

# Development of online SPE-GC-MS system with automated SPE-based derivatization method for metabolome analysis.



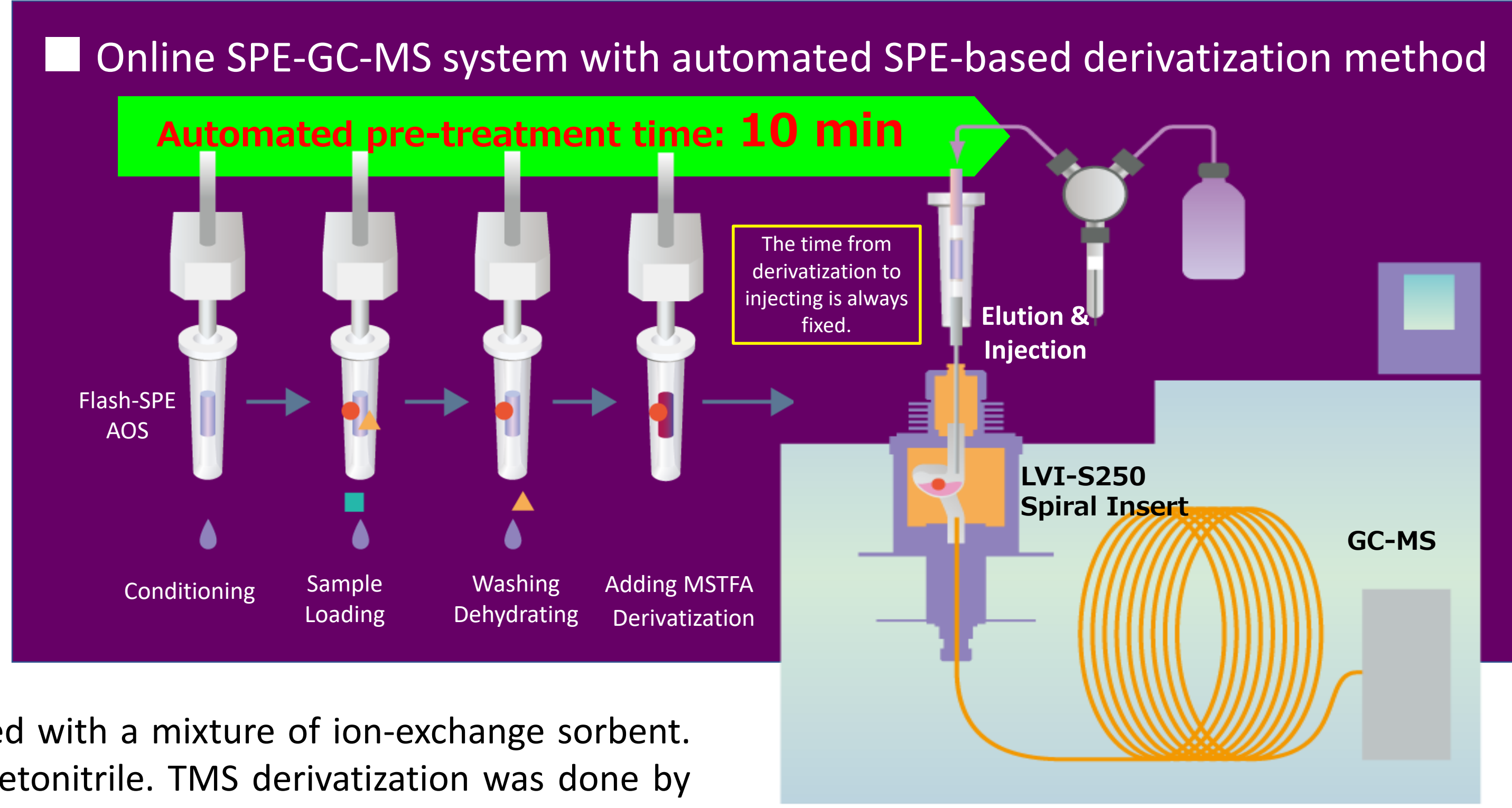
