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GLC ANALYSIS OF BASE COMPOSITION OF  
RNA AND DNA HYDROLYSATES<sup>1</sup>

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INTRODUCTION

Because of the importance of nucleic acids to the genetic code, many researchers have studied the biological function and chemical structure of the various nucleic acid components (purine and pyrimidine bases, nucleosides, and nucleotides). The biological function of DNA (deoxyribonucleic acid) or RNA (ribonucleic acid) depends on the base composition of the polymer and the sequence of the bases in the polymer.

Many methods for the detection of the nucleic acid components have been developed with varying degrees of quantitation obtained. These methods include ion-exchange chromatography by Cohn (1), paper chromatography by Vischer

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and Chargaff (2), paper electrophoresis by Gordon and Reichard (3), thin-layer chromatography by Randerath (16), paper chromatography and time of flight mass spectrometry by Studier et al. (13), and gas-liquid chromatography by MacGee (4), Hashizume and Sasaki (11), Gehrke and Ruyle (5), and the authors of this paper (6).

Many of these methods have been used for the analysis of the base composition of RNA and DNA hydrolysates. However, before analysis, the nucleic acids must be hydrolyzed into bases, nucleosides, or nucleotides, depending on the type of hydrolysis employed. In 1960, Jordan (7) presented the different types of hydrolysis used to obtain the various monomers. Sample plus 70% HClO<sub>4</sub> heated in a closed tube at 100°C-40 min. has been accepted as the best hydrolysis procedure to obtain the purine and pyrimidine bases. Concentrated formic acid or trifluoroacetic acid also has been employed to yield bases. To obtain the nucleosides or nucleotides much milder hydrolysis conditions are necessary, and complete conversion to either the nucleosides or nucleotides is often not achieved.

Many researchers, including Hedgcoth and Jacobon (8), Monjardino (9), and Leech et al. (10), have used thin-layer chromatography (TLC) with spectrophotometric detection and quantitation for the analysis of the base composition. These methods are time consuming, semiquantitative, and the amount of sample is fairly large (more than 100 µg). An electrophoretic method by Borkowski et al. (14) gave a good analysis on a minimum of 50 µg of total DNA. Hiby and Kroger (15) in 1967 used a combination of

TLC and electrophoresis for nucleotide analysis of RNA, but did not obtain quantitative data.

Gas-liquid chromatography (GLC), because of its speed, sensitivity, and quantitative aspects, appeared to be the best method available for the analysis of nucleic acid base composition. In 1966, MacGee (4) reported on the analysis of RNA by GLC. The samples were hydrolyzed with  $\text{HClO}_4$ , followed by ion-exchange cleanup to remove the interfering compounds. MacGee used the N-methyl derivative, which gave multiple peaks for some of the bases, but he was able to obtain quantitative data. Hashizume and Sasaki (11), in 1968, reported the analysis of RNA using the trimethylsilyl (TMS) derivative. The nucleic acid was hydrolyzed with  $\text{HClO}_4$ , and the excess  $\text{HClO}_4$  was precipitated with KOH. Silylation was achieved with hexamethyldisilazane (HMDS) and trimethylchlorosilane (TMCS) in pyridine. Single peaks for all of the bases were obtained, and quantitation was good; but, 20 mg of RNA were needed for each analysis. Gehrke and Ruyle (5), in 1968, presented a method for the analysis of 5.0 mg of RNA. The nucleic acid was hydrolyzed with  $\text{HClO}_4$ , followed by precipitation with KOH and ion-exchange cleanup to remove the phosphate and sugar. The TMS derivatives of the bases were formed with bis(trimethylsilyl)-acetamide (BSA) and chromatographed on an SE-30 column. The method was quantitative, but 20% of the bases were lost during

cleanup. In 1969, Jacobon et al. (12) reported on the analysis of RNA using the TMS derivative of the nucleosides. The method was quantitative, but the sample size was large.

Since many biological samples are available only in microgram quantities, these methods are not useful to determine the base composition. A method was needed that could determine the base composition of RNA or DNA at a biologically significant level. We reported a GLC method for the silylation and chromatography of the purine and pyrimidine bases at macro (100  $\mu\text{g}$  @), semimicro (10  $\mu\text{g}$  @), and micro (500 ng @) levels with good quantitation at all levels (6). The purpose of this investigation was to develop a method for the analysis of nucleic acid hydrolysates at macro, semimicro, and micro levels. This would include the development of a cleanup procedure which would give quantitative recovery of the bases at these levels. This cleanup method, with the silylation and GLC chromatographic method developed earlier, would provide a simple, quantitative, and fast method for the analysis of the base composition of RNA and DNA in a sample size as small as 5  $\mu\text{g}$  of nucleic acid.

## EXPERIMENTAL

## CLEANUP AND ANALYSIS OF RNA AND DNA

I. Apparatus

An F and M 402 Biochemical gas chromatograph (F and M Scientific, Division of Hewlett Packard, Avondale, Pennsylvania), equipped with dual hydrogen flame detectors, was used in this investigation.

For elevated temperature reactions, a sand bath with a variable temperature control ( $\pm 2.0^{\circ}\text{C}$ ) was constructed.

Standards and ion-exchange cleaned nucleic acid hydrolysates were dried on a  $60^{\circ}\text{C}$  hot plate with an IR (infrared) lamp or a  $60^{\circ}\text{C}$  hot plate with a stream of pure  $\text{N}_2$  gas.

The ion-exchange columns used in this study were 4 x 150 mm, 9 x 150 mm, and 15 x 150 mm pyrex glass with teflon stopcocks and were obtained from Fischer and Porter Company, Warminster, Pennsylvania.

The other apparatus used in this study was described in a previous paper (6).

II. Reagents and Materials

The micro reaction vials were obtained from Analytical BioChemistry Laboratories, Inc., Box 1097, Columbia, Missouri.

The purine and pyrimidine bases (uracil, thymine, cytosine, adenine, and guanine) were obtained from Mann Research Laboratories, New York, New York, and were chromatographically pure.

The bis(trimethylsilyl)trifluoroacetamide (BSTFA) was purchased from Regis Chemical Company, 1101 North Franklin Street, Chicago, Illinois, in teflon lined screw cap vials. Acetonitrile, methylene chloride, and dichloroethane were of "nanograde" purity and were purchased from Mallinckrodt Chemical Works, St. Louis, Missouri, as well as formic acid, acetic acid, and perchloric acid.

Dowex 1-X2 anion exchange resin was obtained from Dow Chemical Company, Midland, Michigan; and AG 1-X2, Bio-Rex 9, and AG 3-X4 anion exchange resins were purchased from Bio-Rad Laboratories, Richmond, California. Amberlite IR-4B and Amberlite CG-120 resins were obtained from Mallinckrodt Chemical Works. The water was triply distilled from an all glass distillation apparatus. The other reagents used were of the highest purity available.

The yeast RNA I was obtained from Dr. James Ross, Department of Plant Pathology, University of Missouri; Yeast RNA II and Tobacco Mosaic Virus RNA (TMV-RNA) were obtained from Dr. Om Sehgal, Department of Genetics, University of Missouri. The Salmon Sperm DNA was purchased from Mann Research Laboratories, New York, New York, and the Calf Thymus DNA was purchased from Sigma Chemical Company, St. Louis, Missouri.

### III. Instrumental and Chromatographic Conditions

The chromatographic columns used were 10 w/w% CG SE-30 (straight chained polymethylsiloxane) on 100/120 mesh Supelcoport

(chromatographic W type). The column materials were packed in glass columns (borosilicate), which were 1.0 meter long with an inside diameter (I.D.) of 4.0 mm. The columns were held in the chromatographic oven by front and back teflon ferrules on normal Swagelok fittings. For column preparation and conditioning procedures, see our previous paper (6).

The instrumental conditions were a 7.5°C/min temperature program with a 4 minute initial hold. The program ran from 90°C to 260°C. The detector was operated in the 280°C to 320°C region, and the injection heater was at approximately 200°C. The gas flow rates were as follows: N<sub>2</sub> - 40 ml/min., H<sub>2</sub> - 30 ml/min., and air - 300 ml/min. The attenuation for macro samples was 10 x 32 (1.2 x 10<sup>-9</sup> amps full scale deflection, AFS), for semimicro samples it was 10 x 8 (3.2 x 10<sup>-10</sup> AFS), and for micro samples it was 10 x 2 (8.0 x 10<sup>-11</sup> AFS).

#### IV. Development of a Cleanup Procedure for the Analysis of the Purine and Pyrimidine Bases from a Nucleic Acid Hydrolysate

Before the analysis of the base composition of a nucleic acid could be performed, it was necessary to hydrolyze the nucleic acid into its various monomers. To hydrolyze a nucleic acid to the bases, MacGee used 70% HClO<sub>4</sub> in a closed tube at 100°C-40 min. Hashizume and Sasaki (11) and Gehrke and Ruyle (5) also used this procedure in their investigations with good success.

Because the perchlorate interfered with the silylation of the bases, it was necessary to first remove it from the sample. Hashizume and Sasaki precipitated the perchlorate with KOH before silylation with HMDS and TMCS, and they were able to obtain good results for macro samples. Gehrke and Ruyle also precipitated the perchlorate with KOH, but because BSA was a more powerful silylating reagent, an ion-exchange cleanup was needed to completely remove the interfering compounds from the sample, including the phosphate and degradation products of ribose. They found that approximately 20% of each base was non-selectively lost during precipitation, transfer, and ion-exchange cleanup. The development of a quantitative method for the analysis of the base composition of RNA and DNA would require 95 to 100% recovery of the bases, thus it was necessary to develop a cleanup method that would give this recovery without adding impurities and removing the perchlorate and phosphate from the sample.

#### A. Two Column Method

The perchlorate used for the hydrolysis and the phosphate can be removed by anion exchange chromatography. The perchlorate and phosphate free bases can then be dried, made alkaline with KOH, and placed on another anion exchange column for the removal of neutral (sugar) compounds.



With this outline, the following two column method was developed for the cleanup of a nucleic acid hydrolysate. The method was developed with standards of each base, ribose, and  $H_3PO_4$ .

### Two Column Method

#### 1. Hydrolysis

- a. Add 0.5 ml of 70%  $HClO_4$  to 0.1 mg each of U, T, C, A, G, ribose, and  $H_3PO_4$  in a 16 x 75 mm culture tube.
- b. Seal the tube with a teflon lined cap and heat it at  $100^\circ C$ -40 min.
- c. Cool the tube to room temperature and dilute the sample to 3.0 ml with triply distilled water.

#### 2. Removal of Anions

- a. Place the hydrolyzed sample on a 15 x 70 mm anion exchange column of Dowex 1-X2 formate (50/100 mesh).
- b. Wash the column with 7 x 3 ml triply distilled water at a rate of 1 ml/min.
- c. Discard the first 3.0 ml.
- d. Collect the next 6 x 3 ml in a culture tube (8.5 ml total capacity), evaporating while collecting with a  $90^\circ C$  sand bath and a stream of pure  $N_2$  gas.
- e. Evaporate to dryness.

