strongly polarized than CO, e.g., O₂, such interactions could serve to catalyze rearrangement of the ligands such as proposed in Scheme I.

Conclusions

In this paper it is proposed that the ion–molecule reaction between Cr(CO)₆ and O₂ to produce Cr(CO)₅O⁻ and Cr(CO)₅O²⁻ occurs by a competitive reaction mechanism. The two mechanisms involve (i) simple ligand exchange to produce the Cr(CO)₅O⁻ anion and (ii) addition of O₂ to Cr(CO)₅ followed by intramolecular nucleophilic addition of O⁻ to a CO ligand to form Cr(CO)₅O²⁻ and CO plus CO₂.

A surprisingly large temperature dependence for the rate of reaction of Cr(CO)₅ with O₂ is observed. The strong temperature dependence of the reaction rate is attributed to formation of a high-energy [Cr(CO)₅⁻] species. The high-energy Cr(CO)₅⁻ anion may be formed by thermal decomposition of Cr(CO)₆ to give a high spin state of Cr(CO)₅, which is subsequently ionized by electron attachment to give [Cr(CO)₅⁻]⁺.

A particularly important result of this study is the proton and electron affinity data obtained for Cr(CO)₅O⁻ and Cr(CO)₅O²⁻. Although the oxygen ligand in these two ions differs significantly, the fact that both ions have the same proton and electron affinities suggests that the oxygen atom and molecule interact with the Cr(CO)₅ moiety in an analogous manner. We propose that in both Cr(CO)₅O⁻ and Cr(CO)₅O²⁻, the Cr atom is best described as a Cr⁺ oxidation state and the oxygen ligand as O⁻ and O²⁻, respectively. These results suggest that proton and electron affinity data may be extremely useful as diagnostic tools for probing the electronic environment of metal centers in gas-phase organometallic systems. A similar suggestion has been reported by Squires on the interplay between electron and proton affinities of metal atoms and ions.¹³

Acknowledgment. This research is supported by the U. S. Department of Energy, Office of Basic Energy Sciences (DE-FG05-85ER13434). The FTMS-1000 system was purchased from funds provided by the Texas A&M University Center for Energy and Mineral Resources, Office of University Research, and Texas Agriculture Experiment Station.


A Parallel Right-Handed Duplex of the Hexamer d(TpTpTpTpTpT) with Phosphate Triester Linkages

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Contribution from The Department of Organic Chemistry, Eindhoven University of Technology, 5600 MB Eindhoven, The Netherlands. Received November 3, 1986

Abstract: We show in this work that stable parallel thymine–thymine (T–T) base pairs can be formed in aqueous solution. Initially, this observation was made with 3',5'-di-O-acetylthymidine in water which showed an imino resonance at 13.45 ppm in the ¹H NMR spectrum. Using the nucleoside diphosphate d(pTp), the formation of T–T base pairs could only be induced via methylation of the phosphate groups. This leads to the suggestion that intermolecular electrostatic phosphate–phosphate repulsion precludes T–T base pairing for unmodified d(pTp). It is shown that T–T pairing is also manifest on the dinucleotide level, provided that the phosphate groups are methylated. Using the dinucleoside phosphate I which was separated in its diastereomeric forms, it was shown that the imidiplex melts at Tₘ = 30 °C. Furthermore, it was shown that the duplex of I is parallel. From the detailed conformational analysis of the individual diastereomers it follows that the duplex has a right-handed helical sense, since the backbone bonds C₆₋₋₋₋₋₋₋₋₋₋ and C₆₋₋₋₋₋₋₋₋₋₋ are preferentially y⁺ and β⁻, and the furanoses reside primarily in the south conformation. With the hexamer d(TpTpTpTpTpT), it was shown that T–T pairing also occurs on the hexanucleotide level, after methylation of the phosphate groups. The resulting duplex has a Tₘ value of approximately 65 °C as was established with UV hyperchromicity and with variable-temperature 500-MHz ¹H NMR. It could be clearly established that the duplex is parallel. Molecular modelling studies on the duplex of phosphate-methylated d(TpTpTpTpT) yielded a remarkably slim, parallel structure with about eight residues per turn. The possible relevance of these alternative DNA-like duplexes is briefly mentioned.