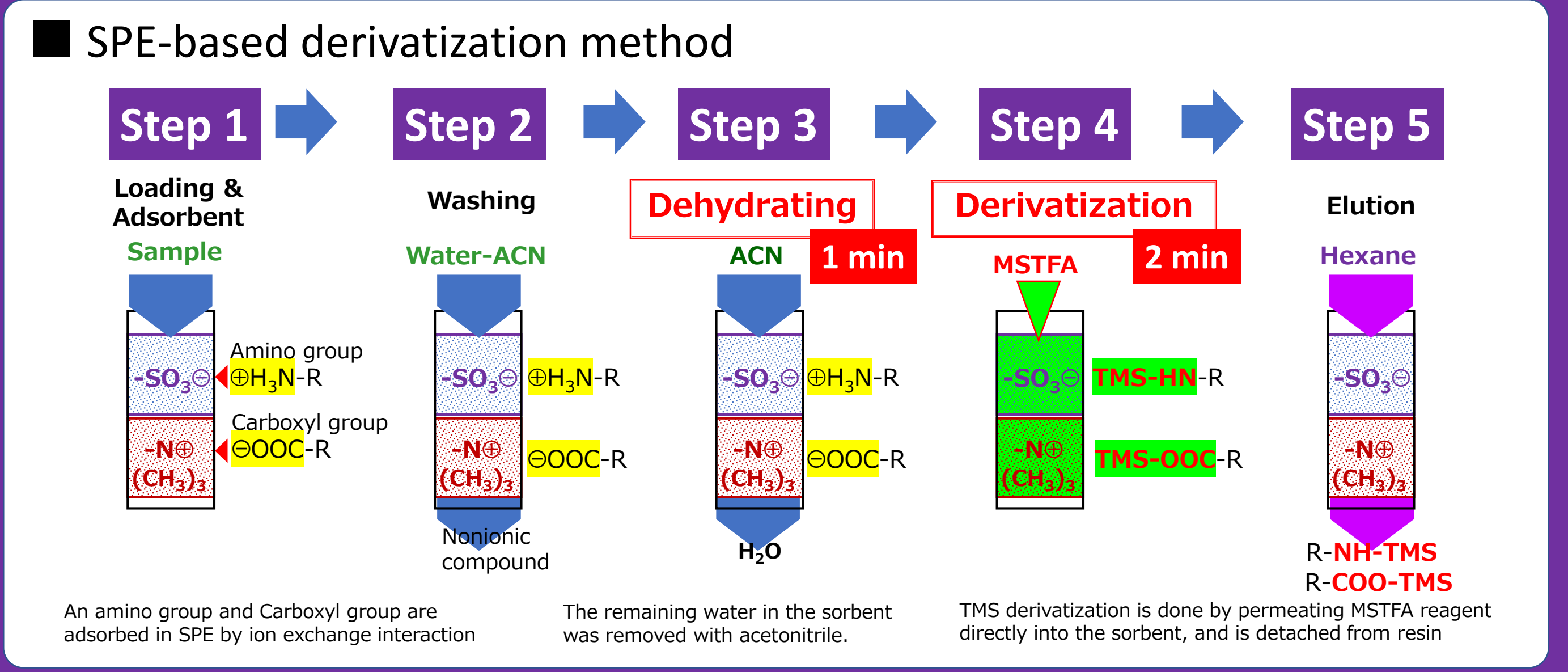
Ryoichi SASANO<sup>1</sup>, Koji MACHITANI<sup>2</sup>, Shusuke OSAKI<sup>2</sup>, Masahiro FURUNO<sup>3</sup>, Eiichiro FUKUSAKI<sup>3</sup>

