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Supporting Information

Tables [Ia], [Ib], [Ic], [Id]: Major cleavage fragments detected in MALDI-TOF mass experiments for CLB-HyM-10 versus U4A-L4T, CLB-HyM-10 versus XU4A-XL4T, CLB-HyQ-10 versus U4A-L4T, CLB-HyQ-10 versus XU4A-XL4T, respectively. The sequence of the cleavage fragments are arranged in order of decreasing mass peak intensity.

 $5'-T_1 - A_2 - G_3 - G_4 - A_5 - G_6 - A_7 - A_8 - A_9 - A_{10} - T_{11} - A_{12} - C_{13} - 3'$ $3'-A_{26} - T_{25} - C_{24} - C_{23} - T_{22} - C_{21} - T_{20} - T_{19} - T_{18} - T_{17} - A_{16} - T_{15} - G_{14} - 5'$ 5'-A₁- A₂- G₃ - G₄ - A₅- G₆- A₇- A₈ - A₉- A₁₀-T₁₁-A₁₂-C₁₃-3 3'-T₂₆-T₂₅-C₂₄- C₂₃- T₂₂-C₂₁-T₂₀-T₁₉-T₁₈-T₁₇-A₁₆-T₁₅-G₁₄-5'

Duplex U4A-L4T

Duplex XU4A-XL4T

Figure [I]. Autoradiographs showing cleavage of 158-mer (left panels) and 135-mer (right panels) of pBR322 DNA fragment induced by DNase I (footprinting) in the presence of peptide HyQ-10 (upper panels), or induced by incubating with conjugate CLB-HyQ-10 in 5 mM sodium cacodylate buffer (pH 6.5) at 37°C for 30 min (lower panels).

Figure [II]. CD spectra: Panel A: Titration of duplex U4A-L4T versus peptide HyQ-10 at peptide concentrations of 0.5, 1.0, 2.2, 2.4, 2.6, 2.8, 3.0, 3.2, 3.4, 4.0, 5.0, 7.0 μ M at 37°C. Panel B: Corresponding CD difference spectra with the contribution of free duplex and peptide HyQ-10 subtracted. Panel C: Titration of U4A-L4T versus conjugate CLB-HyQ-10 at conjugate concentrations of 0.5, 1.0, 1.5, 1.8, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 3.0, 3.5, 4.0, 5.0 μ M at 37°C. Panel D: Corresponding difference spectra with the contribution of free duplex and conjugate CLB-HyQ-10 subtracted.

Figure [III]. Plots of relative intensity of MALDI-TOF mass peaks of major cleavage fragments induced by conjugates CLB-HyM-10, (panel A) and CLB-HyQ-10 (panel B) on the oligonucleotide duplex U4A-L4T; and plots of relative intensity of MALDI-TOF mass peaks of major cleavage fragments induced by conjugates

CLB-HyM-10 (panel C), and CLB-HyQ-10 (panel D) on the oligonucleotide duplex XU4A-XL4T. Representative MALDI-TOF mass peaks of major cleavage fragments induced by conjugate CLB-HyM-10, (panel E); and conjugate CLB-HyQ-10, (panel F) on the oligonucleotide duplex XU4A-XL4T

Figure [IV]. Proposed DNA cleavage mechanism via depurination and carboxonium ion intermediates induced by CLB-peptide conjugates.