Thymine–thymine (T–T) base pairing was recently observed in the crystal structures of 3',5'-di-O-acetylthymidine¹ and cis-thymidine-3',5'-N,N-dimethylphosphoramidate.² Both crystal structures display an approximate twofold rotational symmetry, which is due to the fact that the T-bases are linked via two virtually identical N₇₋₋₋₋₋₋₋₋₋₋₋₋₋₋₋₋ and O₋₋₋₋₋₋₋₋₋₋₋₋₋₋₋₋ hydrogen bonds (Figure 1). Following the convention of Rose et al.,³ it is easily seen that the α faces of the coupled bases are on the same side; i.e., the T-bases are parallel. Therefore, the 5' → 3' vectors run in the same direction on both sides of the T–T pair. The present work is focused on the formation of T–T base pairs in solution. It was found that parallel T–T pairing readily occurs on, e.g., the mono-, di-, and hexanucleotide level, provided that the phosphate groups are triesterified. In a previous communication,⁴ we already published our preliminary results on the phosphate-methylated hexanucleotide duplex. Various physico-chemical techniques (high-resolution proton NMR, UV hyperchromicity) were used in order to characterize these non-Watson–Crick parallel duplexes.

Results and Discussion

T–T Pairing on the Mononucleotide Level. We first studied T–T pairing using the acetylated nucleoside 3',5'-di-O-acetylthymidine⁵ (vide supra) and the nucleoside diphosphate d(pTp). In fact, 3',5'-di-O-acetylthymidine provided the first indication that T–T pairing may occur in aqueous solution, since the imino proton NMR signal was found at a remarkably low-field position (13.45 ppm) in comparison with unlinked thymidine bases (11.2

Reference:

Parallel Thymine-Thymine Base Pairs


The observation of a single, degenerate spectrum for both model systems proves that the hydrogen-bonded nucleotides are symmetric and upfield shifting are observed, which is consistent with gradual dissociation of the dimeric structure.

Using the high-resolution IH NMR spectra of the dimers of 3',5'-di-O-acetylthymidine and phosphate-methylated d(pTp), it was also found that the chemical shift of the imino protons is strongly concentration dependent. At higher dilution, broadening and upfield shifting are observed, which is consistent with gradual dissociation of the dimeric structure.

Figure 2 shows the imino chemical shift as a function of $C_0$, the primitive concentration of phosphate-methylated d(pTp). ppm[5]. Using the d(pTp) system, which contains charged phosphomonoester moieties, no indication for T-T pairing was found. This suggests that electrostatic phosphate-phosphate repulsions reduce the propensity for T-T pairing. Indeed, methylation on the phosphate groups with methyl methanesulphonate results in a distinct imino resonance in water at 13.5 ppm, thus indicating T-T pairing. For the phosphate-methylated d(pTp), it was found that the chemical shift of the imino protons is strongly concentration dependent. At higher dilution, broadening and upfield shifting are observed, which is consistent with gradual dissociation of the dimeric structure.

Table I. Spectral Data of Both Diastereomers of 1, as Determined from the Two-Dimensional $J$-Resolved 300-MHz 1H NMR Spectra

<table>
<thead>
<tr>
<th></th>
<th>slow fraction$^a$</th>
<th>fast fraction$^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\delta^{1H}$</td>
<td>$\delta^{31P}$</td>
</tr>
<tr>
<td></td>
<td>top</td>
<td>bottom</td>
</tr>
<tr>
<td>$J_{H_{1}'H_{2}'}$</td>
<td>8.2 7.2</td>
<td>8.4 7.6</td>
</tr>
<tr>
<td>$J_{H_{1}'H_{2}''}$</td>
<td>6.0 6.6</td>
<td>6.4 6.4</td>
</tr>
<tr>
<td>$J_{H_{1}'H_{3}'}$</td>
<td>6.2 7.0</td>
<td>6.4 6.4</td>
</tr>
<tr>
<td>$J_{H_{1}'H_{4}'}$</td>
<td>2.8 3.6</td>
<td>2.6 3.6</td>
</tr>
<tr>
<td>$J_{H_{2}'H_{3}'}$</td>
<td>2.6 2.8</td>
<td>2.4 3.2</td>
</tr>
<tr>
<td>$J_{H_{2}'H_{4}'}$</td>
<td>4.0 2.6</td>
<td>4.0 2.6</td>
</tr>
<tr>
<td>$J_{H_{3}'H_{4}'}$</td>
<td>4.4 4.0</td>
<td>4.4 4.0</td>
</tr>
<tr>
<td>$J_{H_{3}'H_{4}''}$</td>
<td>5.9</td>
<td>6.4</td>
</tr>
<tr>
<td>$J_{H_{4}'H_{5}'}$</td>
<td>6.0</td>
<td>6.0</td>
</tr>
<tr>
<td>$J_{H_{4}'H_{5}''}$</td>
<td>5.6</td>
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$^a$See ref 11. Obtained by simulation.

