CD Measurements Show That fd and IKe Gene 5 Proteins Undergo Minimal Conformational Changes upon Binding to Poly(rA)†

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ABSTRACT: Circular dichroism (CD) measurements were made on both fd and IKe gene 5 proteins in solution. The difference between the CD spectra of these two proteins was interpreted as being the result of an enhanced tyrosine contribution in the IKe gene 5 protein spectrum. There was no spectral evidence for significant α-helical structures in either of the two gene 5 proteins. CD measurements were also made on complexes of the two gene 5 proteins with poly(rA). The long-wavelength region (300–250 nm) of the CD spectra of both complexes was essentially like that of free poly(rA) at a high temperature. With the assumption that the poly(rA) components of the complexes had the same CD at all wavelengths as did free poly(rA) at a high temperature, it was possible to separate the CD spectra of the complexes into protein and nucleic acid components. Except for the tyrosine CD band at 229 nm, there were no significant changes in the CD bands of either protein upon binding to poly(rA). Thus, each protein appeared to maintain essentially the same overall secondary conformation when complexed with poly(rA) as when in its free state.

In living cells, protein–nucleic acid interactions play fundamental roles in the regulation of gene replication and expression. The G5P[1] from the F-plasmid-specific filamentous phage fd has been extensively studied as a defined system to elucidate the structural basis for protein interactions with single-stranded nucleic acids (Kowalczykowski et al., 1981). The fd G5P binds strongly and cooperatively to single-stranded nucleic acids (Bulsink et al., 1985). The accumulation of this protein in infected cells initiates synthesis of single-stranded viral DNA (Salstrom & Pratt, 1971; Van Drop et al., 1979). Additionally, fd G5P translationally controls the intracellular concentrations of gene 2 and gene 10 proteins by binding to their mRNAs (Model et al., 1982; Yen & Webster, 1982). Finally, the fd G5P forms an intracellular complex with nascent phage single-stranded DNA molecules prior to their maturation into phage particles coated by the gene 8 protein and other minor proteins (Rasched & Oberer, 1986).

Recently, another single-stranded DNA binding protein was isolated from phage IKe-infected *Escherichia coli* cells and was shown to be encoded by gene 5 of the phage (Peeters et al., 1983, 1985). IKe phage, an N-plasmid-specific filamentous phage, exhibits a life cycle similar to that of fd phage (Khatoon et al., 1972). IKe G5P, like fd G5P, binds strongly and cooperatively to single-stranded DNA (de Jong et al., 1987a). A 58% homology in the gene nucleotide sequences suggests that the fd and IKe G5Ps are evolutionarily related (Peeters et al., 1983). The fd G5P consists of 87 amino acid residues, 1 less residue than is in the IKe G5P. There are 39 amino acid residues located at identical positions in both proteins if Gln-21 of the IKe protein is considered to be the extra residue (Peeters et al., 1983).

In solution, fd G5P exists predominantly as a dimer (Cavalieri et al., 1976). Crystallographic data reveal that fd G5P is composed almost entirely (>80%) of β-structure with no α-helix (Brayer & McPherson, 1983). Brayer and McPherson (1983) suggest that the overall fd G5P dimer structure would not significantly change upon binding to DNA because of the degree of monomer–monomer overlap and rigidity of the hydrophobic core in the free G5P dimer structure. The IKe G5P structure predicted from the protein sequence (Peeters et al., 1983) or by modeling procedures (Brayer, 1987) corresponds well with the 3-dimensional structure of fd G5P deduced from X-ray crystallography.

To compare the IKe G5P conformation in solution with that for fd G5P, we have investigated the CD spectra of both proteins. More importantly, the secondary conformational changes of fd and IKe G5Ps upon complex formation have not been previously characterized. This has been difficult to do by CD measurements because of the overlapping spectral contributions of the protein and nucleic acid in complexes. Moreover, Kansy et al. (1986) found that DNAs complexed with fd G5P generally have induced CD spectra that do not clearly correspond to spectra of free states of the nucleic acids; this is true for complexed fd DNA, poly(dA), poly(dT), and poly[d(A-T)]. While complexed poly(dI) and poly(dC) have CD characteristics of single-stranded polymers, the CD band above 250 nm is only slightly changed in the case of poly(dI) and is red-shifted in the case of poly(dC). On the other hand, poly(rA) complexed with either the fd or IKe gene 5 protein has a CD spectrum above 250 nm that is clearly like that of the polymer at a high temperature, which provides an exceptional opportunity for spectral analysis. As shown below, the overlapping CD contributions of the protein and poly(rA) in the complexes were separable on the basis of one simple assumption. This allowed us to determine the CD spectra of

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[1] Abbreviations: CD, circular dichroism; G5P, gene 5 protein.

