2-Aminopurine as a fluorescent probe for DNA base flipping by methyltransferases

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ABSTRACT

DNA base flipping, which was first observed for the C5-cytosine DNA methyltransferase \textit{M}\textsubscript{Hha}I, results in a complete removal of the stacking interactions between the target base and its neighbouring bases. We have investigated whether duplex oligodeoxynucleotides containing the fluorescent base analogue 2-aminopurine can be used to sense DNA base flipping. Using \textit{M}\textsubscript{Hha}I as a paradigm for a base flipping enzyme, we find that the fluorescence intensity of duplex oligodeoxynucleotides containing 2-aminopurine at the target site is dramatically enhanced (54-fold) in the presence of \textit{M}\textsubscript{Hha}I. Duplex oligodeoxynucleotides containing 2-aminopurine adjacent to the target cytosine show little fluorescence increase upon addition of \textit{M}\textsubscript{Hha}I. These results clearly demonstrate that duplex oligodeoxynucleotides containing 2-aminopurine at the target site can serve as fluorescence probes for base flipping. Another enzyme hypothesized to use a base flipping mechanism is the N6-adenine DNA methyltransferase \textit{M}\textsubscript{Taq}I. Addition of \textit{M}\textsubscript{Taq}I to duplex oligodeoxynucleotides bearing 2-aminopurine at the target position, also results in a strongly enhanced fluorescence (13-fold), whereas addition to duplex oligodeoxynucleotides containing 2-aminopurine at the 3′- or 5′-neighbouring position leads only to small fluorescence increases. These results give the first experimental evidence that the adenine-specific DNA methyltransferase \textit{M}\textsubscript{Taq}I also flips its target base.

INTRODUCTION

Specific binding of proteins to DNA often leads to drastic conformational changes in the DNA structure. Proteins can bend, kink, unwind and melt the DNA or can flip out a whole base (nucleotide) from the double helix. Base flipping was initially observed by X-ray crystallography for the C5-cytosine DNA methyltransferase from \textit{Haemophilus haemolyticus} (\textit{M}\textsubscript{Hha}I) (1). Subsequently, a second C5-cytosine DNA methyltransferase, \textit{Haemophilus aegypticus} (\textit{M}\textsubscript{Hae}III) (2), the thymidine glycosylase (3), uracil-DNA glycosylase (4) were seen to use a base flipping mechanism. In each instance, base flipping appears to be necessary to bring the active site amino acid residues in close proximity to the target deoxynucleotide.

A similar example is the N6-adenine DNA methyltransferase from \textit{Thermus aquaticus} (\textit{M}\textsubscript{Taq}I), which catalyses the methyl group transfer from S-adenosyl-L-methionine (AdoMet) to the exocyclic amino group of adenine within the double-stranded (ds) 5′-TCGA-3′ DNA sequence (4). The structure of \textit{M}\textsubscript{Taq}I in complex with its cofactor consists of two domains which form a cleft wide enough to accommodate dsDNA (15). However, modelling of B-DNA into the \textit{M}\textsubscript{Taq}I structure showed that the distance between the target adenine and the activated methyl group of the cofactor is 15 Å, which is too large for direct methyl group transfer (16). By rotating the adenine out of the DNA helix towards the cofactor, the distance between the methyl group donor and acceptor can be significantly reduced, and hence a base flipping mechanism was proposed for \textit{M}\textsubscript{Taq}I. A structural comparison of \textit{M}\textsubscript{Taq}I with the base flipping C5-cytosine DNA methyltransferase \textit{M}\textsubscript{Hha}I showed that the catalytic domains of both enzymes have a very similar fold (17), although primary structural similarities between the two enzymes are limited to a few sequence motifs (18,19). In a superimposition of the catalytic domains of \textit{M}\textsubscript{Taq}I and \textit{M}\textsubscript{Hha}I both the cofactors and the catalytic motifs (N/D P P Y/F/W-motif for N6-adenine DNA methyltransferases and PC-motif for C5-cytosine DNA methyl-
transfersases) overlay very well (17). Because of the similar architecture of their catalytic domains a shared base flipping mechanism seems likely.

In general, X-ray crystallography of protein–DNA complexes provides the absolute proof of DNA base flipping. However, cocystalization of proteins with their DNA substrates is often cumbersome, and in some cases cocystals might never be obtained. Therefore, other methods suitable to detect DNA base flipping would be of great value. Recently, tighter binding of the two C5-cytosine DNA methyltransferases M.HhaI and M.HpaII to duplex oligodeoxynucleotides containing mismatched bases at their target sites (20,21) and of the N6-adenine DNA methyltransferase M.EcoRV to duplexes containing unnatural bases with reduced hydrogen bonding capabilities at the target site (22) was reported. An alternative approach to detect base flipping might be useful to study the N6-adenine DNA base flipping enzyme, which was suggested for this enzyme (43).

