**Abstract**

The most promising anti-HIV integrase class falls into the category of selective strand transfer inhibitors with representatives already in advanced clinical studies. Chemical structures of selected molecules investigated in this study are depicted in Figure 1. Different patterns of mutations are selected under selective pressure despite a common mechanism of action shared by these inhibitors. A number of recombinant HIV-1 containing mutations known to confer resistance to selected integrase inhibitors were engineered and drug susceptibility testing performed for potential cross-resistance evaluation.

**Results**

The results of drug susceptibility testing are presented in Table 1. The susceptibility of recombinant integrase mutant HIV-1 strains harboring various mutations to different chemical series of integrase inhibitors was assessed in the MT-2 cell line. All compounds were generally found to be associated with a reduced susceptibility to the viruses (10 to 145-fold change) when compared to the wild-type virus in the MT-2 cell line with all compounds examined with the exception of GS-9137 where a 48-fold reduction in potency against the HIV-1 T66I harboring the E92Q mutation was observed (Table 1, Figure 2c).

**Conclusion**

In this study, phenotypic analysis of recombinant viruses harboring selected mutations within the integrase gene has demonstrated significant cross-resistance with the compounds investigated.

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**References**

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