

## Poster Sessions – Abstract P138

# Analysis of transmitted drug resistance and HIV-1 subtypes using dried serum spots of recently HIV-infected individuals in 2013 in Germany

Andrea, Hauser<sup>1</sup>; Alexandra, Hofmann<sup>2</sup>; Claudia, Santos-Hoeverner<sup>2</sup>; Ruth, Zimmermann<sup>2</sup>; Osamah, Hamouda<sup>2</sup>; Norbert, Bannert<sup>1</sup> and Claudia, Kuecherer<sup>1</sup>

<sup>1</sup>HIV and Other Retroviruses, Robert Koch Institute, Berlin, Germany. <sup>2</sup>HIV/AIDS and Other Blood Borne Infections, Robert Koch Institute, Berlin, Germany.

**Introduction:** The Robert Koch Institute (RKI) aimed to assess a molecular surveillance strategy based on filter-dried serum spots (DSS) of all newly diagnosed HIV infections in Germany. In 2013, diagnostic laboratories sent DSS to the RKI representing 55% of the newly diagnosed HIV infections reported to the RKI (protection against infection act). DSS were first tested serologically to identify recently acquired infections (< 140 days duration of infection); those classified as “recent infection” were processed for HIV-1 genotyping. The aim of this study was to assess the level of TDR and the current HIV-1 subtypes in the main HIV transmission group categories (TrGrpC) in 2013: men who have sex with men (MSM), women/men with heterosexual contacts (HET) and injecting drug users (IDUs).

**Material and Methods:** DSS were tested for recency of infection using the BED capture EIA. Viral RNA from “recent infections” was amplified by HIV-1 group M generic pol-RT-PCR covering all resistance-associated positions in the HIV-1 protease (AS1-99) and reverse transcriptase (AS1-252) if viral loads were  $\geq 6,500$  copies/mL. PCR amplicons were sequenced (Sanger) to analyze genotypic resistance and the HIV-1 subtype. Results were merged to data from the HIV report, i.e. the TrGrpC.

**Results:** In 2013, 1027 DSS were classified as recent HIV infections (506 MSM, 118 HET, 31 IDUs, 6 others, 366 unknown). RNA was extracted from 703 recent cases and 389/503 samples with sufficient viral load were PCR-positive. By June 2014, 276/389 samples were sequenced: TDR was identified in 13% (35/276) of the recent infections including single (PI, NRTI, NNRTI) and dual drug class resistant strains (NRTI/NNRTI; NNRTI/PI). 18% (51/276) of recent HIV-1 infections were caused by non-B subtypes (A1, C, CRF01\_AE, CRF02\_AG, D, F, G, URFs). TDR was observed at comparable levels in all TrGrpC. Proportions of non-B infections were significantly higher in HET (78%; 14/18) and IDUs (60%; 3/5) compared to MSM (8%; 14/169) ( $p < 0.01$ ).

**Conclusions:** The proportion of TDR was similar but the proportion of HIV-1 subtype non-B infections was higher as previously described for Germany based on results from the German HIV-1 Seroconverter Cohort [1],[2]. This difference could be the result of a broadened inclusion of HET and IDUs due to the sampling method used making this study representative for molecular surveillance of HIV-1 in Germany.

### References

1. Meixenberger K, Scheufele R, Somogyi S, Jansen K, Bartmeyer B, Dupke S, et al. Pronounced potential of resistance mutations to persist in transmitted drug resistant HIV-1 strains. 12th European Workshop on HIV & Hepatitis – Treatment Strategies, Spain; 26–28 March 2014; Poster P\_11.
2. Somogyi S, Meixenberger K, Bartmeyer B, Jansen K, Scheufele R, Dupke S, et al. Continued rising prevalence of HIV-1 non-B subtypes in Germany: Update from the HIV 1 Seroconverter Study; 12th European Workshop on HIV & Hepatitis – Treatment Strategies, Spain; 26–28 March 2014; Poster P\_18.

Published 2 November 2014

**Copyright:** © 2014 Andrea H et al; licensee International AIDS Society. This is an Open Access article distributed under the terms of the Creative Commons Attribution 3.0 Unported (CC BY 3.0) License (<http://creativecommons.org/licenses/by/3.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.