Complicated 1H NMR spectra would be obtained, since the coupled nucleotides then reside in different magnetic environments.

T-T Pairing on the Dinucleotide Level. T-T base pair formation on the dinucleotide level was studied with the dinucleoside phosphate 1. This system was synthesized via a slight modification of the common phosphate triester method, devised originally by Caruthers et al.[9] Initially, I was obtained as a mixture of the $R_P$ and $S_P$ diastereomers. In water, this mixture corresponds to a two-line 31P NMR spectrum (2.14 and 2.04 ppm), and a highly crowded 1H NMR spectrum. The $R_P/S_P$ mixture was separated by reversed-phase HPLC, according to the procedure of Stec et al.[10] (see Experimental Section). The diastereomer which was eluted first corresponds to the downfield 31P peak at 2.14 ppm, whereas the slower fraction is found uphill at 2.04 ppm.[11] For each of the diastereomers in water, at 20 °C, the imino protons were found at 13.1 ppm in the 1H NMR spectrum,[12] i.e., I is also present in the duplex form. We observed that increasing the sample temperature results in substantial broadening and upfield shifting of the imino resonance toward 12.5 ppm, which indicates dissociation (melting) of the duplex structure. From the melting curves (imino chemical shift vs. temperature, not shown) we concluded that the melting temperature ($T_m$) of I is roughly 30 °C. The detailed 1H NMR spectra of the diastereomers of I at 20 °C show that the coupled strands give rise to identical spectra:

![Diagram of the diastereomers of I](https://example.com/diagram.png)


(12) Measured on a Bruker WM 500 spectrometer of the Dutch National NMR Facility at Nijmegen, the Netherlands.

(4) Measured at 500 MHz on the Bruker WM 500 spectrometer of the Dutch National 500/200 MHz NMR Facility at Nijmegen, the Netherlands.


(6) Exclusive methylation of the phosphate groups was accomplished according to: Rhese, H.; Freese, E. Biochim. Biophys. Acta 1969, 190, 418.

(7) The primitive concentration $C_0$ equals the concentration of the free monomer plus twice the concentration of the duplex.

i.e., the structure is highly symmetric. Therefore, the spectra are consistent only with a duplex with parallel T-T pairing (vide supra). For the individual diastereomers, it was possible to analyze the conformations of the 2'-deoxyribose ring and, in part, the phosphate backbone in great detail by means of high-resolution 1H NMR. In order to obtain a complete set of vicinal proton-proton coupling constants, we measured a two-dimensional J-resolved 1H NMR spectrum at 300 MHz\(^1\) for both structures. The results of these experiments are summarized in Table I. It is well-known, that the 2'-deoxyribose ring in nucleosides and nucleotides is involved in a rapid two-state conformational equilibrium between a south form (C2'-endo/C3'-endo twist), and a north form (C2'-exo/C3'-endo twist). According to Altona\(^2\), the population of the south form can be accurately estimated on the basis of JH1H2HS and JH2H3H5:

\[
x_{(sou)} = \frac{17.8 - J_{H1H2HS} - J_{H2H3H5}}{10.9}
\]

As can be seen in Table II, the south conformation dominates for the two furanose rings in each of the diastereomers. The coupling constants JH1H2HS and JH2H3H5 were used to analyze the conformation around the C2'-C3' (\(\gamma\)) bond. The formula\(^3\):

\[
x_{(\gamma+)} = \frac{13.1 - J_{H4H5HS} - J_{H5H3HS}}{9.7}
\]

was used for this purpose. Clearly, the \(\gamma\) conformation (in which O2' is located above the 2'-deoxyribose ring) dominates in both the top (5'-O-acetyl) and the bottom (5'-O-phosphate) residues in the diastereomers. The three-bond phosphorus-proton coupling constants JPH5 and JPH45 were used to describe the conformation around the central C2'-O5' (\(\beta\)) bond of the R\(_F\) and S\(_F\) structures. For this, we used the formula\(^4\):

\[
x_{(\beta+)} = \frac{23.9 - J_{PH5} - J_{PH45}}{18.9}
\]

