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Cationic phosphoramidate α-oligonucleotides efficiently target single-stranded DNA and RNA and inhibit hepatitis C virus IRES-mediated translation

Thibaut Michel, Camille Martinand-Mari¹, Françoise Debart*, Bernard Lebleu¹, Ian Robbins¹ and Jean-Jacques Vasseur

Laboratoire de Chimie Organique Biomoléculaire de Synthèse, UMR 5625 CNRS-UMII, CC 008, Université Montpellier II, Place Eugène Bataillon, 34095 Montpellier Cedex 05, France and ¹UMR 5124 CNRS-UMII, IGMM, Centre National de la Recherche Scientifique, 1919 Route de Mende, 34293 Montpellier Cedex 05, France

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ABSTRACT

A potential means to improve the efficacy of steric-blocking antisense oligonucleotides (ON) is to increase their affinity for a target RNA. The grafting of cationic amino groups to the backbone of the ON is one way to achieve this, as it reduces the electrostatic repulsion between the ON and its target. We have examined the duplex stabilising effects of introducing cationic phosphoramidate internucleoside linkages into ON with a non-natural α-anomeric configuration. Cationic α-ON bound with high affinity to single-stranded DNA and RNA targets. Duplex stabilisation was proportional to the number of cationic modifications, with fully cationic ON having particularly high thermal stability. The average stabilisation was greatly increased at low ionic strength. The duplex formed between cationic α-ON and their RNA targets were not substrates for RNase H. The penalty in \( T_m \) inflicted by a single mismatch, however, was high; suggesting that they are well suited as sequence-specific, steric-blocking, antisense agents. Using a well-described target sequence in the internal ribosome entry site of the human hepatitis C virus, we have confirmed this potential in a cell-free translation assay as well as in a whole cell assay. Interestingly, no vectorisation was necessary for the cationic α-ON in cell culture.

INTRODUCTION

Antisense (AS) oligonucleotides (ON) are ligands of choice to target RNA sequences and diminish, or abrogate, the expression of specific genes (1,2). Indeed, over 42 AS-ON are currently being screened as potential drugs and one is currently an FDA-approved drug (3).

The inherent instability of phosphodiester ON in biological media, and the problems often encountered with the widely used phosphorothioate analogue, have led to the elaboration of a large panoply of novel DNA analogues that possess vastly augmented nuclease resistance (4,5). The potential pharmacological benefits of such analogues are, however, tempered by their incapacity to form a substrate for RNase H, a cellular enzyme that degrades the RNA strand of the DNA:RNA heteroduplex formed between the AS-ON and its target RNA. Despite this, a number of studies have shown that RNase H-incompetent ON can efficiently down regulate specific gene expression by steric hindrance of a specific stage in the processing of information from DNA to protein (6).

An obvious means to increase the efficacy of these so-called ‘steric-blocking’ ON is to improve their affinity for the RNA target sequence. The grafting of cationic amino groups to the ON is a potential means to increase the thermal stability of the duplex formed between the ON and the RNA target, as it can reduce the electrostatic repulsion between the phosphate moieties of the two strands of the duplex.

Cationic groups can be introduced via nucleobase (7–10), sugar (11–13) or backbone modifications (14–23). However, cationisation of the internucleoside linkage has the clear advantage that it can be achieved with only minor adaptations to existing automated DNA synthesis protocols. Furthermore, whilst the grafting of cationic groups on nucleobases or sugars allows the formation of zwitterionic ON, backbone modifications can lead to both zwitterionic as well as fully modified cationic ON.

Although backbone-modifications generally confer a good resistance to nuclease degradation, in most cases, modifications of phosphate groups induce a destabilisation of the duplex. This presumably results from the diastereoisomery due to phosphorus chirality (24), compared with unmodified phosphodiester (PO)-ON. Such stereoisomeric constraints also apply to cationic backbone-modified ON (21). For example, Letsinger has shown that an ON with alternating anionic phosphodiester and cationic stereo-uniform phosphoramidate linkages formed a stable duplex with its DNA target whereas a similar ON containing the other stereoisomer did not bind efficiently (16). Despite this chirality problem, zwitterionic
hybridisation as compared to natural anionic gated. We have also examined the base pairing specificity of cationic linkages within an anionic effects on duplex stability of the number and distribution of ON bind with high affinity to their single-stranded targets. The and diagnostic purposes, we demonstrate that these cationic RNA. Of special interest, with respect to potential therapeutic properties of the phosphoramidate internucleotide linkage on the hybridisation more stable duplexes than their -ON, which were pioneered by our group, form stable parallel-stranded duplexes with parallel orientation with respect to the target. It is well established that α-ON, and their backbone modified phosphorothioate, methylphosphonate and phosphoramide analogues, hybridise to their nucleic acid targets with a parallel orientation (25–30). For this reason, all the PNHDMAP α-ON, were able to elicit Escherichia coli RNase H hydrolysis of a complementary RNA target. Despite this, they were capable of specifically inhibiting translation initiated at the internal ribosome entry site (IRES) of the human hepatitis C virus (HCV) in vitro and in intact cells.

