P0023
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Transmitted drug resistance (TDR) in newly diagnosed HIV-1-infected subjects in Estonia in 2013

Pilleriin Soodla*[1], Kristi Huik[1], Pauskar Merit[1], Eveli Kallas[1], Ene-Ly Jõgeda[1], Heli Rajasaar[1], Matti Maimets[2], Irja Lutsar[1], Radko Avi[1]

[1]*University of Tartu, Tartu, Estonia*

[2]*Tartu University Hospital, Tartu, Estonia*

Background: Estonian HIV epidemic is typical to Eastern Europe being driven by people who inject drugs (PWID). The antiretroviral treatment (ART) adherence in this population is problematic. TDR has been 0, 5.5% and 4.5% in 2006, 2008 and 2010, respectively. Non-nucleoside reverse transcriptase inhibitors, with low resistance barrier, are still first line agents while integrase inhibitors are rarely used. We aimed to evaluate the level and character of TDR in newly diagnosed HIV positive subjects in 2013.

Material/methods: Study included all 324 newly diagnosed HIV cases between 1st of January 2013 and 31st of December 2013. Resistance testing was performed for 295 (91%). Viral RNA was sequenced in *pol* region. HIV-1 drug resistance mutations (DRMs) were determined by Stanford HIV Drug Resistance database (SDRM 2009, CPR v6.0). Phylogenetic analysis was conducted using the maximum likelihood method. Demographical and clinical data was obtained from Estonian Health Board and Estonian HIV-positive patients' database. LAg-avidity EIA testing was performed to categorize patients to recent (median duration of 130 days) or long term infection.

Results: In total 224 (76%) samples were successfully sequenced. The population median age was 32 years (IQR 27-35) and 199 (61%) were male. 77 (55%) patients were infected heterosexually, 70 (22%) via intravenous drug use, 6 (2%) homosexually and in 70 (22%) transmission route was unknown. 128 (44%) were recent infections. At the time of diagnosis, median CD4 cell count was 366 cells/µl (IQR 206-540) and HIV viral load in $\log_{10}$ 4.9 (IQR 4.2-5.5) copies/ml. In phylogenetic analysis 83% of sequences clustered with CRF06_cpx and 11% with subtype A1 reference sequences (Figure 1). Altogether, 15/224 strains (6.7%; 95% CI 3.9% - 11.0%) had a DRM with; no dual or triple class resistance observed. The total number of different mutations was small - K103N (n=8, 53%); M41L (n=2, 13%); M46L (n=2, 13%); and G190E, Y181C L90M, each in one case (7%). Out of 15 potential transmission subclusters (bootstrap>70%), one involved two K103N DRM-possessing viruses (Figure 1). Most of the cases with DRM (11/15) were long term infections according to LAg-avidity testing. The prevalence of TDR in recent infections was 3.1% vs 6.8% in long term infections. There was no correlation between TDR and gender, risk group, viral load, CD4 cell count or duration of the infection.

Conclusions: In Estonia the prevalence of TDR is steadily raising similarly in all risk groups but there is almost no transmission clusters. As TDR has exceeded 5% implementation of resistance testing prior to initiation of antiretroviral treatment is recommended.

Figure 1. Phylogenetic tree with DRMs (blue arrows) and one potential transmission subcluster (bootstrap=91) with two K103N DRM-possessing viruses (red arrows)