<sup>1</sup>; Aisti Science co., Ltd., <sup>2</sup>; Industrial Technology Center of Wakayama prefecture, <sup>3</sup>; Osaka University

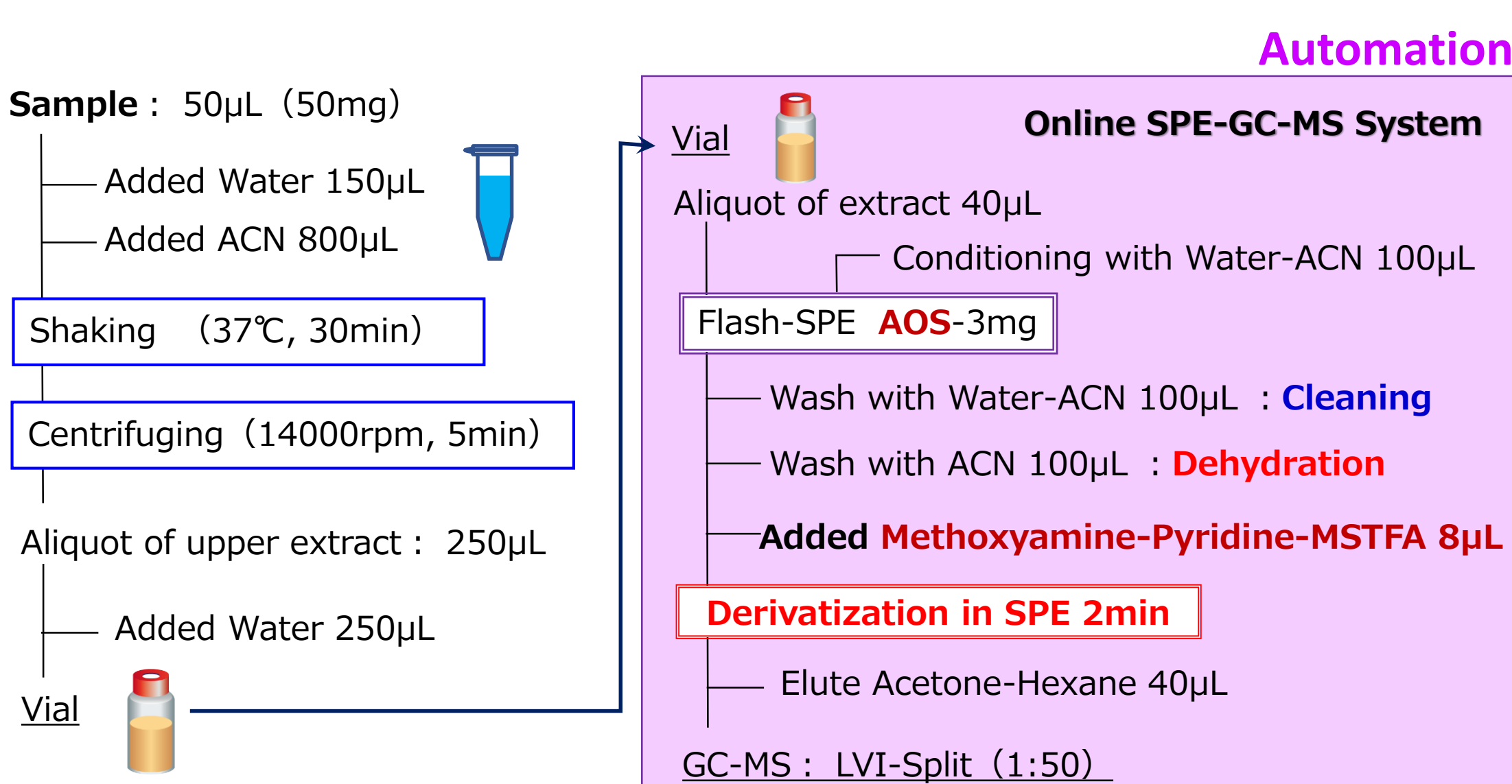
## [Abstract]

Due to complicated sample preparation procedures that include centrifugal concentration, freeze-drying and derivatization, the current metabolomics protocol using GC-MS, requires not only longer processing time but also advanced technical skill. In addition, some silylated metabolites are unstable and the time required for complete silylation varies depending on the metabolite. Therefore, the time gap between derivatization and actual GC-MS analysis can potentially be a source of error. In this study, **automated SPE-based derivatization** method coupled with GC-MS was developed to accomplish an extremely rapid sample preparation. The derivatization method using SPE-gel has a high reaction efficiency and can provide sequential sample introduction to keep the interval from silylation to GC-MS injection constant.