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the complexed proteins for comparison with the spectra of the free proteins.

Materials and Methods

Fd G5P and IKe G5P were isolated and purified as previously described (Sang & Gray, 1987). Protein concentrations were determined from absorption measurements with the extinction coefficient of 0.73 $mg^{-1}\cdot cm^2$ at 276 nm (Day, 1973). Poly(rA) was purchased from Sigma Chemical Co. An extinction coefficient of 10000 $L\cdot mol^{-1}\cdot cm^{-1}$ at 258 nm (Riley et al., 1966) was used to determine poly(rA) concentrations.

Absorption spectra were measured by using a Cary Model 118 spectrophotometer. CD spectra were obtained by using a Jasco Model J500A instrument calibrated with *d*-10-camphorsulfonic acid (Aldrich Chemical Co.) to give a value within 2% of 0.336° ellipticity at 290.5 nm for a 0.1% (w/v) solution (Chen & Yang, 1977). The ratio of the magnitudes of the peaks at 192.5 and 290.5 nm was −2.05 ± 0.03. CD spectra over the range 300–240 nm were measured in a 1 cm path length cell with instrument settings of 1-nm spectral band width, 1-s time constant, and 10 nm/min scan speed. CD spectra from 250 to 190 nm were measured in a 0.1 cm path length cell with an increased time constant of 4 s and a reduced scan speed of 1 nm/min. Digitized data were obtained every 0.1 nm with a Jasco DP-500N data processor. The data were smoothed twice by a sliding 7 point third-order polynomial, and every 10th point was transferred to a Hewlett-Packard 9816S computer. The data were then smoothed by a sliding 13-point quadratic-cubic function (Savitzky & Golay, 1964). CD spectra were plotted as $\epsilon_L - \epsilon_R$ in units of $L\cdot mol^{-1}\cdot cm^{-1}$. Sample temperatures were maintained within ±0.2 °C with an accuracy of ±0.5 °C.

Titrations of poly(rA) with the G5Ps were conducted as previously reported for other polymers (Kansy et al., 1986). The buffer used for experiments with the fd G5P was 2 mM sodium phosphate, pH 7.0. Since the IKe G5P precipitated under these conditions, the buffer for experiments with the IKe G5P was 25 mM sodium phosphate and 25 mM NaF, pH 6.4; the higher salt concentration combined with a lower pH prevented protein aggregation.

Curve-fitting analysis was performed by using a program written by Dr. F. S. Allen (University of New Mexico, Albuquerque). This program uses linear programming techniques to fit measured protein CD spectra with a set of reference spectra. The fractions of the reference spectra used for the fit were constrained to be positive but were not required to sum to 1.0. The reference spectra were those derived by Chang et al. (1978) for α-helix, β-sheet, β-turns, and random components of globular proteins. In addition, we used the CD spectrum of *N*-acetyl-L-tyrosinamide (Shiraki, 1969) to account for the large Tyr bands of both G5Ps. Spectra were fitted over the range 240–190 nm at 2-nm intervals. A spectral fit standard deviation, σ, was obtained from the differences between the measured CD values $[\Delta\epsilon(\lambda)_{meas}]$ and the calculated CD values $[\Delta\epsilon(\lambda)_{calc}]$ at N wavelengths:

$$\sigma = [\sum(\Delta\epsilon(\lambda)_{meas} - \Delta\epsilon(\lambda)_{calc})^2/(N-1)]^{0.5}$$

The spectral contribution of poly(rA) to the CD spectra of each of the protein–poly(rA) complexes over the full wavelength range 300–190 nm relied on an analysis of the spectra above 250 nm, where the proteins had a negligible CD contribution. First, six spectra A_i were obtained for free poly(rA) at temperatures of 0, 20, 50, 60, 70, and 80 °C over the range 300–190 nm:

$$A_i(300\text{–}190) \qquad i = 1\text{–}6 \tag{1}$$

Second, six orthogonal basis vectors B_j were derived from the A_i spectra over the truncated range 300–250 nm by using the singular value decomposition method (Lloyd, 1969; Compton & Johnson, 1986). Three of these were determined to be sufficient to fit the set of poly(rA) spectra over this range. Each of these three significant basis vectors could be expressed as a function of the poly(rA) spectra with factors f_{ji}:

$$B_j(300\text{–}250) = \sum_{i=1}^{6} f_{ji}A_i(300\text{–}250) \qquad j = 1\text{–}3 \tag{2}$$

