Protein Modifications by Activated Carcinogens

I. THE ACETYLATION OF RIBONUCLEASE BY N-ACETOXY-2-FLUORENYLACETAMIDE*

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SUMMARY

The postulated fragmentation of RNase by N-acetoxy-2-fluorenylacetamide (N-acetoxy-2-FAA), an activated metabolite of the carcinogen, N-hydroxy-2-fluorenylacetamide, has been investigated. The interaction of N-acetoxy-2-FAA with RNase resulted in the formation of two new proteins separable from RNase by electrophoresis and ion exchange chromatography. These proteins contained no new NH₂-terminal amino acids, and their amino acid composition was identical with that of native RNase, indicating that the protein had not been modified by cleavage of the peptide chain. The alternative possibility that the formation of the additional proteins was due to a decrease in the positive charge of RNase was examined by the determination of the incorporation of ³H and ¹⁴C from N-[³H]acetoxy-[⁹-¹⁴C]2-FAA into RNase. The ratio of bound ³H to bound ¹⁴C, which measures the relative extent of acetylation and arylamidation in the modified proteins, suggested that acetylation rather than arylamidation was the predominant reaction modifying RNase. The conclusion that the acetyl group of N-[³H]acetoxy-[⁹-¹⁴C]2-FAA had been transferred to RNase was confirmed (a) by the recovery of [³H]acetic acid from the hydrolysates of the modified protein and (b) by the isolation of e-N-acetyl-L-lysine from enzymatic hydrolysates of the modified protein. The isolation of the N-acetylated amino acid accounted in part for the decrease in the positive charge of RNase after reaction with N-acetoxy-2-FAA. The results indicate that N-acetoxy-2-FAA is an acetyl donor and modifies proteins primarily by acetylation rather than arylamidation.

The biological activity of certain hepatocarcinogenic arylamides appears to depend on a two-step mechanism of metabolic activation. The arylamide is first N-hydroxylated (2) and then esterified to an N-sulfate (3), and possibly also to an N-phosphate (4) or N-acetate (5). These esters are highly unstable and decompose spontaneously to an electrophilic arylamidonium ion which arylamidates DNA, RNA, and proteins (6, 7). Although these macromolecular interactions have been documented in detail, the critical reaction that initiates the malignant transformation of the cell is not known. In a previous study, we have described the arylamidation of nuclear proteins, including histones, of rat liver by N-2-fluorenylacetamide in vivo (8). These data prompted us to suggest that arylamidation might alter the histones in such a way that they were no longer able to inhibit the transcription of nuclear DNA (9). However, the arylamidation of the nuclear proteins under these conditions was of such a low order that the elucidation of the structural modifications of the nuclear proteins by presently available analytical techniques was not feasible. We have reinvestigated the problem of the structural modification of proteins by arylamidation in a model system in which we reacted N-acetoxy-2-fluorenylacetamide (N-acetoxy-2-FAA) with RNase. This model system was chosen because it had been reported that N-acetoxy-2-FAA, an ester that is well characterized and available in pure form, reacts through arylamidation with methionine residues of RNase (10). Our objective was to determine whether this would cleave the peptide chain of RNase as had been suggested (7, 11), and, if so, whether histones that had been modified by arylamidation were fragmented in a similar manner. Although we were able to demonstrate arylamidation of RNase by N-acetoxy-2-FAA, to a minor extent, no cleavage of the protein was observed. Further examination of the modified protein showed that acetylation, rather than arylamidation, appeared to be the predominant reaction between N-acetoxy-2-FAA and RNase and that it accounted, at least in part, for the altered properties of RNase that had been exposed to the ester. The experiments leading to these conclusions form the basis of this report.

EXPERIMENTAL PROCEDURE

Labeled and Unlabeled Compounds—N-Acetoxy-[⁹-¹⁴C]2-FAA¹ was prepared by the acetylation of a mixture of N-hydroxy-[⁰-¹⁴C]2-FAA (10.3 mg, lot 485-120, 10 mCi per mmole, New England Nuclear) and N-hydroxy-2-FAA (403 mg) in 10 ml of pyridine with 0.2 ml of acetic anhydride (12). The compound

¹ The following abbreviations are used: N-acetoxy-2-FAA, N-acetoxy-2-fluorenylacetamide; N-hydroxy-2-FAA, N-hydroxy-2-fluorenylacetamide; 3-CH₃-S-2-FAA, 3-methylthio-2-fluorenylacetamide; TEMED, N,N,N',N'-tetramethylethlenediamine; FDNB, 2,4-dinitrofluorobenzene; o CH₃, o 2-FAA, o methylthio-2-fluorenylacetamide.