## [Experimental]

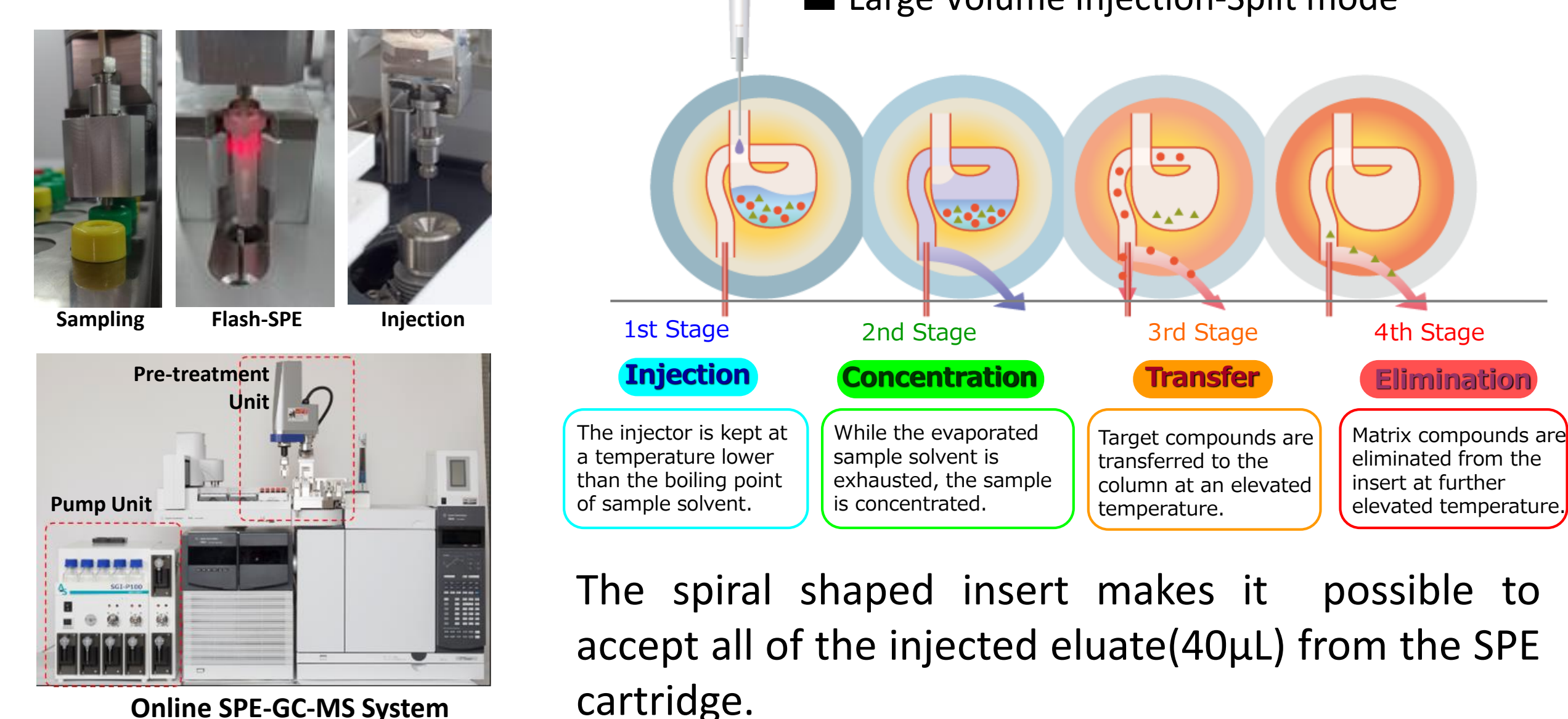


Amino acids and organic acids from the extracted samples were loaded into the SPE column filled with a mixture of ion-exchange sorbent. After washing with acetonitrile/water, the remaining water in the sorbent was removed with acetonitrile. TMS derivatization was done by permeating MSTFA reagent directly into the sorbent. A needle was automatically connected to the SPE cartridge and inserted into the GC-MS. Then, the TMS-derivatized metabolites were eluted with n-hexane, and injected directly into GC-MS with LVI spiral insert.