Then, the spectrum of a G5P·poly(rA) complex (spectrum U) was fitted with the basis vectors (B_j) as described by Johnson (1988) to obtain the factors h_j:

$$U(300\text{–}250) = \sum_{j=1}^{3} h_jB_j(300\text{–}250) \tag{3}$$

By combining eq 2 and 3, the spectrum of the complex could be expressed in terms of the original six poly(rA) spectra (A_i) over the range 300–250 nm:

$$U(300\text{–}250) = \sum_{j=1}^{3} h_j \sum_{i=1}^{6} f_{ji}A_i(300\text{–}250) = \sum_{i=1}^{6}(\sum_{j=1}^{3} h_jf_{ij})A_i(300\text{–}250) \tag{4}$$

As will be shown, the spectra of the complexes above 250 nm were closely fitted by the poly(rA) spectra. Finally, the fractions of A_i obtained from eq 4 (i.e., $\sum_{j=1}^{3} h_jf_{ij}$) were used to calculate the poly(rA) spectral component over the entire 300–190-nm wavelength range

$$A_{calc}(300\text{–}190) = \sum_{i=1}^{6} K_iA_i(300\text{–}190) \tag{5}$$

where $K_i = \sum_{j=1}^{3} h_jf_{ij}$. The G5P spectral component was then obtained [for each G5P·poly(rA) complex] by subtracting the poly(rA) spectral component, $A_{calc}(300\text{–}190)$, from the spectrum of the complex, $U(300\text{–}190)$.

Results and Discussion

Conformations of Free fd and IKe G5P. To compare IKe G5P with the well-studied fd G5P, CD spectra of the two free G5Ps were measured down to 188 nm and are shown in Figure 1. Both fd and IKe G5Ps had two positive CD bands at 229 and 201 nm and a negative CD band at about 190 nm. Neither protein had significant CD bands above 250 nm on the scale shown. Even with a similar predicted secondary structure from amino acid sequences (Peters et al., 1983), the two proteins still showed differences in their CD spectra. The spectrum of fd G5P had a negative CD band between 219 and 207 nm, while the spectrum of IKe G5P was positive in the same wavelength region. Also, the CD band at 201 nm was almost twice as large for IKe G5P compared with that for fd G5P. The 228- and 201-nm bands in the CD spectra of the fd G5P have been assigned to one or more tyrosine residues (Day, 1973), of which the proteins each have five. The tyrosine CD bands were actually the most dominant feature of the spectrum of the IKe G5P, since the shape of this spectrum was almost identical with that of *N*-acetyl-L-tyrosinamide (Shiraki, 1969).

We fitted the CD spectra of fd and IKe G5Ps with the reference spectra derived by Chang et al. (1978) for the secondary structure of globular proteins. In a second set of analyses, we added the spectrum of *N*-acetyl-L-tyrosinamide (Shiraki, 1969) to the reference spectra. In agreement with the results reported by Day (1973), inclusion of a tyrosine component improved the fit to the spectrum of the fd G5P (σ was reduced from 0.32 to 0.23 $L\cdot mol^{-1}\cdot cm^{-1}$). The improve-