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was crystallized from ethanol-water (400 mg, 82% yield, m.p. 110-111.5°, 0.23 μCi per μmole). N-[II]Acetoxy-2-FAA was prepared by reacting N-hydroxy-2-FAA (100 mg) with [II]acetic anhydride (25.0 mg, 25 μCi per mg, New England Nuclear) in pyridine (10 ml) (12). The ester (97 mg, 82% yield, m.p. 110-111°, 16.5 μCi per μmole) gave an ultraviolet absorption spectrum superimposable on that of an authentic sample. 3-Methylthio-2-FAA (m.p. 167-168°) was obtained by reacting dl-methionine with N-acetoxy-2-FAA (10).

e-N-Acetyl-L-lysine (m.p. 247-249°) was prepared by the acetylation of the copper complex of L-lysine (13). α-N-Acetyl-L-lysine (m.p. 245-249°) was obtained from ε-N-benzoylcarbonyl-α-N-acetyl-L-lysine (13, 14). The infrared spectrum of the product was identical with that of an authentic sample.

O-Acetyl-l-serine was prepared by the acetylation of l-serine (2.0 g, 19 mmoles, Calbiochem) in glacial acetic acid saturated with HCl (15). The acetylation of the amino acid was carried out in suspension, instead of in solution as reported (15) because we found that l-serine is only very slightly soluble in glacial acetic acid saturated with HCl. The hydrochloride of O-acetyl-L-serine in ethanol was treated with triethylamine and O acetyl l-serine was obtained after recrystallization from water-ethanol (0.97 μ, m.p. 163-165°, [α]D = +17.2°, c = 2% in 0.1 N HCl).

γKDL 3000 (NH₃⁺), 1730 (−C−O−), 1600 (−C−O−), 1500 (NH₃⁺), 1235 (CH₃ C=O) cm⁻¹.

C₂H₅O₂N
Calculated: C 40.82, H 6.12, N 9.51
Found: C 40.72, H 6.35, N 9.68

The characteristic infrared absorption band at 3450 cm⁻¹ (−OH−) present in l-serine was absent in O-acetyl-L-serine.² O-Acetyl-L-threonine³ was prepared by the acetylation of L-threonine (1.6 g, 14 mmoles) with acetylchloride (0.35 mole) (16). The compound did not have the configuration of O-acetyl-D-threonine, m.p. 130° (16). However, the compound did have the configuration of O-acetyl-D-threonine (m.p. 125-127°, 91% yield, [α]D = -2.22°, c = 2% in H₂O).³

C₆H₁₅NO₂
Calculated: C 44.71, H 6.88, N 8.69
Found: C 44.49, H 6.65, N 8.65

__Refereces__

1. Sheehan et al. (15) reported [α]D = +9.15°, c = 1.8% in 0.1 N HCl, for O-acetyl-L-serine. We have consistently obtained products with infrared spectra superimposable on that of our analytical sample that gave the specific rotation listed in the text.

2. The enantiomorph, O-acetyl β-threonine, [α]D = 21.25° has been reported (17).

3. Sheehan et al. (15) reported [α]D = +9.15°, c = 1.8% in 0.1 N HCl, for O-acetyl-L-serine. We have consistently obtained products with infrared spectra superimposable on that of our analytical sample that gave the specific rotation listed in the text.

4. Fujiiwara et al. reported a compound, m.p. 103-104°, [α]D = +1.5°, c = 2% in H₂O, which they obtained by the rearrangement of N-acetyl-D-threonine in 0.5 N NH₄OH and regarded as N-acetyl-D-threonine (16). However, the compound did not have the correct elementary composition. Moreover, in our experience, the O → N acetyl shift in 0.5 N NH₄OH results in racemization.
carried out at 1.5 m a per tube for 1.5 hours. The proteins were stained with Amido Black (0.25%) in 7.5% acetic acid and de-
stained electrophoretically in the same acid. The absorbance pro-
file of the proteins was measured with the use of a micro-
densitometer (Canako, model F).

