1. 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, brewmaster 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 paper, by metabolomics profiling using GC-MS and GC-FID, we introduce a new approach towards classification and visualization of beer quality by identifying how specific components influence taste from plant to plant.

2. Introduction

In food science, global metabolite analysis, or ‘metabolomics’, is increasingly applied to a wide variety of fields including food safety assessment, quality control, food authenticity, origin and processing. GC-MS are widely used for measuring 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 repeatability.

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.

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 (INFOTCM CORPORATION) was used.

4. Results

4.1- Study1: Classification of different brand beers

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

4.2- Study2: Classification of same brand beers

Principal component analysis for GC-MS/MS

5. Conclusions

6. Acknowledgment

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