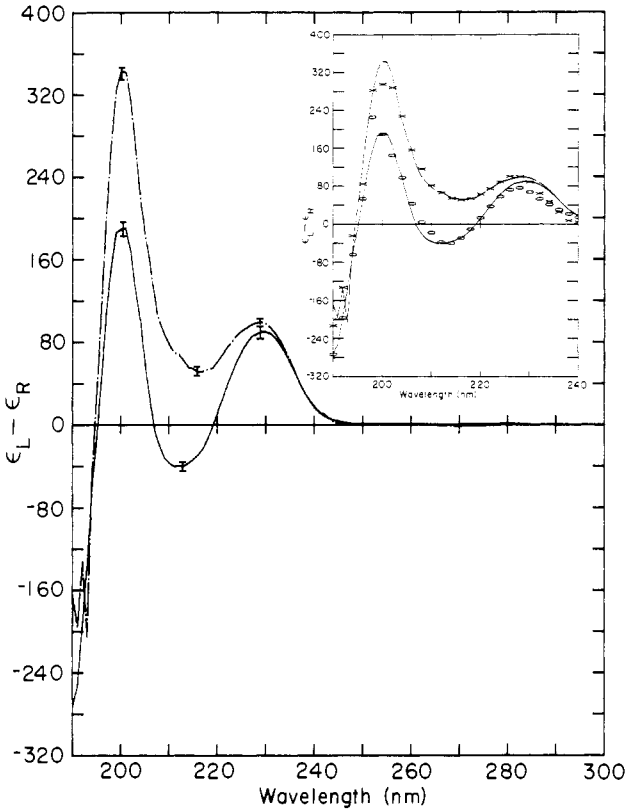

FIGURE 1: Measured CD spectra of fd G5P in 2 mM sodium phosphate, pH 7.0 (—), and IKe G5P in 25 mM sodium phosphate with 25 mM NaF, pH 6.4 (-·-), both at 20 °C. Error bars indicate the range of two measurements. (Inset) Spectral fits to the measured CD spectra of fd G5P (—) and IKe G5P (-·-) using the reference spectra from Chang et al. (1978) plus the spectrum of *N*-acetyl-L-tyrosinamide (Shiraki, 1969); fits to spectra of fd G5P (O) and IKe G5P (×).

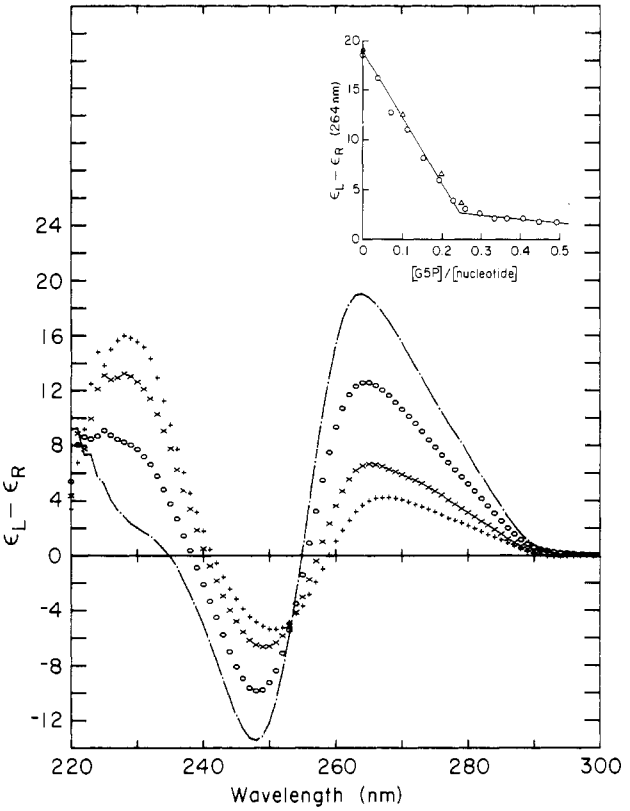

FIGURE 2: CD titration of poly(rA) with fd G5P. Free poly(rA) (-·-) and poly(rA) with added fd G5P to give [protein]/[nucleotide] ratios of 0.10 (O), 0.20 (×), and 0.25 (+). The buffer was 2 mM sodium phosphate, pH 7.0. (Inset) CD at 264 nm versus the molar ratio of G5P to nucleotide.

ment was even greater for the IKe G5P, for which σ was reduced from 1.13 to 0.23 L·mol^{-1}·cm^{-1}, a consequence of the fact that the tyrosine 201-nm band was more prominent in the IKe G5P spectrum than in the fd G5P spectrum. The better fits, with the inclusion of the tyrosine component, are shown in the inset to Figure 1.

Fractions of various protein secondary structures cannot generally be determined from a CD spectral analysis down to 190 nm, the exception being the α-helical secondary structure (Hennessey & Johnson, 1981; Woody, 1985; Yang et al., 1986). For both the fd and IKe G5Ps, the fraction of α-helix was 0.00 for the fits shown in the inset to Figure 1. Since the spectrum of an α-helix is large and unique, the absence of an α-helix component in the G5P spectra was probably significant, although there were large contributions to the G5P spectra from tyrosine and the sums of the fractions of the components were much less than 1.0 ($\sum f_i = 0.59$ and 0.29 for fd and IKe G5Ps, respectively). The absence of an α-helix component in the fd G5P spectrum was in agreement with the G5P secondary structure as determined from X-ray crystallography, which showed that the crystallized protein is predominantly a β-structure with no α-helix (Brayer & McPherson, 1983).