Recently, duplex oligodeoxynucleotides containing 2-aminopurine have been used to study the Klenow fragment of DNA polymerase I (32,33), T4 DNA polymerase (34–36), T7 RNA polymerase (40) and helicases (41,42). The 2-aminopurine fluorescence is highly quenched in polydeoxynucleotides (29), due to stacking interactions with neighbouring bases (30,31) and would be expected to increase dramatically if the 2-aminopurine base is flipped out of the DNA helix. Furthermore, the 2-aminopurine fluorescence excitation and emission maxima are well separated from those of tryptophan and tyrosine residues in proteins, increasing its usefulness for studying protein–DNA interactions. Duplex oligodeoxyxynucleotides containing 2-aminopurine have been used to study the Klenow fragment of DNA polymerase I (32,33), T4 DNA polymerase (34–36), T7 RNA polymerase (37–39), Escherichia coli RNA polymerase (40) and helicases (41,42). Recently, duplex oligodeoxyxynucleotides containing 2-aminopurine have been used to study the N6-adenine DNA methyltransferase M.EcoRI, and a DNA base flipping mechanism was suggested for this enzyme (43).

Using the C5-cytosine DNA methyltransferase M.HhaI as a paradigm for a base flipping enzyme, we demonstrate that 2-aminopurine incorporated in DNA serves as an excellent spectroscopic probe for DNA base flipping. M.HhaI recognizes the specific tetranucleotide DNA sequence 5′-GCCC-3′ (44) and catalyses the methyl group transfer from AdoMet to the 5-position of the first cytosine (45). Titration with M.HhaI of a duplex oligodeoxyxynucleotide, in which the first cytosine is replaced with 2-aminopurine, yields a large increase in the 2-aminopurine fluorescence intensity. In addition, the N6-adenine DNA methyltransferase M.TaqI, which was suggested to use a base flipping mechanism, also shows a strongly enhanced 2-aminopurine fluorescence after addition to a duplex oligodeoxyxynucleotide, in which the target adenine is replaced by 2-aminopurine. Thus, duplex oligodeoxyxynucleotides containing 2-aminopurine can serve as spectroscopic probes for DNA base flipping in protein–DNA complexes. In addition, these duplex oligodeoxyxynucleotides should be very useful to study the dynamics of DNA base flipping.

**MATERIALS AND METHODS**

UV absorption spectra were measured in H2O using a Varian Cary 3E spectrometer. HPLC was performed using a Beckman System Gold equipped with a programmable solvent module 125, a diode array detector module 168, an analog interface module 406 and a Shimadzu spectrophotometric detector RF-551. Fluorescence data were collected with a SLM-Aminco AB2 spectrophotometer. The excitation and emission bandwidths were adjusted to 2 and 8 nm, respectively. Displayed emission spectra were corrected for lamp intensity fluctuations. Fluorescence titrations were performed with an excitation wavelength of 320 nm and an emission wavelength of 381 nm to lower the influence of the natural DNA base absorption and the protein tryptophan fluorescence. Emission spectra were recorded with an excitation wavelength of 320 nm. Due to the optical arrangement of the SLM AB2 all 2-aminopurine emission spectra show an extra shoulder at around 380 nm.

**Oligodeoxynucleotide synthesis, purification and evaluation**

Oligodeoxynucleotides were synthesized on an Applied Biosystems 392 DNA/RNA synthesizer, using standard β-cyanoethyl phosphoramidite chemistry or were purchased from MWG Biotech. 2-Aminopurine, C5-methylcytosine and N6-methyladenine phosphoramidites were purchased from Glen Research. Phosphoramidites for the normal bases and the synthesizer chemicals were obtained from Applied Biosystems and MWG Biotech. Phosphoramidites were dissolved manually in dry acetonitrile at 0.1 M concentration. Sequences of synthesized oligodeoxynucleotides are given in Table 1.

Evaluation of the coupling yield using the dimethyltrimethyl cation assay gave an average of 98.5% per step. Deblocking was achieved by heating in aqueous ammonia (33%, Baker) at 55°C for 8 h. Syntheses were performed ‘trityl on’, and oligodeoxynucleotides containing the dimethoxymethyl group were purified by reversed phase HPLC (Hypersil ODS, 5 μm, 120 A, 250 × 8 mm column, Bischoff) with a linear acetonitrile gradient (13–31% in 20 min, 2.5 ml/min) in triethylammonium acetate buffer (0.1 M, pH 7.0). After detritylation with acetic acid (80%) and ethanol precipitation oligodeoxynucleotides were desalted by gel filtration (NAP column, Pharmacia). Concentrations of oligodeoxynucleotides were determined by UV absorbance at 260 nm using the sum of the extinction coefficients of the individual bases.