From Table II, it appears that both diastereomers have a dominant contribution of \(\beta\) (in which the phosphorus is in a trans orientation with respect to C2') to the conformational equilibrium around the central C2'-O5' backbone bond. The data in Table II do not show significant conformational differences between the diastereomers. For both structures, the combination of south (2'-deoxyribose), \(\gamma\) (C2'-C3'), and \(\beta\) (central C2'-O5') is preferred. It should be mentioned that the same conformation is encountered in standard right-handed B DNA structures, both in solution and in the solid state. In summary, from the overall structural information on the diastereomeric forms of L, we conclude that both systems exist as stable symmetric miniduplexes with right-handed parallel phosphate–sugar backbone strands. It should be mentioned that one- and two-dimensional NOE spectroscopy cannot bolster this structural model. The symmetry of the structure implies that any interstrand NOE contact has a stronger and overlapping intrastrand counterpart. Therefore the use of NOEs for interatomic distance estimation is essentially excluded.

### T-T Pairing on the Hexanucleoside Level

In order to investigate T-T base-pair formation also on the hexanucleoside level, we used the hexanucleoside pentaphosphate d(TpTpTpTpTpT).\(^5\) The methylation of the phosphate groups with methyl methane-sulfonate\(^6\) was essentially complete (99%), as was shown by precipitation of only 1% of the unmethylated starting material with ethanol/water (75:25 v/v). However, since the phosphate methylation is not stereospecific, a multicomponent mixture of diastereomers is obtained, which could not be separated by means of HPLC techniques. Nonetheless, it could be clearly shown that the phosphate-methylated d(TpTpTpTpTpT) is present as a stable duplex in aqueous solution. This conclusion was based on the observation that the imino protons resonate at 13.3 ppm in the 1H NMR spectrum.\(^4\) Furthermore, increasing the sample temperature results in a double helix → coil transition, as was observed with UV hyperchromicity and variable-temperature NMR experiments. Using the UV hyperchromicity technique, we observed a reversible dissociation of the double helix at a \(T_m\) of approximately 67 °C, for a substrate concentration of 1.3 × 10^{-5} M in water.\(^7\) It was found that the melting behavior is identical in aqueous Tris/EDTA buffer solutions (pH 7.5) of 20 mM and 0.2 M. The fact that \(T_m\) is not influenced by the ionic strength of the solution is consistent with the absence of a formal negative charge on the phosphate groups. The neutral character of the methylated substrate also enabled us to study the melting behavior in less polar solvents. The same \(T_m\) value of approximately 67 °C was found in a 80:20 (v/v) mixture of ethanol and water. No melting point in the temperature range 10–80 °C was found using the hydrogen-bond disrupting solvent hexamethylphosphoric triamide (HMPT).\(^8\) This means that in the latter case only the single strand is present, which is confirmed by an imino chemical shift of 2.5 ppm in HMPT.\(^9\) In the case of phosphate-methylated d(TpTpTpTpTpT), it was not possible to determine the conformation of the phosphate–sugar backbone from the high-resolution 1H NMR spectrum. Evidently, this is due to the fact that the duplex contains 10 chiral phosphate groups, and therefore exists as a complex diastereomeric mixture with a highly crowded 1H NMR spectrum. However, the subspectra of the imino- and base-methyl protons are well-defined (Figure 3), since these protons are located at an appreciable distance from the chiral phosphate groups. In both subspectra, three peaks in the approximate ratio 1:1:4 are observed. Most likely, the terminal base pairs are associated with the lower peaks, whereas the imino- and base-methyl resonances of the inner base pairs practically coincide at 13.29 and 1.32 ppm, respectively. We have used these simple subspectra in two ways for further characterization of the duplex structure of phosphate-methylated d(TpTpTpTpTpT).