**Condition of SPE-GC-MS System**

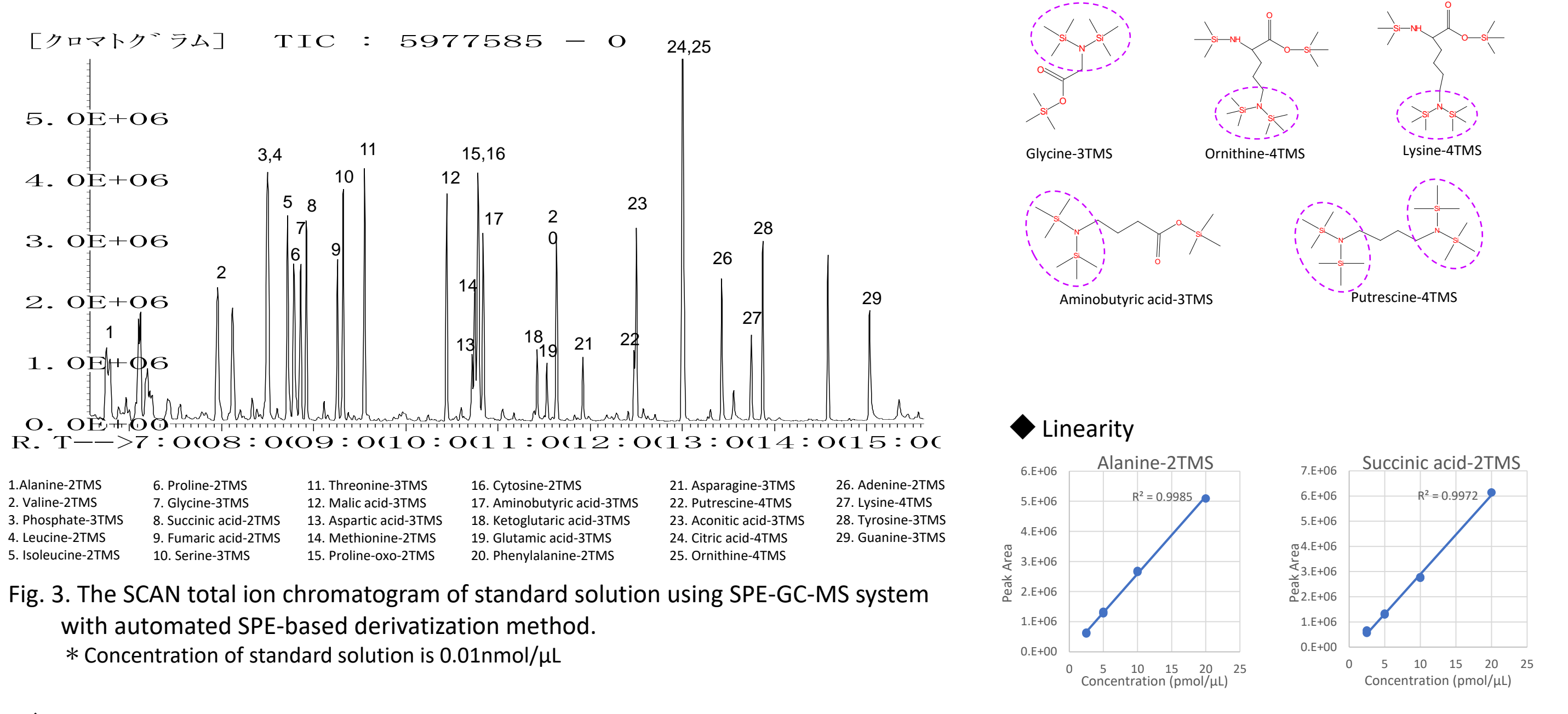
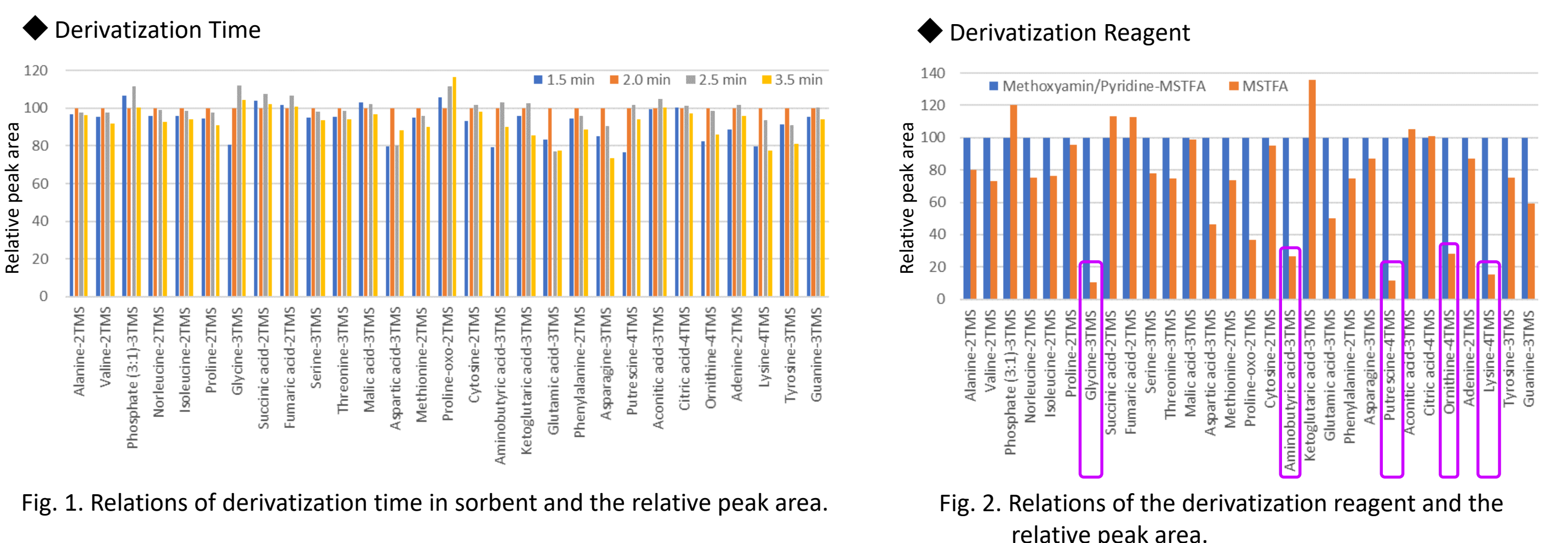
SPE-GC Interface	SGI-M100 ; AISTI Science
SPE Cartridge	Flash-SPE AOS ; AISTI Science
Sample Volume	40μL
PTV Injector	LVI-S250 ; AISTI Science
Insert	Spiral Insert ; AISTI Science
Injector Temp.	80°C(0.2min)-50°C/min-290°C(38min)
GC	Agilent 7890B
Pre-column	Deactivated silica capillary tube, 0.25mm×0.3m
Column	DB-5MS, 0.25mm i.d.×30m, df: 0.25μm
Column Oven Temp.	60°C(2min)-15°C/min-240°C-20°C/min-310°C(1min)
Inlet Mode	Split
Split ratio	50
Gas Saver Flow	15 mL/min
Gas Saver Time	6 min
MS	Agilent 5977B
Detector Temp.	290°C
MS Method	SCAN, 70 - 500 m/z