Base composition of oligodeoxynucleotides was analysed by enzymatic digestion with snake venom phosphodiesterase and alkaline phosphatase followed by analytical reversed phase HPLC (26,46). Normalized peak areas of UV absorption at 254 nm correlated well with the expected base composition of the individual oligodeoxynucleotides. Oligodeoxynucleotides were labelled with treatment with T4 polynucleotide kinase (New England Biolabs) and γ[32P]ATP (0.4 MBq/μl, Hartmann Analytik) and analysed by denaturing PAGE. Radioactivity was quantified using a PhosphorImager (Molecular Imager System GS 525, Bio-Rad). All oligodeoxynucleotides showed a purity >95%.

**DNA methyltransferases**

M.HhaI was essentially isolated as described earlier (47); exhaustive dialysis prior to chromatography yielded AdoMet-free enzyme. The enzyme was purified to homogeneity by passing it through a pre-column of Q-Sepharose followed by column chromatography on S-Sepharose.

M.TaqI was expressed in E. coli strain Escherichia coli cells (New England Biolabs) harbouring pAGL15-M13, which carries the gene for M.TaqI under the inducible tac-promoter. pAGL15-M13 was kindly provided by Drs Jack Benner and Cheryl Baxa, New England Biolabs. Cells were grown at 37°C to an optical density of 0.6 at 600 nm and induced with IPTG (0.1 mM final concentration). After induction (4 h) cells were harvested by centrifugation (30 min at 8000 g).
3500 r.p.m.) and lysed by sonication in buffer A (Mes/HEPES/sodium acetate buffer mix, 6.7 mM each, pH 7.5, 1 mM EDTA, 10 mM β-mercaptoethanol and 10% glycerol), containing sodium chloride (200 mM) and phenylmethylsulfonyl fluoride (25 mg/l). After centrifugation (1 h at 35 000 g) the supernatant was loaded onto a cation exchange column (Poros HS/M, 26 × 95 mm, Perseptive Biosystems) and M.TaqI was eluted with a linear gradient of sodium chloride (0.2–1.0 M) in buffer A. Fractions containing M.TaqI were pooled, 3-fold diluted with buffer A and loaded onto a heparin column (heparin Sepharose CL 6B, 26 × 95 mm, Pharmacia). M.TaqI was eluted with a linear gradient of sodium chloride (0.2–1.0 M) in buffer A. Fractions containing M.TaqI were pooled, and the protein solution was concentrated by ultrafiltration (Centriprep 10, Amicon). The concentrated protein solution (10 ml) was loaded onto a gel filtration column (Superdex 75, 26 × 600 mm, Pharmacia) and eluted with a Tris–HCl buffer (20 mM, pH 7.4) containing potassium chloride (600 mM), EDTA (0.2 mM), DTE (2 mM) and glycerol (10%). Fractions containing M.TaqI were pooled, 2-fold diluted with glycerol and stored at –20°C. M.TaqI was at least 95% pure as judged by polyacrylamide gel electrophoresis in the presence of sodium dodecyl sulfate (48) and staining with Coomassie Blue. However, it was found that some fraction of the protein still contained the cofactor AdoMet. AdoMet bound to M.TaqI was removed as previously described (49). Concentrations of M.HhaI and M.TaqI were estimated by the method of Bradford (50) (Coomassie Protein Assay Reagent, Pierce) using bovine serum albumin as standard. Concentrations were calculated using molecular weights of 37 100 g/mol for M.HhaI and 47 900 g/mol for M.TaqI.

**Gel mobility shift assays**

DNA binding studies with M.HhaI were performed by incubating M.HhaI (50 nM) with 5'-32P-labelled duplexes oligodeoxynucleotides (5 nM) in buffer B (10 mM Tris–HCl, pH 7.4, 50 mM sodium chloride, 0.5 mM EDTA and 2 mM β-mercaptoethanol) supplied with glycerol (5%) and, where applicable, S-adenosyl-L-homocysteine (100 µM) for 30 min at 8°C. Aliquots (5 µl) were loaded onto a non-denaturing polyacrylamide gel (13%, acrylamide: bisacrylamide = 19:1) and electrophoresis was carried out in Tris–borate (45 mM, pH 8.3) and EDTA (1 mM) at 8°C for 2 h. Dried gels were autoradiographed to an X-ray film and the films were scanned with a ScanMaker E6 densitometer (Microtek). DNA binding of M.TaqI was analysed by incubation of M.TaqI (30 nM) with 5'-32P-labelled duplexes oligodeoxynucleotides (1 nM) in buffer C (10 mM Tris–acetate, pH 7.9, 50 mM potassium acetate, 10 mM magnesium acetate, 1 mM DTT and 0.01% Triton X-100) supplied with BSA (0.1 mg/ml) and glycerol (10%) at 0°C for 10 min. Aliquots (10 µl) were loaded onto a non-denaturing polyacrylamide gel (10%, acrylamide: bisacrylamide = 19:1) and electrophoresis was carried out in a buffer (pH 8.5) containing Tris–HCl (25 mM), glycine (192 mM) and EDTA (1 mM) at 0°C for 2 h. Radioactivity in the gel was visualized by autoradiography using a Bio-Rad Phosphoimager.