MATERIALS AND METHODS

Oligonucleotides

It is well established that α-ON, and their backbone modified phosphorothioate, methylphosphonate and phosphoramide analogues, hybridise to their nucleic acid targets with a parallel orientation (25–30). For this reason, all the PNHDMAP α-ON described here were designed with a parallel orientation with respect to the target.

Modified α-ON 3–5 and 11 (Table 1) were synthesized (1 μmol scale) with an ABI Model 381A DNA synthesizer using phosphoramide chemistry (31). Protected deoxy-2'-α-ribonucleoside-3'-phosphoramidites (α-dT, α-dC<sub>Bz</sub> and α-dA<sub>Bz</sub>) were prepared according to published procedures (32). The phosphoramide linkages were introduced into the α-analogues 3–5 through 3'-phosphoramide diminoleside building blocks containing a PNHDMAP linkage (T+T, C+T, T+C), prepared according to a procedure described in the literature for the synthesis of β-analogues (17) and further used by us for α-analogues (25). Oligomers 3–5 were synthesised following standard phosphoramidite chemistry except that extended coupling times (3 × 3 min) were applied.
for the coupling step of the α-dinucleotides. The elongation of chimeric α-ON 6, 7, 12, 12*, 13, 16 and 17 (Table 1), containing mixed PO and PNHDMAP domains, was performed in blocks on an ABI Model 394 DNA synthesizer using hydrogen phosphonate chemistry (33) with protected α-nucleoside 3′-H-phosphonates (25,34) (Scheme 1). The oxidation of each block was carried out manually by the syringe technique outside the synthesizer (22). The phosphodiester bonds were generated by oxidation of the corresponding H-phosphonate diester block with standard iodine–pyridine–water treatment, whereas the PNHDMAP linkages were obtained by oxidation with anhydrous CCl₄ (450 μl) in the presence of pyridine (450 μl) and N-dimethylaminopropylamine (100 μl) (Aldrich) (Scheme 1). In the same way, fully backbone-modified ON 18, 19 and 20 were prepared via H-phosphonate chemistry. The H-phosphonate diester linkages were then manually oxidized by CCl₄ in the presence of 2-methoxethylamine for ON 19 or N-dimethylaminopropylamine for ON 18 and 20. After deprotection with concentrated aqueous ammonia (30%) at 40°C for 5 h, α-ON were purified by preparative HPLC. For ON 3–6, 12, 12*, 16 and 17, purification was performed with a Nucleogel SAX 1000-8 column (50 × 4.6 mm; Macherey Nagel) using a 30 min linear gradient of 0–300 mM NaCl in 5 mM NaOH (pH 12) at a flow rate of 1.5 ml/min. ON 7, 13, 14, 18 and 20 were purified with a Nucleogel SCX 1000-8 column (50 × 4.6 mm; Macherey Nagel) using a 25 min linear gradient of 0–1 M NaCl in 20 mM KH₂PO₄ (pH 6) containing 20% CH₃CN at a flow rate of 1.5 ml/min. Purification of ON 19 was performed by preparative RP–HPLC as previously described (25). All ON were further desalted with Chroma®x PS-RP cartridges (Macherey-Nagel). Their final purity was confirmed by HPLC and their characterization was performed by MALDI-TOF mass spectrometry (data not shown). Unmodified ON 1, 2, 8, 8a–c, 9, 9a–c, 10, 15 (Table 1) were purchased from Eurogentec (Seraing, Belgium).

