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ENGINEERING PREFERENCES OF HAIRPIN PNA BINDING TO COMPLEMENTARY DNA: EFFECT OF N7G IN aeg/aep PNA BACKBONE

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ABSTRACT

AegPNA and aepPNA monomeric units bearing the N7-guanine nucleobase as a substitute for C⁺ have been demonstrated to bind to a GC base-pair of a duplex in a pH-independent manner when placed in the third strand. The aepPNA backbone exerts a preference for binding in the antiparallel Hoogsteen mode over the parallel Hoogsteen mode.

Aminoethylglycyl (*aeg*) Peptide Nucleic Acids (PNAs) are a class of DNA mimics that are neutral and achiral and bind to complementary DNA/RNA sequences with high affinity and sequence specificity (1). Homopyrimidine PNA₂: DNA triplex formation is pH-dependent due to the requirement of N3-protonation of cytosine for the Hoogsteen (HG) mode of recognition. PNA, with no configurational and conformational constraints, accommodates both Watson-Crick (WC) & HG binding modes in either antiparallel or parallel orientations (2). Aminoethylprolyl (*aep*)PNA recently reported by us (3) is a chiral positively charged PNA analogue and oligothymine *aep*PNAs show excellent binding properties with complementary DNA sequences. Chiral *aep*PNA is homomorphous with DNA and may induce orientational preferences in binding to DNA sequences. Mixed polypyrimidine sequences using this chiral backbone are therefore expected to display orientation-selective binding to DNA.

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Figure 1. Hydrogen bonding schemes.

In this communication, we describe the synthesis of triplex forming mixed polypyrimidine sequences using the aepPNA units at predetermined positions and study of their effect on directing the orientation selectivity. N7G is known to mimic C⁺ in its hydrogen bonding pattern (4) in the HG mode (Fig. 1) and hence, aeg/aepPNA-N7G monomeric units are introduced to circumvent the requirement of acidic pH for stable triplex formation.

The aegPNA-N7G ester 2 was synthesized by alkylation of N²-isobutyrylguanine GiBu with the ethyl N-Boc-aminoethyl-N-chloroacetyl glycinate in presence of K₂CO₃. The protected monomer units, (2S, 4S) aepPNA-N7G^{iBu} **6b** and (2S, 4S) aepPNA-C^{CBz} 6a were synthesized similarly, by alkylation of G^{iBu} and C^{CBz} with the common intermediate 5. The compound 5 was prepared by mesylation of the known compound 4 (3) (Scheme 1). The products were purified by column chromatography and characterized (5) by ¹H, ¹³C and mass spectrometry. The ester hydrolysis in all cases was effected with 1N NaOH in aq. MeOH to get the monomer synthons 3, 7a & 7b. The PNA sequences (PNA 9–11) incorporating these new monomers are listed in Scheme 2. The other aegPNA monomers, N-Boc- ϵ -aminohexanoic acid and protected lysine units were synthesized according to the literature procedures (6). The PNA oligomers synthesized by standard protocols (6) were purified by FPLC and characterized by MALDI-TOF mass spectrometry (5).

The designed control bisPNA sequence (PNA 8) with aegPNA-C units in both arms binds to both DNA 12 and DNA 13 sequences without discrimination as studied by UV melting experiments ($\Delta Tm = 0^{\circ}C$, Table 1). A higher Tm was observed at acidic pH in both the cases ($\Delta Tm \sim 7^{\circ}C$) indicating equally efficient HG and WC modes of recognition in either orientation (Scheme 2) of the target strand. Replacement of aegPNA-C in one of the arms by aegPNA-N7G (PNA 9) allows pH-independent triplex formation with the target DNA strands 12 & 13, again, without any orientation selectivity ($\Delta Tm = 2^{\circ}C$). This may be possible, as N7G is capable of recognizing a GC base pair in HG mode with either parallel or antiparallel orientation of the third strand.