First, the chemical shifts of the imino- and base-methyl protons were measured as a function of the sample temperature. The melting curves that were obtained are given in Figure 4. All curves show a melting transition at \(T_m = 64 \pm 0.2\) °C.\(^10\) Remarkably, the UV hyperchromicity measurements (vide supra) resulted in virtually the same \(T_m\) value. This means that the dilution from 10 mM (NMR sample) to 13 mM (UV sample) does not induce a measurable degree of dissociation of the duplex, which confirms the stability of the parallel structure. Secondly, the subspectra were used to discriminate between the symmetric, parallel T-T and the asymmetric, antiparallel T-T coupling (Figure 5). The appearance of only two lower peaks in the subspectra is characteristic for a parallel duplex with a twofold symmetry. In this case, each base pair corresponds with exactly one imino- and one base-methyl peak. In contrast, antiparallel T-T base pairing would result in far more complex subspectra, since this structure lacks any symmetry elements (see Figure 5). For instance, the terminal base pairs are expected to correspond with four methyl and four imino resonances. The fact that the phosphate-methylated d(TpTpTpTpTpT) exists as a complex mixture of diastereomers precludes the use of two-dimensional NOE spectroscopy as a reliable tool for structural elucidation. However, we did perform one-dimensional double resonance experiments in which one of the lower base-methyl resonances was

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1. Measured on a Bruker CXP 300 spectrometer at the Eindhoven University of Technology.
5. (13) Measured on a Bruker CXP 300 spectrometer at the Eindhoven University of Technology.
10. (18) The exchange of the imino protons with the solvent is remarkably slow; broadening of the imino proton resonances is only observed above 75 °C. Chemical shifts could be determined accurately for temperatures up to 85 °C.
with the solvent; i.e., the nucleosides are not coupled. Also on solution at 20 °C no low-field resonances of the NH₂ proton, the hexanucleotide level of phosphate-methylated d-

cytidine (2'-dC) also show the formation of a C-C pair with a parallel arrangement. However, we found for 2'-dC in aqueous solution at 20 °C no low-field resonances of the NH₂ protons, which implies that these protons are involved in a rapid exchange with the interior of the parallel duplex is most stable in the case of T-bases, whereas base-solvent bonding in the single strand form is preferred for C-bases. We considered it of interest to synthesize the phosphate-methylated dodecamer (CpCpCpCpCpCpTpTpT), which represents a combination of phosphate-methylated (CpCpCpCpCpC) and (dTpTpTpTpT). Duplex formation of the dodecamer would result in either a parallel duplex with six T-T and six C-C base pairs, or in a parallel duplex with six T-T base pairs and dangling, nonpaired C-bases. However, since no double helix was coil transition was found in the temperature range 10–90 °C (based on UV hyperchromicity experiments), it can be concluded that the dodecamer is present in the single-strand form; i.e., the C-bases actually preclude the formation of a parallel duplex via T–T pairing.

Structural Model. A molecular model of the phosphate-triesterified (dTpTpTpTpT) was constructed with computer graphics using the structural information provided by the X-ray data of 3',5'-di-O-acetylthymidine, and the detailed NMR data of 3',5'-di-O-acetylthymidine, and the detailed NMR data on both diastereomers of the dinucleoside monophosphate 1. Figure 6 shows a top and side view of the proposed structure. We found that the parallel T–T base pairs indeed fit excellently in a right-handed double helix with γ' and β' backbone torsion angles, south conformation of the 2'-deoxyribose rings, and anti conformation of the T-bases. The inherent symmetry results in the formation of two identical grooves, instead of the minor and major grooves that are found in right-handed B DNA. The structure has approximately eight residues per turn, and a rise per base pair of 3.6 Å. The combination of two thymidine bases results in a helix diameter of 15 Å, whereas the purine–pyrimidine base pairs in B DNA correspond with the much greater helix diameter of 21 Å. Interestingly, our structural model also provides a more plausible explanation for the X-ray diffraction pattern of the dinucleoside phosphate (dTpT), as was recently observed by Tollin et al.1 It was found that this structure crystallizes as a helical structure with about seven units per turn and a rise per base pair of 3.8 Å. The structural model as proposed by Tollin et al. essentially comprises antiparallel T–T base pairs, and a head-to-tail alignment of d(TpT) residues:

(CpCpCpCpCpC) no NH₂ resonances could be detected in the low-field region of the ¹H NMR spectrum recorded at 20 and 4 °C. Additionally, no melting transition was observed in a UV hyperchromicity experiment in the temperature range 10–90 °C. It must be concluded that base–base hydrogen bonding in the interior of the parallel duplex is most stable in the case of T-bases, whereas base-solvent bonding in the single strand form is preferred for C-bases. We considered it of interest to synthesize the phosphate-methylated dodecamer (CpCpCpCpCpCpTpTpT), which represents a combination of phosphate-methylated (CpCpCpCpCpC) and (dTpTpTpTpT). Duplex formation of the dodecamer would result in either a parallel duplex with six T-T and six C-C base pairs, or in a parallel duplex with six T-T base pairs and dangling, nonpaired C-bases. However, since no double helix = coil transition was found in the temperature range 10–90 °C (based on UV hyperchromicity experiments), it can be concluded that the dodecamer is present in the single-strand form; i.e., the C-bases actually preclude the formation of a parallel duplex via T–T pairing.