### 3. Removal of Natural Molecules

- a. Dissolve the dried sample in 2.0 ml of 0.5 N KOH.
- b. Place the sample on a 9 x 60 mm anion exchange column of Dowex 1-X2 formate (50/100 mesh).
- c. Wash the column with 12 x 4 ml triply distilled water at a rate of 1 ml/min. and discard.
- d. Elute the column with 6 x 3 ml of 1.0 N HCOOH.
- e. Discard the first 3.0 ml.
- f. Collect the next 5 x 3 ml in a culture tube (4.5 ml total capacity), evaporating while collecting with a 90°C sand bath and a stream of pure N<sub>2</sub> gas.
- g. Evaporate the sample to complete dryness.

Note: CH<sub>2</sub>Cl<sub>2</sub> was used to azeotrope the last traces of water.

### 4. Silylation

- a. Add 0.2 ml BSTFA and 0.2 ml CH<sub>3</sub>CN containing 100 µg phenanthrene (internal standard).
- b. Tightly seal the vial and silylate at 150°C-15 min.
- c. Cool and inject 3 to 4 µl into the GC.

To evaluate the procedure, each column was analyzed independently, and as a two column method. For these analyses, 12 standards of 100 µg of each base were pipetted from a stock solu-

tion (3.3 mg of each base/100 ml 0.1 N HCl  $\approx$  0.10 mg each base/3.0 ml) and dried on a 60°C hot plate with a stream of pure N<sub>2</sub> gas. Four of the samples were hydrolyzed with 70% HClO<sub>4</sub> and cleaned by the first anion exchange column only. Another four of the samples were dissolved in 2.0 ml of 0.5 N KOH and cleaned by the second anion exchange column only. Then, 0.4 mg ribose and 0.4 mg H<sub>3</sub>PO<sub>4</sub> were added to four of the samples, which were carried through the total two column anion exchange cleanup method.

The dried samples were silylated and analyzed by GLC (for development of the silylating conditions and instrumental settings, refer to our previous paper (6)). The chromatographic peak areas were integrated, and the RMR<sub>B/IS</sub> values were calculated as follows:

$$\text{RMR}_{\text{B/IS}} = \frac{\frac{\text{Area}_{\text{Base}}}{g_{\text{B}} / \text{MW}_{\text{B}}}}{\frac{\text{Area}_{\text{IS}}}{g_{\text{IS}} / \text{MW}_{\text{IS}}}}$$

$$\text{RMR}_{\text{B/IS}} = \frac{A_{\text{B}}}{A_{\text{IS}}} \times \frac{g_{\text{IS}}}{g_{\text{B}}} \times \frac{\text{MW}_{\text{B}}}{\text{MW}_{\text{IS}}}$$

Area<sub>Base</sub> = Area of the chromatographic peak for the base

Area<sub>IS</sub> = Area of the chromatographic peak for the internal standard

MW = Molecular weight

Cytosine gave two chromatographic peaks, and the  $RMR_{C/PHEN}$  was calculated by integrating each peak separately and adding the areas to obtain the total area.

From the  $RMR_{B/IS}$  values for the 12 samples and the  $RMR_{B/IS}$  values for standards not carried through the cleanup steps, the % recovery was calculated as

$$\% \text{ recovery} = \frac{RMR_{B/IS} \text{ (after cleanup)}}{RMR_{B/IS} \text{ (standards)}} \times 100$$

The average % recoveries for the four samples for each experiment are presented in Table I

#### B. One Column Method

As the two column method presented was time consuming, modifications in the procedure were made to speed up the cleanup for simplification, without affecting the recovery of the bases.

Drying of the Sample. The evaporation of the sample while collecting the eluate from the anion exchange column was very time consuming. A faster method for drying the eluate, which did not affect the sample, was needed. Thus, to determine the best drying method for the column eluate, the following drying methods were evaluated: rotary evaporation, lyophilization, a hot plate with an IR lamp, and a hot plate with a stream of pure  $N_2$  gas. Each method was studied by diluting four aliquots (100  $\mu\text{g}$  of @ base) in 3.0 ml of 0.1 N HCl with

20 ml of triply distilled water. The samples were concentrated to approximately 2.0 ml and then transferred to a culture tube before evaporation to complete dryness, derivatization, and chromatography.

Ion-Exchange Columns. Even with modifications of the drying step, the total method was still fairly time consuming. To further modify the method, each anion exchange column was evaluated with ribose and phosphoric acid added to all samples. It appeared that the second anion exchange column was not needed as the analysis of standards with added ribose and  $H_3PO_4$  showed that the ribose was completely degraded by the hydrolysis, and the phosphate and perchlorate were removed by the first anion exchange column. Thus, the following one column method was developed.

#### One Column Method

##### 1. Hydrolysis

$HClO_4$  plus sample at  $100^\circ C$ -40 minutes.

##### 2. Anion Exchange Cleanup

- a. Place the hydrolyzed sample on a 100 x 15 mm anion exchange column of Dowex 1-X2 formate (50/100 mesh).
- b. Wash the column with 16 x 3 ml of triply distilled water at 1 ml/min.
- c. Discard the first 3.0 ml.

- d. Collect the next 15 x 3 ml fractions in a 50 ml beaker.
- e. Concentrate the sample to 2.0 ml on a 60°C hot plate with an IR lamp.
- f. Transfer the sample to a culture tube (4.5 ml total capacity), washing the beaker with 2 x 1.0 ml of 0.1 N HCl.
- g. Evaporate the sample to dryness on a 60°C hot plate with a stream of pure N<sub>2</sub> gas.

### 3. Silylation

The samples were derivatized with BSTFA at 150°C-15 minutes.

Using this procedure, four 100 µg standards of each base with 0.4 mg ribose and 0.4 mg H<sub>3</sub>PO<sub>4</sub> were carried through the entire cleanup method. The % recoveries are given in Table II.

Anion Exchange Resin. A small amount of interference, due to "fines" from the Dowex 1-X2 formate anion exchange resin passing through the porous glass disc, was noticed on the chromatograms of the cleaned standards. A regeneration procedure was developed for the preparation of the resins to prevent further contamination by "fines," and another anion exchange resin was used, AG 1-X2 (a purified and sized Dowex 1-X2) resin in the acetate form.

### Regeneration of Resin

1. Place 300 ml of the dry resin (AG 1-X2) in a 500 ml graduated cylinder.
2. Add 3.0 N KOH (to the 500 ml mark).
3. Invert the cylinder, mixing the resin and 3.0 N KOH.
4. Allow the larger resin particles to settle, then pour off the excess KOH and resin "fines."
5. Wash the resin five times with distilled water, mixing each time, allowing to settle, then pouring off the "fines."
6. Repeat steps 2 to 5 at least three times.
7. Wash the resin to neutral with distilled water.
8. Add 3.0 N acetic acid (to the 500 ml mark).
9. Thoroughly mix, allow to settle.
10. Pour off the excess acetic acid and "fines."
11. Wash five times with distilled water as in Step 5.
12. Repeat steps 8 to 11 at least three times.
13. Wash the resin to neutral with distilled water.

Using this resin regeneration procedure and AG 1-X2 anion exchange resin, the one column method was again evaluated by cleaning four 100  $\mu\text{g}$  standards of each base plus 0.4 mg ribose and 0.4 mg  $\text{H}_3\text{PO}_4$ . The dried samples were silylated and analyzed. The % recovery for each sample is given in Table II.

### C. Cleanup of Semimicro Standards

Using the one column cleanup method described above and the silylation conditions and instrumental settings developed for semimicro standards in our previous paper (6), four semimicro standards (10  $\mu\text{g}$  each base) plus 40  $\mu\text{g}$  ribose and 40  $\mu\text{g}$   $\text{H}_3\text{PO}_4$  were carried through the cleanup procedure. A further refinement of the one column method was employed; a 1/4" plug of glass wool was placed in the ion-exchange column on the coarse porosity, fritted disc, then the anion exchange resin added. The glass wool prevented the resin particles from passing through the glass disc and causing extraneous peaks on the chromatograms.

### V. Analysis of RNA and DNA at Macro and Semimicro Levels

Using this technique for sample cleanup and the silylating conditions presented in our previous paper (6), several types of RNA and DNA samples were analyzed at the macro (ca. 100  $\mu\text{g}$  of each base) and the semimicro (ca. 10  $\mu\text{g}$  of each base) levels. For macro samples 1.0 mg and for semimicro samples 100  $\mu\text{g}$  of nucleic acid were used. The mole % composition for each nucleic acid was calculated as follows:

$$\text{Mole \% Composition} = \frac{\mu\text{mole}_{\text{Base}}}{\mu\text{mole}_{\text{total}}} \times 100$$

$$\mu\text{moles}_B = \mu\text{g}_B / \text{MW}_B$$

$$\mu\text{g}_B = \frac{A_B}{A_{\text{IS}}} \times \frac{\text{MW}_{\text{IS}}}{\text{MW}_B} \times \frac{\mu\text{g}_{\text{IS}}}{\text{RMR}_{B/\text{IS}}}$$



$$\text{RMR}_{\text{B/IS}} \text{ (standard)} = \frac{\text{Area}_{\text{B}} / \text{Moles}_{\text{B}}}{\text{Area}_{\text{IS}} / \text{Moles}_{\text{IS}}}$$

The average mole % composition for each nucleic acid and standard deviations are presented in Tables III and IV. Figures 1 to 8 show typical chromatograms for RNA and DNA samples at the macro and semimicro levels.

#### VI. Micro Sample Cleanup Procedure

Initial experiments showed that, as in the silylation and chromatography of micro standards, the cleanup of micro sample hydrolyates would require changes from the cleanup method developed for macro and semimicro sample hydrolysates. Many types of ion-exchange cleanup were available, but since the one column method using AG 1-X2 acetate anion exchange resin developed for macro samples had worked satisfactorily it was fully evaluated first.

##### A. One Column Method

Using the one column method, 8 micro (ca. 500 ng @ base) standards were analyzed. The dried samples were silylated with 50  $\mu\text{l}$  BSTFA, 25  $\mu\text{l}$   $\text{CH}_3\text{CN}$ , and 25  $\mu\text{l}$   $\text{ClCH}_2\text{CH}_2\text{Cl}$  at 150°C-30 min. (for development of silylating conditions, refer to our previous paper (6)), and analyzed by GLC. The chromatograms obtained from these analyses contained many extraneous peaks and had bad bleed rates. To remove as much contamination as possible, the AG 1-X2 acetate resin was again regenerated,

but greater care was used to remove all of the resin "fines." The reagents used for the sample preparation were redistilled to remove contamination, and the BSTFA was evaluated to determine the best lot, i.e. the lot that gave the best chromatograms. The chromatographic column was conditioned at 270°C until there was little column bleed at 240°C. Using these refinements and very careful techniques to prevent sample contamination, the 500 ng of each base standards were again carried through the one column method and analyzed by GLC.

The purines were not quantitatively recovered from the anion exchange column, thus modifications in the procedure were made. One modification was elution of the purines from the column with dilute acid, another was to place the standards on an acidic column, and a third was to evacuate the resin before sample application to remove trapped air because the air could form pockets which would prevent the bases from passing through the resin at a uniform rate.

#### B. Evaluation of Other Ion-Exchange Resins

Since the one column method with AG 1-X2 acetate anion exchange resin did not give good recoveries for the purines, adenine and guanine, other ion-exchange resins were studied which would possibly give better recovery. The following resins were carefully regenerated and evaluated as possible replacements for AG 1-X2: AG 3-X4, Bio-Rex 9, Amberlite IR-4B, and Amberlite CG-120. These resins were chosen because they

have different polymer lattices or functional groups than AG 1-X2. Four standards (10  $\mu$ g, 2.0  $\mu$ g, and two 500 ng @ base) were cleaned by each resin, and the samples were silylated and chromatographed.

