Anal. Chem. **2000,** *72,* 4865−4873

In Situ Derivatization/Solid-Phase Microextraction for the Determination of Haloacetic Acids in Water

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An in situ derivatization solid-phase microextraction method has been developed for the determination of haloacetic acids (HAAs) in water. The analytical procedure involves derivatization of HAAs to their methyl esters with dimethyl sulfate, headspace sampling using solid-phase microextraction (SPME), and gas chromatography-ion trap mass spectrometry (GC/ITMS) determination. Parameters affecting both derivatization efficiency and headspace SPME procedure, such as the selection of the SPME coating, derivatization−extraction time and temperature, and ionic strength, were optimized. The commercially available Carboxen-poly(dimethylsiloxane) (CAR-PDMS) fiber appears to be the most suitable for the determination of HAAs. Moreover, the formation of HAA methyl esters was dramatically improved (up to 90-fold) by the addition of tetrabutylammonium hydrogen sulfate (4.7 μmol) to the sample as ion-pairing agent in the derivatization step. The precision of the in situ derivatization/HS-SPME/GC/ITMS method evaluated using an internal standard gave relative standard deviations (RSDs) between 6.3 and 11.4%. The method was linear over 2 orders of magnitude, and detection limits were compound-dependent, but ranged from 10 to 450 ng/L. The method was compared with the EPA method 552.2 for the analysis of HAAs in various water samples, and good agreement was obtained. Consequently, in situ derivatization/HS-SPME/GC/ITMS is proposed for the analysis of HAAs in water.

Chemical oxidants, such as chlorine, ozone, chloramines, chlorine dioxide, etc., are used in the treatment of drinking water in many parts of the world, mostly for disinfection and removal of obnoxious chemical compounds or potential toxicants. However, water treatment practices also generate disinfection byproducts (DBPs) due to reactions of these oxidants with natural organic matter present in water. Nowadays, the most common drinking water disinfectant worldwide is chlorine, which produces trihalomethanes (THMs) and haloacetic acids (HAAs) as the most prevalent groups of chlorination byproducts. The levels and speciation of these compounds depend on the water quality conditions (such as total organic content, bromide concentration, temperature, and pH), as well as on the disinfection conditions (such as dose of chlorine and free chlorine contact time).[1] In the early days of DBP research, trihalomethanes (THMs) received almost exclusive attention, because chloroform was shown to be an animal carcinogen. However, awareness that HAAs present serious human health hazards has increased. The U.S. Environmental Protection Agency (USEPA) has classified dichloroacetic acid as a group B2, probable human carcinogen, on the basis of positive carcinogenic findings in the liver of two animal species, male $B6C3F_1$ mouse[2] and male rats,[3] and trichloroacetic acid as a group C, possible human carcinogen, on the basis of limited evidence of carcinogenicity to the liver in animals.[2,4] Accordingly, in the first stage of the D/DBP rule, the USEPA has established a maximum contamination level (MCL) of 60 μg/L for the sum of five HAAs: monochloroacetic acid, dichloroacetic acid, trichloroacetic acid, monobromoacetic acid, and dibromoacetic acid.[5] Under stage II of this rule, this MCL is expected to be reduced to 30 μg/L. Consequently, efforts must be made to develop fast and accurate analytical methods of monitoring concentration, behavior, and distribution of HAAs in water.

Most of the methods used to determine HAAs involve gas chromatography (GC) with electron capture detection (ECD) or coupled with mass spectrometry (GC/MS). For the analysis of these compounds by GC, a prior derivatization step is necessary because of their low volatility and high polarity. Liquid−solid or liquid−liquid extraction (LLE) is commonly used for the isolation of HAAs. After an extraction step, the derivatization of HAAs to short-chain esters using different reagents, such as diazomethane,[6] acid-alcohol,[7,8] or BF_3-methanol,[9] is often applied. Other authors

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10.1021/ac000479d CCC: $19.00
Published on Web 09/14/2000

proposed simultaneous extraction−derivatization[10] or a derivatization step prior to the extraction.[8,11,12] The derivatization is performed either in dry conditions by evaporation of the matrix sample or directly in water, and in both cases the derivatives are then extracted by organic solvents[8,11] or directly analyzed by the headspace technique.[12] On the other hand, the Grob closed-loop stripping analysis (CLSA) technique has recently been employed for the determination of the most common nonpolar and polar halogenated DBPs using GC-ECD analysis, but only results for dichloroacetic acid and dibromoacetic acid have been reported.[13] Determination of HAAs without derivatization is possible by using liquid chromatography,[6,14−16] especially ion chromatography[15,16] or capillary zone electrophoresis.[17] Some of these methods are able to achieve detection limits for HAAs similar to or even better than GC methods, but multistep procedures, involving trace enrichment processes, are also necessary, which is tedious and time-consuming.

Solid-phase microextraction (SPME), pioneered by Pawliszyn and co-workers,[18−20] is a rapidly growing technique. It involves the partitioning of organic analytes from the aqueous or gaseous medium onto the stationary-phase coating of a SPME fiber. The analytes can be determined by GC via thermal desorption at the GC injector port, or by HPLC via a special interface. SPME has been used successfully for the analysis of a wide range of organic compounds in water samples,[21,22] and recently, it has been applied for the determination of various DBPs in water samples, such as trihalomethanes and halogenated solvents,[23−25] iodinated halomethanes,[26,27] carbonyl compounds,[28] cyanogen halides,[29] and also for compounds causing taste and odor in water supplies, such as geosmin and 2-methylisoborneol.[30] To our knowledge, only two studies report HAAs analysis by SPME. Aikawa and co-workers[31] described the analysis of HAAs in drinking water by in situ acidic derivatization to the methyl esters with HCl/methanol followed by headspace SPME (HS-SPME) and GC-ECD determination using a poly(dimethylsiloxane) fiber. Although this method is rapid, a high limit of detection was obtained for monochloroacetic acid (400 μg/L) and only three chlorinated acetic acids were studied. More recently, a new method for the analysis of the six HAAs included in EPA method 552 using HS-SPME/GC coupled to ion-trap mass spectrometry (ITMS) was developed in our laboratory.[32] Acid-catalyzed ethylation instead of methylation was used to form volatile esters with high partition constants on the fiber in order to obtain low detection limits. The method showed good sensitivity (detection limits from 10 to 200 ng/L), but was relatively time- and labor-intensive.