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\[
\begin{align*}
\text{TP} & \text{TP TP TP TP}
\end{align*}
\]

\[
\begin{align*}
\text{TP Tp Tp Tp Tp Tp}
\end{align*}
\]

However, it was necessary to invoke unlikely conformational characteristics as a syn orientation of the T-bases and a γ'–γ' pair.


(20) Molecular mechanics calculations using the AMBER program confirm this structural model. See: van Genderen, M. H. P.; Koole, L. H.; Aagaard, O. M.; van Lare, C. E. J.; Buck, H. M. Biopolymers, in press.

conformation around the C4'-C5' bond in order to construct an antiparallel helix. On the basis of our present data, we feel that a head-to-tail structure with parallel T-T pairing gives a more adequate explanation for the fiber X-ray diffraction pattern of d(TpT). The resulting double helical structure has backbone strands that are regularly interrupted. Consequently, phosphate groups are not found in opposite positions, which minimizes electrostatic repulsion. Essentially, this situation parallels the phosphate-methylated system d(TpTpTpTpTpT) in which the phosphate repulsions are completely eliminated.

Concluding Remarks

It has been shown that the formation of T-T base pairs may occur readily in aqueous solution, provided that interstrand phosphate-phosphate repulsions are eliminated via methylation of the phosphate groups. The resulting duplex structures are parallel and highly symmetric. Detailed conformational analyses of a phosphate-methylated d(TpT) model, for which the Rp and Sp diastereomers were separated, revealed that the backbone conformations are standard; i.e., a close resemblance with respect to right-handed B DNA is seen. The phosphate-methylated hexamer d(TpTpTpTpTpT) exists as a duplex with an exceptional stability in aqueous solution. Since the duplex is essentially uncharged, the stability of the structure is not influenced by the ionic strength of the medium. However, d(TpTpTpTpTpT) exists in the single strand form in the hydrogen-bond disrupting solvent HMPT. We feel that the present model systems may be useful as simple artificial probes for phosphate backbone-protein interactions (recognition) in which the negative charges on the phosphate groups are (partially) neutralized. In this context it is therefore of interest that complex formation between polylysine or polyarginine and DNA leads to an increased stability of the duplex as was reflected in the elevated values of Tm with respect to uncomplexed DNA.23 Our results now show that neutralization of the phosphate groups may also result in the formation of parallel DNA structures. Finally, it can be concluded that the proposed parallel structures for the phosphate-methylated thymine oligomers differ markedly from familiar DNA systems, and may therefore be considered as a valuable contribution to the design of new DNA-like structures.

Experimental Section

Synthesis. 3',5'-Di-O-acetyltidine.14 This compound was prepared by adding acetic anhydride (16.5 mmol, 1.55 mL) to a solution of thymidine (8.2 mmol, 2.0 g) in 50 mL of anhydrous pyridine. The solvent was evaporated after 3 h, and the resulting viscous glass was chromatographed on a Woelm silica gel column, using dry 2-butanone as eluent (Rf = 0.65). The product was obtained as a white crystalline solid in 41% yield. Anal. Calcd for C14H18O6N2: C, 51.50; H, 5.50; N, 8.61. Found: C, 51.84; H, 5.62; N, 8.61.

Thymidine 3',5'-di(dimethylphosphate).6 Thymidine 3',5'-diphosphate (sodium salt, purchased from P-L Biochemicals) was treated with methyl methanesulfonate according to Rhaese and Freese.6 Methylation of the phosphate groups was essentially complete, as was shown with 31P NMR spectroscopy. The methylated structure corresponds with two 31P NMR resonances, at 0.4 and 0.6 ppm, whereas two signals, at 3.8 and 4.1 ppm are found for the unmethylated compound.