Mass	Strand	Cleavage fragments	Proposed cleavage
			mechanism
2033.9	Lower	T ₁₉ T ₂₀ C ₂₁ T ₂₂ C ₂₃ C ₂₄ dr 5' HO ₃ PO P P P P P P OH 3' (Na ⁺)	Depyrimidination of T ₁₈ and
			T ₂₅
2337.3	Upper	G4 A5 G6 A7 A8 A9 A10 5' HO3PO ↓ P↓ P↓ P↓ P↓ P↓ P↓ OPO3H 3' (Na ⁺)	Depurination of G_3 and
			depyrimidination of T ₁₁
2643.2	Upper	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Depyrimidination of T ₁ and
			depurination of A ₁₀
1732.3	Upper	T ₁ A ₂ G ₃ G ₄ A ₅ dr 5' CH ₃ P P P P P OH 3'	Depurination of G ₆
1597.9	Lower	T ₁₇ T ₁₈ T ₁₉ T ₂₀ C ₂₁ 5' HO ₃ PO P P P P OPO ₃ H 3'	Depurination of A ₁₆ and
			depyrimidination of T_{22}
998.3	Lower	G ₁₄ T ₁₅ A ₁₆	Depyrimidination of T ₁₇
		5' CH ₃	
2943.8	Lower	T ₁₅ A ₁₆ T ₁₇ T ₁₈ T ₁₉ T ₂₀ C ₂₁ T ₂₂ C ₂₃ dr 5'HO P P P P P P P P P P P P P OPO3H 3' (Na ⁺)	Depurination of G ₁₄ and
			depyrimidination of C ₂₄
806.3	Upper	A ₈ A ₉ dr 5' HO ↓ P ↓ P ↓ OH 3' (Na [*])	Depurination of A_{10} and A_7
1442.2	Upper	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Depurination of A ₅
1948.7	Lower	T ₁₅ A ₁₆ T ₁₇ T ₁₈ T ₁₉ T ₂₀ 5' HO ₃ PO P P P P P P OPO ₃ H 3' (Na ⁺)	Depurination of G_{14} and C_{21}

Table [1a]. CLB-HyM-10 versus U4A-L4T

Mass	Strand	Cleavage fragments	Proposed cleavage
			mechanism
998.6	Lower	G ₁₄ T ₁₅ A ₁₆ 5' CH ₃ ↓ P ↓ P ↓ OPO ₃ H 3' (Na ⁺)	Depyrimidination of T ₁₇
1948.5	Lower	T ₁₅ A ₁₆ T ₁₇ T ₁₈ T ₁₉ T ₂₀ 5' HO ₉ PO \P \P \P \P \P \P \OPO ₃ H 3' (Na ⁺)	Depurination of G_{14} and depyrimidination of C_{21}
1597.9	Lower	T ₁₇ T ₁₈ T ₁₉ T ₂₀ C ₂₁ 5' HO ₃ PO P P P P P OPO ₃ H 3'	Depurination of A_{16} and depyrimidination of T_{22}
1960.3	Upper		Depyrimidination of C_{13} and depurination of G_6
711.0	Upper	A10 T11 5' HO3PO P OPO3H 3'	Depurination of A_9 and A_{12}
926.3	Lower		Depurination of A_{16} and depyrimidination of T_{20}
806.1	Upper	A ₈ A ₉ dr 5' HO ↓ P ↓ P ↓ OH 3' (Na ⁺)	Depurination of A_{10} and A_7
2025.2	Upper	G4 A5 G6 A7 A8 A9 5'H03P0 PPPPPPPPPPPPOP03H 3' (Na ⁺)	Depurination of G_3 and A_{10}
2033.1	Lower	Т ₁₉ Т ₂₀ С ₂₁ Т ₂₂ С ₂₃ С ₂₄ dr 5' HO ₃ PO / P / P / P / P / P / P / OH 3' (Na ⁺)	Depyrimidination of T_{18} and T_{25}
2186.9	Upper	A1 A2 G3 G4 A5 G6 A7 5' CH3 P P P P P P P P P O	Depurination of A ₈