Identification and Measurement of o-Methylthio-2-FAA—The amounts of the o-methylmercaptoamidc released spontaneously from the protein during the reaction of RNAse with N-acetoxy-
\[ ^{[9-14}C\]2-FAA were measured by inverse isotope dilution (23). Carrier 3-CH\(_3\)S-2-FAA (0.4 g) was added to the reaction mixture, and the proteins were precipitated with acetone and removed by centrifugation. The supernatant liquid was concentrated at reduced pressure, and the residue was extracted with a mixture of benzene-\(n\)-hexane (15:85). The solvent was evaporated at reduced pressure, and the 3-CH\(_3\)S-\([9-14]C\]2-FAA was purified by thin layer chromatography.

Enzymatic Activity and Amino Acid Composition of Modified RNAse—The enzymatic activity of the modified protein was assayed by the method of Roth with ribonucleic acid (type XI, Sigma) as the substrate (24). The hydrolysis of RNA by ribo-
nuclease A (type XII, Sigma) served as a control.

The amino acid analyses of the proteins were carried out on duplicate samples with a Beckman/Spinco amino acid analyzer model 120B (25, 26). The proteins were hydrolyzed in sealed tubes with 6 N HCl (3 mg of protein per ml) at 110° for 22 hours.

The NH\(_2\)terminal amino acids of the modified proteins were identified by reacting the proteins with FDNB (27). The pro-
teins were hydrolyzed in 6 N HCl (2 ml) at 110° for 16 hours. The DNP amino acids were extracted with ether and chromato-
graphed on Silica Gel GF\(_{254}\) with ethanol-water (63:37) as solvent (28). The acet-
ate residue was dissolved in citrate buffer, and \([14]C\) aspartic acid,
\(\text{\[14]C\]glycine, and \(\text{\[14]C\]leucine were added as markers. The acet-
alyzed amino acids were then resolved by chromatography on a Beckman-Spinco 120B amino acid analyzer. The effluent was split into two equal portions. One of these was used for amino acid analysis. The other was analyzed for \(\text{H}\) and \(\text{^{14}C}\) by liquid
scintillation spectrometry. The \(\text{[H]}\)amino acid in the elution
profile was tentatively identified by its position relative to the positions of the markers.

Estimation of \(\epsilon\)-N-Acetyl-\(\epsilon\)-lysine—The amount of \(\epsilon\)-N-[\(\text{\[3H]\]}
acetyl-\(\epsilon\)-lysine in the enzymatic hydrolysates of the modified proteins was measured by inverse isotope dilution (29). \(\epsilon\)-N-Acetyl-
\(\epsilon\)-lysine (30 mg) was added to a portion of the radioactive eluate that had been obtained by chromatography of the hydrolysates on AG 50W-X4. The solution was brought to a boil, and basic
empyc carbonate was added. The copper complex was collected and decomposed with \(\text{H}\text{S}\). The \(\epsilon\)-N-[\(\text{\[3H]\}\
acetyl-\(\epsilon\)-lysine was iso-
lated by thin layer chromatography on silica gel and purified to
constant specific radioactivity by successive thin layer chroma-
tographies with three different solvents (30).

Protein and Radioactivity Measurements—Protein contents were estimated by the modified Folin method with RNAse A (type XII, Sigma) as the standard (33).

Radioactivity was determined using a Packard liquid scintilla-
tion spectrometer (model 3875). The solutions (1 ml) were
added to vials containing 15 ml of Scintisol-Complete (Isolab Inc.,
Akron, Ohio). All samples were counted in duplicate and cor-
corrected for quenching by means of an external standard.

Radiochromatograms were scanned with a Berthold thin layer
chromatography scanner (Drickmann, Westbury, N. Y.).

