

Algorithm (www.hivdb.stanford.edu; HIVdb version 6.1.1F; 2012 webService version beta-1.0.1) to identify mutations and to determine drug susceptibility. Sequences were analysed by using different lists of mutations (Bennett D. 2009; Johnson V. 2011). Trends in the prevalence of drug resistance mutations were calculated by logistic regression.

Results A total of 9,528 patients from five study centres were included into analysis. 4,989 viral sequences were collected from 34% (3,267/9,528) of these patients. 47% (2,365/4,989) of sequences were produced from patients being treatment naïve and 50% (2,495/4,989) from patients under treatment. TDR was identified in 10% (203/1,950) of viral strains. The prevalence of TDR over time was stable at 10.4% (95% CI 9.1–11.8; OR: 0.98; 95% CI 0.92–1.04; $p_{\text{for trend}} = 0.6$; 2001–2011). NRTI-resistance was determined in 7% (128/1,950), followed by 3% NNRTI- and PI-resistance, respectively (NNRTI: 61/1,950; PI: 56/1,950). Prevalence of ADR in treated patients was high (61%; 1,500/2,453 of sequences) but declined significantly over time (OR: 0.8; 95% CI 0.77–0.83; $p_{\text{for trend}} < 0.001$; 2001–2011). Within drug classes NNRTI-resistance was predominant (56%; 834/1503), followed by NRTI-resistance in 52% (1,139/2,194) of sequences of patients with ADR exposed to these drug classes. PI-resistance was identified in 30% (543/1773). Integrase-resistance was determined in 8% (13/161) of integrase-sequences.

Discussion Prevalence of TDR is highly stable in this unselected study population, whereas ADR declined significantly over the time, indicating that this decline was presumably influenced by ART related effects, broader resistance testing and resistance test guided therapy.

019.3 ESTIMATE OF THE PREVALENCE OF TRANSMITTED DRUG RESISTANCE (TDR) AND ACQUIRED DRUG RESISTANCE (ADR) IN A HIV RESISTANCE STUDY OF THE GERMAN CLINSURV-HIV COHORT

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Aim To estimate the prevalence of HIV-TDR and ADR in one resistance study of the German ClinSurv-HIV cohort.

Method The ClinSurv study is a national open multi-centre long term observational cohort with 15 participating clinical centres (n = 16,750 patients; 31.12.2011). In a resistance study all ClinSurv patients in five centres were identified. Sequences were processed through the Stanford University Genotypic Resistance Interpretation

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