Changes in the Poly(rA) and G5P CD Spectra upon Complex Formation. CD changes upon titration of poly(rA) with fd G5P or IKe G5P are shown in Figures 2 and 3, respectively. The large positive CD band at 264 nm due to poly(rA) decreased as the molar ratio of protein to poly(rA) increased. Also, the negative 248-nm band decreased, the crossover at 255 nm shifted to longer wavelengths, and the 229-nm CD increased, the effects below 250 nm being at least partly due to the G5P added during the titration. These CD changes upon forming the fd G5P·poly(rA) complex have been reported previously by Anderson et al. (1975). The protein-induced changes in the CD of poly(rA) above 250 nm were essentially identical with the CD changes observed upon heating poly(rA) (Figure 4).

Titration plots showing the CD changes at 264 nm as a function of [G5P]/[nucleotide] ratio are shown as insets in Figures 2 and 3. The titrations of poly(rA) were linear up to a break point at a [G5P]/[nucleotide] ratio of 0.25 in the case of fd G5P titrations and of 0.20 in the case of IKe G5P titrations. Since small CD changes continued to occur at higher protein concentrations, the actual stoichiometries of binding to poly(rA) could not be determined with certainty from these data. The fd G5P first binds to DNA polymers in an $n = 4$ mode at low salt concentrations (Kansy et al., 1986). It seems likely that the fd G5P binds to poly(rA) in a predominantly $n = 4$ mode up to the break point. IKe G5P also binds to poly(rA) with an $n = 4$ stoichiometry at salt concentrations below 0.75 M NaCl (KCl) (de Jong et al., 1987a). For the present study, we simply wished to determine the [G5P]/[nucleotide] ratio that would give us the maximum CD changes for each complex and still be within the primary binding mode. Therefore, G5P·poly(rA) complexes were prepared for the CD analysis by adding G5P to poly(rA) solutions to give molar [G5P]/[nucleotide] ratios of 0.25 for the fd G5P·poly(rA) complex and of 0.18 for the IKe G5P·poly(rA) complex.

The long-wavelength CD region (>250 nm) of both complexes (Figures 2 and 3) compared with the CD of heated poly(rA) (Figure 4) showed that the poly(rA) in the complexes was similar to free poly(rA) at high temperatures. To make an exact comparison, the singular value decomposition method was applied to determine an orthogonal set of basis vectors

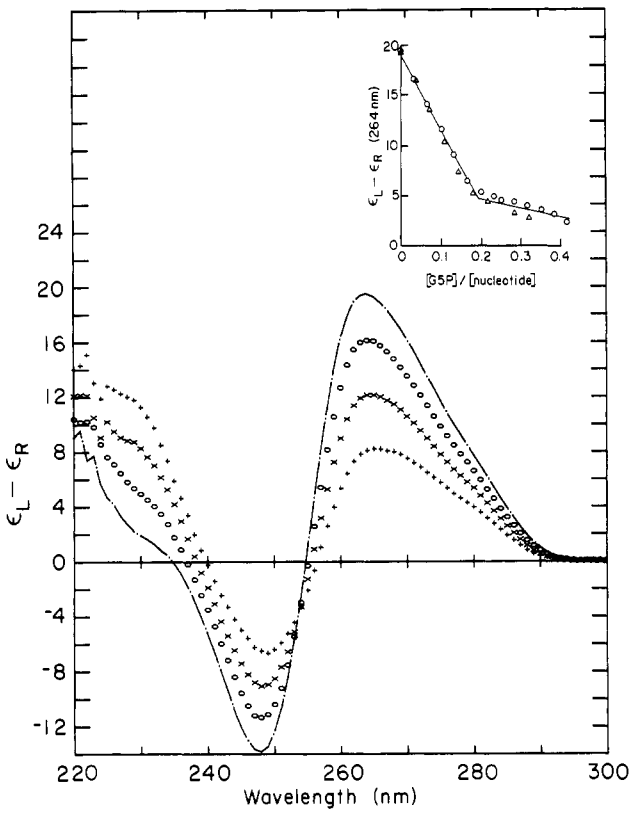

FIGURE 3: CD titration of poly(rA) with IKe G5P. Free poly(rA) (-·-) and poly(rA) with added IKe G5P to give [protein]/[nucleotide] ratios of 0.05 (O), 0.10 (×), and 0.15 (+). The buffer was 25 mM sodium phosphate with 25 mM NaF, pH 6.4. (Inset) CD at 264 nm versus the molar ratio of G5P to nucleotide.