**Steady-state fluorescence measurements**

Fluorescence measurements were performed in 5 × 5 mm cuvettes at 25°C. Titrations of duplex oligodeoxynucleotides (20 and 250 nM) with M.HhaI were performed in buffer B and with M.TaqI in buffer C (see gel mobility shift assays). S-adenosyl-L-homocysteine (50 µM) was added to buffer B for titrations of 2GC and GC2G with M.HhaI. Duplex oligodeoxynucleotides were made by mixing strands containing 2-aminopurine or non-fluorescent control strands with a 1.1-fold molecular excess of methylated complementary strands in the appropriate buffer and heating at 95°C for 2 min followed by cooling to room temperature over a period of 4 h. Enzymatic digestion of the duplex oligodeoxynucleotide G2GC was done by addition of DNase I (0.1 µg, Boehringer Mannheim) and snake venom phosphodiesterase (2 µg, Boehringer Mannheim) to a solution (400 µl) containing G2GC (250 nM) and buffer B supplemented with magnesium chloride (5 mM).

**Table 1. Sequences of duplex oligodeoxynucleotides and their abbreviations used in this publication**

| (i) Duplex oligodeoxynucleotides for M.HhaI | x | y | z | C | G | CMe | G | TGGCCCAACGATCCGG-3' |
| 5'-GACTGGTAGCAGATCGAG | x | y | z | C | G | CMe | G | ACTGGCTGAGTAGGTG-5' |
| 3'-TGACCATATCACGTC | T | C | AMe | G | T | C | AMe | AGCGC |

| (ii) Duplex oligodeoxynucleotides for M.TaqI | x | y | z | C | G | T | AMe | G | TCCTGGGTCAGACCG-5' |
| 5'-GCTGTGAGATCAGTGCT | x | y | z | C | G | T | AMe | G | TGGCTGAGTAGGTG-5' |
| 3'-CGCAGACTGAGTCAG | T | C | AMe | G | T | C | AMe | AGCGC |

*The bases targeted by M.HhaI and M.TaqI are bold in the following symbols are used for modified nucleosides: 2', 2-aminopurine-1-β-D-2',deoxynucleoside; CMe, 5-methyl-2'-deoxycytidine and AMe, 6-methyl-2'-deoxyadenosine.
Fluorescence data processing

All fluorescence emission spectra and fluorescence intensities from titrations were corrected for protein tryptophan fluorescence by subtraction of control spectra and control titrations, where the 2-aminopurine fluorophor was replaced by adenine in the duplex oligodeoxynucleotides. In addition, fluorescence data were corrected for variable background emission of the solutions. This was necessary, because the 2-aminopurine fluorescence is highly quenched in duplex oligodeoxynucleotides and its fluorescence intensity at low duplex concentration used in this study (20 and 250 nM) is small compared with the background. Therefore, the fluorescence intensities of the various duplex oligodeoxynucleotides were measured at higher concentrations (typically between 0.5 and 4 µM). Fluorescence intensities of all duplex oligodeoxynucleotides containing 2-aminopurine showed a linear dependence on their concentrations. Fluorescence intensities at 20 and 250 nM concentration free of background were calculated from the obtained slopes. Titration data (fluorescence intensities as a function of total enzyme concentrations) were fitted to the real solution of the quadratic binding equation for one binding site on their concentrations. Fluorescence intensities at 20 and 250 nM concentration were measured at higher concentrations (typically between 0.5 and 4 µM). Fluorescence intensities of the various duplex oligodeoxynucleotides containing 2-aminopurine showed a linear dependence on their concentrations. Fluorescence intensities at 20 and 250 nM concentration free of background were calculated from the obtained slopes. Titration data (fluorescence intensities as a function of total enzyme concentrations) were fitted to the real solution of the quadratic binding equation for one binding site (51) using the data analysis program GraFit (52).