RESULTS

Modification of RNAse by N-Acetoxy-2-FAA—The initial reac-
tions of RNAse with N-acetoxy-2-FAA were carried out in media consisting of 0.1 m Tris-HCl (pH 7.4), 7\text{\[\mu\]} urea, and 50\% acetone. These conditions were selected so as to unfold the RNAse and to expose the amino acid residues of the protein to the ester (34). Furthermore, this concentration of acetone insured the solubility of the ester as well as that of the protein. N-Acetoxy-2-FAA and RNAse are soluble in media with an acetone content between 18
and 65\%. The molar ratio of ester to protein in these experi-
ments was 80. At the completion of the incubation the RNAse was precipitated by excess acetone, and the precipitate was found to contain 86\% of the initial protein. The precipitated protein was resolved by disc electrophoresis into three components, designated A, B, and C (Fig. 1), whereas native RNAse moved largely as a single component. The acetone-precipitable, heterogeneous RNAse is subsequently referred to as modified RNAse. Protein A had the same mobility as unreacted RNAse and accounted for
45\% of the absorbance of the electrophoretic profile. Proteins B and C were less basic than protein A and accounted for 42 and
13\%, respectively, of the total stained protein. The electro-
phoretic profiles of equal amounts of untreated RNAse and of modified RNAse (Fig. 1) indicated that proteins B and C were formed at the expense of native RNAse.

The possibility that proteins B and C were products of the
clavage of RNAse was investigated in four different experiments. First, we compared the hydrolysis of RNA by native and by mod-
ified RNAse. These measurements showed that modified RNAse had retained 96\% of the enzymatic activity of native RNAse. Second, we analyzed the supernatant liquid of the de-
proteinized reaction mixture for the presence of o-CH\(_3\)S-\([9-14]C\]2-
FAA. If the mercaptoamide were found, it would indicate that N-acetoxy-2-FAA had reacted with methionyl residues of RNAse and that the resulting sulfonium ion had decomposed spontane-
The proteins (100 µg per gel) were resolved in polyacrylamide gels as described in the text. —, RNase purified by gel chromatography on Sephadex G-25; ———, proteins precipitated by acetone from the reaction of RNase with N-acetoxy-2-FAA.

The isolation of the compound and its purification was carried out as described in the text. The figure shows the migration of the radioactivity in comparison to that of authentic 3-CH₃-S-2-FAA during the first chromatography on Silica Gel GF₂₅₄ with petroleum ether:chloroform:methanol (50:45:5) as the solvent (23). o-CH₃-S-2-FAA moves on thin layer chromatography at the same rate as 3-CH₃-S-2-FAA (6).

The concentration gradient of NaCl used is shown by -----. The eluate was collected in 5-ml fractions at a rate of 19 ml per hour, and the proteins were located by their absorbance at 280 nm.

As an alternative, we considered the possibility that the interaction of N-acetoxy-2-FAA with RNase yielded three proteins which differed only in their net positive charge. This would account for the electrophoretic separation of modified RNase into three components. If the above explanation were correct, it would also be expected that modified RNase would be resolvable by ion exchange chromatography. Accordingly, we chromatographed modified RNase on Bio-Gel CM-30 with a linear gradient of increasing NaCl concentration (36). As shown in Fig. 4, the modified RNase was fractionated into three components which appeared to be comparable in their relative charge and amounts greater than that of the 14.6% gel (35), the similarity of the patterns eliminated the possibility that proteins A, B, and C were separated on the basis of differences in molecular size. All of these data led us to conclude that the modification of the RNase that we had observed was not attributable to cleavage of peptide bonds and fragmentation of the native RNase.

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to proteins A, B, and C obtained by electrophoresis. Therefore, we retained the same designation (A, B, and C) for the three proteins resolved by ion exchange chromatography. Protein A was eluted in the same position as native RNase (Fig. 4). Proteins B and C were eluted with lower concentrations of NaCl than protein A and were therefore more acidic than protein A or RNase. It appeared very plausible from disc electrophoresis and ion exchange chromatography that protein B differed from protein A by 1 charge unit per molecule, and protein C differed from protein A by at least 2 charge units per molecule.

The conditions for the formation of proteins A, B, and C from N-acetoxy-2-FAA and RNase are summarized in Table I. The reaction of N-acetoxy-2-FAA with RNase in 0.005 M Tris-HCl + 7 M urea yielded progressively larger amounts of protein B, as the molar ratio of ester to protein was increased from 1 to 5. Protein C was formed only at the higher concentration of the ester. However, these experiments were complicated by the fact that native RNase, even after purification by gel chromatography, still contained a second protein (<5%) that was eluted in the same position as protein B and that appeared to be increased in amount by exposure of the RNase to 7 M urea (Table I). This protein was largely eliminated by chromatography of native RNase on Bio-Gel CM-30 and by omission of urea from the medium. Under these conditions, the formation of proteins B and C was demonstrated unequivocally (Experiments 2 and 3, Table I).

