	148.04891	Isomer	-	C9 H8 O2	none	148.05188	-2.97	0.87	100	924	Furan, 2,2'-methylenebis-	C9 H8 O2	148	
056	7.10	82837	✓	109.05169	Isomer	-	C6 H7 N O	none	109.05222	-0.53	0.93	88	908	1H-Pyridine-2-carboxaldehyde	C6 H7 N O	109	
057	7.16	186554	✓	138.06500	-	-	Multi Hits	-	-	-	-	-	768	Butanoic acid, 4-hydroxy-	C4 H8 O3	104	
058	7.22	3727421	✓	98.03622	Isomer	-	C5 H6 O2	none	98.03623	-0.01	0.99	100	917	2-Furanmethanol	C5 H6 O2	98	
059	7.26	49053	✓	162.06372	Isomer	-	C10 H10 O2	none	162.06753	-3.81	0.90	100	829	Furan, 2-(2-furanylmethyl)-5-	C10 H10 O2	162	
060	7.45	43569	✓	156.07328	-	-	Multi Hits	-	-	-	-	-	716	4(1H)-Pyridine, N-acetyl-	C7 H9 N O	123	
061	7.52	38838	✓	124.05078	-	-	C7 H8 O2	none	124.05188	-1.10	0.69	100	656	3-Ethenyl-3-methylcyclopent-	C8 H12 O	124	
062	7.86	107521	✓	147.05464	Isomer	-	C9 H9 N O	none	147.05797	-3.23	0.94	100	931	1H-Pyridine, 1-(2-furanylmethyl)-	C9 H9 N O	147	
063	8.00	118217	✓	124.05024	Isomer	-	C7 H8 O2	none	124.05188	-1.64	0.90	100	930	Phenol, 2-methoxy-	C7 H8 O2	124	
064	8.41	99222	✓	178.05741	-	-	Multi Hits	-	-	-	-	-	672	Furan, 2,2'-(oxybis(methylene))	C10 H10 O3	178	
065	8.50	109257	✓	94.04121	Isomer	-	C6 H6 O	none	94.04132	-0.11	0.96	100	949	Phenol	C6 H6 O	94	
066	8.60	84932	✓	152.07936	Isomer	-	C9 H12 O2	none	152.08318	-3.82	0.84	64	818	Phenol, 4-ethyl-2-methoxy-	C9 H12 O2	152	
067	9.14	46160	✓	150.06385	Isomer	-	C9 H10 O2	none	150.06753	-3.68	0.87	100	896	2-Methoxy-4-vinylphenol	C9 H10 O2	150	

Figure 3. Integrated qualitative analysis results on msFineAnalysis

The msFineAnalysis Auto Analysis function detected 67 components in the GC/EI and GC/FI measurements (Figure 2) that were automatically linked using their retention time. The Auto Analysis function then automatically used the steps in Figure 1 to analyze the linked data, and the results were output as a color-coded table as shown in Figure 3. Each color indicates a level of confidence for the identity of the compound:

- Green: A molecular formula candidate was uniquely identified.
- Orange: Multiple molecular formula candidates were identified.
- White: No significant molecular formula candidates were identified.

The components classified as orange or white can be further reviewed manually to potentially identify a unique candidate formula. In this example, the software was able to automatically determine a unique molecular formula for 63 of the 67 components in the coffee headspace sample.

[Conclusions]

The msFineAnalysis software produces highly accurate qualitative analysis results by automatically combining the EI library search results and soft ionization (SI) molecular formula determinations. Additionally, this software makes it possible to determine molecular formulas for unknown components not registered in library (match factor score: low), which can not be identified by database search alone (Figure 1, left side). The effectiveness of the msFineAnalysis integrated analysis method effectiveness for GC/MS qualitative analysis was demonstrated by automatically determining molecular formulas from exact masses, regardless of the level of match factor score, to limit the candidate formulas.

