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EFFECT OF SUBSTITUTING ARABINONUCLEOSIDES FOR DEOXYNUCLEOTIDES IN THE DNA PRIMING STRAND ON THE POLYMERASE ACTION OF HIV-1 RT

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EFFECT OF SUBSTITUTING ARABINONUCLEOSIDES FOR DEOXYNUCLEOTIDES IN THE DNA PRIMING STRAND ON THE POLYMERASE ACTION OF HIV-1 RT

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ABSTRACT

The ability of 5'-DNA-araN-3' chimeras to serve as primers during HIV-1 RT-catalyzed DNA synthesis was assessed. It is shown that while the structural changes imparted by the arabinose units are minimal, the biological outcome is significant. For example, a DNA strand with arabinocytidine (araC) at the 3'-terminus was found to serve as a primer of DNA synthesis but significant pausing of HIV-RT was observed after the addition of 4 dNTP's. This phenomenon was not observed for the analogous DNA primer containing a riboC unit or an all-DNA strand.

Arabinonucleosides are stereoisomers of the naturally occurring ribonucleosides, differing only in the configuration at the 2'-position of the sugar ring (Fig. 1A). This seemingly "minor" alteration of the sugar ring leads to nucleoside analogues with remarkable biological activities, including anticancer and antiviral activities (1,2). Recent reports on arabinonucleic acids (ANA) are rapidly drawing attention with the main emphasis being the impact of 2'-stereochemistry (RNA *versus* ANA)

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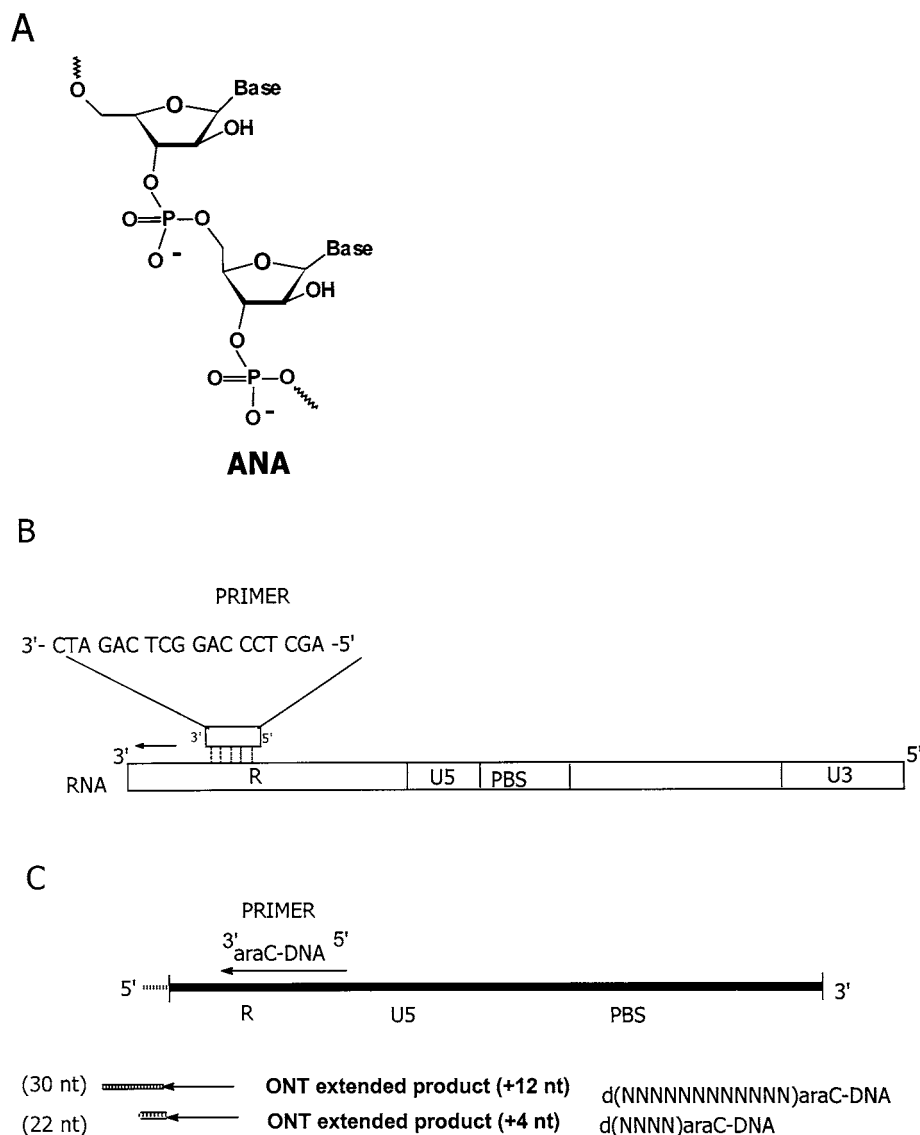