In this paper, a new method for analysis of HAAs in water using HS-SPME/GC/ITMS is proposed. Direct derivatization of HAAs in water by dimethyl sulfate or diethyl sulfate was tested in order to obtain low detection limits, to avoid tedious preconcentration steps, and to reduce the analysis time. Experimental conditions to obtain high efficiency in the derivatization step were established and HS-SPME parameters were optimized to achieve good sensitivity in the GC. The optimized procedure was applied to the analysis of nine HAAs (EPA method 552.2) in tap water and swimming-pool water.

EXPERIMENTAL SECTION

Chemicals and Materials. Monochloroacetic acid (MCAA, 99%), monobromoacetic acid (MBAA, 99%), dichloroacetic acid (DCAA, 99%), dibromoacetic acid (DBAA, 98%), trichloroacetic acid (TCAA, 99.5%), and tribromoacetic acid (TBAA, 99%) were obtained from Fluka (Buchs, Switzerland); bromodichloroacetic acid (BDCAA, 99%) and chlorodibromoacetic acid (CDBAA, 99%) were purchased from Supelco (Bellefonte, PA), and finally, bromochloroacetic acid (BCAA, 98%) was supplied by Chem Service (West Chester, PA). All standards were used as received. A commercially available EPA 552.2 esters calibration mixture in methyl *tert*-butyl ether (MtBE), containing the methyl esters of the 9 HAAs at a purity higher than 97% and concentrations between 200 and 2000 μg/mL, was obtained from Supelco (Bellefonte, PA). The derivatization reagents dimethyl sulfate (DMS) and diethyl sulfate (DES), as well as the ion-pairing agent, tetrabutylammonium hydrogen sulfate (TBA-HSO_4), and the dechlorinating agent, ammonium chloride, were obtained from Fluka at a high purity (≥99%). *The derivatization reagents, as well as some HAAs are carcinogenic or toxic and were handled in accordance with the most current material safety data sheets.* The compounds, 2,3-dibromopropionic acid (98%) and 1,2-dibromopropane (97%), used as the surrogate standard and internal standard were purchased from Fluka and Sigma-Aldrich (Milwaukee, WI). Methanol of residue analysis grade and sulfuric acid for analysis were supplied by Merck (Darmstadt, Germany), whereas MtBE of residue analysis grade was obtained from Fluka. Anhydrous sodium sulfate and copper (II) sulfate pentahydrate were purchased from Panreac (Barcelona, Spain) and Probus (Badalona, Spain), respectively. Water from the Milli-Q water purification system (Millipore Corp., Bedford, MA) was used.

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SPME experiments were performed with a manual fiber holder supplied from Supelco (Bellefonte, PA). Five commercially available fibers, Poly(dimethylsiloxane), PDMS, 100 μm; Polyacrylate, PA, 85 μm; Carboxen-Poly(dimethylsiloxane), CAR-PDMS, 75 μm; Poly(dimethylsiloxane)-divinylbenzene, PDMS-DVB, 65 μm; and StableFlex Divinylbenzene-Carboxen-Poly(dimethylsiloxane), DVB-CAR-PDMS, 50/30 μm were purchased from Supelco. Before use, each fiber was conditioned in a heated GC split/splitless injection port under helium flow according to the manufacturer's instructions. Screw-capped vials (10, 30, and 40 mL), sealed with a Teflon-lined silicon septum and used for storing the standard solutions as well as for sample derivatization and extraction in both HS-SPME and LLE procedures, were obtained from Wheaton (Millville, NJ). The vials were cleaned with AP-13 Extran alkaline soap (Merck) for 24 h; rinsed consecutively with (i) deionized water, (ii) 1:10 HCl/water, (iii) again with deionized water, and (iv) finally with Milli-Q water; and baked at 110 °C overnight. Volumetric glassware was washed as described above, but was air-dried. Anhydrous sodium sulfate was heated to 400 °C overnight to remove phthalates and other interfering organic substances and then stored at 110 °C until use.

Stock standard solutions of each HAA (2000 μg/mL) were prepared by weight in Milli-Q water. Standard mixtures were prepared weekly or daily, depending on their concentration, except for TBAA, which was prepared daily because it decomposes spontaneously at 25 °C.[6] All solutions were stored frozen in the dark at −17 °C until use. For evaluating the SPME procedure, water standards containing 200 μg/L of each HAA were prepared by adding 50 μL of a standard mixture of 45 μg/mL into 10 mL of Milli-Q water and then sealing them in a 30-mL screw-capped vial.

Barcelona tap water and swimming-pool water samples were analyzed using the proposed HS-SPME protocol as well as the EPA method 552.2. The samples were collected in 250-mL amber glass bottles with PTFE-faced septa and polypropylene screw caps containing ammonium chloride, avoiding the presence of headspace at the top of the bottles. All analyses were performed within 2 days of sampling. Ammonium chlorine was added as a dechlorinating agent to preserve the samples by converting the highly reactive free chlorine to the less reactive monochloramine. Thus, the free chlorine was prevented from reacting with precursor organic matter to form additional DBPs.

Instrumentation. All analyses using SPME procedures were carried out with a Varian 3400 CX GC capillary gas chromatograph coupled to a Saturn 3 GC/MS ion trap mass spectrometer (Sugar Land, TX). Separations were conducted on a DB-5 MS fused-silica capillary column, 30 m × 0.25 mm i.d. × 0.25 μm (J&W Scientific, Folsom, CA), with helium as carrier gas, at a linear velocity of 34 cm/s. The column was held at 40 °C for 1 min, ramped at 20 °C/min to 60 °C, then up to 120 °C at 5 °C/min, held for 3 min, and finally ramped at 25 °C/min to 280 °C and held for 10 min. Desorption time and injection port temperature were set at the optimum values.