The spiral shaped insert makes it possible to accept all of the injected eluate(40μL) from the SPE cartridge.

## [Results]

### Evaluation with the standard solution



**Reproducibility**

Table 1. Reproducibility of peak area with standard solution using SPE-GC-MS system.

No.	Compound	1	2	3	4	5	6	7	8	9	Ave.	RSD, %
1	Alanine-2TMS	2,780,202	2,814,678	2,805,838	2,870,446	2,863,343	2,876,876	2,832,581	2,892,127	2,718,118	2,708,045	3.0
2	Valine-2TMS	3,231,804	3,290,271	3,270,689	2,966,049	3,107,665	3,112,760	3,054,983	3,085,131	3,160,769	3,144,654	3.4
3	Phosphatate (3:1)-3TMS	1,980,261	1,945,488	1,840,146	1,762,489	1,746,163	1,658,940	1,595,771	1,679,471	1,591,253	1,739,088	8.3
4	Norleucine-2TMS	3,860,754	3,995,800	3,961,145	3,572,341	3,750,253	3,758,730	3,712,869	3,739,371	3,834,508	3,801,252	3.4
5	Isoleucine-2TMS	3,136,213	3,281,486	3,263,795	2,942,720	3,111,611	3,105,804	3,057,182	3,062,330	3,129,208	3,124,559	3.4
6	Proline-2TMS	3,325,565	3,442,716	3,432,215	3,055,493	3,245,563	3,222,235	3,230,614	3,241,932	3,297,586	3,288,078	3.6
7	Glycine-3TMS	2,170,640	2,352,241	2,218,378	2,229,077	2,288,729	2,328,562	2,291,359	2,432,007	2,270,036	2,270,036	4.3
8	Succinic acid-2TMS	3,026,526	3,101,538	3,047,596	2,891,528	2,874,284	2,777,718	2,840,856	2,917,358	3,180,044	2,950,282	5.2
9	Fumaric acid-3TMS	1,768,634	1,813,725	1,793,816	1,636,001	1,697,384	1,608,388	1,635,895	1,710,549	1,825,272	1,718,697	4.9
10	Serine-3TMS	2,012,774	2,110,285	2,078,505	1,857,116	1,869,420	1,978,512	1,918,379	1,950,455	1,968,792	1,982,700	3.9
11	Threonine-3TMS	1,040,407	1,085,291	1,075,400	963,085	1,015,290	1,028,004	988,509	997,181	1,024,209	1,024,597	3.8
12	Malic acid-3TMS	485,209	496,725	505,695	464,693	471,484	446,942	451,563	459,884	497,251	478,694	4.5
13	Aspartic acid-3TMS	527,945	521,172	605,941	439,870	548,152	689,805	622,430	590,812	358,848	544,997	18.3
14	Methionine-2TMS	1,317,135	1,376,552	1,320,877	1,165,099	1,233,662	1,299,449	1,267,142	1,274,606	1,279,034	1,281,506	4.6
15	Proline-oxo-2TMS	1,972,285	2,178,513	2,198,272	2,213,001	2,171,464	2,218,260	2,143,150	2,348,329	2,286,991	2,252,380	6.1
16	Cytosine-2TMS	1,164,055	1,199,619	1,211,399	1,081,564	1,154,429	1,175,900	1,130,354	1,140,346	1,191,227	1,161,433	3.5
17	Aminobutyric acid-3TMS	1,993,218	2,080,359	1,832,270	1,718,333	1,911,994	1,983,878	1,952,195	1,884,295	2,036,145	1,922,616	5.6
21	Asparagine-3TMS	364,587	393,568	385,785	215,347	280,091	284,791	258,735	240,746	363,337	292,988	7.9
19	Glutamic acid-3TMS	486,088	482,193	528,880	375,004	494,429	585,775	510,207	483,426	320,272	474,030	16.8
20	Phenylalanine-2TMS	1,553,897	1,642,952	1,616,874	1,422,103	1,528,499	1,584,042	1,507,985	1,508,372	1,520,941	1,540,820	4.2
22	Ornithine-3TMS	663,367	673,444	787,729	789,718	711,470	808,655	771,975	652,659	737,745	739,640	8.0
23	Aspartic acid-2TMS	4,077	3,243	3,558	3,410	3,211	2,885	3,216	2,919	3,005	3,205	10.8
23	Lysine-4TMS	384,118	400,570	466,485	466,911	449,562	483,398	450,203	364,748	433,653	433,287	9.5
24	Tyrosine-3TMS	739,551	763,670	838,110	848,309	773,737	850,307	875,807	790,095	852,336	814,659	5.9
25	Guanine-3TMS	3,773	3,789	3,207	3,438	2,485	2,720	2,968	3,136	2,457	3,108	16.1