C. Evaluation of a Charcoal Column Cleanup Procedure

Since ion-exchange chromatography gave poor recoveries for adenine and guanine, a different type of cleanup was attempted. Saxinger (17) used a charcoal column cleanup for the purine and pyrimidine bases and reported good recoveries on 200 ng of radioactive adenine by counting the adenine before and after cleanup.

The charcoal column cleanup method was evaluated for nucleic acid hydrolysates at the micro level. The charcoal column was initially prepared by refluxing a 1/1 w/w mixture of Norit A charcoal and Celite 545 for 2.0 hours with the following solvents: 2 N HCl; 6 N  $\text{NH}_4\text{OH}$ ; pyridine/water (1/1); pyridine; water; methanol; a mixture of benzene-methanol-water; benzene; formic acid; and water. The charcoal-celite mixture was thoroughly washed with each reagent before refluxing with that reagent. The prepared charcoal was placed in a 9 x 150 mm ion-exchange column, column size 9 x 9 mm. The hydrolyzed standard of the purine and pyrimidine bases was placed on the column and washed with 12 x 4 ml of triply distilled water and 12 x 4 ml 1.0 N HCl. The bases were then eluted with 6 x 4 ml of concentrated formic acid.

The samples were dried, silylated, and analyzed by GLC. Semimicro standards ( ca. 10  $\mu\text{g}$  @ base) were used to evaluate this cleanup method. Initial experiments showed that the background from the charcoal procedure was not satisfactory. After the charcoal was exhaustively washed with formic acid, it was then evaluated at the semimicro and micro levels.

D. Evaluation of Small Ion-Exchange Column

Since the sample size for micro samples had been greatly reduced (ca. 500 ng @ base), the large anion exchange column (100 x 15 mm) had prevented the purines from being recovered. The AG 1-X2 acetate anion exchange resin or the glass wool used to prevent resin "fines" from contaminating the sample were probably adsorbing the purines, thus preventing their recovery. By using a smaller amount of resin and a "silanized" glass wool plug, the purines would have less sites for adsorption and would be recovered at least semi-quantitatively.

To evaluate the small column and "silanized" glass wool plug, four micro standards were hydrolyzed with 50  $\mu\text{l}$  70%  $\text{HClO}_4$ , placed on the anion exchange column (column size 100 x 4 mm), and washed through the column with 25 x 1 ml of triply distilled water. The experiment was repeated a number of times, and the average % recovery for each of the bases was calculated.

## VII. Analysis of RNA and DNA at the Micro Level

### A. RNA Analysis

The three types of RNA (Yeast RNA I and II and Tobacco Mosaic Virus (TMV - RNA) analyzed at the macro level were analyzed at the micro level by the procedure developed above. Approximately 5.0  $\mu\text{g}$  of RNA were used for each analysis. Fifty microliters 70%  $\text{HClO}_4$  were used for the hydrolysis, and the hydrolysate was cleaned by anion exchange chromatography using a 100 x 4 mm column of AG 1-X2 acetate anion exchange resin. The samples were dried, silylated with BSTFA, and analyzed by GLC. The results of these analyses are presented in Table V. Figure 9 shows a typical chromatogram of Yeast RNA II at the micro level.

### B. DNA Analysis

As with the macro samples, a  $\text{HCOOH}$  hydrolysis was used for the Salmon Sperm and Calf Thymus DNA samples to prevent thymine degradation. The anion exchange columns were washed with 25 x 1 ml of 0.5 N acetic acid in place of the water wash. The results of these analyses are presented in Table VI. Figure 10 shows a typical chromatogram of a 5.0  $\mu\text{g}$  Salmon Sperm DNA hydrolysate carried through the procedure.

## RESULTS AND DISCUSSION

I. Anion Exchange Cleanup MethodsA. Two Column Method

The evaluation of the two column cleanup method showed that a nucleic acid hydrolysate at the macro level could be cleaned by anion exchange chromatography without significant loss of any of the bases and with complete removal of the interfering compounds, perchlorate, phosphate, and ribose. The average % recovery of four macro standards for each column and for the total method are presented in Table I. The first anion exchange column gave good recoveries for all the bases, but the second anion-exchange column showed a slight loss for the purines, adenine and guanine. The average % recovery for the total procedure was very good, indicating that the method would be acceptable as a cleanup step for the analysis of the base composition of RNA and DNA hydrolysates.

B. One Column Method

Even though the two column cleanup method gave excellent recoveries of the bases, it was time consuming and thus a more efficient one step column cleanup method was desired.

TABLE I  
 GLC ANALYSIS AND RECOVERY OF THE PURINE  
 AND PYRIMIDINE BASES AT THE MACRO LEVEL  
 TWO COLUMN ION-EXCHANGE CLEANUP METHOD

Column	Recovery <sup>a</sup> , %				
	U	T	C <sup>b</sup>	A	G
First Column <sup>c</sup>	93	—	96	97	97
Second Column <sup>c</sup>	96	95	93	88	82
Total Method <sup>c</sup>	94	—	88	96	99

$${}^a \text{Recovery, \%} = \frac{\text{RMR}_{\text{B/IS after cleanup}}}{\text{RMR}_{\text{B/IS standard}}} \times 100$$

$$\text{RMR}_{\text{B/IS}} = \frac{\text{Area}_{\text{B/Moles}_{\text{B}}}}{\text{Area}_{\text{IS/Moles}_{\text{IS}}}}$$

<sup>b</sup> Cytosine gave two chromatographic peaks, each was integrated separately and the areas were added to obtain the total area.

<sup>c</sup> Average of four independent runs containing 100  $\mu\text{g}$  of each base.

1. Drying of Samples. Various drying methods were evaluated which would eliminate possible contamination of the sample and shorten analysis time. Four drying methods were evaluated: rotary evaporation, lyophilization, and a hot plate with an IR lamp or a stream of pure N<sub>2</sub> gas; and all gave good results with no apparent loss of the bases. The hot plate with an IR lamp was the easiest, fastest, and least likely to add contamination to the sample so it was used to dry large volumes, such as the wash from the anion exchange columns. Also, the hot plate with a stream of pure N<sub>2</sub> gas was used to dry small volumes because of its speed and simplicity.

2. Ion-Exchange Columns. Further evaluation of each column in the two column method indicated that the second anion exchange column was not needed. The perchlorate and phosphate were removed by the first column, and the ribose was completely degraded in the HClO<sub>4</sub> hydrolysis step. The one column cleanup method thus developed was evaluated with four 100 µg standards of each base plus ribose and H<sub>3</sub>PO<sub>4</sub>. The % recovery is given in Table II. No interfering peaks were found on the chromatograms, due to the ribose or phosphate, but a few resin "fines" caused some extraneous peaks that could interfere with the bases at a lower sample level.

3. Anion Exchange Resin. To achieve quantitative recovery and efficiency of cleanup, of the purine and pyrimidine bases, the anion exchange resin was changed from Dowex



TABLE II

GLC ANALYSIS AND RECOVERY OF THE PURINE  
AND PYRIMIDINE BASES AT THE MACRO LEVEL  
ONE COLUMN ION-EXCHANGE CLEANUP METHOD

Sample	Dowex 1-X2 Formate and Recovery <sup>a</sup> , %			
	U	C	A	G
1	95	95	95	92
2	95	101	98	102
3	99	100	97	95
4	96	97	96	95
Average	96	98	96	96

Sample	AG 1-X2 Acetate and Recovery <sup>a</sup> , %			
	U	C	A	G
1	94	94	92	95
2	96	98	98	96
3	94	97	94	92
4	95	100	92	101
Average	95	95	94	96

$${}^a\text{Recovery, \%} = \frac{\text{RMR}_{\text{B/IS}} \text{ through cleanup}}{\text{RMR}_{\text{B/IS}} \text{ standard}} \times 100,$$

$$\text{RMR}_{\text{B/IS}} = \frac{\text{Area}_{\text{B}}/\text{Moles}_{\text{B}}}{\text{Area}_{\text{IS}}/\text{Moles}_{\text{IS}}}, \text{ and}$$

$\text{RMR}_{\text{B/IS}}$  standard was the average of four independent results.

1-X2 formate to AG 1-X2 acetate, and a regeneration procedure of the resin was developed. To evaluate the AG 1-X2 acetate anion exchange resin, four 100  $\mu\text{g}$  standards of each base plus ribose and  $\text{H}_3\text{PO}_4$  were analyzed, and the % recovery is presented in Table II. No resin "fines" were observed in the samples, and the chromatograms were free of extraneous peaks.

### C. Semimicro Samples

Analysis of semimicro (ca. 10  $\mu\text{g}$  @ base)

standards using the single column procedure with AG 1-X2 showed that all of the bases were quantitatively recovered. The following average % recoveries were obtained from four independent semimicro standards plus ribose and phosphate: U - 85%, T - 93%, C - 92%, A - 85%, and G - 86%. No extraneous peaks due to ribose degradation products, phosphate, or resin "fines" were found on the chromatograms.

## II. RNA Analysis

### A. Macro Samples

Three types of RNA, Yeast RNA I, Yeast RNA II, and TMV-RNA, were analyzed at the macro level, 1 mg of RNA, (ca. 100  $\mu\text{g}$  @ base) using the single column procedure described above. The mole % composition for each type of RNA was calculated by the formula presented earlier, and these values, along with the standard deviations, are presented in Table III. The literature values for the Yeast RNA II and TMV-RNA were obtained from TLC data

by Dr. Sehgal, Department of Genetics, University of Missouri. The values obtained by the GLC procedure were in excellent agreement with those obtained by TLC. Figures 1, 3, and 4 show typical chromatograms of the RNA's analyzed. Each peak represents approximately 1.0  $\mu\text{g}$  injected.

#### B. Semimicro Samples

For the analysis of RNA at the semimicro level, 100  $\mu\text{g}$  of RNA (ca. 10  $\mu\text{g}$  @ base) were carried through the single column procedure. The mole % composition plus standard deviations for each type of RNA are given in Table III. The results agree quite well with those obtained from macro samples and with TLC literature values. Typical chromatograms for semimicro samples of RNA are shown in Figures 2 and 5. Each peak represents approximately 250 ng injected. Because of impurities in the RNA, some samples contained as little as 5.0  $\mu\text{g}$  of each base. No problems were encountered due to this decrease in total RNA or from the impurities in the sample analyzed.

### III. DNA Analysis

#### A. Hydrolysis

Initial experiments showed that the hydrolysis of DNA with 70%  $\text{HClO}_4$  was unsatisfactory. Only 20% of the thymine was recovered under the hydrolysis conditions used. Jordan (7) indicated that perchloric acid was not the reagent of choice

for DNA, but that concentrated formic acid plus DNA heated in a closed tube at 175°C-2 hrs. gave good results. The formic acid hydrolysis method was found to be satisfactory for DNA, but not for RNA as uridylic acid was not completely hydrolyzed to uracil.

Also, the one column cleanup method had to be slightly modified for analysis of DNA because the formic acid was not strong enough to keep all the bases as cations. The purines tended to be partially retained by the anion-exchange resin with water as wash, but when 1.0 N acetic acid was used to elute the bases, all were quantitatively recovered.