The ion trap mass spectrometer (ITMS) was operated in electron ionization (EI) positive-mode using automatic gain control (AGC). For EI experiments, the instrumental parameters were set at the following values: a filament emission current of 75 μA, an electron multiplier voltage of 1850 V, and a modulation amplitude of 2.5 V, using perfluorotributylamine (FC-43) as reference. The transfer line and the ion trap manifold temperatures were maintained at 270 and 220 °C, respectively. For ethylation experiments, the instrument was operated in full-scan mode and the mass range was from m/z 27 to 325 at 0.8 s/scan. For quantification, two selected ions of each ethyl haloacetate were monitored: m/z 77/94 for MCAA, 83/85 for DCAA, 117/82 for TCAA, 121/138 for MBAA, 174/120 for DBAA, 251/172 for TBAA, 129/109 for BCAA, 163/161 for BDCAA, and 209/205 for CDBAA. For methylation experiments, the mass spectrometer was operated in full-scan mode between m/z 29 and 260 at 0.8 s/scan, with an ionization time of 100 ms. After establishing the optimized conditions, different acquisition segments during each chromatographic run were applied using a narrow mass range and different scan rates. To enhance the response, ionization times of 200 or 400 ms, depending on the compound, were used. The ions of the methyl haloacetates used for quantification were as follows: m/z 59/108 for MCAA, 83/85 for DCAA, 117/119 for TCAA, 93/95 for MBAA, 173/171 for DBAA, 251/253 for TBAA, 129/127 for BCAA, 163/161 for BDCAA, and 209/205 for CDBAA. For MCAA m/z 59 instead of 77 was used to prevent interference from the fiber. Saturn version 5.2 software was used for data acquisition.

Analyses of HAAs by EPA method 552.2 were performed on a Carlo Erba 5300 Mega Series gas chromatograph (Milan, Italy), equipped with a ^{63}Ni electron capture detector (ECD). A 60 m × 0.25 mm i.d. × 0.25 μm DB-1701 fused-silica capillary column (J&W Scientific, Folsom, CA) was used. The column temperature program was 36 °C, held for 21 min, then increased at 10 °C/min to 140 °C, held for 3 min, up to 240 °C at 20 °C/min, held for 5 min, and finally increased at a rate of 20 °C/min to 280 °C and held for 10 min. Carrier gas was hydrogen (32 cm/s at 36 °C), and nitrogen was used as makeup gas (50 mL/min). A 30-m DB-17 (50% phenyl, 50% methylpolysiloxane) fused-silica capillary column with 0.25-mm i.d. and 0.25-μm film thickness (J&W) was used for confirmation. Injector and detector temperatures were kept at 200 and 330 °C, respectively, and splitless injection mode (1 min) was used in all analyses. ChromCard version 1.3 software (Fisons Instruments, Spain) was used for data acquisition. Confirmation of analytes in the more complex sample, swimming-pool water, was performed by GC/MS.

HS-SPME Procedure. In situ derivatization/HS-SPME was optimized using different derivatization reagents such as DES and DMS in order to obtain the ethyl and methyl haloacetates prior to the analysis by HS-SPME. Briefly, 10 mL of Milli-Q water containing 200 μg/L of each compound (total amount of HAAs, 0.12 μmol) was placed in a 30-mL screw-cap glass vial containing a 10 × 5 mm Teflon-coated stir bar and 5 g (3.5 M) of anhydrous sodium sulfate. After addition of an ion-pairing agent (TBA-HSO_4, 2.3 μmol, as aqueous solution), the vial was closed. One hundred microliters of derivatization reagent (DES, 0.73 mmol, or DMS, 1.05 mmol, i.e., high excess) was then injected through the septum, and the vial was clamped inside a water-thermostatized bath, which was placed on a hot plate/stirrer. After 5 min at 55 °C, the fiber was exposed to the headspace above the aqueous solution for the desired extraction time. Magnetic stirring at 1200 rpm was applied during both stabilization and extraction. Finally, the fiber was desorbed in the injection port of the gas chromatograph for 2 min, at different temperatures depending on the fiber coating (splitless injection mode). Several parameters affecting

both derivatization and HS-SPME were then studied: derivatization reagent (DMS or DES) and fiber stationary phase type, derivatization−extraction temperature (from 35 to 70 °C), derivatization−extraction time (up to 60 min), volume of derivatization reagent (between 10 and 160 μL of DMS) and amount of ion-pairing agent (up to 6.6 μmol). Other parameters affecting the HS-SPME procedure, such as desorption temperature (280 and 300 °C), desorption time (up to 2 min), and the effect of ionic strength in the aqueous solution (from 0 to 5 M of anhydrous sodium sulfate) were also optimized. Possible carryover was prevented by keeping the fiber in the injector for an additional time with the injector in the split mode (purge on). Moreover, blanks were run periodically during the analysis to confirm the absence of contaminants. For optimization, all determinations were performed in duplicate, and the average values are reported.

Liquid−Liquid Extraction Procedure (EPA Method 552.2). Liquid−liquid extraction for the determination of HAAs in tap water and swimming-pool water was performed in triplicate following EPA method 552.2[7] with minor modifications. Briefly, 11 μL of a MtBE solution of 2,3-dibromopropionic acid 22 μg/mL, as surrogate standard, 3 mL of concentrated sulfuric acid (to obtain pH < 0.5), 12 g of anhydrous sodium sulfate, 3 g of copper (II) sulfate pentahydrate, and 2 mL of MtBE were added to a 30-mL water sample placed in a 40-mL vial. The vials were then sealed with Teflon-faced septa, shaken for 15 min in a rotary mixer, and allowed to stand for 5 min. To derivatize the HAAs, 1 mL of the MtBE extract and 2 mL of methanol/sulfuric acid (9:1) were transferred to a 10-mL vial, which was placed in a thermostatic water bath at 50 °C for 1 h. After cooling to 4 °C, 5 mL of a $CuSO_4$/Na_2SO_4 solution was added and the mixture was shaken by hand for 2 min. An aliquot of 300 μL of MtBE extract was transferred to a 2-mL vial, and 3 μL of a MtBE solution of 1,2-dibromopropane, of 10 mg/L, was added as internal standard. Finally, 1 μL of the MtBE extract was injected into the GC.

RESULTS AND DISCUSSION

The objective was to develop and optimize both the in situ derivatization and the extraction conditions for the quantification of HAAs from water. To derivatize carboxylic acids, an esterification reaction is frequently used. For instance, NaOH or K_2CO_3 catalyzes in situ methylation of diols, phenols, or even aliphatic acids with low molecular weight, but cannot be used for direct analysis of halogenated acids in water, such as HAAs, because they decompose to halogenated hydrocarbons in acidic or alkaline media. Another possibility of in-matrix derivatization of organic acids involves the alkylation with dimethyl sulfate[12,33] to the corresponding methyl ester. The addition of modifiers, such as ion-pairing agents, which activate the analytes during derivatization, increases esterification yields and thus improves the sensitivity of the procedure.[12] Ammonium quaternary salts, such as tetrabutylammonium bromide or tetrabutylammonium chloride, can be used as ion-pairing agents for the analysis of HAAs in water. However, they react with the derivatization reagents, dimethyl sulfate or diethyl sulfate, to form halogenated hydrocarbons, which could compete with HAAs derivatives for the fiber. So, tetrabutylammonium hydrogen sulfate (TBA-HSO_4) was used as the ion-pairing agent. In addition, ethylation was initially used instead of methylation in order to form relatively high molecular weight volatile esters, with expected high partition constants on the fiber.