The separation of modified RNase into three components on the basis of charge would require that a reactive species derived from N-acetoxy-2-FAA had reacted with functional groups of the amino acids in RNase that confer a net positive charge on the protein. However, amino acid analyses indicated that the composition of proteins A, B, and C was virtually identical and the same as that of RNase A. It appeared as if the molecular species that had interacted with proteins B and C was removed during acid hydrolysis. Based on the known reactivities of N-acetoxy-2-FAA (6, 7) we considered two mechanisms as being consistent with this interpretation of the data. First, an amionic ion arising from the spontaneous decomposition of N-acetoxy-2-FAA might react with a lysine residue that formed a hydrogen bond with a carboxyl group (34). The arylamination would abolish the hydrogen bond, thereby liberating an additional carboxylate ion and decreasing the net positive charge of the protein. Alternatively, N-acetoxy-2-FAA might acetylate the ε-amino group of lysine, which would also have the effect of decreasing the positive charge on the protein. There is a precedent for the nonenzymatic transfer of acetyl groups from N-acetoxy-4-acetylaminobiphenyl and by N-acetoxy-4-acylaminothreonate (6).

In order to decide whether N-acetoxy-2-FAA modified RNase by arylamination or by acetylation we reacted the protein with N-[3H]acetoxy-[9-14C]2-FAA. The incorporation of 14C and of 3H into proteins A, B, and C was measured for the nonenzymatic transfer of acetyl groups from N-acetoxy-2-FAA (6, 7) we considered two mechanisms as being consistent with this interpretation of the data. First, an amionic ion arising from the spontaneous decomposition of N-acetoxy-2-FAA might react with a lysine residue that formed a hydrogen bond with a carboxyl group (34). The arylamination would abolish the hydrogen bond, thereby liberating an additional carboxylate ion and decreasing the net positive charge of the protein. Alternatively, N-acetoxy-2-FAA might acetylate the ε-amino group of lysine, which would also have the effect of decreasing the positive charge on the protein. There is a precedent for the nonenzymatic transfer of acetyl groups from N-acetoxy-4-acetylaminobiphenyl and by N-acetoxy-4-acylaminothreonate (6).

<table>
<thead>
<tr>
<th>Experiment no.</th>
<th>Reaction medium</th>
<th>Percent of total protein eluted from Bio-Gel CM-30 in*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>[N-acetoxy-2-FAA/RNase]</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Tris-HCl, acetone</td>
<td>95.7 4.3</td>
</tr>
<tr>
<td>2</td>
<td>Tris-HCl, acetone</td>
<td>88.7 11.3</td>
</tr>
<tr>
<td>3</td>
<td>Tris-HCl, acetone</td>
<td>79.0 21.0</td>
</tr>
<tr>
<td>4</td>
<td>Tris-HCl, acetone</td>
<td>55.0 35.1 9.4</td>
</tr>
<tr>
<td>5</td>
<td>Tris-HCl, acetone</td>
<td>97.7 2.3</td>
</tr>
<tr>
<td>6</td>
<td>Tris-HCl, acetone</td>
<td>97.6 2.2</td>
</tr>
<tr>
<td>7</td>
<td>Tris-HCl, acetone</td>
<td>47.5 ± 0.7 36.5 ± 3.8 16.0 ± 1.2</td>
</tr>
<tr>
<td>8</td>
<td>Tris-HCl, 2.4% EtOH</td>
<td>54.5 ± 13.2 35.7 ± 6.4 17.9 ± 8.7</td>
</tr>
</tbody>
</table>