#### B. Macro Samples

Two types of DNA, Salmon Sperm DNA and Calf Thymus DNA, were analyzed by the method proposed above. One milligram of DNA was hydrolyzed with 0.5 ml of 98 to 100% HCOOH at 175°C-2.0 hrs. The samples were carried through the one column method using 1.0 N acetic acid to elute the column. The average mole % composition for each DNA was calculated and these values plus the standard deviations are given in Table IV. The literature values were obtained from Sober's Handbook of Biochemistry. The values obtained for the Salmon Sperm DNA agreed closely with the literature values, but the Calf Thymus DNA values for thymine were low and for cytosine were high as compared to the literature. It is possible that some deamination of cytosine occurred during hydrolysis giving low cytosine data for the literature values, and incomplete hydrolysis of the DNA would give low thymine

TABLE III  
MOLE PERCENT COMPOSITION OF RNA SAMPLES

Weight <sup>a</sup>	RNA	Mole % Composition <sup>b</sup>			
		U	C	A	G
100 µg	Yeast RNA I	20.6	24.2	26.5	28.7
	S. D. <sup>c</sup>	±1.4	±1.3	±0.9	±1.4
10 µg	Yeast RNA I	20.8	23.9	26.3	28.0
	S. D.	±2.3	±1.0	±1.7	±1.2
100 µg	Yeast RNA II	21.2	25.1	26.0	27.6
	S. D.	±2.0	±0.9	±0.6	±1.1
10 µg	Yeast RNA II	21.7	26.5	27.0	24.8
	Literature Value <sup>d</sup>	20.1	24.6	25.0	30.1
100 µg	TMV-RNA	26.5	20.2	30.2	23.1
	S. D.	±2.3	±0.8	±2.7	±1.0
10 µg	TMV-RNA	25.8	20.0	31.3	22.3
	S. D.	±1.5	±2.2	±1.2	±0.7
	Literature Value <sup>d</sup>	26.3	18.5	29.8	25.3

<sup>a</sup> Approximate weight of each base in sample of RNA analyzed.

<sup>b</sup> Mole % Composition =  $\frac{\mu\text{Moles}_B}{\mu\text{Moles}_{\text{Total}}} \times 100$

<sup>c</sup> S. D. = standard deviation. Four or more independent analyses.

<sup>d</sup> Literature values obtained from TLC data by Dr. Sehgal, Department of Genetics, University of Missouri.

