Analysis of Tetrahydrofuran and Methanol in Distillation Residue Samples by Automated Headspace Solid-Phase Microextraction–Gas Chromatography with Flame Ionization Detection

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Abstract

Automated headspace solid-phase microextraction (SPME) coupled with gas chromatography and flame ionization detection is used to determine the amounts of methanol and tetrahydrofuran (THF) in distillation residue samples from a proprietary chemical reaction. A 65-µm polydimethylsiloxane/divinylbenzene SPME fiber is used to perform the extractions. Optimized extraction conditions for each analyte are determined using a parts-per-million-level methanol in water standard and a parts-per-billion-level THF in water standard. The amount of methanol and THF in distillation residue samples is quantitated by both standard addition and external standard calibration curve. The two methods of quantitation are compared.

Introduction

Chemical reactions are often performed in solvent systems that contain a high amount of organic compounds or are totally nonaqueous. In order to make such reactions economically viable, a key component of process development work is in the area of solvent recovery. If the nonaqueous solvent can be effectively recovered, then it can be recycled in the process and thus reduce solvent usage and waste disposal costs. One way to remove solvents on a process scale is through distillation. The distillate is often analyzed using a typical liquid-injection-based gas chromatographic (GC) method. The distillation residue, however, is more difficult to analyze, because it may contain nonvolatile reaction components, a catalyst, residual volatile solvents, and nonvolatile solvents. To further complicate the analysis, the distillation residue is often left as a slurry to facilitate easier handling of the material in the process.

Methanol and tetrahydrofuran (THF) are common reaction solvents that can be removed and recycled through distillation and are usually analyzed using GC methods. However, normally straightforward GC analyses take on added complexity when methanol and THF are present at parts-per-million levels in a distillation residue. Some type of sample preparation must be performed before methanol and THF analyses using GC can be performed.

Dynamic headspace analysis (1,2) and static headspace analysis (3,4,5) are common ways to analyze volatile compounds in matrices that are not readily amenable to GC analysis. Dynamic headspace analysis (often called purge-and-trap) typically involves the use of a carrier gas to purge volatile compounds out of the sample matrix, where they are then collected using some type of trap. The analytes are then desorbed from the trap and analyzed by GC. This technique has the advantage of transferring all of the volatile compounds from the sample to the trap, which can result in low detection limits. The disadvantages include a complex purge-and-trap instrument that can cause contamination and carryover problems. Also, the technique is typically used with aqueous samples, and the water vapor generated during the purge step can cause analysis problems. Static headspace analysis involves the equilibration of the sample with its headspace and then direct sampling of the headspace. The headspace sample is then analyzed by GC. A static headspace instrument, which can accurately control the sample temperature, is needed to perform the analysis. The main advantage of this technique is that it presents a sample to the GC that is free of nonvolatile matrix components. The disadvantages of the technique include the need to determine equilibrium conditions for the matrix and possible carryover and adsorption problems with the static headspace instrument.

Headspace solid-phase microextraction (SPME) is a straightforward extraction procedure that allows for the extraction of volatile analytes from various matrices. The advantages of SPME include relatively simple instrumentation, no use of extraction solvent, the ability to concentrate analytes, and the capability to be automated when the appropriate autosampler and software combination is used. The ability to automate the extraction allows for the sample preparation to occur while the

chromatographic analysis is being performed, thus greatly reducing sample preparation time. Information concerning the theory and practice of SPME can be found in a recent book by Pawliszyn (6), the inventor of the technique.

In this work, parts-per-million levels of methanol and THF were determined in distillation residue samples. These slurry-type samples presented a sample preparation challenge that was handled through a headspace SPME sample preparation approach prior to GC analysis. SPME was chosen, rather than dynamic or static headspace analysis, because headspace instruments were not available, and automated SPME could be performed using existing instrumentation for relatively little additional cost. Also, SPME has been successfully applied to the analysis of methanol in matrices such as whole blood (7), a proprietary liquid containing 40% NaOH (8), hexane (9), gasoline (9), and water (9), and SPME has been successfully applied to the analysis of THF in water (9). The use of automated headspace SPME–GC to determine residual volatile solvents in distillation residues represents a new application of the technique.