Optimization of the SPME Conditions. (a) Derivatization Reagent and Fiber Selection. Ethylation of HAAs with DES was initially tested, and the analysis of the derivatives formed using HS-SPME with different stationary phases was evaluated to obtain high sensitivity and selectivity. Five fibers were tested: PDMS, 100 μm; PA, 85 μm; PDMS-DVB, 65 μm; CAR-PDMS, 75 μm; PDMS-DVB, 65 μm; and StableFlex DVB-CAR-PDMS, 50/30 μm. SPME conditions are described in the Experimental Section. A long extraction time (60 min) was applied to select the fiber coating, to ensure that a large amount of ethyl derivatives was formed and extracted. The desorption temperatures were within the recommended operating range for each fiber: 250 °C for PDMS, 290 °C for PA, 260 °C for PDMS-DVB and DVB-CAR-PDMS, and 280 °C for CAR-PDMS. No carryover on second desorptions was found for any of the fibers, indicating complete removal of analytes at these temperatures. The results showed that these fibers were not suitable for all the analytes because only small amounts of MBAA, DCAA, and DBAA ethyl haloacetates were detected. Moreover, all fibers showed an extremely broad peak close to those of the TCAA and BCAA ethyl esters, which interfered with the determination of these compounds. Since these problems were hard to overcome, methylation was performed using DMS, and the fiber coating was optimized. The relative responses obtained for methyl haloacetates using the fibers are shown in Figure 1. Homogeneous polymer coatings, such as PDMS and PA fibers, did not extract HAAs methyl esters; only small amounts of di- and trihalogenated HAAs derivatives (from 0.03 to 3.7% respect to maximum response area for DBAA with the CAR-PDMS fiber) were extracted. For coatings formed by porous polymeric phases such as PDMS-DVB, CAR-PDMS, and the dual-coated DVB-CAR-PDMS, the HAAs methyl esters were successfully extracted (Figure 1). This may be due to the strong retention of the analytes into the pores. Generally, the high molecular weight derivatives showed best extraction efficiencies for these three fibers, except TBAA, which showed low sensitivity. This could be explained by the fact that TBAA undergoes spontaneous decomposition to bromoform[6] in aqueous solution even at 25 °C, or could have undergone thermal degradation during esterification with DMS.[12] The presence of bromoform was confirmed by identification in the chromatogram. Moreover, peaks corresponding to the decomposition of BDCAA, CDBAA, and TCAA to the respective halogenated hydrocarbons were also observed in the chromatogram, but the yield of formation was low. On the other hand, only the dual-coated DVB-CAR-PDMS and CAR-PDMS fibers extracted all HAAs, including the monohalogenated species; CAR-PDMS showed the highest extraction efficiency for all the compounds (responses were 1.7−8 times higher than those obtained with dual-coated DVB-CAR-PDMS fiber). The mean micropore diameter (10 Å) of Carboxen is lower than that of divinylbenzene (17 Å), so it would be ideal for SPME analyses of small molecules in the C_2−C_6 range,[22] such as HAAs methyl esters. In terms of selectivity, it should be noted that some additional peaks appeared at the beginning of the chromatogram with CAR-PDMS fiber in comparison with those with PDMS-DVB and DVB-CAR-PDMS fibers. However, these peaks did not

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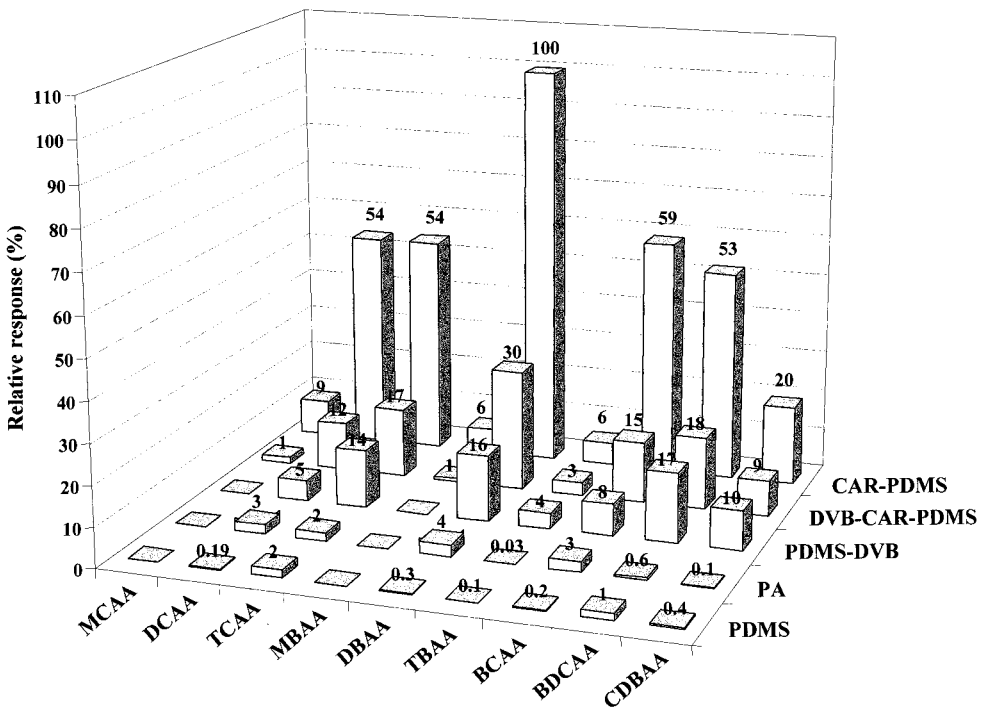

Figure 1. Extraction efficiency of five commercial SPME fibers. All recoveries are normalized to the maximum area response obtained. Milli-Q water containing 200 μg/L of each HAA; DMS, 100 μL; TBA-HSO_4, 2.3 μmol; sodium sulfate, 3.5 M; extraction time, 60 min; extraction temperature, 55 °C.

interfere with the detection of our derivatives, so CAR-PDMS coating was selected for all subsequent experiments. As mentioned above, 60 min was the time used to compare the behavior of the fibers. To reduce extraction time, the efficiency of extractions conducted for 25 min was compared with those conducted for 60 min with the CAR-PDMS fiber. Mean responses were similar for all the derivatives, except that for DBAA methyl ester, which showed an increase of 12% in the area after the 60-min extraction. Therefore, a sampling time of 25 min was used for optimization purposes.