FIGURE 1

## GLC CHROMATOGRAM OF THE BASES IN YEAST RNA-I MACRO ANALYSIS

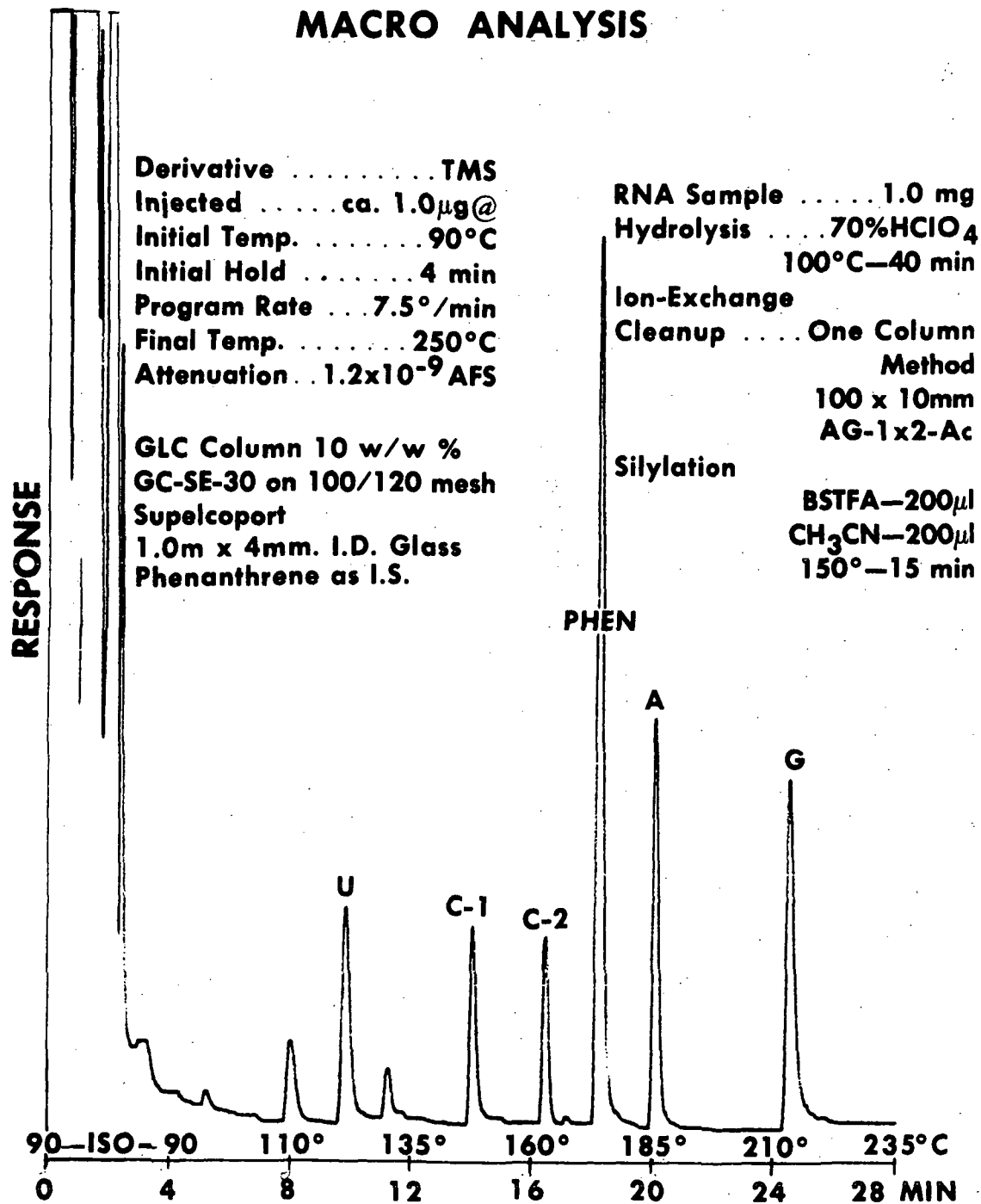


FIGURE 2

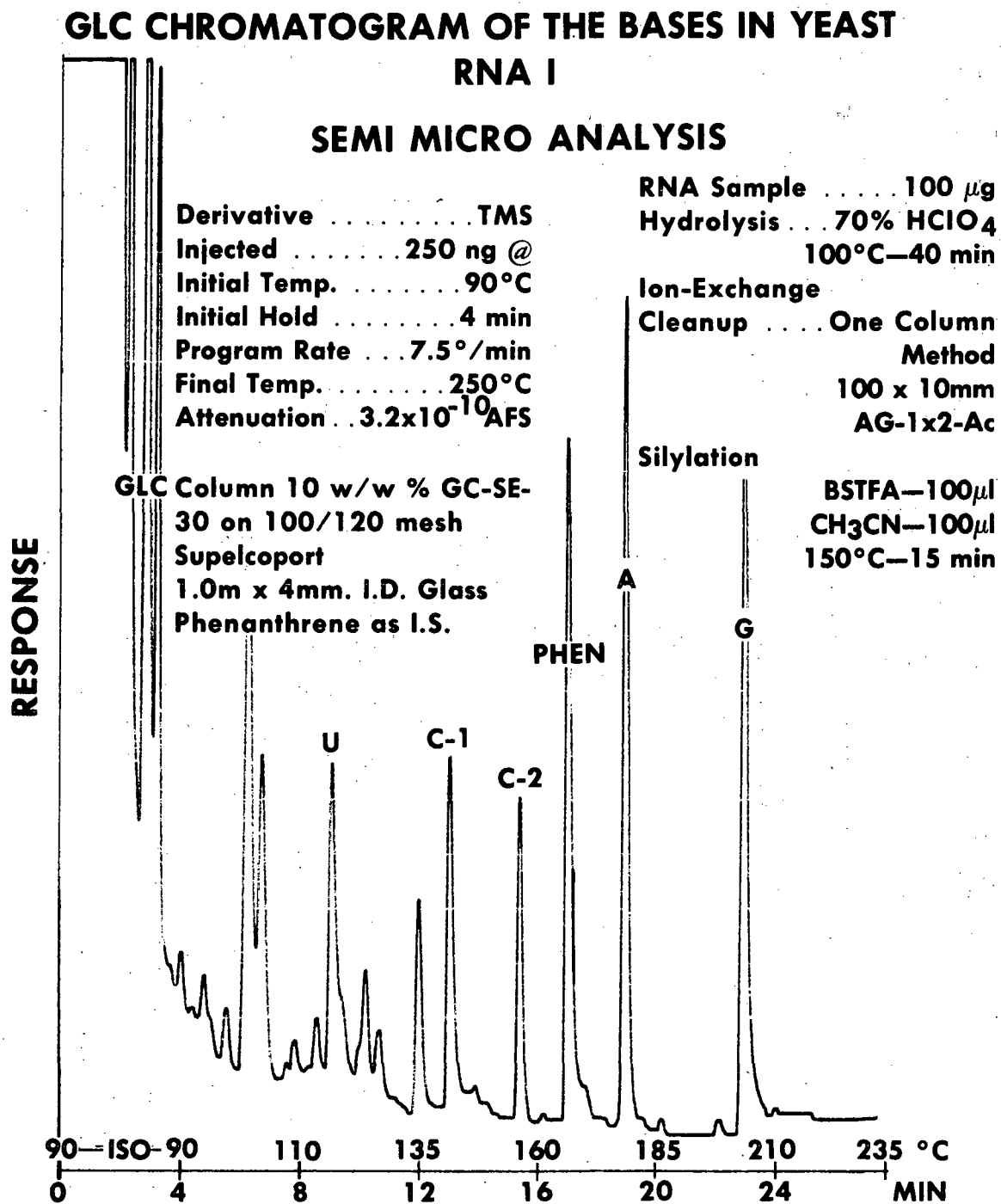


FIGURE 3

## GLC CHROMATOGRAM OF THE BASES IN YEAST RNA II MACRO ANALYSIS

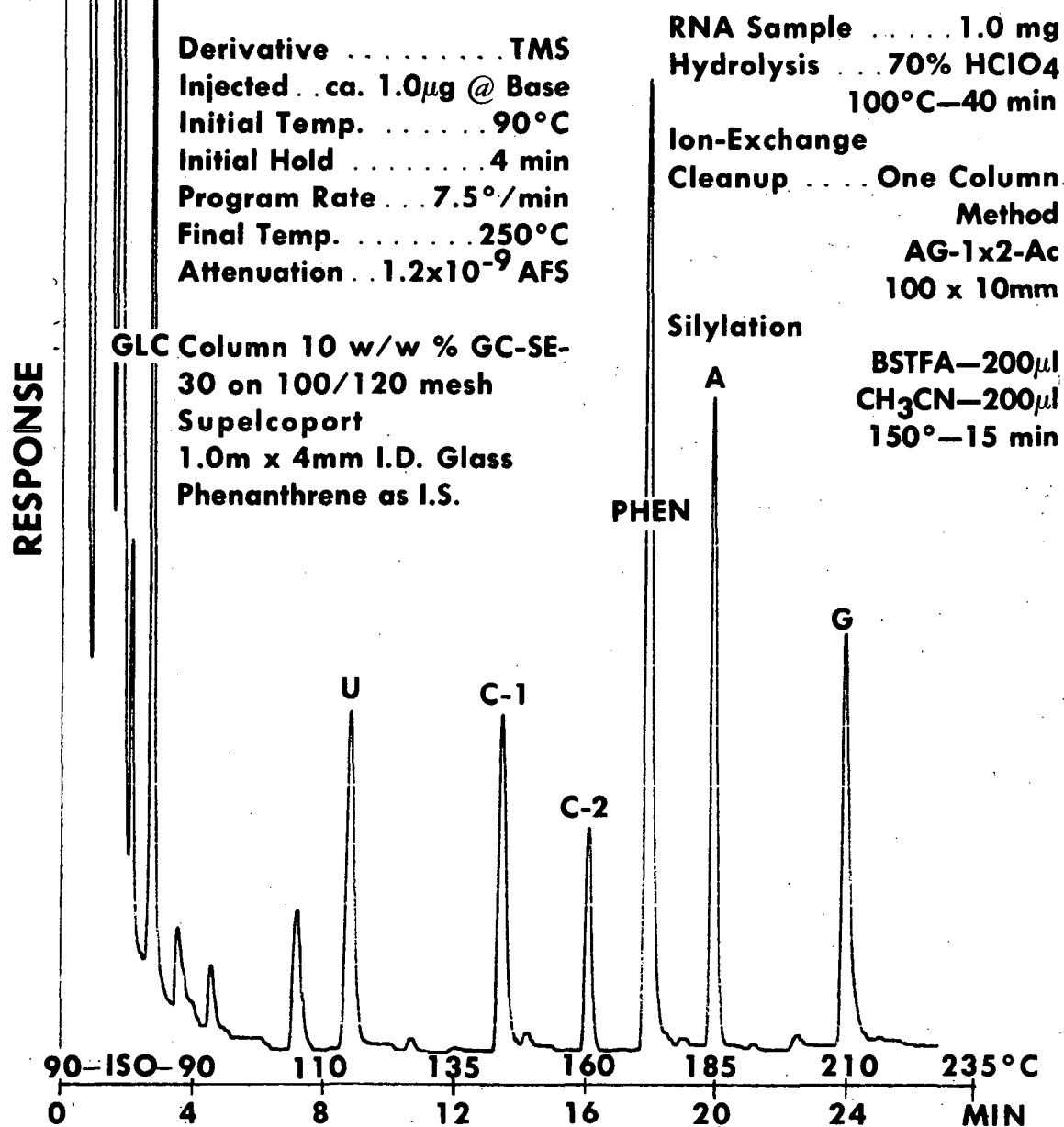




FIGURE 4

## GLC CHROMATOGRAM OF THE BASES IN TMV-RNA MACRO ANALYSIS

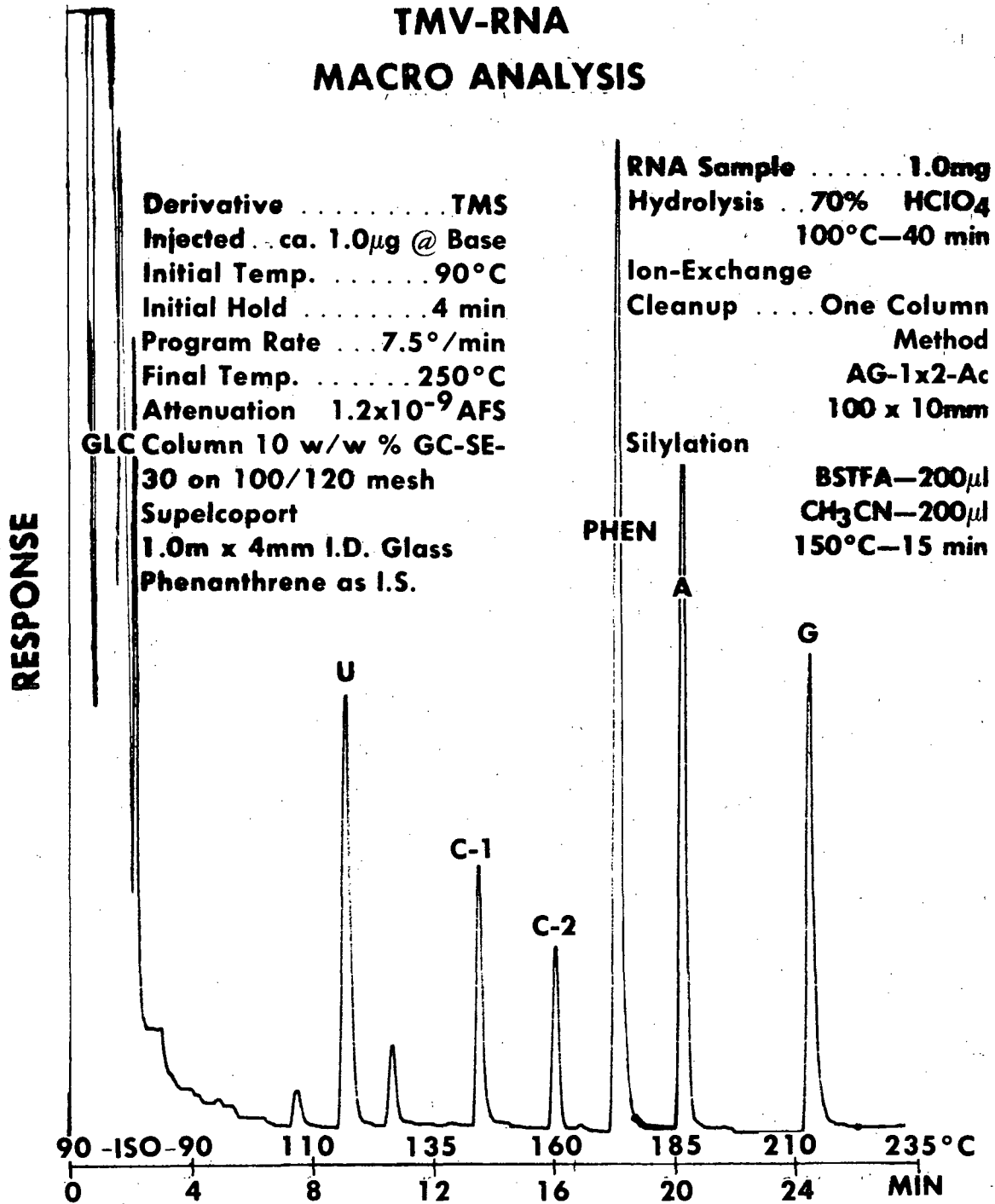


FIGURE 5

## GLC CHROMATOGRAM OF THE BASES IN TMV-RNA SEMIMICRO ANALYSIS

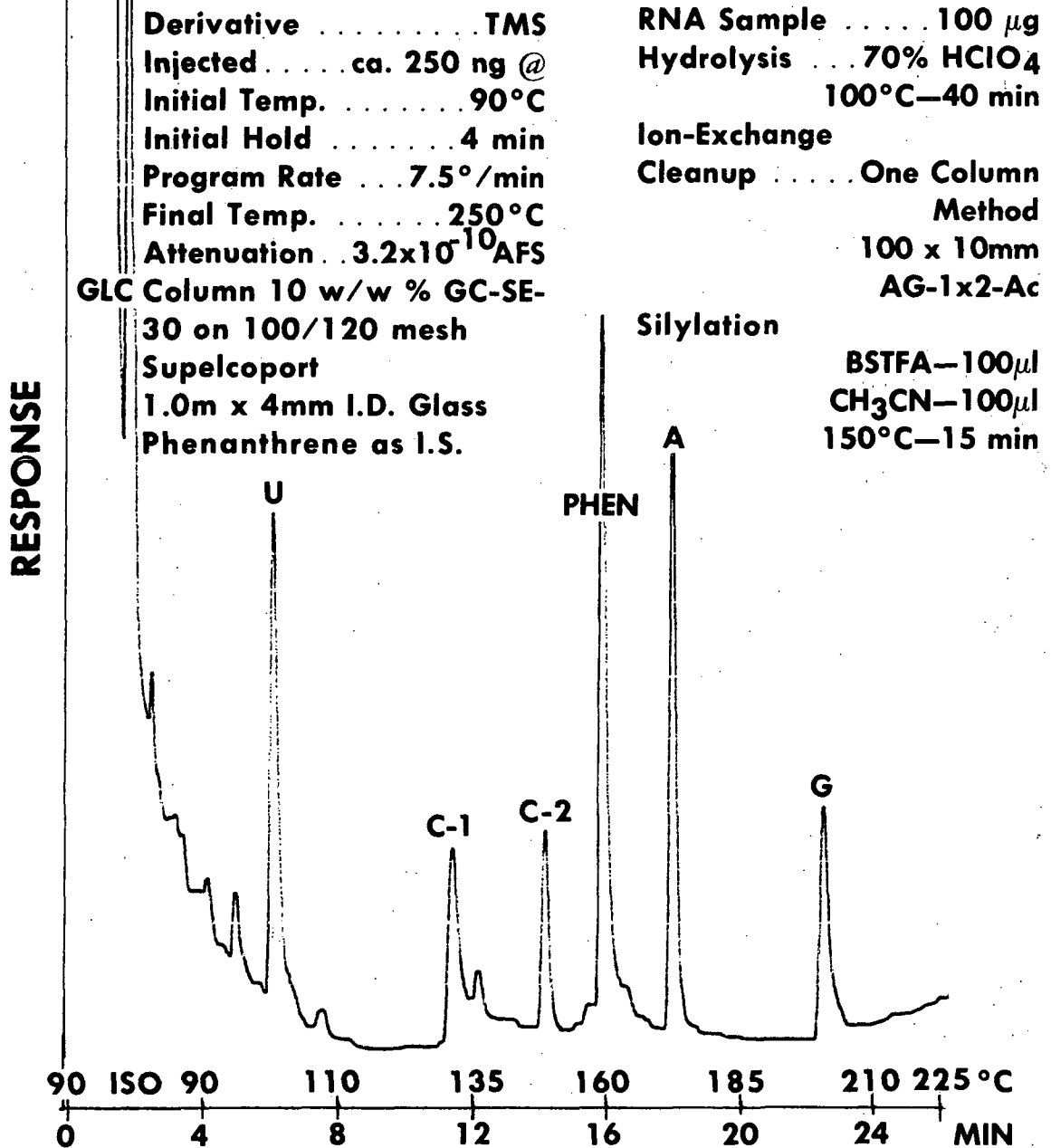


TABLE IV  
MOLE PERCENT COMPOSITION OF DNA SAMPLES

Weight <sup>a</sup>	DNA	Mole % Composition <sup>b</sup>			
		T	C	A	G
100 μg	Salmon Sperm DNA	28.9	21.9	28.8	20.6
	S. D. <sup>c</sup>	±1.4	±1.6	±0.7	±0.5
10 μg	Salmon Sperm DNA	26.8	20.5	31.2	22.3
	S. D.	±1.1	±1.7	±0.2	±1.4
	Literature Value <sup>e</sup>	28.5	21.1	28.7	22.3
	S. D. <sup>d</sup>	±1.5	±0.8	±0.9	±0.7
100 μg	Calf Thymus DNA	23.6	24.4	30.4	21.6
10 μg	Calf Thymus DNA	24.6	22.8	28.9	23.5
	Literature Value <sup>e</sup>	28.2	21.2	28.4	21.8

<sup>a</sup> Approximate weight of each base in sample of DNA analyzed.