Experimental

Reagents and samples

High-performance liquid chromatography-grade water and methanol (> 99.9% purity) were obtained from Burdick and Jackson (Muskegon, MI). THF (> 99.5% purity) was obtained from EM Science (Gibbstown, NJ). These chemicals were used to prepare standard solutions. The reaction solvent system was comprised of approximately 60% THF, 20% water, 5% acetic acid, and less than 1% methanol. The remaining mass balance consisted of proprietary reactants and reaction products. Distillation residue samples were collected at four different time points during the distillation process.

Instrumental conditions

A 30-m DB-5 column (J&W Scientific, Folsom, CA) with a 0.54-mm internal diameter and 5-µm film thickness was used in a Varian (Walnut Creek, CA) 3800 GC. The pressure was programmed to maintain a constant helium flow rate of 5 mL/min through the column. The split/splitless injector was operated with the split vent closed, and a Varian SPME injection port insert was installed. The GC was equipped with a Varian 8200 autosampler capable of SPME injections. The autosampler rack used 2-mL sample vials, which allowed for unattended extraction and subsequent GC analysis of up to 48 samples. Varian Star software was used for extraction and instrument control and data collection. A polydimethylsiloxane/divinylbenzene (PDMS/DVB) SPME fiber with a 65-µm film thickness (Supelco, Bellefonte, PA) was used for the extractions. The recommended operating temperature for the PDMS/DVB fiber is 200–270°C with a conditioning temperature of 260°C. Each new fiber was conditioned for 45 min at 260°C before use. Fibers were used for approximately 40 extractions for methanol analysis and approximately 75 extractions for THF analysis before peak shape degradation was noted.

For the THF analyses, the initial column oven temperature was set to 50°C and held there for 2 min. It was then increased at a rate of 20°C/min to 240°C, where it was held for 2 min. The flame ionization detector (FID) was set to the most sensitive range and was held at 250°C.

For the methanol analyses, the initial column oven temperature was set at 40°C and held there for 3 min. It was then increased at a rate of 15°C/min to 240°C, where it was held for 5 min. The FID was set to the most sensitive range and was held at 260°C.

Results and Discussion

Separate aqueous THF and aqueous methanol standards were used to optimize the headspace SPME conditions for the analysis of THF and methanol, respectively. Aqueous analyte standards were chosen for the optimization work, because the actual sample matrices varied, making it impractical to optimize with respect to each matrix. The SPME conditions were optimized with respect to extraction time, desorption time, desorption temperature of the GC injection port, and sample volume in 2-mL autosampler vials. All extractions were performed at room temperature, because the autosampler did not have an extraction temperature control feature.

THF analysis

Optimization of THF analysis conditions

An aqueous 254-ppb THF standard was used to optimize the THF SPME conditions. The extraction time with respect to response was investigated for times ranging from 1 to 15 min. An extraction time of 9 min was chosen based on the data presented in Figure 1. An increase in response of over 50% was found for a 9-min extraction time versus a 1-min extraction time, whereas minimal increases in response were found for extraction times greater than 9 min. In each case, a desorption time of 2 min was used, because no THF carryover was observed with this desorption time. Injection port temperatures of 200, 225, and 250°C were investigated for the desorption temperature. No difference in THF response was observed for the three temperatures, so 200°C was chosen as the desorption temperature. When performing headspace SPME with the Varian autosampler, the maximum recommended volume

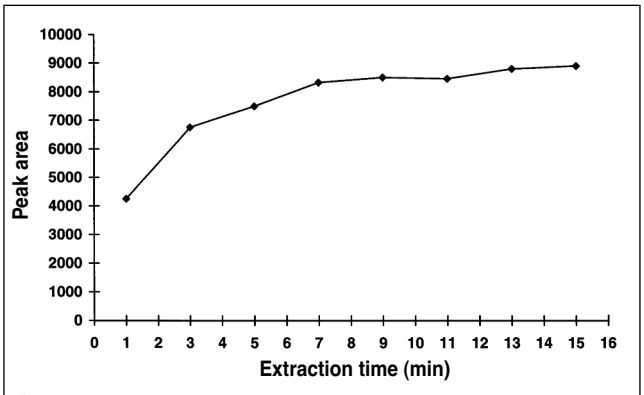

Figure 1. Extraction time optimization for THF analysis.

is 0.8 mL in a 2-mL autosampler vial. Three volumes (0.2, 0.5, and 0.8 mL) were investigated. No difference was observed for the three volumes. A 0.5-mL sample was chosen in order to conserve samples yet still provide a reasonable volume in terms of sample handling.