* In Experiments 1 to 4, commercial RNase was purified by gel filtration on Sephadex G-25 with 0.10 M Tris-HCl (pH 7.4) as the eluent. In Experiment 1, the purified RNase was rechromatographed on Bio-Gel CM-30 without incubation. In Experiments 2 to 4, the eluate containing the purified RNase was made 7 M with respect to urea, an equal volume of acetone was added, and the mixtures were incubated as described in the text. In Experiments 3 and 4, the acetone contained the appropriate amount of N-acetoxy-2-FAA. In Experiments 5 to 8, commercial RNase was purified by chromatography on Bio-Gel CM-30 as described in the text. In Experiment 5, the purified protein was rechromatographed on Bio-Gel CM-30 without incubation. In Experiments 6 and 7, the purified protein was titrated to pH 7.4 and diluted with an equal volume of acetone, and the mixtures were incubated as described in the text. In Experiment 7, the acetone contained the appropriate amount of N-acetoxy-2-FAA. In Experiment 8, the N-acetoxy-2-FAA in 0.5 ml of ethanol was added over a period of 3 hours to 20.0 ml of a magnetically stirred solution of RNase purified by chromatography on Bio-Gel CM-30 and titrated to pH 7.4. The reaction mixture was then incubated as described in the text. At the completion of the incubations, the proteins were precipitated with acetone, and the modified RNase was chromatographed on Bio-Gel CM-30.

The designation of the isolated proteins is that shown in Fig. 4 and described in the text.

The specific radioactivities of proteins isolated from reaction of RNase with N-[3H]acetoxy-[9-14C]2-FAA.

<table>
<thead>
<tr>
<th>Experiment no.</th>
<th>Reaction medium</th>
<th>Proteins isolated</th>
<th>(atoms 3H)/(100 mole RNase)</th>
<th>(atoms 14C)/(100 mole RNase)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Tris-HCl, acetone</td>
<td>A 1.2 B 61.5 C 108.5</td>
<td>2.6 4.7 12.0</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Tris-HCl, acetone</td>
<td>A 4.4 ± 1.2 B 67.2 ± 20.0 C 113.9 ± 20.7</td>
<td>6.9 ± 2.9 10.7 ± 4.6 20.9 ± 6.6</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Tris-HCl, 2.4% EtOH</td>
<td>A 5.8 ± 1.0 B 59.0 ± 15.0 C 97.7 ± 17.7</td>
<td>11.5 ± 1.9 16.3 ± 3.0 31.9 ± 9.5</td>
<td></td>
</tr>
</tbody>
</table>

TABLE I

Formation of proteins B and C by reaction of N-acetoxy-2-FAA with RNase

TABLE II

Specific radioactivities of proteins isolated from reaction of RNase with N-[3H]acetoxy-[9-14C]2-FAA.
TABLE III

Release of [3H]acetyl groups from modified RNase by alkaline and acid hydrolysis

RNase (80 mg, 5.8 amoles) purified by chromatography on Bio-Gel UM-30 was reacted with N-[3H]acetoxy-2-FAA (8.2 mg, 29 amoles, 7.2 X 10^6 dpm) as described in the text and in Experiment 7 of Table I. The modified RNase was precipitated and hydrolyzed as indicated in the text. The [3H]acetic acid in the hydrolysate was determined by inverse isotope dilution as described in the text.

<table>
<thead>
<tr>
<th>Hydrolytic conditions</th>
<th>Protein-bound 3H</th>
<th>Steam distillate 3H</th>
<th>Fraction of bound 3H recovered as [3H]acetic acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medium</td>
<td>Time</td>
<td>Temperature</td>
<td>dpm x 10^-3</td>
</tr>
<tr>
<td>2 N NaOH</td>
<td>2</td>
<td>25°</td>
<td>50</td>
</tr>
<tr>
<td>2 N NaOH</td>
<td>18</td>
<td>25°</td>
<td>50</td>
</tr>
<tr>
<td>6 N H2SO4</td>
<td>6</td>
<td>100°</td>
<td>50</td>
</tr>
</tbody>
</table>