**UV melting experiments**

The concentration of each ON was determined spectrophotometrically at 260 nm and at 80°C assuming that the molar extinction coefficient of each ON is the sum of the molar extinction coefficients of the constitutive deoxynucleotides. Optical measurements were carried out on a Uvikon 943 spectrophotometer (Kontron). The temperature of the cell was controlled by a Huber temperature programmer (Ministat) connected to a refrigerated ethyleneglycol/water bath. The cell compartment was continuously flushed with dry nitrogen when the temperature was below room temperature. Prior to the experiments, the ON, each at a final concentration of 3 μM, were mixed in 100 mM NaCl, 10 mM sodium cacodylate (pH 7) and allowed to incubate at 90°C for 30 min. During the melting experiments the heating rate was 0.5°C/min. Digitised absorbance and temperature values were stored in a computer for subsequent plotting and analysis. Tₘ values were determined from the maxima of the first derivative plots of absorbance versus temperature.

**Hydrolysis of RNA heteroduplexes with *E.coli* RNase H**

RNA target 15 was 5′-end labeled using [γ³²P]ATP (ICN 3000 Ci/mmol) and T4 Polynucleotide Kinase (Invitrogen) following the manufacturer’s protocol. Control PO β-ODN or modified PNHDMAP ON 16–18 (200 pmol) and RNA 15 (0.2 pmol) were incubated in 10 μl of assay buffer (20 mM Tris–Cl, pH 8, 50 mM KCl, 10 mM MgCl₂, 1 mM dithiothreitol) for 30 min at 37°C in the presence of 2 U of *E.coli* RNase H (Sigma). Reactions were stopped by heating to
90°C for 2 min and adding 2 μl of 80% formamide gel loading buffer containing tracking dyes. Cleavage products were separated on a 20% polyacrylamide/7M urea sequencing gel. Radioactive bands were visualised by autoradiography.

Plasmids
The bi-cistronic plasmid pRL-HL was kindly provided by S. Lemon (Galveston, Texas), and is outlined in Figure 2. Cistrons 1 and 2 code for Renilla and firefly luciferases, respectively, and are separated by the HCV IRES. The plasmid is more fully described by Honda et al. (35).

RNA production
5'-capped RNA (to prime in vitro translation assays) was transcribed in vitro from the T7 promoter of pRL-HL using the Ribomax-T7 kit (Promega) following the manufacturer’s protocol. The plasmid was linearised immediately after the 3'-end of the required transcript, using HindIII restriction enzyme, purified on 1% agarose gels and electro-eluted from the excised gel bands. Five micrograms of purified plasmid were used as a template in 100 μl transcription reactions. DNase-treated RNA transcripts were purified using RNeasy mini columns (Qiagen). Purity and integrity were verified on 1% agarose gels.

In vitro translation
Translation assays were performed as described by Robbins and LeBlu (36), using nuclease-treated rabbit reticulocyte lysate (Promega) and [35S]methionine (Amersham-Pharmacia biotech; 1000 Ci/mmol) in 10 μl reactions. The translation reactions were primed with 200 ng of capped RNA in all cases. ON were added, on ice, prior to the addition of the lysate, with no specific prehybridisation step. Translated products were resolved on 12% running/4% stacking polyacrylamide–SDS gels. Vacuum-dried gels were analysed by autoradiography using Kodak Biomax films. Protein bands were quantified using NIH Image software (version 1.62).

Cell culture and establishment of stable transfectants
The hepatocyte cell line HepG2 was maintained in DMEM supplemented with non-essential amino acids (Gibco BRL), 20 mM HEPES pH 7.5 (Gibco BRL) and 10% fetal calf serum, at 37°C and 5% CO2.

pRL-HL was purified using an endotoxin-free plasmid maxiprep column (Qiagen) and transfected into HepG2 cells using FuGENE-6 (Roche) following the manufacturer’s instructions. Stably transfected clones were selected using G418 (1 mg/ml).

Intact cell assays
pRL-HL-expressing HepG2 cells (5.10⁵) were plated to each well of six-well plates and allowed to grow overnight, giving a confluency of between 60 and 80% at time of loading. Cells were incubated with ON and harvested after 24 h, by scraping into Passive Lysis Buffer (Promega). Luciferase activities were assayed using dual-luciferase chemistry (Promega) and an EG & G Berthold MicroLumat LB96P luminometer.

