The Philippines has the fastest growing HIV epidemic in the Asia-Pacific. Concurrent with this is a subtype shift from B to CRF01_AE. We have previously documented transmitted drug resistance (TDR) locally. However, the lack of drug pressure and the insensitivity of Sanger-based sequencing (SBS) may leave archived drug-resistance mutations (DRMs) undetected. To better detect TDR, we performed next-generation sequencing (NGS) on treatment-naïve patients and compared this with SBS.

Methods

Following ethics approval, newly-diagnosed adult Filipino HIV patients were recruited from the Philippine General Hospital HIV treatment hub. Demographic data was collected, and blood samples underwent SBS with a WHO-approved protocol. Whole-genome NGS was performed using Illumina HiSeq through a commercial provider (Macrogen, Korea). Genotype and DRMs were analyzed and scored using the Stanford HIV Drug Resistance Database.

Results

113 patients were analyzed. Median age was 29 years (range 19-68), mean CD4 count was 147 cells/µL (range 0-556) and median viral load was 2.8 x 10^6 copies/mL. Genotype distribution was: CRF01_AE (93), B (13), possible CRF01_AE/B recombinants (5), CRF02_AG (1), possible URF (1). TDR prevalence by SBS and NGS at different minority variant cutoffs are shown in Table 1.

Conclusion

NGS is a more sensitive tool for detecting TDR compared to SBS. Nearly double the DRMs were found at an NGS cutoff of ≥5%, including INSTI DRMs. With increasing HIV drug resistance worldwide, switching to NGS may help decrease rates of initial treatment failure, especially in settings with limited repertoires of ARVs.

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