

sample directly into a Janis dewar from room temperature to 6 K.

RESULTS AND DISCUSSION

Fig. 1 shows the absorption and fluorescence spectra of the free thionin and the thionin mixed with each of the oligonucleotides of AT and GC at room temperature. The red-shift of the absorption maxima upon interacting with AT and GC has been reported previously and has been attributed to dyenucleotide base stacking interactions by Tuite and Kelly.¹¹ Fig. 1 shows that fluorescence is quenched by a factor of ~70% upon binding with AT and greatly quenched by a factor of > 99% upon binding with GC. Such base dependent

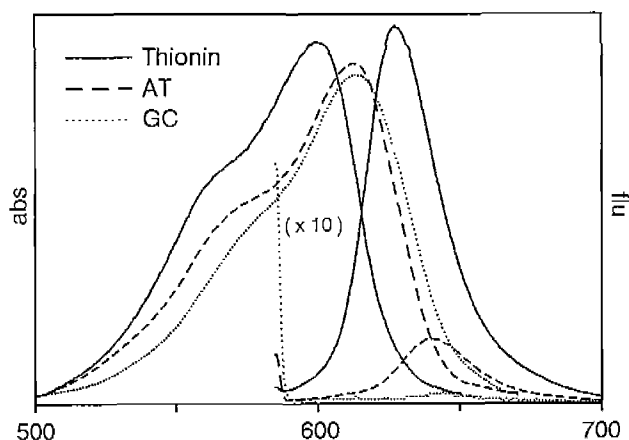


Figure 1. Absorption and fluorescence spectra of the free thionin and the thionin mixed with each of the oligonucleotides of AT and GC at room temperature. The excitation of the fluorescence is located at 585 nm.

effects has been attributed to stacking of the dye heterocycle next to a G than an A residue since G base is more polarizable, giving a larger perturbation of dye optical properties.¹⁰ The large fluorescence quench is consistent with the sandwich model for thionin intercalated in the base pairs of GC.

Fig. 2 shows the low temperature preburn and postburn SH spectra of thionin and thionin mixed with AT, GC and CT-DNA doped in Gl:H₂O glass taken at $\lambda_B \sim 600$ nm. It is found that the two absorption bands of thionin at ~613 and ~625 nm upon interacting with GC and CT-DNA. The absence of these two bands at room temperature is probably due to thermal broadening effect. The ~603 and ~617 nm bands have been assigned to the amino-form and imino-form of thionin, respectively.³ Fig. 2 shows that the relative intensity of the absorption band of the imino-form to that of the amino-form of thionin decreases appreciably upon interacting with GC and CT-DNA than with AT. Furthermore, significant reduction of the hole depths of thionin upon interacting with GC than AT implies that binding of the thionin to GC is stronger than AT.

Figs. 3a-3d show the corresponding SH spectra obtained

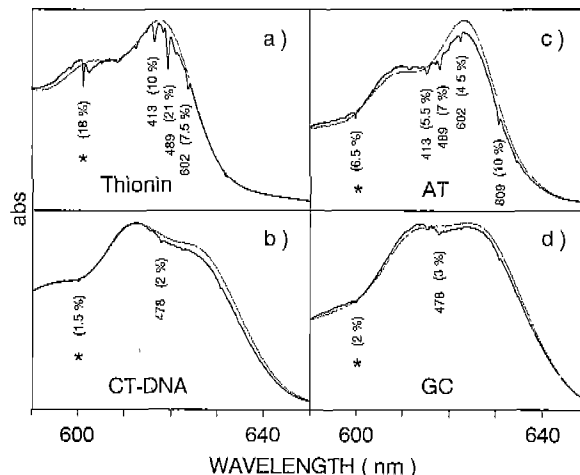


Figure 2. Preburn and postburn spectra of thionin (a) and the thionin mixed with each of the oligonucleotides of CT-DNA (b), AT (c), and GC (d) dissolved in 5:4 glycerol:water solution at $T \sim 6$ K. Prominent satellite holes with the ratios of hole depths are labelled with excited-state vibrational frequencies.

from the difference between each set of spectra in Figs. 2a-2d. It is important to observe different NRHs at 478 and 489 cm⁻¹ in Fig. 3, indicating that the appearance of 478 cm⁻¹ NRH in Figs. 3b and 3d is not due to residues of the free thionin. In addition, the occurrence of the 908 cm⁻¹ NRH in Figs. 3b-3d results from the thionin-DNA interaction since it is not observed in Fig. 3a. When the burning wavelength is tuned to 605 nm, the 809 cm⁻¹ NRH disappears in the spectrum of free thionin, but appears in the spectra of thionin upon interacting with these polynucleotides, as shown in Figs. 4a and 4d. We believe that the contribution from residues of the free thionin to the NRHs appeared in Figs. 3b-3d can be neglected.

In order to investigate the binding sites of thionin to AT, mode assignment is required for comparing the relative changes of the hole depths. In our previous study,³ the normal mode calculations suggested that the (478, 798) and (489,

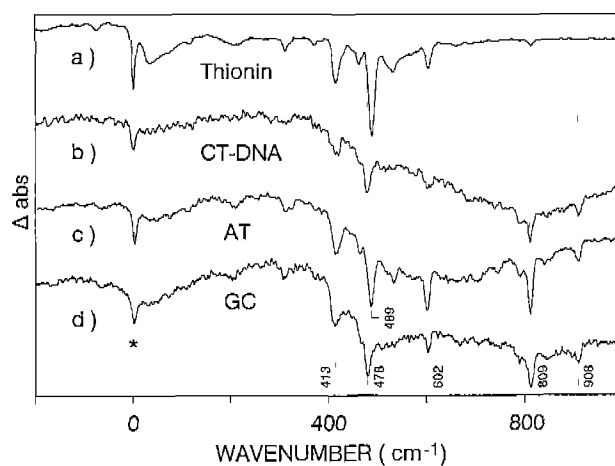


Figure 3. The corresponding SH spectra obtained from the difference between each set of spectra in Figs. 2a-2d.