RESULTS

Duplex oligodeoxynucleotides used

For fluorescence measurements with HhaI, which catalyses the methylation of the first cytosine within the ds 5'-GCGC-3' DNA sequence, we used three hemimethylated duplex oligodeoxynucleotides, which are derived from the recognition sequence (for abbreviations of duplex oligodeoxynucleotides see Table 1). In G2GC the target cytosine, in 2GC its 5'-neighbour and in G2C its 3'-neighbour, is replaced with the fluorescent base 2-aminopurine. Since the recognition sequence of HhaI is palindromic, HhaI can, in principle, bind in two orientations. In order to direct binding of HhaI in the orientation, in which 2-aminopurine (G2GC) or cytosine (2GC and G2C) is targeted, the complementary strand in these duplexes contained 5-methylcytosine at the other target position. Such a preference for single binding orientation was observed in co-crystals of HhaI with hemimethylated DNA (53).

Analogous hemimethylated duplex oligodeoxynucleotides were used for the fluorescence measurements with TaqI, which catalyses the methylation of the adenine within the ds 5'-TCGA-3' DNA sequence. In the duplex oligodeoxynucleotides TCG2 and TC2A the target adenine and its 5'-neighbour are replaced by 2-aminopurine, whereas in TCGA2 2-aminopurine occupies the 3'-neighbour position outside the recognition sequence. In order to direct binding in the desired orientation the complementary strands in these duplex oligodeoxynucleotides contained N6-methyladenine at the other target position.

The various duplex oligodeoxynucleotides containing 2-aminopurine showed quite different fluorescence intensities (Table 2). In general, the fluorescence intensities of duplex oligodeoxynucleotides, in which the 2-aminopurine base can form a Watson–Crick-like base pair with thymine, are lower than those having 2-aminopurine in a mismatch position. Apart from base pairing, the 2-aminopurine fluorescence in these duplex oligodeoxynucleotides is also quite sensitive to the sequence context.

Table 2. Fluorescence intensities of duplex oligodeoxynucleotides containing 2-aminopurine before and after titration with HhaI or TaqI

<table>
<thead>
<tr>
<th>Duplex containing 2-aminopurine</th>
<th>Fluorescence before titration (a.u.)</th>
<th>Fluorescence after titration (a.u.)</th>
<th>Relative fluorescence increase</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 G2GC</td>
<td>4.76 ± 0.04</td>
<td>255.3 ± 3.1</td>
<td>53.6 ± 2.1</td>
</tr>
<tr>
<td>2 2GC</td>
<td>5.91 ± 0.05</td>
<td>8.7 ± 0.8</td>
<td>1.5 ± 0.2</td>
</tr>
<tr>
<td>3 GC2C</td>
<td>9.90 ± 0.40</td>
<td>18.0 ± 1.5</td>
<td>1.8 ± 0.2</td>
</tr>
<tr>
<td>4 TCG2</td>
<td>1.77 ± 0.06</td>
<td>23.0 ± 0.8</td>
<td>13.0 ± 0.9</td>
</tr>
<tr>
<td>5 TC2A</td>
<td>5.81 ± 0.27</td>
<td>9.9 ± 0.2</td>
<td>1.7 ± 0.1</td>
</tr>
<tr>
<td>6 TCGA2</td>
<td>4.45 ± 0.07</td>
<td>9.0 ± 0.1</td>
<td>2.0 ± 0.1</td>
</tr>
</tbody>
</table>

*For the fluorescence titrations with HhaI (rows 1–3) and TaqI (rows 4–6) duplex oligodeoxynucleotides containing 2-aminopurine-1-β-D-2' deoxyribofuranosyl (2) were used at 250 nM concentration and the excitation and emission wavelengths were set to 320 and 381 nm, respectively. Fluorescence intensities are given in arbitrary units (a.u.) and errors as standard deviations.

Binding of HhaI and TaqI to duplex oligodeoxynucleotides

Binding of HhaI and TaqI to the various duplex oligodeoxynucleotides was analysed in gel mobility shift assays. The results obtained with HhaI are shown in Figure 1. Duplex oligodeoxynucleotides were incubated with HhaI and the free duplex oligodeoxynucleotides (lower bands) separated from the HhaI-bound duplexes (upper bands) by non-denaturing gel electrophoresis. Under these conditions HhaI completely bound to G2GC, partly to the specific duplex oligodeoxynucleotide GCGC and no binding was observed with 2GC and GC2G (lanes 1–4). However, addition of S-adenosyl-L-homocysteine (AdoHcy) to the incubation mixture resulted in nearly complete binding of all duplex oligodeoxynucleotides (lanes 5–8). Binding of TaqI to specific duplex oligodeoxynucleotide TCGA and the various duplex oligodeoxynucleotides containing 2-aminopurine is demonstrated in Figure 2. The electrophoretic mobilities of the duplex oligodeoxynucleotides alone are shown in lanes 1, 3, 5 and 7. Addition of TaqI (30 nM) prior to electrophoresis resulted in nearly complete formation of complexes for all four duplex oligodeoxynucleotides even in the absence of AdoHcy (upper bands in Figure 1).
emission spectrum in the presence of M.