Table 2. Thermal stability (Tm and ΔTm) of duplexes formed between homopyrimidines ON 2–7 and their DNA target 1 and salt concentration dependence of the duplexes stability

<table>
<thead>
<tr>
<th>ON</th>
<th>DNA target 1</th>
<th>100 mM NaCl</th>
<th>ΔTm (°C)</th>
<th>No NaCl</th>
<th>Tm (°C)</th>
<th>ΔTm (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>35.5</td>
<td>20.6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>48.0</td>
<td>+12.5</td>
<td>39.0</td>
<td>+18.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>54.5</td>
<td>+19.0</td>
<td>47.5</td>
<td>+26.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>60.0</td>
<td>+24.5</td>
<td>58.2</td>
<td>+37.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>58.5</td>
<td>+23.0</td>
<td>55.5</td>
<td>+34.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>69.0</td>
<td>+33.5</td>
<td>78.5</td>
<td>+57.9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Experiments were carried out at 3 μM concentration for each strand in a buffer containing 10 mM sodium cacodylate, pH 7 at the indicated NaCl concentration. ΔTm = Tm modified ON – Tm 2.

RESULTS
Cationic internucleoside linkages stabilise hybrids
The stability of the double-stranded helix formed between an ON and a complementary ssDNA or RNA target is a compromise between hydrogen bonding and the electrostatic repulsion between the negatively charged phosphate moieties of the two strands. To investigate the extent to which the introduction of cationic internucleoside bonds (which reduce the net negative charge) into the backbone could stabilize duplexes, we evaluated melting temperatures (Tm) by thermal denaturation and renaturation experiments. We observed no differences between the thermal association and dissociation curves of the ON/DNA complementary strands tested. The introduction of cationic PNHDMAP linkages into homopyrimidine α-ON 3–7 (Tables 1 and 2), as well as into α-heteropolymers 12–14 (Tables 1 and 3), greatly increased the thermal stability of the duplexes, see for example unmodified phosphodiester β-ON 2 or 10 and α-ON 11. This stabilisation is proportional to the number of modifications. The average stabilisation was 4.4°C per modification in duplexes obtained with the homopyrimidine ON (Table 2) and 2°C in duplexes with the heteropolymer (Table 3). The average stabilisation was greatly increased at low ionic strength (6.7°C per modification) (Table 2).

The effect of cationic charge distribution on duplex formation was evaluated by comparison of the ΔTm per modification calculated for each modified ON. The homopyrimidine α-ON 6, harbouring an internal stretch of five contiguous PNHDMAP linkages, formed a slightly less stable hybrid (ΔTm/mod + 4.6°C) than an isosequential ON 5 that harbours five PNHDMAP alternated with phosphodiester linkages (ΔTm/mod + 4.9°C) (Table 2). On the other hand, ON 12, which also has a central window of five PNHDMAP linkages, formed a more stable duplex on DNA target 8 than ON 13, which has the cationic linkages in the 5' and 3' wings, even though there is one additional PNHDMAP linkage in this ON (Table 3). The sharpness of the melting curves with the DNA targets was slightly affected with increasing modifications. The higher the number of cationic linkages, the broader the temperature range over which the duplexes melted (Fig. 1A and B).

As with DNA targets, no differences between the thermal association and dissociation curves were observed with RNA
targets. The stability of the hybrids formed between the RNA target 9 and α-ON 12 and 13, containing respectively five and six cationic linkages, was only slightly higher than that with the corresponding PO α-ON 11 (ΔTm +1.2°C), but somewhat lower than the duplex formed with the natural PO β-ON 10 (ΔTm +1.6°C) (Table 3). The fully modified ON 14, however, showed a substantial enhancement of duplex stability, compared with both PO β-ON 10 and α-ON 11 (ΔTm +10.4°C and +13.2°C, respectively). The decrease in Tm observed between α-ON 12 and 13 hybridised to an RNA target when compared with a DNA target was considerably greater (ΔTm –12°C and –11°C, respectively) than the decrease observed with either PO α-ON 11 (ΔTm –1.7°C) or with PO β-ON 10 (ΔTm –0.9°C) (Table 3). In contrast with the DNA targets, all duplexes formed with RNA exhibited the same cooperativity of melting, regardless of the number of modifications and their distribution (Fig. 1C and D).

The replacement of one α-2'-deoxyadenosine, in the central cationic linkages window of α-ON 12, with a 2-amino-α-2'-deoxyadenosine (ON 12*) (37) had no effect on the duplex stability with DNA, but increased the Tm with an RNA target by 3°C.

