O1. Increasing prevalence of transmitted drug resistance mutations in patients diagnosed with HIV in Sweden 2010 – 2014

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Background
Transmitted drug resistance (TDR) may lead to failure of antiretroviral treatment (ART). The prevalence of TDR varies geographically according to ART practices and history. In Sweden the prevalence has been lower than in many other high-income countries; 5.6% was reported in patients diagnosed 2003-2010. TDR was then associated with men who have sex with men (MSM) and subtype B infection. In Sub-Saharan Africa (SSA) the prevalence of TDR has increased after roll-out of ART, especially for non-nucleoside RT inhibitors (NNRTIs). Patients diagnosed with HIV in Sweden today are mainly migrants from high-endemic areas and Swedish born MSM. In this study, we investigated the prevalence, characteristics and trends of TDR in ART naïve patients diagnosed in Sweden 2010-2014.

Methods
InfCare HIV is a clinical decision tool and research database covering all HIV clinics in Sweden. Clinical data, laboratory parameters and pol sequences from resistance testing are routinely entered into the system. 1882 patients with either first positive serology or first CD4 entry 2010-2014 were recorded. 1284 patients had complete data including a pol sequence within 180 days of diagnosis and before start of ART. The Stanford CPR v 6.0 tool was used to screen for surveillance drug resistance mutations (SDRMs) according to the WHO 2009 SDRM list. Subtyping was done with Rega HIV-1 subtyping tool and PhyML phylogenetic tree analysis. Statistical analysis was carried out in StataSE 12 and Statistica.

Results
Of 1284 patients, 91 patients had one or more SDRMs, representing a TDR prevalence of 7.1% (95% CI: 5.7% - 8.5%), with a significant increase (p=0.003) during the period from 4.9 % (CI 95%: 2.4% - 7.5%) in 2010 to 12.1% (CI 95%: 7.9% - 16.2%) in 2014. The prevalence of NRTI, NNRTI and PI SDRMs were 4.1% (95% CI: 3.0% - 5.2%), 3.2% (95% CI: 2.2% - 4.2%) and 1.5% (95% CI: 08% - 2.1%), respectively. Both NNRTI and PI SDRMs, but not NRTI SDRMs, increased significantly during the study period (p=0.04 and p=0.03, respectively).
TDR was higher in MSM than in heterosexually infected (p=0.02). NRTI SDRMs were more common in patients infected in Sweden (p=0.003), with M41L being the most common mutation (n=11).Sequences from eight MSM with the M41L mutation formed a phylogenetic cluster. NNRTI SDRMs were more common in patients infected in SSA than elsewhere (p=0.048). Of 19 patients from SSA with NNRTI SDRMs, 10 harboured the K103N mutation.

Conclusions
We found a significant increase in the prevalence of TDR over the study period. This is due both to clonal spread of virus with NRTI mutations among MSM in Sweden and increase of TDR among

migrants from SSA. An increase of TDR in SSA has been anticipated and has been described from local TDR surveillance studies in Africa. Our findings emphasize the value of resistance testing at diagnosis.