The column was washed with deionized water, and the neutral and acidic amino acids were chromatographed on Silica Gel GF254 (1-mm thickness) with ethanol-water (63:37) as the solvent.
The release of $^3$H-acetyl groups from modified RNase by alkaline hydrolysis indicates that N-acetoxy-2-FAA esterified hydroxylamino acids in RNase, although the particular amino acids have not been identified. O-Acetyl-l-tyrosine can be eliminated from consideration since it is deacetylated in 1 hour by $2 \times \text{NaOH}$ at 25° (40). In our experiments, only trace amounts of $^3$H-acetyl groups were obtained from modified RNase under these conditions (Table III). l-Serine and l-threonine would also be available for esterification to O-acetyl-l-serine and O-acetyl-l-threonine (34). These acetylated amino acids were not found in enzymatic hydrolysates of modified RNase despite the fact that 11% of bound $^3$H-acetyl groups were liberated from the modified protein by alkaline hydrolysis (Table III). The absence of the O-acetylated amino acids might have been due to their rearrangement to the N-acetylated derivatives at the pH maintained during enzymatic hydrolysis (16). If rearrangement had occurred, the N-acetylated compounds would have been washed through AG 50W-X4 and would have appeared in the minor radioactive fraction eluted from the resin with water (Fig. 5). Because O-acetylation of serine and threonine by N-acetoxy-2-FAA represents a relatively minor reaction in comparison to N-acetylation of lysine and because the charge properties of RNase would not be affected by O-acetylation, the identification of the products of the rearrangement, i.e., N-acetyl-l-serine and N-acetyl-l-threonine, was not further pursued.

It has been postulated that N-acetoxy-2-FAA decomposes to an arylamidonium ion through an activated ion pair in which the acetoxy group is spatially separated from the remainder of the molecule (37). It has also been shown that the rate of formation of the amidonium ion is a function of the water content of the medium (37). Our data are in agreement with these findings since alkylation of proteins B and C was increased by 50% when the reaction between N-acetoxy-2-FAA and RNase was carried out in 2.4% ethanol instead of in 50% acetone (Table II).

It has been reported that certain N-acetoxy-N-arylamides, such as N-acetoxy-4-acetylaminobiphenyl and N-acetoxy-2-acetylaminophenanthrene, acetylate, rather than arylamidate, guanosine (6). It, also, has been inferred that the acetylation proceeds through an ion pair similar to that proposed for arylation (37). However, our data indicate that acetylation of RNase by N-acetoxy-2-FAA was decreased by 11% under conditions which increased the extent of arylation by 50%. Because of the lack of correspondence between arylation and acetylation, it appears unlikely that acetylation proceeds through an activated ion pair resembling that proposed for arylation. The possibility remains to be explored whether the mechanism of the acetylation of proteins by N-acetoxy-2-FAA consists instead of a nucleophilic attack of the nitrogen of the e-amino group of lysine on the partially positively charged carbonyl carbon atom of N-acetoxy-2-FAA, as shown in Fig. 8.

Heretofore, efforts to explain the mode of action of the carcinogenic $N,O$-diacetylarylhydroxylamines and their phosphate and sulfate analogues have centered on the arylation of proteins and of nucleic acids. In this report, we present evidence that $N$-acetoxy-2-FAA is an acyl donor for proteins and that its capacity for acetylation exceeds that for arylation by several orders of magnitude. It seems possible, also, that the phosphate and sulfate analogues of $N$-acetoxy-2-FAA which are considered to be biologically active forms of $N$-hydroxy-2-FAA may phosphorylate or sulfonate, or both, proteins. If the chemical reactions underlying the action of carcinogenic esters of hydroxamic acids were the transfer of the acetyl, phosphoryl, or sulfonyl group from the ester to cellular receptors, the hydroxamic acid would be
regenerated and be available for re-esterification as indicated in Fig. 8. By a repetition of this cyclic process, a few donor molecules could modify a large number of receptors. In contrast, in modification by acetylation the hydroxamic acid is not regenerated and a cyclic process is, therefore, not operative. The limiting factor in modification by acetylation would be the amount of activated carcinogen present in the cell.

We have previously presented evidence that $N$-2-fluorenylacetamide or its activated metabolite(s) arylamidate rat liver histones at a trace level (8). On the basis of our present data, it seems possible that the histones and other nuclear proteins were extensively modified in these earlier experiments by the mechanism suggested above. There is evidence that reversible acetylation or phosphorylation, or both, of histones and acidic nuclear proteins removes the inhibition that these proteins exert on the transcriptional process (9). Further experiments are needed to determine whether $N$-acetoxy-2-FAA and related carcinogens donate acetyl, phosphoryl, or sulfonyl groups to chromosomal proteins and whether the transfer of these groups affects the control of transcription by these proteins.

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