In contrast to the aegPNA backbone, introduction of aepPNA-C units in this sequence (PNA 10) led to a stronger binding with DNA 13 ($Tm = 48^{\circ}C$) as compared to **DNA 12** (Tm = 37.5°C) at neutral pH exhibiting a significant bias in



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boc-N OEt
$$(i)$$
 boc-N OR (ii) 2 . $R = CH_2CH_3$ 3 . $R = H$

(i) N2-iBuG, K2CO3, DMF. (ii) NaOH, CH3OH, H2O.

Scheme 1a.

(iii) Ms-Cl, pyridine. (iv) B, K₂CO₃, DMF. (v) NaOH, CH₃OH, H₂O.

Scheme 1b.

the directionality of binding ($\Delta Tm \sim 10^{\circ}C$). This selectivity was less pronounced $(\Delta Tm \sim 5^{\circ}C)$ at acidic pH, which can be explained on the basis of the differential protonation of cytosine N3 in aegPNA-C and aepPNA-C units in the HG strand. The aepPNA backbone being protonated even at physiological pH, N3-protonation of cytosine in aepPNA-C is probably less pronounced at pH 5.8 and is reflected

Scheme 2. PNA Oligomer Sequences.





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Table 1.

DNA		DNA 12	DNA 13
PNA		Tm (°C)	Tm (°C)
aegPNA-C	PNA 8	45 (52.7)	45 (52)
aegPNA-N7G	PNA 9	45 (47)	47 (45)
aepPNA-C	PNA 10	37.5 (47)	48 (52)
aepPNA-N7G	PNA 11	42 (43)	51 (49)

Figures in parentheses denote the Tm at 5.8 pH. Tm studies were performed in 0.01 M sodium phosphate buffer, pH 7.4 with a heating rate of 0.5° C per min. The Tm values were obtained from the peaks in the first derivative plots of % hyperchromicity at 260 nm Vs temperature and are accurate to $\pm 1^{\circ}$ C. Each experiment was repeated at least twice.

in the corresponding Tm values. This result indicates that the presence of chiral aepPNA units stabilizes the PNA:DNA complex when the HG strand containing these units is in the antiparallel orientation with respect to the DNA central strand. The aepPNA-N7G units in this sequence (**PNA 11**) confirm the selectivity for the antiparallel HG mode of binding of the third strand (Δ Tm \sim 9°C). The aegPNA-C units of this sequence (**PNA 11**) are consequently in the WC mode of binding and hence, no change was observed in Tm at lower pH (Δ Tm \pm 1°C).

In summary, the introduction of *aepPNA* units in the backbone of triplex forming PNA oligomers strongly influences the recognition of DNA in an orientation selective manner. The triplex formation is pH-dependent when *aepPNA*-C units are used, while *aepPNA*-N7G units permit triplex formation at physiological pH.

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- 5. Characteristic signals: **2**: ¹H NMR (CDCl₃) δ: 10.1 (s, 1H, *G*-N*H*), 7.9 (s, 1H, *G-H*8). ¹³C NMR δ: 167.2 (*G-C*H₂-CO), 162.9 (*G-C*2), 156.4 (*G-C*4), 148.0 (*G-C*6),



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145.2 (*G*-*C*8), 112.2 (*G*-*C*5). **6b**: ¹H NMR (CDCl₃) δ : 12.1 (br s, 1H, *G*-N*H*), 8.4 (s, 1H, *G*-*H*8), 5.6 (m, 1H, *H*4). ¹³C NMR δ : 156.4 (*G*-*C*2), 156.0 (*G*-*C*4), 147.5 (*G*-*C*6), 142.3 (*G*-*C*8), 111.5 (*G*-*C*5), 59.5 (*C*4). MALDI-TOF: **PNA 8:** [M]_{obs} = 4499.75, [M]_{calc} = 4495.64; **PNA 9:** [M]_{obs} = 4580.88, [M]_{calc} = 4575.69.

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