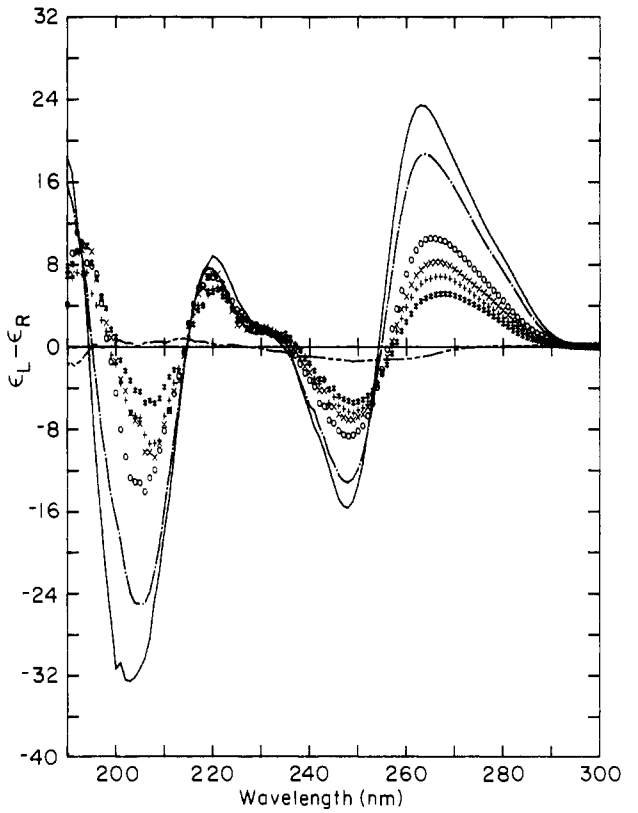

FIGURE 4: CD spectra of poly(rA) in 2 mM sodium phosphate, pH 7.0, at different temperatures: 0 °C (—); 20 °C (-·-); 50 °C (O); 60 °C (×); 70 °C (+); 80 °C (*). Also included is the CD spectrum of 3′-rAMP at 0 °C (- - -) in 10 mM sodium phosphate and 0.1 M NaF, pH 7.0 (provided by K. H. Johnson, The University of Texas at Dallas).

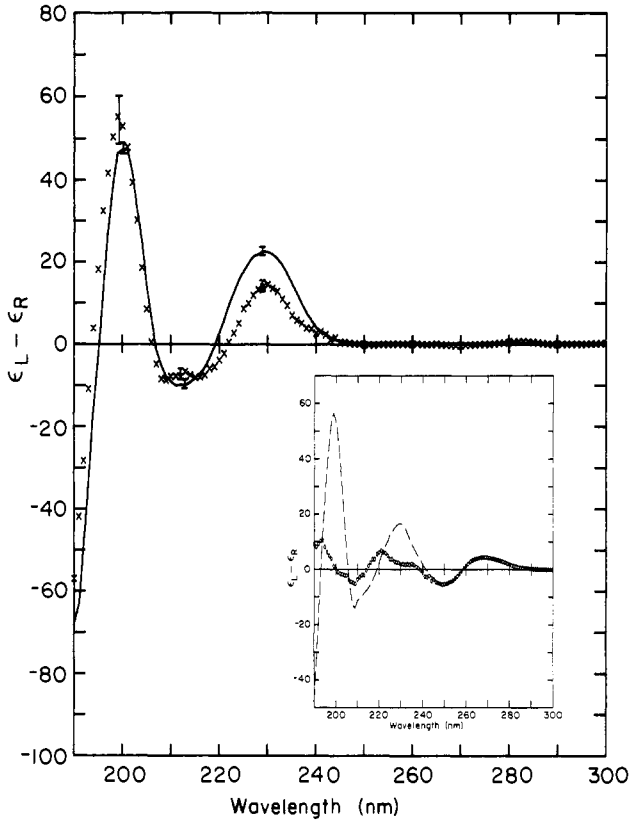

FIGURE 5: Comparison of the CD spectrum of free fd G5P (—) and the spectral component of poly(rA)-bound fd G5P (×) obtained from the spectrum of the fd G5P·poly(rA) complex by subtracting the poly(rA) component. The error bars indicate the range of three measurements. (Inset) Spectrum of the fd G5P·poly(rA) complex (- - -) and the component poly(rA) spectrum (O) obtained by fitting the region above 250 nm.

(over a truncated range of 300–250 nm) from the set of poly(rA) spectra at different temperatures shown in Figure 4. We determined that three basis vectors were needed to reconstitute all the poly(rA) spectra obtained from 0 to 80 °C, to within the error of measurement. These basis vectors were then fitted to the spectra above 250 nm of the fd G5P·poly(rA) and IKe G5P·poly(rA) complexes. Thus, as explained under Materials and Methods, we obtained factors by which the poly(rA) spectra could be multiplied to fit the spectra of the complexes above 250 nm. The insets to Figures 5 and 6 show the measured CD spectra of the fd G5P·poly(rA) and IKe G5P·poly(rA) complexes together with the fitted poly(rA) spectral components.

