

Supporting Information

Derivatives of 5-nitro-furan-2-carboxylic acid carbamoylmethyl ester inhibit RNase H activity associated with HIV-1 reverse transcriptase

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Text

We studied the purified reverse transcriptases of HIV-1 clade C Indie-C1^{S1} and CRF01_AE 93JP-NH1^{S2}. Alignment of reverse transcriptase amino acid sequences of the clade B B.FR.x.pNL43, clade C Indie-C1, and 93JP-NH1 is provided in Figure S1 (Fig. S1). The unique amino acids of 93JP-NH1 RT, namely Ser447 His499 Arg512 Val517 Glu524 Lys550, may be responsible for its higher susceptibilities toward compounds 1 and 2 (Fig. 3B and Table 1).

Figure legends

Figure S1. Alignment of reverse transcriptase amino acid sequences of the clade B B.FR.x.pNL43, clade C Indie-C1, and 93JP-NH1, a representative of CRF01_AE. Sequences were aligned using CLUSTAL W software.

References

- (S1) Mochizuki, N.; Otsuka, N.; Matsuo, K.; Shiino, T.; Kojima, A.; Kurata, T.; Sakai, K.; Yamamoto, N.; Isomura, S.; Dhole, T.N.; Takebe, Y.; Matsuda, M.; Tatsumi, M. An infectious DNA clone of HIV type 1 subtype C. *AIDS Res Hum Retroviruses* **1999**;15(14):1321-4.
- (S2) Sato., H.; Tomita., Y.; Ebisawa., K.; Hachiya., A.; Shibamura., K.; Shiino., T.; Yang., R.; Tatsumi., M.; Gushi., K.; Umeyama., H.; Oka., S.; Takebe., Y.; Nagai., Y. Augmentation of human immunodeficiency virus type 1 subtype E (CRF01_AE) multiple-drug resistance by insertion of a foreign 11-amino-acid fragment into the reverse transcriptase. *J Virol* **2001**;75:5604-13.

Figure S1.

B.FR.x.pNL43 PISPIETVPV KLKPGMDGPK VKQWPLTEEK IKALVEICTE MEKEGKISKI GPENPYNTPV FAIKKKDSTK WRKLVDFREL [80]
 C.Indie-C1TA..D.II. [80]
 AE.93JP_NH1 D.I. T T..K. E..... R [80]

B.FR.x.pNL43 NKRTQDFWEV QLGIPHPAGL KQKKSVTVLD VGDAYFSVPL DKDFRKYTAF TIPSINNETP GIRYQYNVLP QGWKGSPAIF [160]
 C.Indie-C1 K..... YE..... [160]
 AE.93JP_NH1 K..... ES..... [160]

B.FR.x.pNL43 QCSMTKILEP FRKQNPDIVI YQYMDDLYVG SDLEIGQHRT KIEELRQHLL RWGFTTPDKK HQKEPPFLWM GYELHPDKWT [240]
 C.Indie-C1 ..S..IR.... A..EI..... I..... E... K..... [240]
 AE.93JP_NH1 ..S..... .IK..EM.. R..I ..A.. S..... R.. [240]

B.FR.x.pNL43 VQPIVLPEKD SWTVDNIQKL VGKLNWASQI YAGIKVRQLC KLLRGTKALT EVVPLTEEAE LELAENREIL KEPVHGVVYD [320]
 C.Indie-C1 Q..... P..... A... DI..... [320]
 AE.93JP_NH1 E..... K..... A... DI..... T..... [320]

B.FR.x.pNL43 PSKDLIAEIQ KQGQGQWTYQ IYQEPMFKNLK TGKYARMKGA HTNDVKQLTE AVQKIATESI VIWGKTPKFK LPIQKETWEA [400]
 C.Indie-C1 D..... KRRT. M... R..... T [400]
 AE.93JP_NH1 V..V. D..... KRS. R... V..... R... R... T [400]

► RNase H domain

B.FR.x.pNL43 WWTEYWQATW IPEWEFVNTP PLVKLWYQLE KEPIIGAETF YVDGAANRET KLGKAGYVTD RGRQKVPLT DTTNQKTELQ [480]
 C.Indie-C1 T..... D..A.V... I.S. E..... [480]
 AE.93JP_NH1 M..... D..V... S... S. E..... H [480]

B.FR.x.pNL43 AIHLALQDSG LEVNIIVTDSQ YALGIIQAQP DKSESELVSQ IIEQLIKKEK VYLAWVPAHK GIGGNEQVDT LVSAGIRKVL [560]
 C.Indie-C1 ..Y..... S..... N. R... S... S..... [560]
 AE.93JP_NH1 S..... R... V.N. E... S... K ... S..... [560]