<sup>b</sup> Mole % Composition =  $\frac{\mu\text{Moles}_B}{\mu\text{Moles}_{\text{Total}}} \times 100$

<sup>c</sup> S. D. = standard deviation. Four or more independent analyses.

<sup>d</sup> S. D. = standard deviation of four literature values.

<sup>e</sup> Literature Value = average of eighteen results.

FIGURE 6

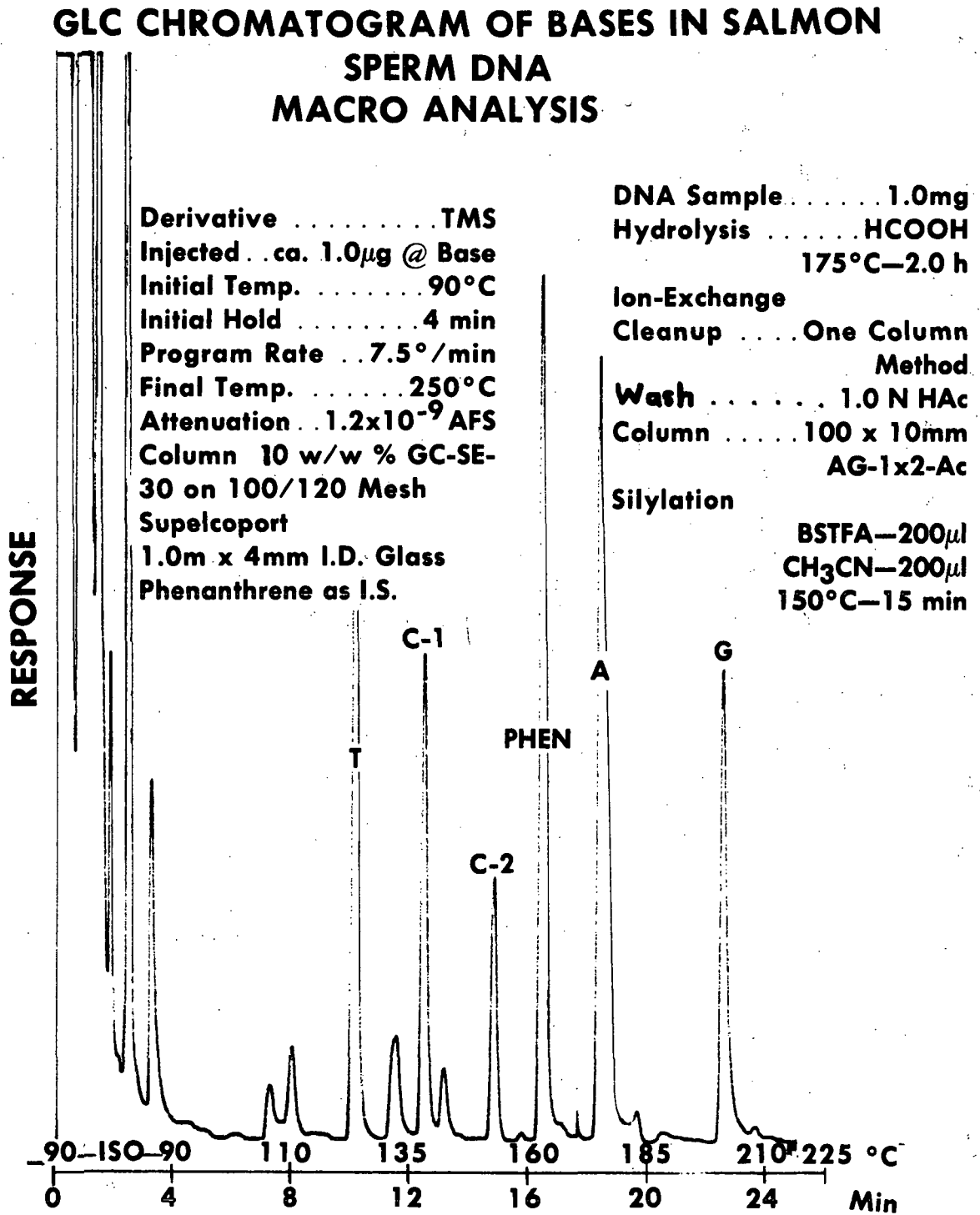


FIGURE 7

## GLC CHROMATOGRAM OF THE BASES IN SALMON SPERM DNA SEMI MICRO ANALYSIS

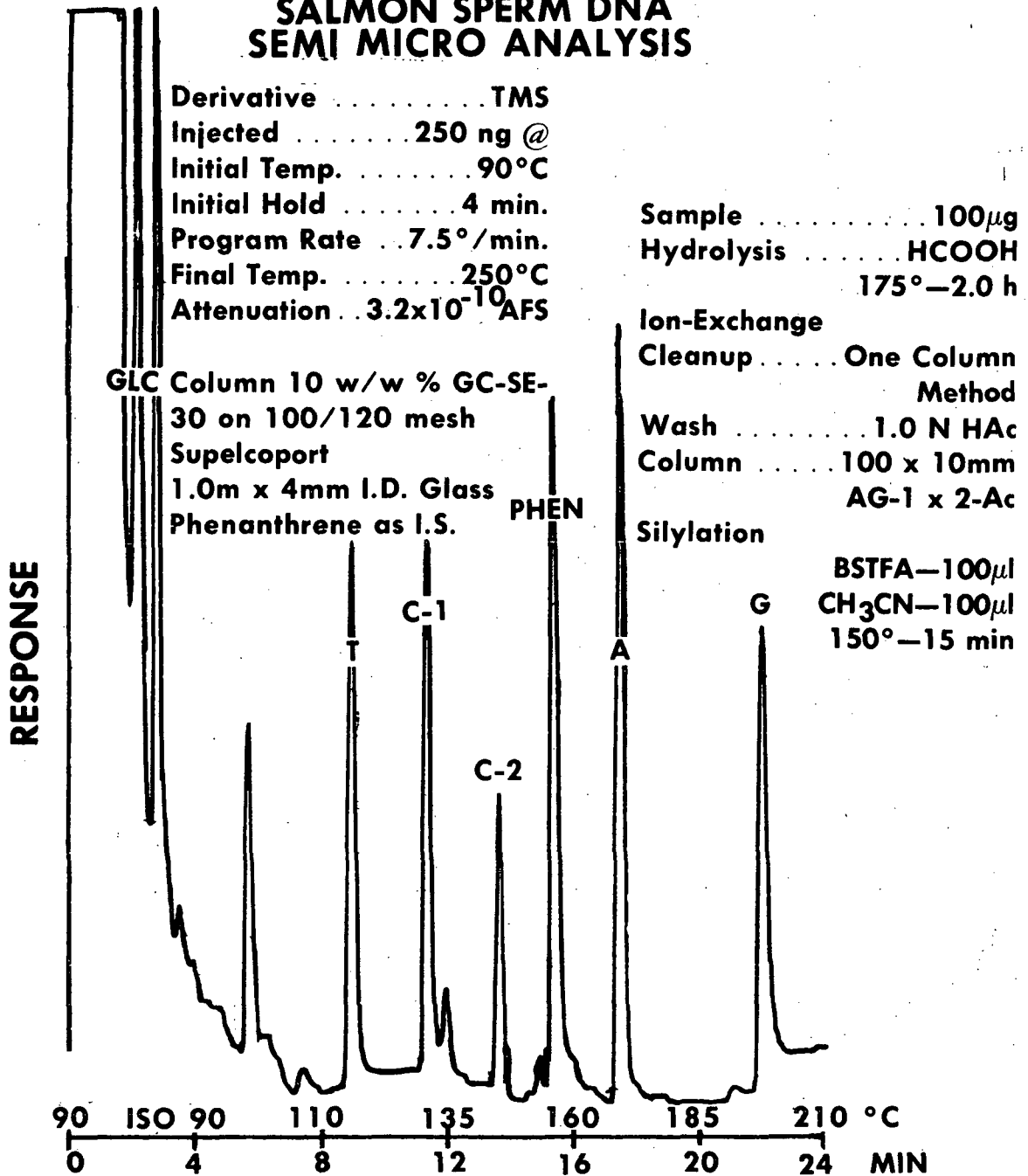
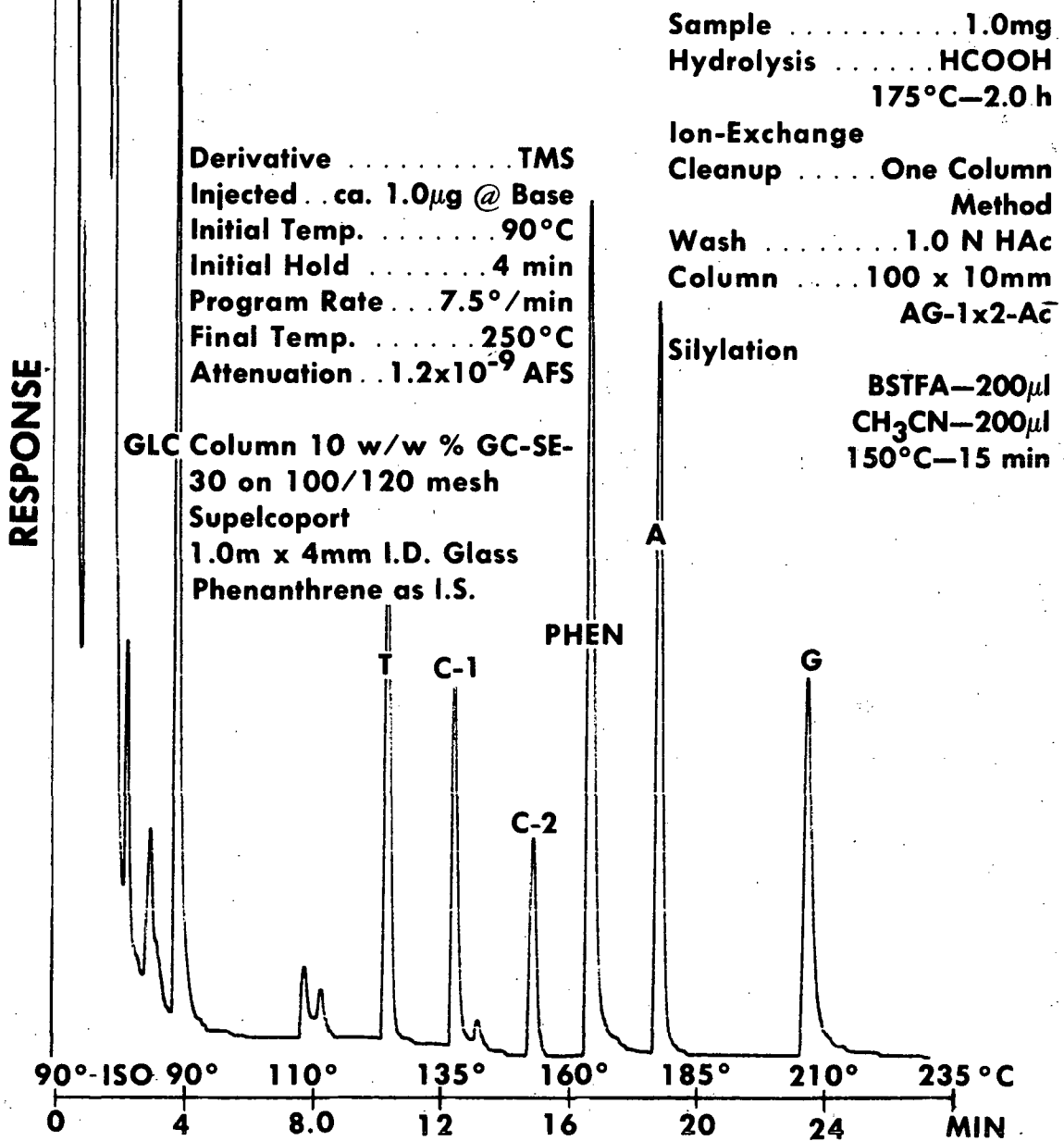


FIGURE 8

## GLC CHROMATOGRAM OF THE BASES IN CALF THYMUS DNA MACRO ANALYSIS



values. Figures 6 and 8 show typical chromatograms obtained for DNA at the macro level. Each peak represents ca. 1.0  $\mu\text{g}$  injected.