It can be seen that the spectra of poly(rA) at high temperatures adequately described the 300–250-nm region of the CD spectra of the two protein-poly(rA) complexes. Therefore, the observed change in the long-wavelength CD band (>250 nm) when a complex was formed between poly(rA) and either protein was mainly due to a change in the poly(rA) conformation. This was in agreement with previous studies of the CD changes upon binding of fd G5P to single-stranded DNA polymers that led to the conclusion that there was no significant CD above 250 nm arising from an induced optical activity of the protein aromatic residues during complex formation (Kansy et al., 1986).

The present work also provided a clear indication that the state of G5P-bound poly(rA) was optically similar to that of poly(rA) unstacked by heating. This differed from the cases of most complexes formed between fd G5P and DNA polymers, which show CD changes during complexation that are generally more complicated than those ascribed to simple base

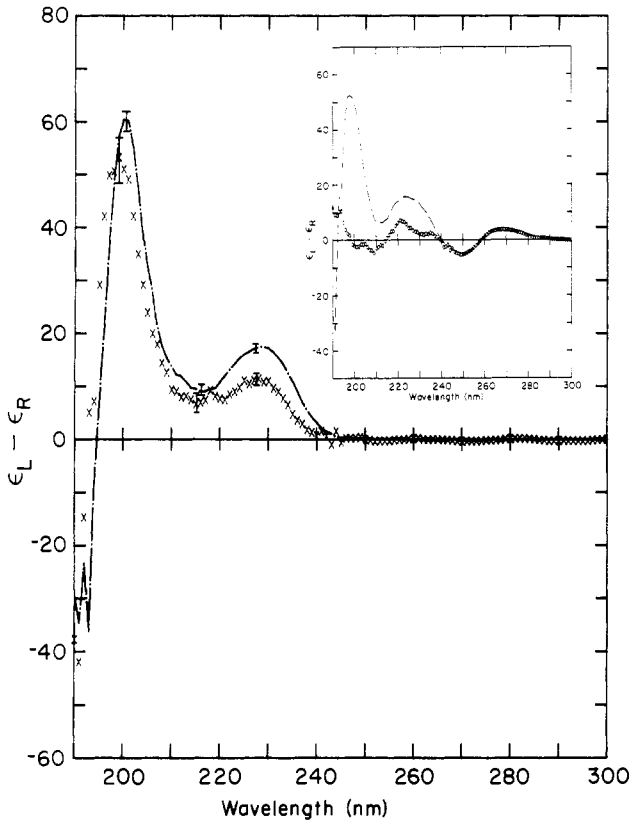

FIGURE 6: Comparison of the CD spectrum of free IKe G5P (-·-) and the spectral component of poly(rA)-bound IKe G5P (×) obtained from the spectrum of the IKe G5P·poly(rA) complex by subtracting the poly(rA) component. The error bars indicate the range of two measurements. (Inset) Spectrum of the IKe G5P·poly(rA) complex (---) and the component poly(rA) spectrum (○) obtained by fitting the region aboove 250 nm.

unstacking (Kansy et al., 1986). We estimated that the magnitudes of the poly(rA) CD at 264 nm in the fd G5P·poly(rA) and IKe G5P·poly(rA) complexes prepared for this study were equivalent to those of free poly(rA) at approximately 88 and 87 °C, respectively. The CD spectra of free poly(rA) at these temperatures or for poly(rA) bound to either G5P at 20 °C were definitely different from that of the 3′-rAMP monomer at 0 °C, shown in Figure 4. Thus, neighboring nucleotides in the G5P·poly(rA) complexes retained significant residual interaction with each other, as in the polymer at high temperature. In previous work (Kansy et al., 1986), we observed that poly[d(T)] actually became hypochromic when a complex was formed with fd G5P, in agreement with the notion that there is interaction among the bases in the binding site.