Table [Ib]. CLB-HyM-10 versus XU4A-XL4T

Table [Ic]. CLB-HyQ-10 versus U4A-L4T

Mass	Strand	Cleavage fragments	Proposed cleavage
			mechanism
712.4	Upper	A10 T11 5' HO3PO	Depurination of A_9 and A_{12}
998.3	Lower	G ₁₄ T ₁₅ A ₁₆ 5' CH ₃ , P, P, OPO ₃ H 3' (Na ⁺)	Depyrimidination of T ₁₇
1732.7	Upper	T ₁ A ₂ G ₃ G ₄ A ₅ dr 5' CH ₃ \downarrow P \downarrow P \downarrow P \downarrow P \downarrow OH 3'	Depurination of G ₆
2337.5	Upper	G4 A5 G6 A7 A8 A9 A10 5' HO3PO \ P \ P \ P \ P \ P \ P \ OPO3H 3' (Na ⁺)	Depurination of G_3 and depyrimidination of T_{11}
2033.9	Lower	T ₁₉ T ₂₀ C ₂₁ T ₂₂ C ₂₃ C ₂₄ dr 5' HO ₃ PO ↓ P ↓ P ↓ P ↓ P ↓ P ↓ OH 3' (Na ⁺)	Depyrimidination of T_{18} and T_{25}
2642.6	Upper	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Depyrimidination of T_1 and depurination of A_{10}
1442.3	Upper	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Depurination of A ₅
2177.6	Upper	T ₁ A ₂ G ₃ G ₄ A ₅ G ₆ A ₇ 5' CH ₃ P P P P P P OH 3'	Depurination of A ₈
2943.9	Lower	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Depurination of G ₁₄ and depyrimidination of C ₂₄
970.7	Upper	A ₅ G ₆ A ₇ 5' HO ↓ P ↓ P ↓ OPO ₃ H 3'	Depurination of G_4 and A_8
926.7	Lower	T ₁₇ T ₁₈ T ₁₉ 5' HO ↓ P ↓ P ↓ OPO₃H 3'	Depurination of A_{16} and depyrimidination of T_{20}
1140.8	Upper		Depurination of A_{12} and A_8
1948.6	Lower	T ₁₅ A ₁₆ T ₁₇ T ₁₈ T ₁₉ T ₂₀ 5' HO₃PO \ P \ P \ P \ P \ P \ OPO₃H 3' (Na ⁺)	Depurination of G_{14} and depyrimidination of C_{21}

Mass	Strand	Cleavage fragments	Proposed cleavage
			mechanism
712.7	Upper	A10 T11 5' HO3PO P OPO3H 3'	Depurination of A_9 and A_{12}
998.3	Lower	G ₁₄ T ₁₅ A ₁₆ 5' CH ₃ ↓ P ↓ P ↓ OPO ₃ H 3' (Na ⁺)	Depyrimidination of T ₁₇
2024.8	Upper	G4 A5 G6 A7 A8 A9 5'HO3PO↓P↓P↓P↓P↓P↓OPO3H 3' (Na ⁺)	Depurination of G_3 and A_{10}
2033.9	lower	Т ₁₉ Т ₂₀ С ₂₁ Т ₂₂ С ₂₃ С ₂₄ dr 5' HO ₃ PO , P, P, P, P, P, P, OH 3' (Na ⁺)	Depyrimidination of T_{18} and T_{25}
970.7	Upper	A ₅ G ₆ A ₇ 5' HO ↓ P ↓ P ↓ OPO₃H 3'	Depurination of G_4 and A_8
1948.7	Lower	T ₁₅ A ₁₆ T ₁₇ T ₁₈ T ₁₉ T ₂₀ 5' HO₃PO P P P P P OPO₃H 3' (Na ⁺)	Depurination of G ₁₄ and depyrimidination of C ₂₁
1451.2	Upper	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Depurination of A_5
2186.6	Upper	A1 A2 G3 G4 A5 G6 A7 5' CH3 P P P P P P P OH 3'	Depurination of A ₈

Table [Id]. CLB-HyQ-10 versus XU4A-XL4T



Figure [I]

A HyQ-10 / U4A-L4T





C CLB-HyQ-10 / U4A-L4T



D CLB-HyQ-10 / U4A-L4T Difference spectra



Figure [II]



Figure [III]



D



Figure [III]



Figure [III]



Figure [III]



F



Figure [III]

F



Figure [IV]

5'-A₁ - A₂ - G₃ - G₄ - A₅-G₆ - \downarrow A₇ \downarrow -A₈-A₉ - A₁₀-T₁₁- A₁₂- 3' H₂N-KR-(Py)₄-K-R-P_h-M- X X -M-P_h-R-K - (Py)₄-R-K-NH₂

3'-dr - C₂₄- **C**₂₃- **T**₂₂-**C**₂₁ \downarrow -**T**₂₀-**T**₁₉-**T**₁₈-**T**₁₇- **A**₁₆- **T**₁₅-**5'** The chemical nuclease activity, energetics, and stepwise cleavage

mechanism of chlorambucil-peptide conjugates are presented.