Derivatization−Extraction Temperature. The effect of sample temperature on the derivatization/HS-SPME was examined from 35 to 65 °C (Figure 2). An increase in temperature enhanced the derivatization reaction yield. Moreover, the mass transfer process was also favored by increasing the vapor pressure of the analytes in the headspace. On the other hand, the distribution constant of the methyl haloacetates between the headspace and the fiber coating was also temperature-dependent. At high temperatures (above 55 °C), the affinity of the analytes for the fiber coating diminished and the relative responses decreased (Figure 2). Fifty-five degrees Celsius was the optimum temperature for all the methyl haloacetates.

Derivatization Reagent and Ion-Pairing Agent Amount. The concentration of the derivatization reagent also affects the reaction yield of HAAs methyl esters. Amounts of DMS ranging from 10 (0.10 mmol) to 160 μL (1.89 mmol) were tested at 55° (Figure 3). In general, volumes of DMS between 60 (0.63 mmol) and 100 μL (1.05 mmol) gave satisfactory reaction yields for most of the compounds. The relative responses for some HAAs decreased at high amounts of DMS. The addition of 60 μL (0.63 mmol) of DMS ensured the maximum response for MBAA methyl ester.

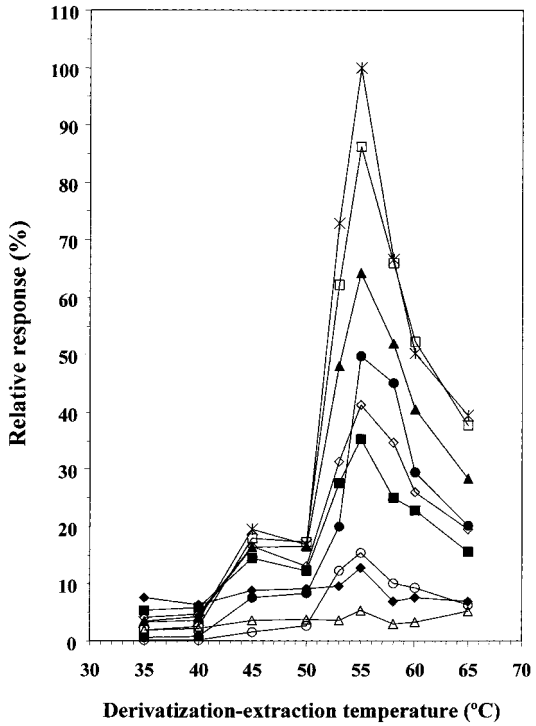

Figure 2. Temperature profiles for in situ methylation HS−SPME of the nine HAAs. Conditions as in Figure 1, with a 25-min extraction time and the CAR-PDMS fiber. Compound identification: (◆) MCAA, (■) DCAA, (▲) TCAA, (△) MBAA, (★) DBAA, (○) TBAA, (◇) BCAA, (□) BDCAA, (●) CDBAA.

The effect of the amount of ion-pairing agent on the derivatization of HAAs was studied by adding TBA-HSO_4 to the water up to 6.6 μmol and using 60 μL of DMS. The responses relative to the maximum value obtained for DBAA methyl ester are given in Table 1. The best results for most compounds were obtained using

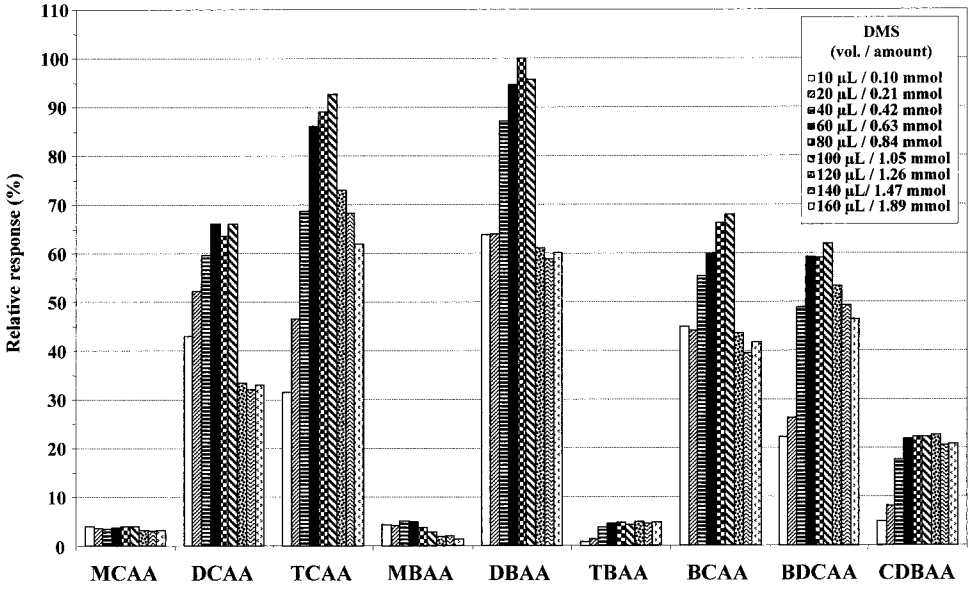

Figure 3. Effect of dimethyl sulfate on the reaction yield of HAAs. Conditions as in Figure 2, extraction temperature 55 °C.

Table 1. Effect of Ion-Pairing Agent (TBA-HSO_4) on HAA Reaction Yields to the Corresponding Methyl Haloacetates[a]

	amt of TBA-HSO_4 (μmol)							area response ratio with[b] without the use of TBA-HSO_4
compd	0	0.23	0.47	2.36	4.72	5.66	6.61	
	relative responses with respect to the maximum area value (%)							
MCAA	0.9	1.2	1.4	4.3	5.7	2.5	1.4	6
DCAA	3.6	24.2	55.4	84.4	82.8	70.3	66.8	23
TCAA	0.8	29.6	63.0	72.0	69.3	69.8	60.3	90
MBAA	1.7	1.5	1.6	3.5	5.7	5.1	4.6	3
DBAA	2.3	15.1	34.8	95.5	95.4	89.6	100	41
TBAA	0.3	1.4	1.5	2.9	2.9	2.2	2.8	9
BCAA	2.7	23.6	46.3	75.3	72.3	64.6	71.0	27
BDCAA	0.4	8.9	16.1	29.9	31.1	26.5	31.1	80
CDBAA	0.5	5.3	7.0	19.2	20.8	17.4	20.1	44

[a] Milli-Q water containing 200 μg/L of each HAA ($\sum$ HAAs = 0.12 μmol). [b] Amount of TBA-HSO_4, 4.72 μmol.

