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Metabolomic Profiling of Beer Using GC-MS and GC-FID

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. Overview

Despite the same brand and identical brewing techniques, it is widely known that beer taste and quality is not consistent from plant to plant. Therefore, brewers normally check beer quality mainly by sensory test method, and in turn, adjust beer taste in order to reduce these differences as much as possible. In this poster, by metabolomics profiling using GC-MS and GC-FID, we introduce a new approach towards classification and visualization of beer quality to identify how specific components influence taste from plant to plant.

2. Introduction

In food science, global metabolite analysis, or 'metabolomics', is increasingly applied to a number of value-added food production areas including food-safety assessment, quality control, food authenticity, origin and processing. GC-MS are widely used for measuring the total amount of metabolites in a sample. Whereas GC-FID might be less utilized in Metabolomics than GC-MS so far. This is because GC-MS is more powerful in peak annotation, and peak annotation is considered necessary for Metabolomics. But GC-FID has a massive feature; low cost, easy to use, and better reputability.



GC-MS(/MS)

- Permits comprehensive measurement of several hundred compounds in a single measurement
- Better peak annotation
- First-choice comprehensive measurement Low cost



- Simple measurement
- Ideal for efficient routine measurement of specific compounds
- Better repeatability

Figure1 Instrument Features

In order to introduce a new approach towards classification and visualization of beer quality, we tried doing the following two studies.

Study1: Classification of different brand beers

Five brand beers were analyzed by GC-FID and GC-MS, and then principal component analysis (PCA) was performed using each GC-FID and GC-MS data. The results of PCA from each GC-FID and GC-MS data were compared. From loading plot of GC-MS data, we can successfully identify how specific components influence this classification.

Study2: Classification of same brand beers

The different plant and lot beers in the same brand were analyzed by GC-FID and GC-MS, and then principal component analysis (PCA) was performed using each GC-FID and GC-MS data. The results of PCA from each GC-FID and GC-MS data were compared. From loading plot of GC-MS data, we can successfully identify how specific components influence this classification.

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3. Methods

3-1. Samples

After metabolites were extracted from beers, they were derivatized. Table 1 shows pretreatment procedure for the sample of GC-MS and GC-FID, and Table 2 shows types of analyzed beer samples.

Tahla1 Dratraatment procedure

Table1 Pretreatment procedure	Table2 Types of analyzed beer samples		
50µL degassed beers	Types of beer	Study1	Study2
An internal standard [*] was added.	Lager A	0	
	Pale ale A (Plant: a)	0	0
Extraction of hydrophilic metabolites.	Pale ale A (Plant: b, Lot: a)		0
Drying	Pale ale A (Plant: b, Lot: b)		0
	Pale ale A (Plant: b, Lot: c)		0
Samples were methoximated and trimethylsilylated.	Pale ale B	0	
	Pale ale C	0	
* 2-Isopropylmalic acid (0.5 mg/mL)	IPAA	0	

Principal component analyses (PCA) for GC-MS/MS and GC-FID data were performed in the following study 1 and 2.

4-1. Study1: Classification of different brand beers

remained.

3-2. Analytical conditions and software

Pretreated beers were analyzed by GC-MS triple quadrupole mass spectrometer and GC-FID. For statistical analysis, SIMCA 15 software (INFOCOM CORPORATION) was used.

Table3 Analytical condition in GC-MS/MS	Table4 Analytical condition in GC	
GC-MS/MS : GCMS-TQ8040	GC : GC-2030	-20
Software :	Column: SH-Rtx-1 (60 m × 0.32 mm I.D., 1.00	-30
Smart Metabolites Database (475 compounds)	μm)	
GC conditions	Carrier Gas: He	
Column: DB-5(30 m ×0.25 mm I.D., 1.00 µm)	Injection Temperature : 280 ° C	
Carrier Gas: He	Control Mode : Linear velocity (25.0 cm/sec)	
Injection Temperature : 280 ° C	Injection Method : Split (1:15)	
Control Mode : Linear velocity (39.0 cm/sec)	Oven Temperature :	
Injection Method : Splitless	40°C-4°C/min-320°C (15min)	
Sampling time: 1min	Detector : FID	
Oven Temperature :	Detector Temperature : 330 ° C	
100°C (4 min) - 10°C/min - 320°C (11 min)		
MS conditions		
Ion Source Temperature : 200 ° C		
Interface Temperature : 280 °C		
Tuning Mode : Standard		Fi
Measurement Mode : MRM		G
Loop Time : 0.25 seconds		0
MRM Transitions : 950 Transitions		

4. Results

Principal component analyses for GC-MS/MS

Figure2 shows Score plot and loading plot from GC-MS/MS data. From Score plot of figure2, we can confirm that five types of beers were successfully classified. Loading plot of figure2 means which compounds are relatively higher concentration among five beers and how specific compounds influence this classification. Table5 shows higher concentration compounds in each beer from loading plot. In IPA A and Pale ale C, a lot of some sugars were

Principal component analyses for GC-FID

Figure3 shows the score plot from GC-FID data. We can get almost the same score plot as one of GC-MS/MS. This result suggest that GC-FID can also used for classification of beers quality. Whereas, it is difficult how specific compounds influence this classification from only FID data, because qualitative analyses performance on GC-FID is less than GC-MS.



Figure2 Score plot and loading plot from C-MS/MS data



Figure3 Score plot from GC-FID data

Table5 Higher concentration compounds in each beer from loading plot

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ypes of beer	Higher concentration compounds
.ager A	Phenylpyruvic acid, Glutaric acid
	Lyxose, Xylose, Arabinose
	Threo-b-hydroxyaspartic acid
	2-Ketoglutaric acid
	2-Hydroxyglutaric acid
Pale ale A	Maleic acid, Cadaverine, Maltitol
	4-Aminobutyric acid, Dopamine
	Tryptophan, Oxalic acid
Pale ale C	Galactose, Galacturonic acid
	Glucose, Mannose, Erythrulose
	Homogentisic acid, Glucuronic acid
	Asparagine
PAA	Sebacic acid, Fructose, Sorbose
	Tagatose, Psicose

Principal component analyses for GC-MS/MS

Figure4 shows score plot and loading plot from GC-MS/MS data. From Score plot of figure4, we can confirm that the same brand beers brewed in different plants were divided. Plus, different lots of same plant can successfully classified in the score plot. Loading plot of figure4 means which compounds are relatively higher concentration among the same brand beers and how specific compounds influence this classification. Table6 shows higher concentration compounds in beers brewed in Plant a and b from loading plot. In the beer brewed in Plant a, a lot of metabolites from sugar were remained. These results suggest that this approach could be a powerful tool for adjusting food quality. Principal component analyses for GC-FID Figure4 shows the score plot from GC-FID data. We can get almost the same score plot as one of GC-





Figure4 Score plot and loading plot from GC-MS/MS data

4-2. Study2: : Classification of same brand beers

MS/MS. This result suggests that GC-FID can also used for classification of beers quality in same bland.

5. Conclusions

 Score plot from GC-MS/MS and GC-FID successfully categorized five brands of beer, different plants and lots in same brand beer.

Phenylpyruvic acid, Tryptamine

2'-Deoxyuridine, Cystamine-d8, Uridine

• From the loading plots in GC-MS/MS, we could identify important compounds which determine differences of beer brands, same brand beers brewed in different plants and product lots. • This study suggest a new approach towards classification and visualization of beer quality.

• In the future, GC-FID potential for this filed will be tested in more detail.

6. Acknowledgment

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