3'-O-Acetyltidine. 5'-Tritidine (15.6 mmol, 7.53 g) and acetic anhydride (16 mL) were dissolved in 70 mL of anhydrous pyridine. This mixture was magnetically stirred overnight. After complete removal

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(22) A syn conformation for thymine has been observed in the left-handed duplex of d(CGCGATCGCG), in which the C-bases are brominated. See: Feigon, J.; Wang, A. H.-J.; van der Marel, G.; van Boom, J. H.; Rich, A. Science 1985, 230, 82.

of the solvent (coevaporation with two 20-mL portions of water), the oily residue was chromatographed on a Woaelm silica gel column, using dry 2-butanol as eluent. The yield of 5'-trityl-3'-O-acetyltymidine (Rf = 0.52) was 8.01 g (98%). 1H NMR (acetone-d6) δ 1.48 (3 H, s, CH3 base), 2.06 (3 H, s, CH3 acetyl), 2.48-2.54 (2 H, m, H2, H4, 3.46-3.50 (2 H, m, H1, H3, 4.18 (1 H, m, H5), 5.50 (1 H, m, H7), 6.38 (1 H, dd, H6), 7.24-7.56 (15 H, m, trityl), 7.64 (1 H, s, H8). A solution of the crude tritylated material (7.8 g) was mixed with water (4:1 v/v) and held for 10 min. After complete evaporation of the acetic acid (coevaporation with two 20-mL portions of water), the white residue was chromatographed on a Woaelm silica gel column, using dry 2-butanol as eluent. 3'-O-Acetyltymidine (Rf = 0.23) was obtained as a white foam; yield 3.03 g (77%); 1H NMR (acetone-d6) δ 1.84 (3 H, s, base), 2.00 (3 H, s, CH3 acetyl), 2.36-2.40 (2 H, m, H2, H4), 2.88 (1 H, bs, OH), 3.83-3.88 (2 H, m, H3, H5), 4.09 (1 H, m, H5), 5.35 (1 H, m, H6), 6.12 (1 H, dd, H7), 7.84 (1 H, s, H8).

3'-[Methoxy-N,N-disopropylaminophosphino]-5'-trityltymidine
5'-Trityltymidine (14.3 mmol, 6.9 g) was suspended in a mixture of acetic acid and water (4:1 v/v) as the eluent. Concentration of the appropriate product (0.17 g, fractions were 38 and 42 min). Chromatographic Separation of the Diastereomers of 1. The separation of the diastereomers of 1 was performed with a Dupont-830 HPLC system which was equipped with a Nucleosil 100-7-C8 column (250 x 20 mm) and a Zeiss EM2D UV detector (set at 265 nm). The product was prepared from acetonitrile (13%, HPLC grade), glacial acetic acid (1%, ethyl hexane), triethylamine (1%, Gold Label grade), and deionized water. The flow rate was 20–25 mL/min. The elution times for the fractions were 38 and 42 min. dNucleotides. The hexamers d(TpTpTpTpT)24 and (CpCpCpCpCpCpCp)2 were synthesized on a 10-μmol scale with an Applied Biosystems 380A DNA synthesizer following a standard phosphite (OCH3) triester synthesis protocol. The purity of the material was carefully checked with gel electrophoresis and HPLC. For d(TpTpTpTpT), methylation of the phosphate groups could be performed in a straightforward manner according to the procedure of Beaucage and Fmee.43 The methylation was essentially complete (99%), as was shown by precipitation on only 1% of the unmethylated starting material with ethanol/water (75:25 v/v). In the case of d(CpCpCpCpCpCpCp), phosphate methylation was accomplished as follows. The product from the synthesizer was dissolved in 1 mL of dry pyridine, benzyl alcohol (10 equiv) was added. After stirring for 24 h, the pyridine was completely removed. The residue was dissolved in 1 mL of water, and methyl methanesulfonate (7 equiv) was added. After standing overnight, the solvent was evaporated, and 1.5 mL of a 5% solution of hydrazine in water was added. Base protection was complete after stirring at 30 °C for 5 h, as was proven with thin layer chromatography. Finally, the appropriate spectral windows (10-15 ppm) were chosen and Fourier hyperchromicity experiments on the phosphate-methylated dodecamer were performed with a Perkin-Elmer 124 spectrophotometer, using 10-mm cuvettes and a wavelength of 260 nm.

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