4.7 μmol (1.6 mg) of TBA-HSO_4. The effect of the ion-pairing agent on the yield of the derivatization is shown by the increase in the peak area obtained with the use of TBA-HSO_4 at the optimized conditions. The responses increased up to 90-fold for some of the compounds (Table 1).

Effect of Ionic Strength. For many organic analytes, aqueous solubility decreases with increasing ionic strength, and thus, the partitioning from the aqueous solution to the headspace is improved.[20] To raise the ionic strength, an inorganic salt is often added to the aqueous matrix. The most common salts used in SPME are sodium chloride and sodium sulfate; however, sodium chloride is not recommended when analyzing DBPs due to the presence of bromide as an impurity which can enhance the amount of bromide-HAAs in the sample.[34] So, sodium sulfate was chosen. As expected, the amount of analyte adsorbed onto the fiber augmented significantly when sodium sulfate concentration increased to 3.5 M. At higher concentrations, constant responses were obtained for some compounds (MCAA, TBAA, BDCAA, and CDBAA) whereas a decrease was observed for others (DCAA, TCAA, MBAA, DBAA, and BCAA). So a concentration of 3.5 M was maintained for subsequent studies.

Derivatization−Extraction Time and Stirring Rate. The extraction time profiles of the methyl haloacetates were then studied up to 60 min (Figure 4). Different equilibration times were obtained for the analytes, depending on the headspace/aqueous sample distribution constant, K_{hs}, and the fiber coating/headspace distribution constant, K_{fh}.[19] Some derivatives (MCAA, BDCAA, and CDBAA methyl esters) achieved equilibration in 5−15 min but other compounds needed 25 or 35 min. Consequently, an exposure time of 35 min was chosen as optimal for all the haloacetates.

The effect of stirring rate on the responses was tested between 900 and 1200 rpm. On the basis of extraction efficiency, similar responses were obtained for MCAA, BDCAA, CDBAA, and TBAA methyl esters at all the rates studied. However, for DCAA, TCAA, MBAA, DBAA, and BCAA methyl esters, equilibrium was not reached for rates below 1200 rpm, indicating that diffusion through the water was the rate-controlling step in the adsorption. In terms of precision, RSDs (n = 3) lower than 7% were obtained for five HAAs at low stirring rate; however, values that were too high were observed for the remaining compounds (up to 15%). So, 1200 rpm was maintained for further studies, taking into account the shorter equilibration time assessed for all the compounds at this rate.

Optimization of Desorption Conditions. Two desorption temperatures, 280 and 300 °C, were evaluated for a desorption time of 2 min. Results showed no differences in the GC responses between the two temperatures. In addition, carryover was not detected at either temperature; therefore, the lower temperature was chosen for further experiments to avoid degradation of the fiber with temperature. All compounds were quantitatively desorbed from the CAR-PDMS fiber in 1 min at 280 °C (Figure 4).

In summary, for optimum in situ derivatization and HS-SPME sampling of HAAs from water, 3.5 M Na_2SO_4, 4.7 μmol of TBA-

(34) Xie, Y. *Effect of sodium chloride on DBP analytical results,* Division of Environmental Chemistry, American Chemical Society Annual Conference; Aug 21−26, 1995, Chicago, IL; Extended Abstract.

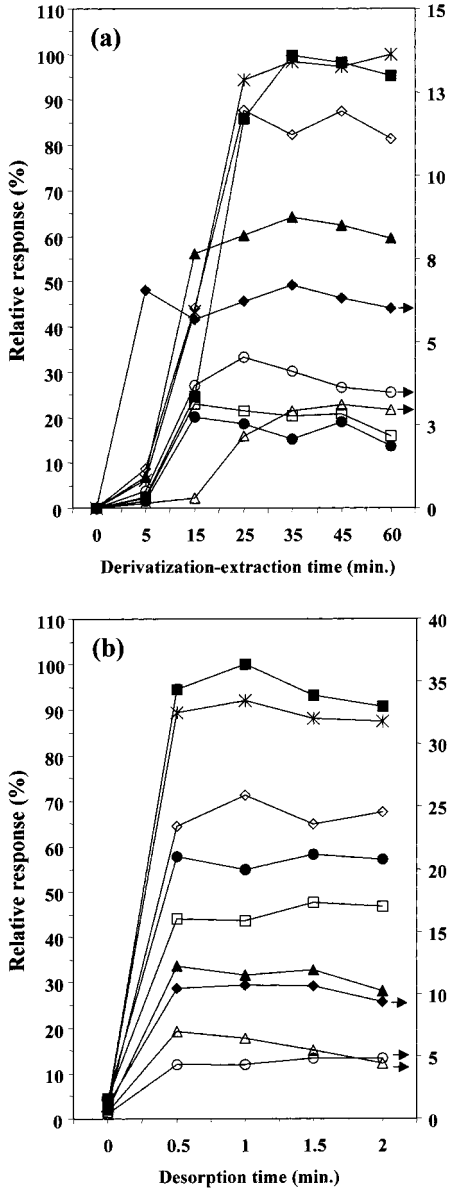

Figure 4. (a) Extraction time and (b) desorption time profiles of methyl haloacetates by in situ methylation HS-SPME/GC/ITMS at 55 °C. Fiber and conditions as in Figure 2, with 60 μL of DMS and 4.7 μmol of TBA-HSO_4 as ion-pairing agent. In (b) extraction time was 35 min. Compound identification: (◆) MCAA, (■) DCAA, (▲) TCAA, (△) MBAA, (★) DBAA, (○) TBAA, (◇) BCAA, (□) BDCAA, (●) CDBAA. For MCAA, MBAA, and TBAA methyl esters, the scale is shown on the right.

HSO_4, and 60 μL of DMS were added to 10 mL of water. The sample was maintained at 55 °C stirred at 1200 rpm and a CAR-PDMS fiber was exposed to the headspace for 35 min.