THF response linearity

A calibration curve was prepared using aqueous THF standards ranging in concentration from 0.595 to 70.9 ppm THF. A linear response was not found over this range, with a suppressed response observed above approximately 5 ppm THF. A calibration curve was then prepared using aqueous THF standards ranging in concentration from 59.2 to 1190 ppb THF, and a linear response was found over this range (R^2 = 0.9981, slope = 39.01, y-intercept = 1495). A typical SPME–GC chromatogram for an aqueous THF standard is shown in Figure 2. The additional peaks noted in the chromatogram are system peaks and are also found when a headspace SPME is performed on an empty autosampler vial, as evidenced by the chromatogram in Figure 3.

THF extraction precision

One sampling from each of six consecutive vials containing an aqueous 254-ppb THF standard yielded a relative standard deviation (RSD) of 1.98%. Six consecutive samplings from the same vial of the 254-ppb THF standard yielded an RSD of 4.25%. It should be noted that the response for the same vial samplings showed a steady decrease, with peak integration values of 9509, 9264, 9155, 8868, 8692, and 8483. This would indicate that the THF was being depleted with each subsequent sampling, and only a single extraction should be performed per vial. One sampling from each of six consecutive vials containing a distillation residue sample containing approximately 1000 ppb THF yielded an RSD of 6.2%.

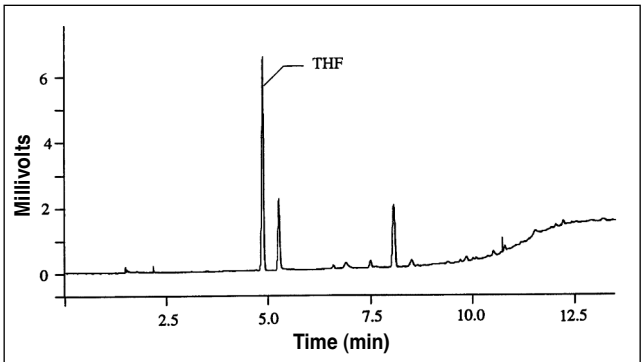

Figure 2. SPME–GC chromatogram of an aqueous 542.2-ppb THF standard.

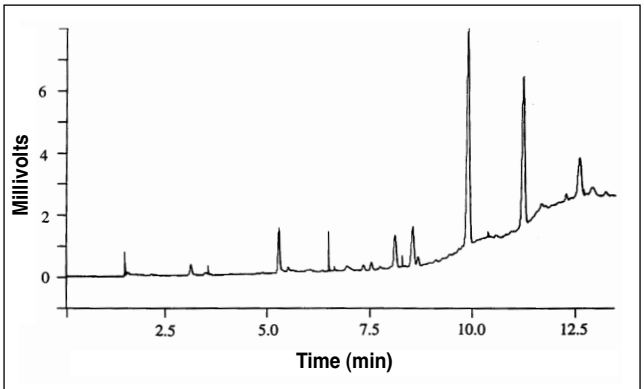

Figure 3. SPME–GC chromatogram of an empty autosampler vial sample.

Distillation residue sample THF analysis

Once both a set of analysis conditions and a linear response range were established, sample quantitation was performed. Because the sample matrix would be changing as the distillation progressed, it would be difficult to prepare a universally representative blank matrix sample into which THF could be added. Instead, a standard addition method of quantitation was compared to an external standard method of quantitation in an effort to determine the best way to determine the amount of THF present and to compare the two methods of quantitation.

Each of four different distillation residue samples were diluted with water so that the THF response was within the response range found for the 59.2- to 1190-ppb THF standards. The samples were then quantitated with respect to an external standard calibration curve generated using a series of aqueous THF standards. Next, two comparable dilutions were made for each sample. In the first dilution, the samples were diluted with an aqueous THF standard solution to add approximately 280 ppb THF to each sample. In the second dilution, the samples were diluted with water to approximately the same matrix concentration as found in the 280-ppb THF spiked samples. These standard addition samples were used to quantitate the amount of THF in the distillation residue samples. Table I contains a summary of the calibration curve and the standard addition quantitation data. The values, expressed in parts-per-million, are the amount of THF found in each sample after dilution factors were taken into account. The results indicate that the matrix influenced parts-per-billion-level THF quantitation and that the standard addition method of quantitation is required for THF analysis. The need for standard addition is minimized when the sample matrix can be diluted to a greater extent, as demonstrated in the Residue 1 sample. Figure 4 is a typical SPME–GC chromatogram of THF in a distillation residue sample.