Fig. 4. Relations of concentration in vial and the peak area.

### Evaluation with the mouse serum

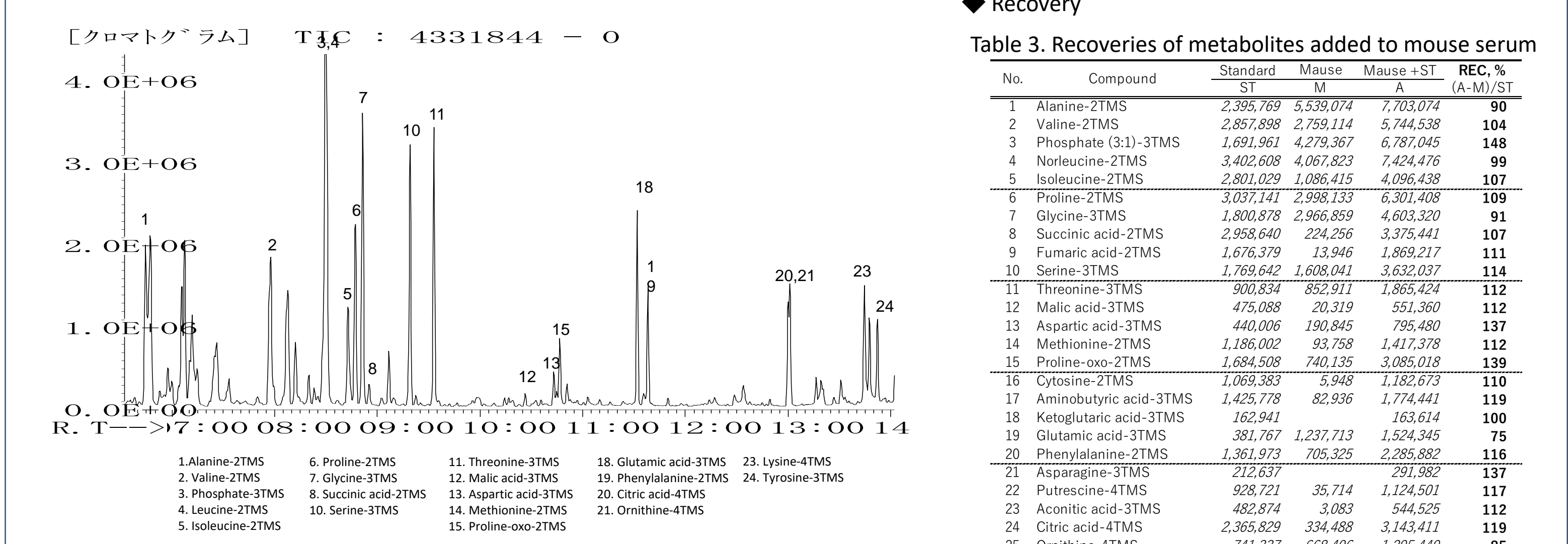
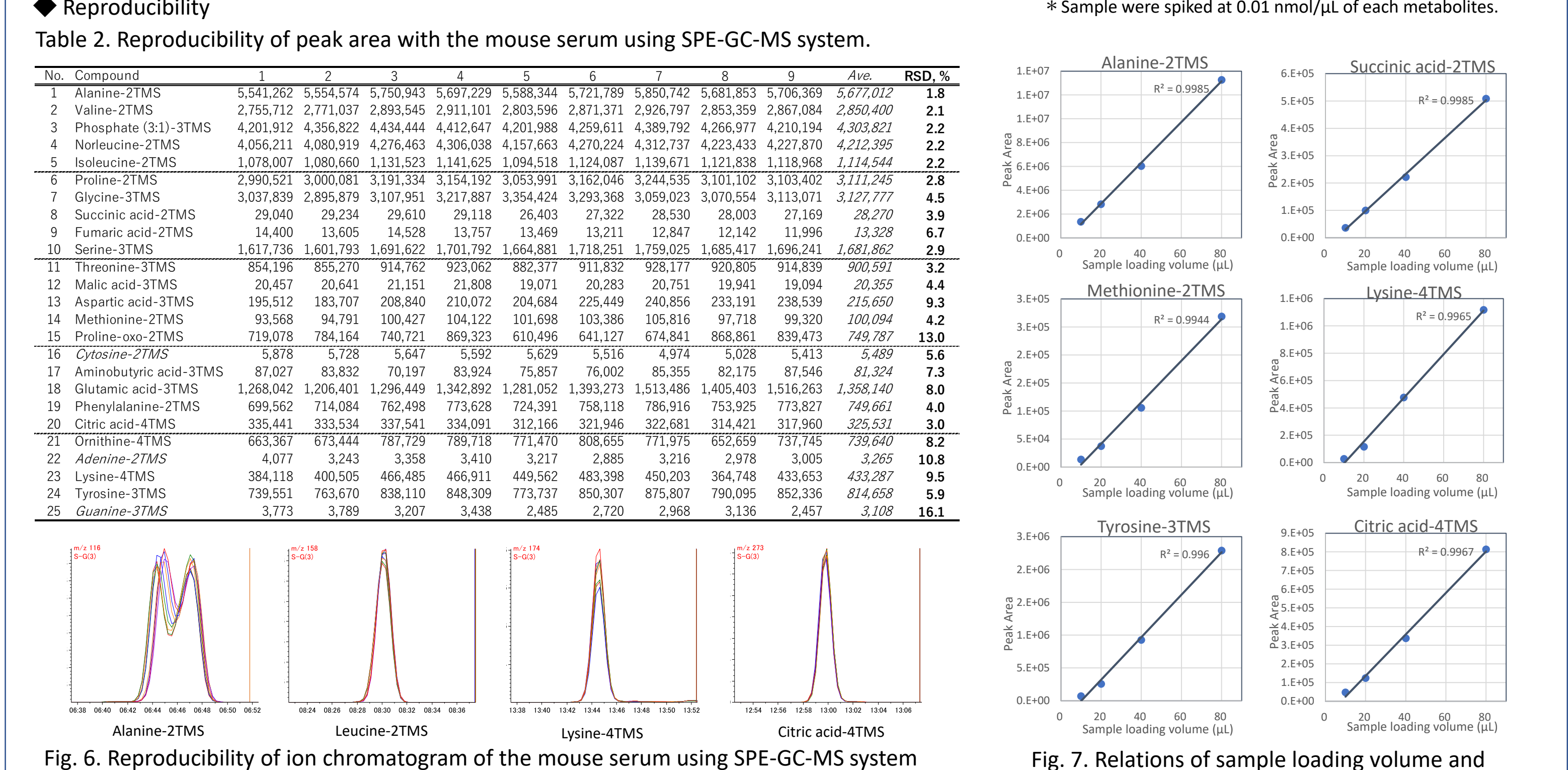


Fig. 5. The SCAN total ion chromatogram of the mouse serum using SPE-GC-MS system with automated SPE-based derivatization method.



## [Conclusion]

Pre-treatment, dehydration and derivatization of the sample was done in 10 minutes. Applying the system to metabolite standard solutions and mouse serums resulted in good reproducibility and robustness. Thus, online SPE-GC-MS system with automated SPE-based derivatization method enables the rapid and reliable analysis of metabolites.

## Acknowledgments

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