Linearity, Precision, and Sensitivity Study. Calibration parameters of the GC/ITMS were determined by conventional injection. Linear dynamic ranges were from 0.45 to 450 ng injected, depending on the compound. Limits of detection (LOD), defined as the concentration of the analyte that produces a chromatographic peak with a signal-to-noise ratio (S/N) of greater than 3, were evaluated in full-scan mode at optimized conditions and ranged from 17 pg for DBAA and BCAA methyl ester to 156 pg for TBAA methyl ester. The run-to-run and day-to-day precision of the system was assessed by consecutively analyzing 10 replicates of a standard mixture containing the nine esters at concentrations between 10.8 and 108 μg/mL on one day and on three different days, respectively. Good precision was achieved with relative standard deviations (RSDs) for run-to-run precision between 2.5 and 6.6% and for day-to-day precision from 4.0 to 8.4%.

Parameters of the in situ derivatization/HS-SPME/GC/ITMS method were evaluated using the optimized conditions. In the first step, quantification with external calibration without internal standard, as is frequently used in SPME, was tested. The precision was determined for a set of five replicates of Milli-Q water spiked with HAAs and analyzed consecutively on one day and on three different days (Table 2). RSDs for run-to-run precision ranged between 9.8 and 13.9% and for day-to-day precision between 10.1 and 15.6%. The run-to-run precision of the optimized SPME method (expressed as RSDs) was not as good as that reported for the EPA method 552.2[7] for water spiked at similar concentrations of HAAs (Table 2).

To increase the precision, the effect of addition of an internal standard was evaluated. In the first step, the use of 1,2-dibromopropane, recommended as an internal standard by the Standard Method 6251B was tested. This compound achieved equilibrium in 30 min, and quantitative desorption from the fiber occurred in 1 min. However, the response depended on the amount of HAAs in the aqueous sample. For instance, a decrease in the 1,2-dibromopropane area of 34% was observed when the concentration of HAAs rose from 18 to 405 μg/L. To eliminate these problems, a compound similar to the HAAs, 2,3-dibromopropionic acid, was then chosen as an internal standard. This compound achieved equilibrium in 35−40 min, and quantitative desorption from the fiber was observed in 1 min. Moreover, satisfactory precision for five determinations (RSD lower than 6%) was obtained. In addition, an invariable response of this compound was observed at different concentrations of HAAs in the water sample. Using this internal standard, all HAAs showed RSD values for run-to-run precision of less than 10%, except for MCAA (10.9%) and day-to-day precisions (RSDs) lower than 11.4%. The linearity of the optimized HS-SPME/GC/ITMS method was examined over the range 0.1−300 μg/L, expressed as the initial concentration of HAAs in water. The linear range was established from the curves obtained by plotting the relative area of each methyl haloacetate to that of the internal standard (A/A_{is}) versus the concentration of each HAA (Table 2). Most methyl haloacetates showed good linearity and correlations ($r^2 \geq 0.995$). Detection limits were calculated using Milli-Q water spiked at low levels of HAAs and analyzed using the optimized procedure. In these experimental conditions, LODs were from 0.01 to 0.45 μg/L, which are 1.8- to 25-fold lower than those obtained with the EPA method 552.2. Moreover, LODs using this procedure were 71 to 2000 times lower than those reported by Aikawa and co-workers[31] for MCAA, DCAA, and TCAA using in situ derivatization with methanol/HCl and GC/ECD determination.

Analysis of Water Samples. To examine the feasibility of the HS-SPME method, two water samples with different amounts of HAAs, one from Barcelona's water distribution system (<10 μg/L) and the other from a swimming pool (10−150 μg/L), were analyzed. HAAs were determined in triplicate using the optimized HS-SPME method as well as LLE (EPA method 552.2). Internal standard calibration was used in both methods. HS-SPME/GC/

Table 2. Linear Range, Detection Limits, and Precision for In Situ Methylation/HS-SPME/GC/ITMS Method

				precision[b]			EPA method 552.2	
					run-to-run[c]	day-to-day[d]		
compd	linear range (μg/L)	corr coeff (r^2)	LOD[a] (μg/L)	target value (μg/L)	with int std (without)	with int std (without)	run-to-run[b,e]	LOD[a,f] (μg/L)
MCAA	1.00−140	0.998	0.20	13.5	10.9 (13.9)	11.4 (14.4)	13	0.60
DCAA	0.50−75	0.998	0.07	6.83	8.0 (12.2)	8.4 (12.9)	11	0.24
TCAA	0.20−100	0.997	0.02	6.80	9.0 (9.8)	9.3 (10.1)	8.3	0.20
MBAA	1.30−150	0.999	0.40	13.5	9.8 (12.1)	10.7 (12.5)	11	0.20
DBAA	0.50−60	0.995	0.01	6.92	7.2 (11.1)	8.6 (13.4)	6.0	0.20
TBAA	1.35−180	0.997	0.45	13.5	9.3 (12.9)	10.0 (15.6)	7.6	1.5
BCAA	0.50−120	0.999	0.01	6.66	6.3 (11.5)	6.8 (13.4)	9.3	0.25
BDCAA	1.00−135	0.996	0.15	6.68	7.8 (11.8)	8.1 (13.8)	9.6	0.40
CDBAA	1.50−250	0.998	0.40	13.3	7.0 (11.1)	7.3 (11.8)	7.6	0.75

[a] LOD, limit of detection. [b] Precisions expressed as RSDs (%). [c] $n = 5$. [d] $n = 5$ replicates × 3 days. [e] $n = 7$ (reagent water spiked between 2.00 and 20.0 μg/L). [f] The LOD is defined as a level of a compound in a sample yielding a peak in the final extract with a signal-to-noise (S/N) ratio of approximately five, whichever is greater.