A single mismatch in a cationic α-ON/target duplex is highly destabilising

As it has been reported that the enhancement of duplex stability by cationic polyamines can be sufficient to counter-balance the instability caused by mismatched bases (38), we evaluated the influence of a single mismatch AX in the DNA 8 or RNA 9 targets on the stability of the hybrids.

Introduction of one AC, AA or AG mismatch in the hybrids between the cationic α-ON 14 and DNA targets 8a-c decreased the Tm by 15.5, 14.0 and 12.5°C, respectively (Table 4). The average destabilisation per mismatch was

Table 3. Thermal stability (Tm and ΔTm) of duplexes formed between tat sequence ON 10–14 and their DNA 8 and RNA 9 targets

<table>
<thead>
<tr>
<th>ON</th>
<th>DNA target 8 Tm (°C)</th>
<th>RNA target 9 Tm (°C)</th>
<th>ΔTm (°C)</th>
<th>ΔTm (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>45.5</td>
<td>44.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>43.5</td>
<td>41.8</td>
<td>–2.0</td>
<td>–2.8</td>
</tr>
<tr>
<td>12</td>
<td>55.0</td>
<td>43.0</td>
<td>+9.5</td>
<td>–1.6</td>
</tr>
<tr>
<td>12*</td>
<td>55.0</td>
<td>46.0</td>
<td>+9.5</td>
<td>+1.4</td>
</tr>
<tr>
<td>13</td>
<td>54.0</td>
<td>43.0</td>
<td>+8.5</td>
<td>–1.6</td>
</tr>
<tr>
<td>14</td>
<td>72.5</td>
<td>55.0</td>
<td>+27.0</td>
<td>+10.4</td>
</tr>
</tbody>
</table>

Experiments were carried out at 3 μM concentration for each strand in a buffer containing 10 mM sodium cacodylate, pH 7, 100 mM NaCl. ΔTm = Tm modified ODN – Tm 10.

Figure 1. (a) UV-melting curves and (b) first derivative plots for the duplexes formed with DNA target 8 and β-PO 10 (green line), ON 12 (blue line), ON 13 (pink line) or ON 14 (red line). (c) UV-melting curves and (d) first derivative plots for the duplexes formed with RNA target 9 and β-PO 10 (green line), ON 12 (blue line), ON 13 (pink line) or ON 14 (red line).
higher for cationic α-ON 14 (ΔTm/mismatch −14.0°C) than for β-ON 10 (ΔTm/mismatch −12.0°C). Nevertheless, it should be noted that the increased stability of the duplex formed by the cationic α-ON compared with the β-ON with the perfect duplex is reflected by more stable hybrids with the corresponding mismatched duplexes (Table 4). In addition, the cationic α-ON 12 and 14 discriminate AG mismatches with either DNA or RNA targets better than the β-ON 10. Surprisingly, with the RNA target, the CA mismatch is less destabilising with the cationic α-ON 14 (ΔTm = −8.5°C) than for the regular β-ON (ΔTm = −11.3°C). The average destabilisation per mismatch for both cationic α-ON 14 and β-ON was identical (ΔTm/mismatch −10.0°C). Here again, the mismatched duplexes formed between the cationic α-ON 14 and the mismatched RNA targets 9a–c were more stable than the corresponding duplexes with the β-ON 10 and, indeed, greater than that of the perfectly matched RNA 9/β-ON 10 duplex (Table 4).

**Cationic α-ON/RNA duplexes are not substrates for RNase H**

Under conditions (37°C for 30 min) where the control PO ON stimulated RNA 15 degradation (data not shown), the chimeric α-ON 16–18/RNA 15 duplexes were not substrates for E.coli RNase H.

**Cationic α-ON arrest HCV IRES-mediated translation in an acellular assay**

ON complementary to the IIIId loop of the HCV IRES were tested in dose-response in an *in vitro* translation assay programmed with a bi-cistronic construction that allows the simultaneous monitoring of translation initiated at the HCV IRES (firefly luciferase) and from a classical, eukaryote, cap-dependent translation initiation site (Renilla luciferase) (Fig. 2A). Cationic α-ON were capable of arresting IRES-dependent translation, whilst having no effect on cap-dependent translation initiation (Fig. 2B). The IC50 was inversely proportional to the number of cationic charges for ON 16–18 (Fig. 2C). The fully cationic ON 18 has a significantly lower IC50 than an isosequential 2′-O-methyl-oligoribonucleotide (2′-O-Me ON). Neither neutral backboned methoxyethylphosphoramidate (PNHME) ON 19 nor a scrambled, fully cationic α-ON 20 affected IRES-mediated translation (Fig. 2C).