Fluorescence studies with M. 

Fluorescence studies with M.

Figure 2. Gel mobility shift analysis of the interactions between M. TaqI and duplex oligodeoxynucleotides (1 nM). Lanes 1, 3, 5 and 7 in the absence of M. TaqI and lanes 2, 4, 6 and 8 in the presence of M. TaqI (30 nM).

Figure 3. Fluorescence emission spectra of G2GC: curve (a) 250 nM duplex oligodeoxynucleotide alone, curve (b) 10 µM duplex oligodeoxynucleotide alone, curve (c) 250 nM duplex oligodeoxynucleotide in the presence of saturating concentration of M.HhaI (2 µM) and curve (d) 250 nM duplex oligodeoxynucleotide after digestion with DNase I and phosphodiesterase.

Figure 4. (A) Fluorescence titrations of G2GC (●), 2CGC (○) and G2C (□) at 250 nM concentration each with M.HhaI. Titrations of 2CGC and G2C were done in the presence of S-adenosyl-L-homocysteine (50 µM). (B) Fluorescence titrations of G2GC at 20 nM concentration in the absence (●) and presence of 50 µM S-adenosyl-L-homocysteine (□) with M.HhaI. Data fitting yielded dissociation constants $K_f$ of 3.9 ± 1.1 and 2.9 ± 0.9 nM in the absence and presence of S-adenosyl-L-homocysteine, respectively.
which carries the 2-aminopurine fluorophor at the target site of M\textit{Taq}I, results in a 13-fold increase of the fluorescence intensity. The titration data were fitted to the real solution of the quadratic binding equation for one binding site and resulted in a $K_d$ of $120 \pm 30 \text{nM}$. This relatively weak binding is in conflict with the apparent $K_d$ determined by 2-aminopurine fluorescence titration. Given the similarities of the $K_d$ determined in the different fluorescence solution assays, we think that the gel mobility shift assay indicates too tight binding for M.

Figure 3 (curve a). This is very similar to the result obtained for the emission spectrum of TCG in the presence of M.

$30 \text{nM}$. This relatively weak binding is in conflict with the apparent binding equation for one binding site and resulted in a $K_d$ of $120 \pm 30 \text{nM}$. This relatively weak binding is in conflict with the apparent $K_d$ determined by 2-aminopurine fluorescence titration. Given the similarities of the $K_d$ determined in the different fluorescence solution assays, we think that the gel mobility shift assay indicates too tight binding for M.

DISCUSSION

We have used the C5-cytosine DNA methyltransferase M\textit{Hha}I as a paradigm for a DNA base flipping enzyme. It was demonstrated by X-ray crystallography of a series of ternary complexes between M\textit{Hha}I, various versions of substrate DNA and the product cofactor AdoHcy that the enzyme flips its target cytosine out of the DNA and into its active site (1,53–55). In addition, there is indirect evidence that base flipping does also occur in the binary M\textit{Hha}I–DNA complex. It was shown that M\textit{Hha}I catalyses exchange of the proton at the 5-position of cytosine with solvent in the absence of cofactor (56).

Base flipping in the binary complex is also supported by the observation that M\textit{Hha}I binds more tightly to duplex oligodeoxynucleotides containing thymine, uracil (20) and even adenine or guanine replacements for the target cytosine (21). This enhanced binding of M\textit{Hha}I to such duplexes is attributed to the lower energy required for opening a mismatched base pair upon formation of the binary complex. Recently, base flipping in the binary complex has been observed by $^{19}$F NMR spectroscopy (57). 2-Aminopurine also forms a mismatch with guanine in the G2GC duplex, and it is therefore not surprising that M\textit{Hha}I binds strongly to this duplex oligodeoxynucleotide in the gel shift assay.

Since base flipping results in a complete removal of the stacking interactions between the target base and its neighbours, and the fluorescence quenching of the 2-aminopurine base in dsDNA is mainly due to base stacking interactions, the 2-aminopurine fluorescence should increase dramatically if the 2-aminopurine base is flipped out of the DNA helix. Thus, the observed 54-fold increase of the 2-aminopurine fluorescence intensity upon addition of saturating amounts of M\textit{Hha}I to such duplexes is attributed to the lower energy required for opening a mismatched base pair upon formation of the binary complex. Recently, base flipping in the binary complex has been observed by $^{19}$F NMR spectroscopy (57). 2-Aminopurine also forms a mismatch with guanine in the G2GC duplex, and it is therefore not surprising that M\textit{Hha}I binds strongly to this duplex oligodeoxynucleotide in the gel shift assay.