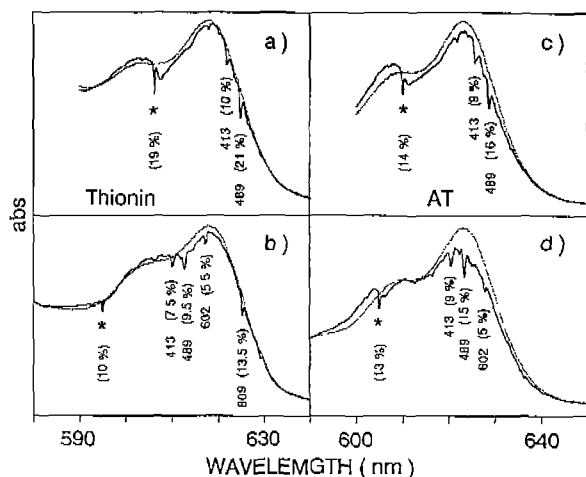


Figure 4. Preburn and postburn spectra of thionin taken at $\lambda_B \sim 605$ nm (a) and $\lambda_B \sim 595$ nm (b) and the thionin mixed with AT taken at $\lambda_B \sim 610$ nm (c), and $\lambda_B \sim 605$ nm (d) at $T \sim 6$ K. Prominent satellite holes with the ratios of hole depths are labelled with excited-state vibrational frequencies.

809) cm^{-1} NRHs are due to the inner ring motion of the amino-form and the imino-form of thionin, respectively. The 602 cm^{-1} NRH is related to ring skeleton motion. Deuteration of the amino group was conducted to distinguish the amino group from ring moiety. Our SH results showed that the 413 cm^{-1} NRH disappears but the 388 cm^{-1} NRH appears upon deuteration (data not shown). Normal mode calculation and deuteration study allow us to assign the 413 cm^{-1} NRH to NH_2 motion of the amino-form.

Since the absorption spectrum contains at least two absorption components, only a qualitative comparison of the reduction of the hole depths is given. Considering the red side of the absorption spectrum is less complicated than the blue side of the absorption spectrum, Fig. 4 shows preburn and postburn spectra taken at $\lambda_B \sim 605$ and ~ 595 nm for free thionin and $\lambda_B \sim 610$ and ~ 605 nm for thionin mixed with AT. Since the 478 and 798 cm^{-1} NRHs are not observed at red side of the absorption spectrum, we compare relative changes of the hole depths among the 413, 602, 489 and 809 cm^{-1} NRHs upon interacting with AT. Taking into account the ~ 5 nm red-shift of the absorption band upon interacting with AT, the SH spectrum taken at $\lambda_B \sim 600$ nm for free thionin is compared to the spectrum taken at $\lambda_B \sim 605$ nm for thionin interacting with AT. Figs. 2 and 4 show that the hole depths of 489 and 809 cm^{-1} related to the imino-form are reduced to a similar ratio of ~ 0.7 . In addition, the hole depth of 602 cm^{-1} related to the amino-form is also reduced to a similar ratio of ~ 0.7 . However, the hole depth of 413 cm^{-1} NRH slightly decreases about 10%. The less reduction of the 413 cm^{-1} NRH indicates that the hydrogen bonding between the exocyclic NH_2 mode of thionin and the OH mode of matrix is less perturbed upon interacting with AT. It further implies that a direct hydrogen bond formed between the amino group of thionin and the phosphate group of DNA is unlikely. However, an indirect hydrogen bonding *via* water between

them cannot be eliminated.

Although the comparison of the hole depths of NRHs upon interacting with GC and CT-DNA is more difficult, the hole depths of the 478 and 489 cm^{-1} NRHs are found to be $\sim 2\%$ and $\sim 1.5\%$ upon interacting with CT-DNA, respectively. Thus, we consider that the binding affinity for the tautomers are similar to both polynucleotides.

The lack of shift in hole frequency implies that the interaction between thionin and these polynucleotides is not dramatic in the bound form compared to the BODIPY-oligonucleotide interactions.^{7,8} However, it is consistent with the intercalation model since the frequency of the in-plane vibrational modes of chromophore is less shifted by the stacking between the ring moiety of dye molecule and the DNA base pairs. Although our spectral results suggest similar binding affinity for the two tautomers of thionin to GC, different binding geometries can occur because of their different dipole moments.³ In addition, we suspect that the amino-form of thionin is partially intercalated with AT or external stacking with AT because of the steric hindrance from the backbone in the minor groove and the methyl group of thymine in the major groove of the B-form DNA structure. The binding site appears to be from the major groove of AT because of the less perturbation on the exocyclic amino group. However, the imino-form can intrude into the base pairs AT with the long axis at certain orientation to the axis of nucleic acids.

In summary, we have demonstrated that two tautomers of thionin exist upon interacting with these polynucleotides. Our results suggest that the binding affinities of these two tautomers are similar to each polynucleotide. Significant reduction of the hole depths upon interacting with GC than AT suggests that either the optical properties of thionin is more perturbed or the thionin molecule is more isolated from the matrix by GC than AT. In addition, we have shown that the exocyclic amino group is less perturbed by AT. Circular dichroism may be useful to probe the details of binding geometries between two tautomers of thionin and these polynucleotides.

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