**Cationic α-ON arrest HCV IRES-mediated translation in cell culture**

In order to establish whether cationic α-ON are capable of blocking IRES-mediated translation in a cellular environment, the bi-cistronic construction used for the cell-free translation
The incorporation of cationic modifications, into both an oligopyrimidine α-ON and a mixed purine/pyrimidine ON, increased the melting temperatures of the duplexes formed with a DNA target in comparison with that of an unmodified phosphodiester β-ON. The increase in \( T_m \) was positively correlated to the number of cationic modifications. Curiously, the increased \( T_m \) observed with DNA targets was only observed with an RNA target when the ON was fully cationic. The lower melting cooperativity of modified duplexes with the DNA target 8 compared to PO duplex accounts for the effect of increasing mixtures of diastereoisomers, when the number of modifications increases, due to the chirality of the phosphorus atom. Indeed, this difference in hybridization abilities between isomers was previously observed in backbone-modified β-ON as well as α-ON (25). In contrast, we observed only a minor difference between isomers with α-ON when the target was RNA.

At low salt concentration, the differences in the affinity of the cationic ON 7 and the natural ON 2 is striking. This reflects the charge repulsion between the two negatively charged PO backbones of 2 and its target 1 and in contrast, the charge attraction between the cationic ON 7 and its anionic target 1. In comparison, hybrids with ON 5 and 6, with a lower net charge (−1), were less sensitive to a change of ionic strength. Compared to previously studied non-ionic PNHME α-ON (25), which induced a slight stabilisation effect, anionic or zwitterionic α-ON 12 and 13 do not improve affinity for RNA target. We have found, however, that the affinity of a PNHDMAP α-ON for the RNA target could be increased by replacing an α-2′-deoxyadenosine by a 2-amino-α-2′-deoxyadenosine (A*) that can potentially form three hydrogen bonds (37) with a complementary thymine and uracil, unlike adenine, which forms only two hydrogen bonds.

Cationic PNHDMAP α-ON exhibit the highest affinity for DNA and RNA targets of all the backbone-modified α-ON studied. This is particularly true of the fully modified cationic α-ON 14 and probably results from electrostatic interactions between cationic PNHDMAP linkages and the anionic PO backbone of the targets.

For the partially cationic α-ON, the distribution of cationic charges appears to influence the affinity for both DNA and RNA targets. A 12mer oligopyrimidine ON with five cationic linkages, for example, has a substantially higher \( T_m \) when the charged linkages are evenly distributed compared with when they are bunched into the central region. Centrally grouped cationic linkages in the mixed purine/pyrimidine α-ON, on the other hand, are more favourable than an ON with cationic linkages restricted to the wings.

It is clear that, as with virtually all second-generation (i.e. not phosphorothioate) analogues described to date, cationic PNHDMAP α-ON are incapable of forming a suitable substrate for RNase H. This is of little surprise as unmodified α-ON are themselves RNase H incompetent (39). This has a major implication for their use as antisense reagents as, unless they are coupled to an RNase activator (40) or contain an RNase H-competent central window (41), their activity is restricted to steric blockade. However, RNase H competence,
although potentially increasing activity is also a source of decreased specificity, as only a few contiguous nucleotides need to hybridise to provoke target cleavage and this reduces their ability to distinguish between a bona fide target sequence and a partially complementary by-stander sequence (42). The advantage of steric blocking by a mismatch (43) is in keeping with similar mismatches in the corresponding duplexes formed with a neutral PNHME α-ON (25) (ΔTm/mismatch ≈15.4°C), indicating that base pairing fidelity is not overwhelmed by the electrostatic attraction between the cationic ON and the anionic backbone of the target. As reported for anionic β-ON (43), for cationic α-ON hybridised to DNA targets, the least stable mismatches are those containing cytosine and the most stable mismatches are those containing guanine.

Cationic α-ON, therefore, fulfill a number of criteria critical to their use as antisense agents; namely high affinity, high stability and good selectivity. We therefore tested their applicability of cationic phosphoramidate ON as simple, non-vectorised antisense agents. We thank the Association pour la Recherche contre le Cancer for financial support (J.-J.V. and B.L.) and the Ligue Nationale pour la Recherche contre le Cancer for a post-doctoral fellowship (C.M.-M.).

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