In contrast with the M\textit{Taq}I–TCG2 complex, complexes between M\textit{Taq}I and duplexes carrying 2-aminopurine at the neighbouring positions (TC2A and TCGA2) show fluorescence emission spectra with a shape similar to those of the duplex oligodeoxynucleotides alone (data not shown).
effect of AdoHcy on the electrophoretic mobility of this complex could be related to our observation that the dissociation constants of G2GC in the presence and absence of AdoHcy are not significantly different (Fig. 4B). It should be pointed out that duplex oligonucleotides with cytosine at the target position do show an increased binding upon addition of AdoHcy in gel mobility shift experiments (21). The insensitivity of the $K_d$ of G2GC to the addition of AdoHcy could be due to the sterically more demanding 2-aminopurine base at the target position, which does not allow an AdoHcy-induced conformational rearrangement of $M_{HhaI}$ to increase binding.

In contrast with G2GC, the duplex oligodeoxynucleotides 2CGC and GC2C, in which the neighbouring bases of the target cytosine are replaced with 2-aminopurine, bound to $M_{HhaI}$ only in the presence of AdoHcy in the gel shift assay and gave only small increases of the 2-aminopurine fluorescence emission upon titration with $M_{HhaI}$ (1.5- and 1.8-fold, respectively). In these complexes base flipping of the target cytosine should lead to a 2-aminopurine which has lost its base stacking interactions to one of its neighbours. This situation can be compared with duplex oligodeoxynucleotides having 2-aminopurine at the 3′-end. Bloom et al. (32) showed that placing 2-aminopurine at the 3′-end of a duplex oligodeoxynucleotide results in a very low fluorescence intensity and thus only one stacking neighbour is sufficient to result in a large fluorescence quenching (25- to 125-fold depending on the nature of the 5′-neighbour of 2-aminopurine). Therefore, the small fluorescence increases in the $M_{HhaI}$–2CGC and $M_{HhaI}$–GC2C complexes are in accordance with the neighbouring cytosine being flipped out of the DNA helix.

$M_{HhaI}$ does not bend its DNA substrate significantly (1.58) and the large 2-aminopurine fluorescence intensity of the $M_{HhaI}$–G2GC complex can solely be attributed to base flipping. Since the 2-aminopurine fluorescence in duplex oligodeoxynucleotides is highly quenched due to stacking interactions with neighbouring bases, DNA bending, kinking and base flipping induced by DNA binding proteins should have different effects on the 2-aminopurine fluorescence intensity. In general, smooth bending does not result in an unstacking of neighbouring base pairs and thus should not lead to a large increase of the 2-aminopurine fluorescence. In contrast, kinking of DNA, as observed in DNA complexes with the catabolite gene activator protein (CAP) (59), the TATA-box binding protein (TBP) (60,61) or the restriction endonuclease EcoRV (62), leads to unstacking of adjacent base pairs (63). This leads to a situation, in which each base at the kink has only one stacking neighbour and may be compared with the $M_{HhaI}$–2CGC and $M_{HbaI}$–GC2C complexes, in which 2-aminopurine has only one stacking neighbour due to base flipping, or to a duplex oligodeoxynucleotide, in which 2-aminopurine is placed at the end. Since the later arrangements do not lead to a large 2-aminopurine fluorescence increase, DNA kinking is also not expected to result in a large fluorescence increase. Only if both stacking neighbours are removed upon DNA binding, e.g. by base flipping, duplex oligodeoxynucleotides containing 2-aminopurine should show a large fluorescence increase. However, it should be noted, that a small 2-aminopurine fluorescence increase due to bending or kinking might also give a valuable fluorescence signal change, which can be used to study DNA binding.

Titrations of duplex oligodeoxynucleotides containing 2-aminopurine with the adenine-specific DNA methyltransferase $M_{TaqI}$ lead to similar results as those with $M_{HhaI}$. Replacement of the target adenine with 2-aminopurine within the recognition sequence of $M_{TaqI}$ (TCG2) yields a strongly enhanced 2-aminopurine fluorescence signal (13-fold) upon titration with $M_{TaqI}$. In addition, the shape of the 2-aminopurine fluorescence emission spectrum in the $M_{TaqI}$–TCG2 complex resembles that of the free 2-aminopurine-2′-deoxynucleotide. Addition of $M_{TaqI}$ to duplex oligodeoxynucleotides bearing 2-aminopurine at the 5′-neighbouring position (TC2A) or at the 3′-neighbouring position (TCG2A) of the target adenine show only a 1.7- and 2.0-fold increase of the fluorescence intensity, respectively. In addition, the shapes of the fluorescence emission spectra are similar to those of the duplex oligodeoxynucleotides alone. The similarities of the results obtained with $M_{HhaI}$ and $M_{TaqI}$ strongly indicate a common base flipping mechanism for both DNA methyltransferases.