Given that the CD spectra of the complexes above 250 nm could be modeled by the CD spectra of poly(rA) at high temperatures, we assumed that the CD component of poly(rA) in the spectrum of a given complex below 250 nm was simply an extension of the poly(rA) component found above 250 nm. We thus obtained an apparent poly(rA) contribution to the region below 250 nm by multiplying the free poly(rA) spectra over the entire 190–300-nm range by the same factors that were derived to fit the region above 250 nm. The poly(rA) components of the spectra of the two complexes are shown in the insets to Figures 5 and 6 along with the spectra of the respective complexes. The differences, attributed to the protein components, are shown in the main panels of Figures 5 and 6, where they are compared with the CD spectra of free fd and IKe G5Ps. Except for differences in the 229-nm band of both proteins, which can be ascribed to changes in the optical activity of one or more tyrosines, the CD components of the proteins in the complexes were not significantly different from the CD spectra of the free proteins. This not only affirms the soundness of the above assumption but the comparisons in Figures 5 and 6 provide the first strong evidence that the G5Ps do not undergo substantial changes in secondary conformation upon binding to a nucleic acid.

The 229-nm tyrosine CD bands of fd and IKe G5Ps decreased by 34–35% in magnitude when the proteins were complexed with poly(rA), compared with these bands for the free G5Ps. These similar reductions of the tyrosine bands were consistent with the fact that the positions of all five tyrosines are conserved between the two protein sequences (Peeters et al., 1983). The tyrosine CD band of fd G5P is reduced 26–43% by binding of the protein to various single-stranded DNAs (Kansy et al., 1986). Since the binding of fd G5P to a short oligodeoxyribonucleotide $d(A)_7$ shows no change in the 229-nm CD band, the decrease of this band upon binding to DNA polymers has been suggested to arise from protein–protein interactions (Gray et al., 1984; Kansy et al., 1986). Cann (1972) has shown that the 230-nm tyrosyl CD band in *N*-acetyl-L-tyrosinamide decreases as the solvent changes from H_2O to 100% dioxane. When fd G5P cooperatively interacts with nucleic acid polymers, a tyrosine engaged in protein–protein contacts may shift to a nonpolar environment and cause the 229-nm band to decrease. A specific tyrosine that might be involved in cooperative binding is Tyr-41, according to NMR studies (King & Coleman, 1988).

CONCLUSION

The present work demonstrates that the residual neighboring base–base interactions in fd or IKe G5P-bound poly(rA) are similar to those in free poly(rA) at a high temperature. This is not inconsistent with Raman spectra that indicate that the poly(rA) sugar–phosphate backbone structural changes induced by fd G5P binding are slightly different from those induced by heating (Otto et al., 1987), since CD measurements are sensitive mainly to interactions between the base chromophores. The similarity we find in the poly(rA) structures in complexes with the two proteins is consistent with the evidence from NMR studies that the DNA binding grooves of the two G5Ps may be almost identical (de Jong et al., 1987b, 1989; Dick et al., 1989). Also, it has been shown by electron microscopy that the two G5Ps form indistinguishable left-handed helical structures with fd DNA (Gray, 1989).

Since the optical activity of poly(rA) is that of a right-handed helix in solution (Bush & Tinoco, 1967; Moore & Williams, 1986) and since there is residual interaction of neighboring bases in the G5P·poly(rA) complexes, as shown by the CD above 250 nm (Figures 5 and 6), the CD and electron microscopy results may be reconciled if only a small fraction of the bases are stacked in a right-handed conformation within the overall left-handed helical structures formed by both DNA·G5P complexes. An alternative possibility is that complexes formed with fd DNA differ in helical sense from those formed with poly(rA).

The CD spectra of both proteins are influenced by the optical activity of tyrosine and have no apparent contribution from an α-helical structure. The tyrosine contribution below 220 nm was much larger in the case of the IKe G5P, although both proteins had 229-nm tyrosine bands that were similar in magnitude and similar in the reduction in magnitude that occurred upon binding to poly(rA). Other than an effect on this tyrosine CD band, the CD measurements provided evidence that neither fd nor IKe G5P has a significantly altered secondary conformation upon complex formation with poly-

(rA). Because of the compact dimer unit of free fd G5P, it has been proposed that no significant structural changes can occur upon binding to DNA (Brayer & McPherson, 1983). A β-ribbon containing residues 15–32 may move like a clamp during DNA binding (Brayer & McPherson, 1984; King & Coleman, 1988); however, such a change would not be detected by CD measurements unless it also involved significant changes in the fractions of the various types of protein secondary structure.

Thus, our CD data support the notation from model binding (Brayer, 1987), electron microscopy (Gray, 1989), fluorescence (Peeters et al., 1983), and NMR studies (de Jong et al., 1987b, 1989) that the homologous IKe and fd G5Ps are similar in their structures and, in particular, have similar nucleic acid binding sites.

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Registry No. Poly(rA), 24937-83-5.

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