### C. Semimicro Samples

Analysis of 100  $\mu\text{g}$  of DNA (ca. 10  $\mu\text{g}$  @ base) using formic acid hydrolysis gave good results. The mole % composition (Table IV) agreed very well with the values obtained from macro samples of DNA. Figure 7 shows a typical chromatogram of a semimicro sample of Salmon Sperm DNA. Each peak represents 250 ng injected.

## IV. Micro Sample Cleanup Method

### A. One Column Method

The single column procedure using AG 1-X2 acetate anion exchange resin developed for cleaning macro and semimicro hydrolysates was fully evaluated as a cleanup method for micro sample analysis. Initial experiments showed that extreme care in handling samples was necessary to prevent contamination. The resin "fines" must be completely removed, the reagents free of impurities, and the BSTFA of excellent quality. Even with these careful techniques, the purines, adenine and guanine, were not recovered from the anion exchange column.

In experiments to recover the purines, the anion exchange columns were eluted with dilute acid (HCl or acetic acid). The purine recovery was slightly better (approximately 20% for adenine and guanine), but still too low for a semi-quantitative

analysis. An acidic anion exchange column was evaluated and the recoveries were improved, but still low. When the resin column was evacuated to remove trapped air, the resulting chromatograms were cleaner, but the recovery was not improved. These experiments indicated that the single column macro or semimicro procedure, even with modifications, would not serve as a cleanup method for the analysis of nucleic acid hydrolysates at the micro level.

#### B. Other Ion-Exchange Resins

The above experiments showed that adenine and guanine at the micro level were lost on passing through the anion exchange column. The Ag 1-X2 acetate resin could have active sites on which the purines were being held, thus preventing them from passing through the column.

Other ion-exchange resins, with a different polymer lattice or a different functional group than AG 1-X2, might give the desired recovery of these bases. The following resins were evaluated as possible replacements for AG 1-X2: AG 3-X4, Bio-Rex 9, Amberlite IR-4B, and Amberlite CG-120. To evaluate each resin, it was carefully regenerated, and the resin "fines" removed. Four standards (10 µg, 2.0 µg, and two 500 ng @ base) were then cleaned by each resin. The AG 3-X4 resin gave very clean chromatograms and good recoveries of all the bases for the 10 µg standard, but the recoveries of adenine and guanine at the 500 ng level were again low. Other experiments with modifications gave similar results



at the micro level. Bio-Rex 9 and Amberlite IR-4B gave poor recoveries at the 10  $\mu\text{g}$  each base level, and the chromatograms contained many extraneous peaks. Even with exhaustive regeneration, the chromatograms were unacceptable. Amberlite CG-120, a cation exchange resin, gave purine recovery of 50% at the micro level, but the pyrimidines were completely lost. Additional experiments did not improve the purine recoveries, and the pyrimidines were not detected.

### C. Charcoal Column Cleanup

The ion-exchange methods gave poor recoveries for the purines, adenine and guanine, at the micro level. A method of cleaning up micro samples of the bases had been developed by Dr. Carl Saxinger, Ames Research Center-NASA, but this method had not been used in conjunction with GLC so the method was fully studied. Initial experiments at the semi-micro (10  $\mu\text{g}$  @ base) level showed the regeneration procedure developed by Dr. Saxinger did not remove all of the impurities from the charcoal, and these impurities interfered with the chromatography of the bases by GLC. Thus, the charcoal was exhaustively washed with concentrated formic acid (the eluting reagent) and with water to remove as much of the impurities as possible. With this prepared charcoal, the semimicro experiment was rerun with good results. The average % recovery for 12 semimicro standards containing  $\text{H}_3\text{PO}_4$  and ribose were: U - 92%, T - 92%, C - 105%, A - 93%, and G - 90%. No extraneous peaks were observed on the chromatogram due to the  $\text{HClO}_4$ ,  $\text{H}_3\text{PO}_4$ ,

or ribose; and only minor peaks were detected as coming from the charcoal.

With this method and the formic acid washed charcoal, experiments were then made to determine the recovery of the bases at the micro (500 ng @ base) level. The contamination from the charcoal observed in the initial semimicro experiment was again present so the recovery could not be ascertained. Further regeneration of the charcoal did not remove the impurities so the method could not be used for micro analysis of nucleic acid hydrolysates, however, the method could be used for semimicro analyses with good success.

#### D. Small Ion-Exchange Column

Since the amount of sample in micro analyses was greatly reduced, the amount of  $\text{HClO}_4$  needed for hydrolysis was also reduced, and the amount of resin needed to remove the interfering compounds could be lowered. The less resin employed for cleanup would offer fewer active sites for possible adsorption of the purines. Also, a "silanized" glass wool plug was used in place of normal glass wool to decrease active sites. With these ideas, experiments were conducted with 50  $\mu\text{l}$   $\text{HClO}_4$  for hydrolysis, an AG 1-X2 acetate anion exchange column of 100 x 4 mm, and 25 x 1 ml of triply distilled water as wash. Initial experiments showed promise with adenine and guanine being recovered at approximately 60%. Using very careful techniques, 12 micro (500 ng @ base) standards were carried

through the method with an average recovery of U - 66%, T - 53%, C - 92%, A - 76%, and G - 65%. In general, these values were too low for good quantitative analysis, but could be used for semi-quantitative data. The mole % composition of RNA or DNA at the micro level could be semi-quantitatively determined.

## V. Micro Analysis of RNA and DNA

### A. RNA Analysis

The three types of RNA (Yeast RNA I and II, and TMV-RNA) analyzed at the macro (1.0 mg RNA) and semimicro (100 µg RNA) levels were analyzed at the micro (5.0 µg RNA) level by the method outlined above. Four independent samples of each type of RNA were analyzed, and the average mole % composition is given in Table V. The values compare well with the mole % composition obtained at the macro level, even though the micro analyses were only semi-quantitative. Figure 9 shows a typical chromatogram for Yeast RNA II at the micro level. Each peak represents approximately 30 ng injected.

### B. DNA Analysis

Two types of DNA (Salmon Sperm DNA and Calf Thymus DNA) that were analyzed at the macro and semimicro levels were analyzed at the micro level. To hydrolyze the DNA, 100 µl of concentrated formic acid were used to prevent thymine degradation, which occurs on hydrolysis with HClO<sub>4</sub>. The anion

exchange column was washed with 0.5 N acetic acid in place of water to prevent the bases from being held on the resin. Standards were recovered using this method at U - 68%, T - 80%, C - 89%, A - 74%, and G - 66%. Four independent samples of each DNA were analyzed and the average mole % composition is given in Table VI. The values for micro analysis of Salmon Sperm DNA compared well with those obtained at the macro level, and the Calf Thymus DNA mole % composition at the micro level compared well with literature values, but not with the values obtained at the macro level for thymine. The hydrolysis at the macro level may have been incomplete due to the composition of DNA, giving low thymine values. Figure 10 shows a typical chromatogram for 5.0  $\mu\text{g}$  of Salmon Sperm DNA hydrolyzed with HCOOH. Each peak represents ca. 30 ng injected.

TABLE V

COMPARISON OF GLC MICRO AND MACRO  
ANALYSES OF RNA SAMPLES

Weight <sup>a</sup>	RNA	Mole % Composition <sup>b</sup>			
		U	C	A	G
5 µg	Yeast RNA I <sup>c</sup>	22.8	22.8	26.8	27.7
1 mg	Yeast RNA I <sup>d</sup>	20.6	24.2	26.5	28.7
5 µg	Yeast RNA II <sup>c</sup>	26.1	21.6	28.6	23.2
1 mg	Yeast RNA II <sup>d</sup>	26.5	20.2	30.2	23.1
5 µg	TMV-RNA <sup>c</sup>	23.3	26.5	24.2	26.2
1 mg	TMV-RNA <sup>d</sup>	21.2	25.1	26.0	27.6

<sup>a</sup>Weight = weight of RNA sample.

<sup>b</sup>Mole % Composition =  $\frac{\text{nMoles}_B}{\text{nMoles}_{\text{Total}}} \times 100$

<sup>c</sup>Four independent analyses for each RNA. Standard deviation ranged from  $\pm 0.5$  to  $\pm 1.7$ .

Average value for each RNA at the macro level.

Note: 500 ng each base standards were carried through cleanup with the RNA's to correct losses of the bases on the anion exchange column.

TABLE VI

COMPARISON OF GLC MICRO AND MACRO  
ANALYSES OF DNA SAMPLES

Weight <sup>a</sup>	DNA	Mole % Composition <sup>b</sup>			
		T	C	A	G
5 $\mu$ g	Salmon Sperm DNA <sup>c</sup>	27.9	20.4	28.9	22.4
1 mg <sup>d</sup>	Salmon Sperm DNA <sup>c</sup>	28.9	21.9	28.8	20.6
5 $\mu$ g	Calf Thymus DNA <sup>c</sup>	29.4	23.0	28.5	19.1
1 mg <sup>d</sup>	Calf Thymus DNA <sup>c</sup>	23.6	24.4	30.4	21.6
	Literature Value	28.2	21.2	28.2	21.8

<sup>a</sup>Weight = weight of DNA sample.

<sup>b</sup>Mole % Composition =  $n \text{ Mole}_B / n \text{ Mole}_{\text{Total}} \times 100$

<sup>c</sup>Four independent analyses for each DNA. Standard deviation ranged from  $\pm 0.3$  to  $\pm 2.7$ .

<sup>d</sup>Average value for each DNA at the macro level.

Note: 500 ng each base standards were carried through cleanup with the DNA's to correct losses of the bases on the anion exchange column.

