

ABSTRACT

Human Immunodeficiency Virus (HIV) is a virus that causes Acquired Immunodeficiency Virus (AIDS) which is still considered a global burden. Japan has not yet been successful in fulfilling the UNAIDS/WHO (90/90/90) target due to the lack of HIV surveillance in the country. HIV is known as a virus with a very high genetic diversity in which the presence of insertions or deletions (indels) and single nucleotide polymorphism in the genome may cause quasispecies formation. This quasispecies development would allow the formation of drug resistant strains while also affecting HIV viral tropism. Hence it is necessary to use sequencing platforms in analyzing the HIV genome to gain information regarding HIV genomic diversity so a more personalized and effective antiretroviral therapy (ART) can be administered to HIV patients. The new PacBio Sequel IIe platform guarantees a 99.99% accuracy in their raw reads; however, an irregular level of indels were found to be present across all samples in the HIV Protease Reverse Transcriptase - Integrase (PRRT-IN) gene which is the most common gene associated with HIV drug resistance mutation. Sanger sequencing was used to confirm the presence of indels in the same gene and it was found that no fragments were present in any of the samples indicating that the new PacBio Sequel IIe platform is yet to be utilized as a suitable platform for indels detection in the HIV genome.

Keyword: Human Immunodeficiency Virus; Indels; Quasispecies; PacBio Sequel IIe; HIV PRRT-IN gene; Sanger sequencing