ITMS was found to be highly selective for the analysis of HAAs in both drinking water and swimming-pool water. No interferences from other compounds that may have been in the sample matrix were detected in these conditions, see Figure 5 for swimming-pool water. The results obtained for the water samples using HS-SPME and LLE are given in Table 3. The total HAAs concentration found in the tap water (~30 μg/L) is lower than the MCL (60 μg/L) established for the USEPA for the sum of 5 HAAs, whereas for swimming pool water the concentration rose to ~300 μg/L, more than 10-fold that of tap water. As for HAA speciation, several factors may influence the results: chlorine dose, reaction time, natural organic matter content, and bromide concentration. Trihalogenated acetic acids, especially TCAA, constituted the greatest fraction of the total HAA concentration in swimming-pool water (81%), whereas for tap water the tri- and dihalogenated species were similar (45 and 50%, respectively) (Table 3). On the other hand, the fraction of monohalogenated species was practically negligible (from 1.2 to 5%) in both samples. To compare the results of HS-SPME with those of LLE, the significance of the mean values was studied statistically using the Student's *t*-test. When unequal variances were obtained (*F*-test), Cochran's test was applied. The significance values (*p*) obtained are given in Table 3. Generally, the results with HS-SPME using internal standard agree with those obtained with LLE in both cases ($P < 0.05$). The reproducibility of both HS-SPME and LLE was generally high for swimming-pool water. The coefficients of variation (up to 17%) can be considered acceptable, considering matrix complexity. In situ methylation/HS-SPME/GC/ITMS showed some advantages over LLE and GC/ECD method, such as the avoidance of organic solvents and labor-intensive sample manipulation steps. Consequently, losses of analytes and analysis time are minimized. In addition, lower detection limits were obtained with the proposed method.

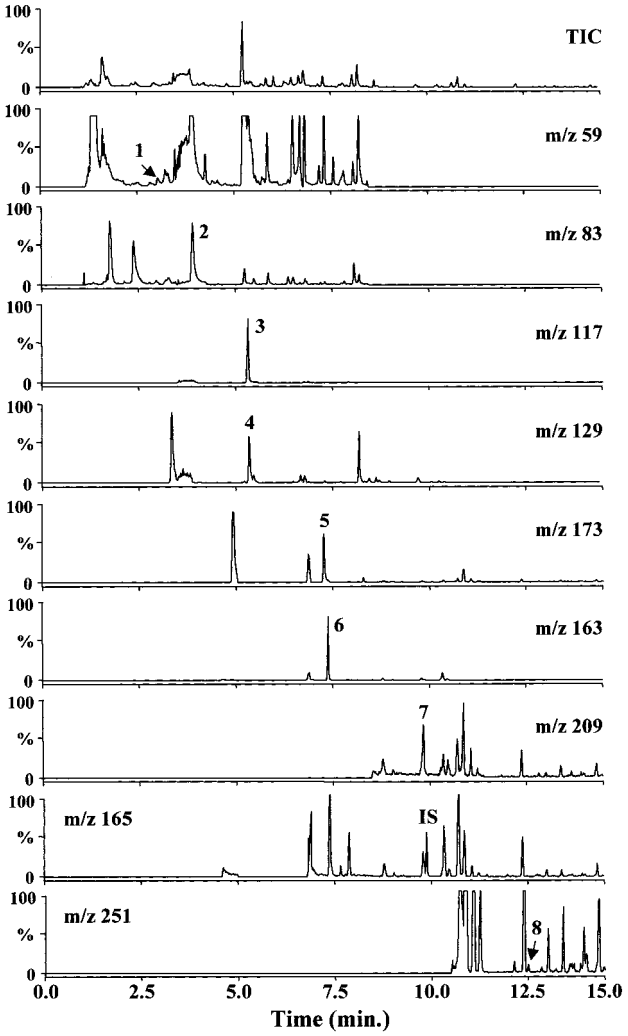

Figure 5. HS-SPME/GC/ITMS total-ion chromatogram and single-ion chromatograms of methyl haloacetates from swimming-pool water. Compound identifications: 1, MCAA; 2, DCAA; 3, TCAA; 4, BCAA; 5, DBAA; 6, BDCAA; 7, CDBAA; and 8, TBAA methyl esters; IS, 2,3-dibromopropionic acid methyl ester.

CONCLUSIONS

The feasibility of HS-SPME/GC/ITMS for the analysis of HAAs in water after in situ derivatization with dimethyl sulfate has been demonstrated. The CAR-PDMS fiber was found to be the most effective coating for the analysis of HAAs methyl esters, especially for monohalogenated ones. Maximum responses were obtained using 10-mL water samples salted with sodium sulfate and set at an equilibration time of 35 min at 55 °C. A large increase in the

Table 3. Quantitation Results for HAAs in Barcelona Tap Water and Swimming Pool Water by SPME and EPA Method 552.2

	tap water				swimming pool water					
	headspace SPME[a,b]		EPA method 552.2[a]		headspace SPME[a,b]		EPA method 552.2[a]		significance level (*P*-value)[c]	
compd	mean (μg/L)	RSD (%)	mean (μg/L)	RSD (%)	mean (μg/L)	RSD (%)	mean (μg/L)	RSD (%)	tap water	swimming-pool water
MCAA	1.43	8.3	1.43	8.6	4.22	14.8	3.73	15.7	0.993	0.377
DCAA	8.27	12.8	9.10	7.6	45.2	16.7	49.4	13.6	0.981	0.520
TCAA	5.64	7.1	6.34	9.9	155	17.0	129	11.6	0.203	0.155
MBAA	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.		
DBAA	1.64	5.5	1.71	3.0	2.76	13.9	2.22	10.9	0.312	0.109
TBAA	n.d.	n.d.	n.d.	n.d.	18.9	15.1	17.5	17.4		0.643
BCAA	4.29	8.9	4.18	3.9	10.5	15.9	11.9	9.8	0.678	0.352
BDCAA	5.28	13.9	6.32	6.8	60.6	10.9	61.2	5.3	0.101	0.617
CDBAA	1.90	5.9	2.22	13.5	32.8	7.1	32.5	8.9	0.161	0.903
total HAAs	28.4		31.3		330		307			

[a] $n = 3$. [b] Int std is 2,3-dibromopropionic acid. [c] Significant differences between procedures for $P < 0.05$ (at the 95% confidence level); n.d., not detected.

reaction yield was obtained using TBA-HSO_4 as modifier for the in situ methylation with dimethyl sulfate. HS-SPME in conjunction with GC/ITMS gave good precision; it was linear over 2 orders of magnitude and the detection limits were at the low ppb level. The method is proposed as an alternative to the liquid−liquid extraction (EPA method 552.2) for the analysis of HAAs in aqueous matrixes containing either low or high HAAs levels.

ACKNOWLEDGMENT

This study was supported by CICYT-Spain project number AMB97-0405 and the Pla de Recerca de Catalunya (Generalitat de Catalunya), project number 1999SGR00049. M.N. Sarrión acknowledges a Ph.D. fellowship from the University of Barcelona.

Received for review April 26, 2000. Accepted July 19, 2000.

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