The lower fluorescence intensity of the $M_{TaqI}$–TCG2 complex compared with the $M_{HhaI}$–G2GC complex might be explained by different chemical environments of the 2-aminopurine base when flipped out of the DNA helix. It was suggested for $M_{TaqI}$, that the target adenine after being flipped out of the DNA will interact with NPPY (105–108), VVP (164–166) and F196 in the $M_{TaqI}$–DNA complex (17). Since the 2-aminopurine quantum yield is reduced in hydrophobic solvents (29) and the putative active site of $M_{TaqI}$ is very hydrophobic, a reduced 2-aminopurine fluorescence intensity is expected. In addition, the 2-aminopurine fluorescence is blue-shifted in hydrophobic solvents (29) and the observed 3 nm blue shift of the 2-aminopurine emission maximum in the $M_{TaqI}$–TCG2 complex compared with the free 2-aminopurine-2′-deoxynucleotide supports this interpretation. Alternatively, the lower fluorescence intensity of the $M_{TaqI}$–TCG2 complex could be explained by different equilibria between an inner- and extrahelical state of the 2-aminopurine base in the $M_{TaqI}$–TCG2 and $M_{HhaI}$–G2GC complexes. 2-Aminopurine can form two Watson–Crick-like hydrogen bonds to the partner thymine in the TCG2 duplex, whereas in G2GC 2-aminopurine forms a mismatch with the partner guanine. Therefore, the equilibrium in the $M_{HhaI}$–G2GC complex could lie more on the extrahelical side compared with that in the $M_{TaqI}$–TCG2 complex, which could explain the higher 2-aminopurine fluorescence intensity of the $M_{HhaI}$–G2GC complex. A third explanation for the lower fluorescence of the $M_{TaqI}$–TCG2 complex could be that a certain fraction of the enzyme docks to the recognition sequence in the alternative orientation, which does not lead to a flipped out 2-aminopurine base. However, this possibility can be excluded, because in studies with a duplex oligodeoxynucleotide, in which the target bases of both strands were replaced with 2-aminopurine, no higher fluorescence intensity is observed upon addition of $M_{TaqI}$ compared with the $M_{TaqI}$–TCG2 complex (data not shown).

Recently, fluorescence studies with duplex oligodeoxynucleotides containing 2-aminopurine and the N6-adenine DNA methyltransferase $M_{EcoRI}$ have been reported (43). Similar to our results with $M_{HhaI}$ and $M_{TaqI}$, addition of stoichiometric amounts of $M_{EcoRI}$ to a duplex oligodeoxynucleotide containing 2-aminopurine at the target site resulted in a large (14-fold) increase of the 2-aminopurine fluorescence. These findings with $M_{TaqI}$ and $M_{EcoRI}$ give experimental evidence that a base flipping mechanism similar to that described for the C5-cytosine DNA methyltransferases $M_{HhaI}$ and $M_{HaeIII}$ also operates in adenine-specific DNA methyltransferases. Since the active site residues of $M_{TaqI}$ as well as other amino acids are highly conserved among N6-adenine DNA methyltransferases and N4-cytosine DNA methyltransferases (18,19,64), a common base flipping mechanism for all DNA
methytransferases seems likely (5). This hypothesis can now be tested experimentally by using duplex oligodeoxynucleotides, in which the target base is replaced by 2-aminopurine.

In conclusion, the C5-cytosine DNA methyltransferase M\textit{HhaI}, which is known to flip out its target base for catalysis, leads to a large increase of the 2-aminopurine fluorescence when added to duplex oligodeoxynucleotides containing 2-aminopurine at the target site. Addition of the N6-adenine DNA methyltransferase \textit{M{TaqI}} to duplex oligodeoxynucleotides, in which the target base is replaced by 2-aminopurine, also results in a strongly enhanced 2-aminopurine fluorescence emission. These results demonstrate that 2-aminopurine can be used as a fluorescence probe for DNA base flipping. In addition, this approach is suitable to determine \(K_D\) in the nanomolar range. Furthermore, it should be possible to use the 2-aminopurine fluorescence signal in stopped flow experiments to monitor DNA base flipping in real time.

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