FIGURE 9

## GLC CHROMATOGRAM OF THE BASES IN YEAST RNA II MICRO ANALYSIS

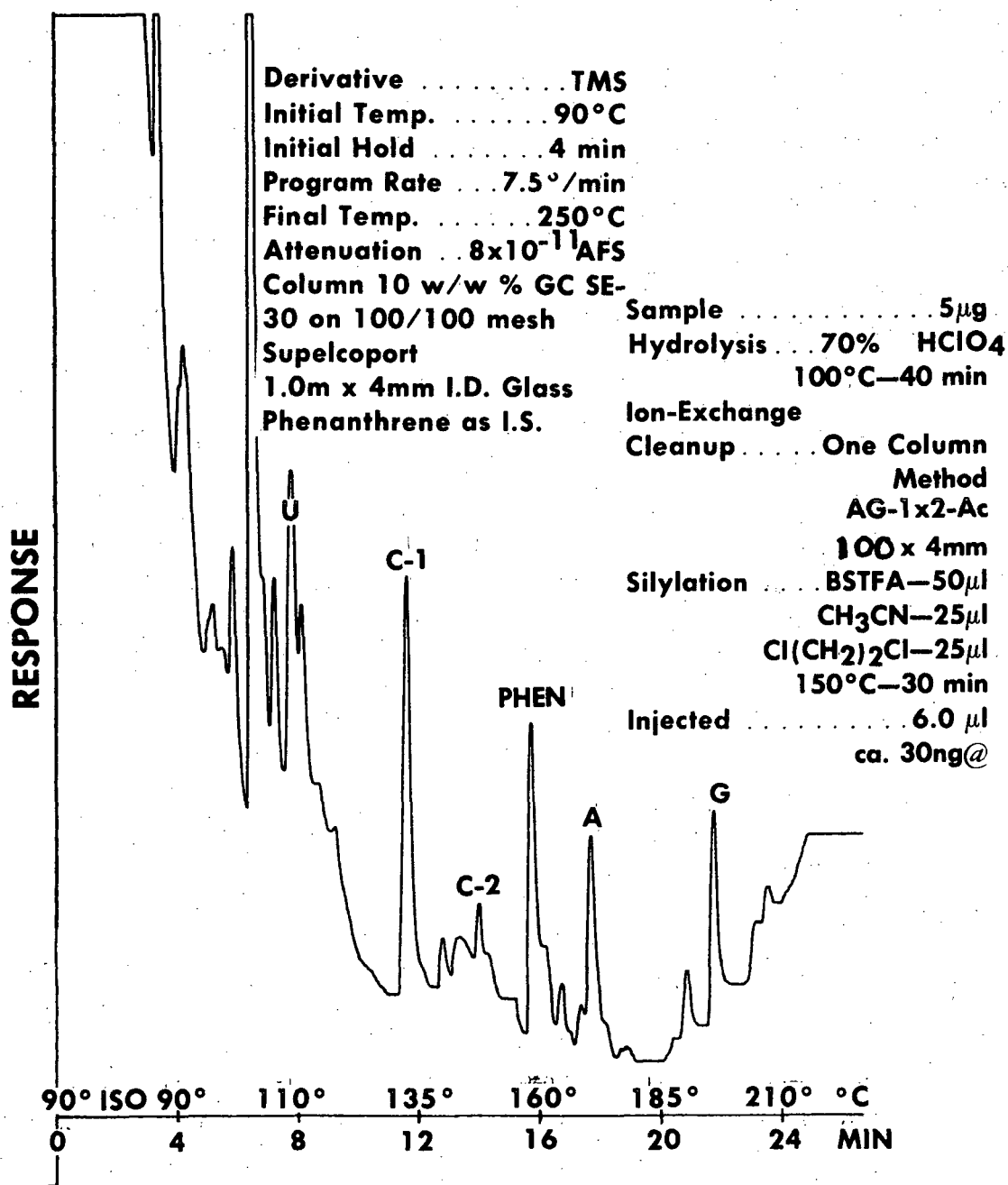
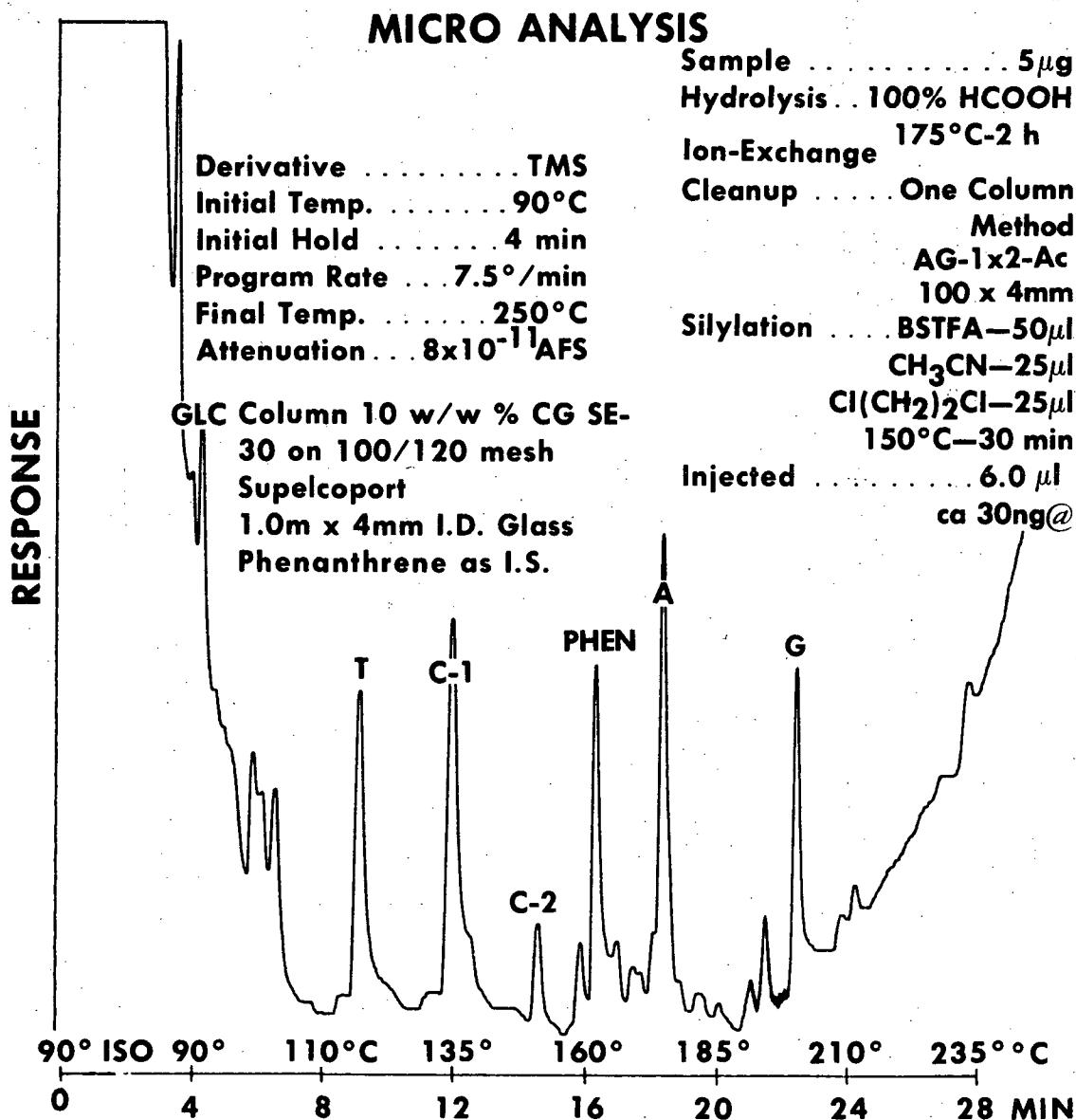


FIGURE 10

## GLC CHROMATOGRAM OF BASES IN SALMON SPERM DNA





## SUMMARY AND CONCLUSIONS

A quantitative GLC method has been developed for the analysis of hydrolysates of nucleic acids at the macro (1.0 mg) and semimicro (100  $\mu$ g) levels of total nucleic acids and a semi-quantitative method for micro samples ( 5.0  $\mu$ g of nucleic acid). An anion exchange cleanup procedure, which gave quantitative recovery of the purine and pyrimidine bases, removed the phosphate and ribose released during hydrolysis of the sample, and did not add interfering compounds which would affect the silylation and chromatography of the bases, was needed. The final cleanup method consisted of a single column procedure using AG 1-X2 acetate anion exchange resin. GLC analysis of the bases was accomplished by first converting them to their TMS-derivative with BSTFA followed by chromatography on a 10 w/w% CG-SE-30 100/120 mesh Supelcoport column.

First, a two column anion-exchange cleanup procedure was developed which gave good recovery of the bases without added contamination. However, this procedure was time consuming and thus was modified.

The modifications gave rise to a single column cleanup procedure using AG 1-X2 acetate anion exchange resin, which gave 95 to 100% recovery of the bases at the macro level (100  $\mu$ g @ base) and 85 to 90% recovery at the semimicro level (10  $\mu$ g @ base).

Using the one column cleanup method, and the silylating and chromatographic conditions developed earlier, three types of RNA (Yeast RNA I and II and TMV-RNA) and two types of DNA

(Salmon Sperm and Calf Thymus) were analyzed at the macro and semimicro levels. The RNA's were hydrolyzed with 70% HClO<sub>4</sub> and the DNA's with 98 to 100% formic acid. DNA could not be quantitatively hydrolyzed with HClO<sub>4</sub> because thymine was partially destroyed, and formic acid did not completely hydrolyze uridylic acid in RNA to uracil. The mole % composition of each RNA and DNA was determined and found to be in good agreement with values reported in the literature.

A number of problems were encountered in the development of a micro method for analysis of nucleic acids (5.0 µg). The one column method used for macro and semimicro samples was unsatisfactory, because the purines adenine and guanine, were not recovered from the ion-exchange column. Some changes, including eluting with dilute acid, using an acidic column, evacuating the resin to remove trapped air, and changing the ion-exchange resin, were tried without success. Recovery at the semimicro level with some of the modifications was good, but at the micro (500 ng @ base) level, the purines were not recovered.

A charcoal column cleanup procedure was evaluated as a possible alternative for micro analysis. Excellent recoveries at the semimicro level (10 µg @ base) were obtained, but at the micro level, impurities from the charcoal column interfered with the silylation and chromatography of the bases.

Even with exhaustive regeneration of charcoal and the very careful techniques, the impurities could not be removed

In micro analyses, the amount of nucleic acid sample used was considerably reduced, thus the amount of  $\text{HClO}_4$  needed for hydrolysis and the anion exchange column size used in the one column method could be correspondingly reduced. Using a 100 x 4 mm AG 1-X2 acetate anion exchange column with a small plug of "silanized" glass wool above the fritted glass disc and 50  $\mu\text{l}$  of  $\text{HClO}_4$  for hydrolysis, all of the bases were semi-quantitatively recovered. Little interference from the anion exchange resin was observed on the chromatograms so the procedure could be used for semi-quantitative determination of the mole % composition of RNA or DNA.

With this method, the three RNA's and two DNA's were analyzed at the micro level (5.0  $\mu\text{g}$  of total nucleic acid). Hydrolysis with  $\text{HClO}_4$  was used for RNA and  $\text{HCOOH}$  for DNA. The mole % composition for all samples was in good agreement with the values obtained at the macro level (1.0 mg of total nucleic acid) and with literature values.

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