Figure 1. (A) Arabinonucleic acids. (B) The R region sequence of the HIV-1 genomic RNA. The sequence of the antisense primer molecule is 5'-AGC TCC CAG GCT CAG ATC-3'. (C) Schematic illustration of DNA polymerization products in the *in vitro* DNA polymerization reactions.

on physicochemical and biological properties (3). For example, both *E.coli* RNase H and HIV-1 RT associated RNase H cleave RNA strands of ANA:RNA duplexes, but not those of RNA:RNA duplexes (3a,c).

Chimeric oligonucleotides serve as excellent probes for studying the mechanism by which polymerases read-through the backbone of nucleic acid double



helices. Recent studies with chimeric RNA-DNA oligonucleotides have increased our understanding of the mechanism of substrate discrimination (rNTP *versus* dNTP) and extension of RNA transcripts by T7 RNA polymerase (4). Similar studies on HIV-1 reverse transcriptase (RT) have been reported (5). It is known that when HIV-1 RT encounters an altered nucleotide on the template strand, the enzyme may read through, pause or terminate synthesis (6). Primer extension may be accomplished with fidelity or with the insertion of a random or particular incorrect base while pausing (6). Termination may also occur before, at or after encountering the modified site on the template strand (6). It is not known whether DNA strands incorporating arabinonucleotides (araN) can serve as primers of RNA-dependent DNA polymerization, nor if they have been used to probe the mechanism of HIV-1 RT translocation.

Here, we describe a study in which chimeric oligodeoxynucleotides containing arabinonucleotide residues (araN) were characterized for hybridization affinity and the ability to prime reverse transcription. Specifically, we wished to assess the efficiency with which HIV-1 RT extended a DNA-araC primer bound to an RNA template. The primers synthesized were 18-mer chimeric oligonucleotides complementary to the R-region of genomic HIV-1 RNA (Fig. 1B), the sequence of which are shown in Table 1. First, the ability of these oligomers to form duplexes with complementary RNA and DNA was determined from UV melting and circular dichroic spectroscopy. T_m values listed in Table 1 indicate that as deoxynucleotides near the middle of the strand were replaced by arabinonucleotides, T_m values with the target RNA were reduced slightly at *ca.* 0.5°C/substitution. The destabilizing effect was greater when the chimeras hybridized to a target DNA (ΔT_m *ca.* -2.3°C/araN). However, it should be noted that the apparent

Table 1. Thermal Stability of Duplexes Formed by DNA-ANA Chimeras with Target RNA and DNA Single Strands