Methanol analysis

Optimization of methanol analysis conditions

An aqueous 200-ppm methanol standard was used to optimize the methanol SPME conditions. The extraction time was investigated for times ranging from 1 to 20 min. An extraction

Table I. Comparison of THF Quantitation in Distillation Residue Samples by External Calibration Curve and Standard Addition Methods of Quantitation

	Calibration curve (ppm THF)	Standard addition (ppm THF)	Calibration curve/ standard addition
Residue 1	269.5	306.0	88.1%
Residue 2	15.8	57.1	27.6%
Residue 3	6.46	13.8	46.8%
Residue 4	8.44	16.1	52.4%

time of 10 min was chosen based on the data presented in Figure 5. The plot of extraction time versus response indicated a minimal difference in response with respect to extraction time, with only a 12% increase when going from a 1-min to a 20-min extraction time. A desorption time of 2 min was chosen, because no methanol carryover was observed when subsequent fiber desorptions were performed. The desorption temperature was evaluated at 200, 225, and 250°C. A 5% increase in response was observed when going from an injection port temperature of 200 to 225°C, but no difference was found when going from 225 to 250°C. An injection port temperature of 225°C was selected as the optimum desorption temperature. Sample sizes of 0.2, 0.5, and 0.8 mL in a 2-mL vial were investigated for headspace SPME analysis. A small 2% increase in response was noted when the sample volume was increased from 0.2 to 0.5 mL, but no increase was noted when the sample volume was increased from 0.5 to 0.8 mL. A sample volume of 0.5 mL was selected as the optimum volume for the 2-mL sample vials.

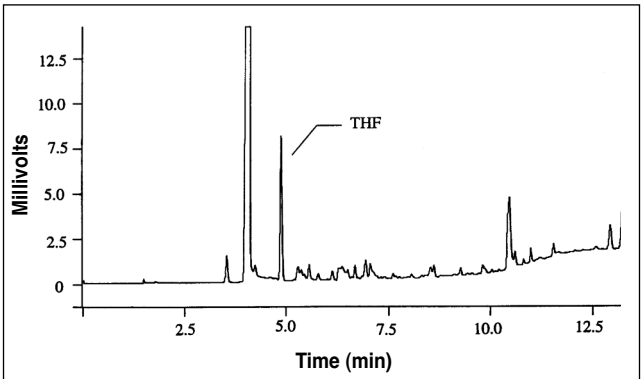

Figure 4. SPME–GC chromatogram of THF in distillation residue sample 2.

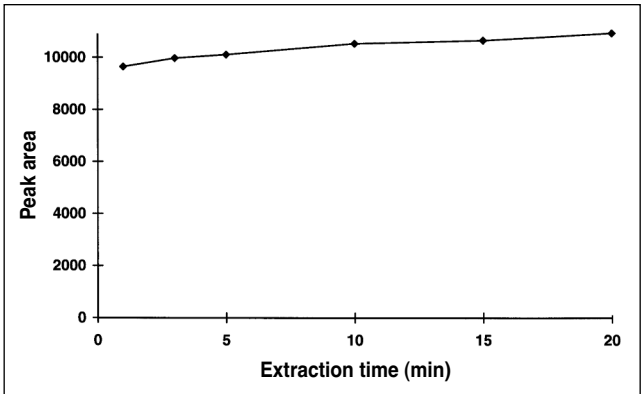

Figure 5. Extraction time optimization for methanol analysis.

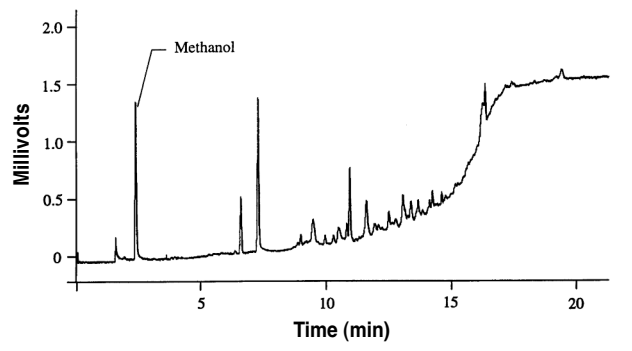

Figure 6. SPME–GC chromatogram of a 97.21-ppm aqueous methanol standard.