| Antisense Oligomer | Code | Antisense Sequence with ARA and Ribo Inserts | T_m (°C) | |
|--------------------|------|--|------------|------|
| | | | RNA | DNA |
| D18 | I | 5'-AGC TCC CAG GCT CAG ATC-3' | 72.3 | 68.0 |
| DNA-araC1 | II | 5'-AGC TCC CAG GCT CAG ATaC-3' | 71.6 | 68.0 |
| DNA-araU2 | III | 5'-AGC TCC CAG GCT CAG AaUC-3' | 71.7 | 65.5 |
| DNA-araA3 | IV | 5'-AGC TCC CAG GCT CAG aATC-3' | 71.7 | 65.5 |
| DNA-araG4 | V | 5'-AGC TCC CAG GCT CAaG ATC-3' | 69.9 | 64.0 |
| DNA-araA5 | VI | 5'-AGC TCC CAG GCT CaAG ATC-3' | 71.7 | 66.2 |
| DNA-araC16 | VII | 5'-AGaC TCC CAG GCT CAG ATC-3' | 71.5 | 65.0 |
| DNA-riboC1 | VIII | 5'-AGC TCC CAG GCT CAG ATrC-3' | 71.1 | 68.0 |
| R18 | IX | 5'-AGC UCC CAG GCU CAG AUC-3' | 84.6 | 66.2 |

All duplexes were 2.3 μ M in concentration. Buffer: 140 mM KCl, 1 mM MgCl₂, 5 mM Na₂HPO₄ (pH = 7.2). Target RNA:GAU CUG AGC CUG GGA GCU, Target DNA:GAT CTG AGC CTG GGA GCT.



destabilization caused by arabino units is significantly smaller than that created by mismatches at similar positions ($\Delta T_m = -5^\circ\text{C}$), suggesting that araN residues in these duplexes retain classical base-pairing interactions. This conclusion is also evident in the work of Beardsley and co-workers, who found that substituting dN for araN residues in the DNA strand of DNA:RNA and DNA:DNA duplexes resulted only in a moderate loss of stability (7).

The CD spectra of the DNA/araN:RNA hybrids closely resemble the spectra of unmodified DNA:RNA hybrids, all of which displayed characteristic "A-helix" patterns. The major difference seen among the spectra of the various DNA/araN:RNA hybrids was the magnitude of the negative Cotton effect at *ca.* 210 nm. The intensity of this peak gradually decreased as the araN insert was moved from the 3'-end towards the middle of the sequence, reaching a minimum when the araN residue was located at position -4. These observations suggest that while helix conformation of DNA/RNA hybrids is not significantly altered by an araN substitution, disruption of this particular hybrid sequence is greatest when the araN residue is located *ca.* 4 to 5 nt upstream from the DNA primer's 3'-end. Remarkably, these observations correlate well with ability of DNA/araC primers to partially block HIV-RT catalyzed DNA polymerization.

Thus, whereas HIV-1 RT readily extends the antisense unmodified DNA primer I to form the expected 30 nt product (Fig. 1C), primer extension is significantly reduced for the DNA primer containing the araC at the 3' end. In this case, significant pausing of HIV-RT was noted after the addition of the 4th DNA residue producing primarily 5'-DNA-araC-dNNNN-3' (" +4 product") and only ~10% of the expected full-length (30 nt) product. Pausing is also observed for the chimeric DNA primers containing araN at internal positions (e.g., -1, -2, -3 and -4). In all cases, the polymerization reactions produced the 'premature' 5'-dN...dN-araN-dNNNN-3' (or " +4") product as well as the expected full-length 30 nt product (Fig. 1C). There seems to be no change in priming relative to the DNA control when the araN residue is placed at, and past, the fifth position (primers VI-VII, Table 1). Interestingly, a primer containing riboC at the 3'-end (DNA-riboC) was fully extended to the 30 nt product without accumulation of the corresponding " +4 product".

In conclusion these results indicate that when araX is located at or near the 3' terminus of a DNA primer, the arabinose 2'-hydroxyl group, while not significantly affecting the stability of the primer terminus, interferes directly with the mechanism by which HIV-1 catalyzes phosphodiester bond formation. In addition, the results suggest that while the arabinose 2'-OH does not cause *immediate* chain termination, the efficiency of subsequent steps, particularly the addition of the 5th dN nucleotide, is very much dependent on the sugar stereochemistry at position 2' (ribo *versus* arabino). This may be due to either "physical blockage" of HIV-RT translocation when the enzyme encounters the arabinonucleotide residues, and/or subtle changes in helix conformation as demonstrated by our CD experiments.



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