Methanol response linearity

A calibration curve was prepared using aqueous methanol standards ranging in concentration from 17.8 to 444.1 ppm methanol, and a linear response was found over this range (R^2 = 1.0000, slope = 42.33, y-intercept = –13.81). A typical SPME–GC chromatogram for an aqueous methanol standard is shown in Figure 6.

Methanol extraction precision

One sampling from each of six consecutive vials containing an aqueous 200-ppm methanol standard yielded an RSD of 0.83%. Five consecutive samplings from the same vial of 200-ppm methanol standard yielded an RSD of 0.85%. These results indicate good precision for the analysis of an aqueous methanol standard at the 200-ppm level. The data from the five consecutive samplings from the same vial of aqueous methanol standard indicate that multiple samples can be taken from the same vial when the methanol concentration is in the 200-ppm range. One sampling from each of five consecutive vials containing a distillation residue sample with approximately 20 ppm methanol yielded an RSD of 2.4%.

Distillation residue sample methanol analysis

Once both a set of analysis conditions and a linear response range were established, sample quantitation was performed. Because the sample matrix would be changing as the distillation progressed, it would be difficult to prepare a universally representative blank matrix sample into which methanol could be added. Instead, a standard addition method of quantitation was compared to an external standard method of quantitation in an effort to determine the best way to determine the amount of methanol present and to compare the two methods of quantitation. Each of four different distillation residue samples were quantitated (undiluted) with respect to an external standard calibration curve generated with aqueous methanol standards. The samples were then diluted 1:1 with water and quantitated with respect to a sample that had been diluted 1:1 with a 50-ppm methanol in water standard solution for the standard addition analysis. Table II contains a summary of the

Table II. Comparison of Methanol Quantitation in Distillation Residue Samples by External Calibration Curve and Standard Addition Methods of Quantitation

	Calibration curve (ppm Methanol)	Standard addition (ppm Methanol)	Calibration curve/ standard addition
Residue 1	70.66	72.28	97.8%
Residue 2	54.30	55.62	97.6%
Residue 3	45.98	47.90	96.0%
Residue 4	51.81	50.42	102.8%

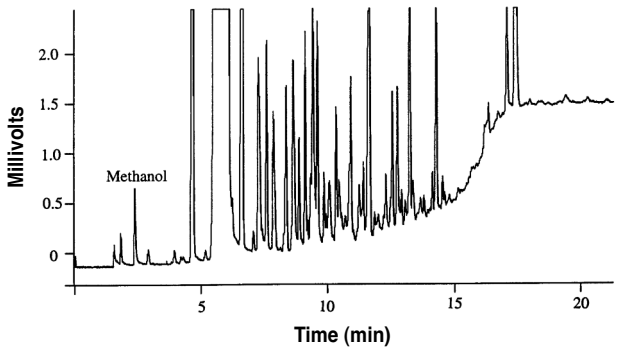

Figure 7. SPME–GC chromatogram of methanol in distillation residue sample 2.

calibration curve and the standard addition quantitation data. For the methanol analysis, reasonable agreement between the external standard and the standard addition methods of quantitation was observed. This would indicate that either method of quantitation could be used for the quantitation of methanol in these samples. Figure 7 is a typical SPME–GC chromatogram of methanol in a distillation residue sample. This chromatogram is more complex than the THF in the distillation residue sample chromatogram found in Figure 4 because the methanol analysis sample is not diluted.

Conclusion

Automated headspace SPME–GC was successfully used to determine the amount of THF and methanol in distillation residue samples. Automated extraction conditions were optimized for both THF and methanol. THF was analyzed over a linear parts-per-billion concentration working range, and methanol was analyzed over a linear parts-per-million concentration working range. Precision, in terms of RSD, was good for each analyte as reflected by values of 1.98% for an aqueous THF standard and 0.83% for an aqueous methanol standard. It was determined that making multiple extractions from the same vial was not possible for the analysis of a parts-per-billion-level THF standard but was possible for the analysis of a parts-per-million-level methanol standard. Distillation residue samples were quantitated by both the standard addition and external standard calibration techniques for THF and methanol. The results indicated that the standard addition technique was necessary for accurate THF quantitation, whereas methanol could be quantitated by either the standard addition or external standard calibration curve techniques.

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