

O268

1-hour Oral Session

Challenges in HIV care in 2016

Dynamics of HIV epidemic and transmission networks within new diagnoses, France 2012-2014

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Background: Transmitted/founder (T/F) viruses isolated at the early stage of infection are indicators of the variants that are spreading within a population. The aim of the study was to combine an immunoassay for very recent infection to a phylogenetic analysis of T/F viruses and sociodemographic information to analyze the dynamics of the HIV epidemic at a country level.

Material/methods: The French reporting system for new HIV diagnoses is linked to a virological surveillance using an assay for recent infection performed on dried serum spots (DSS). A threshold defining very recent infection (VRI) was calibrated on a panel of seroconverters for a mean duration of 31 days. All samples corresponding to a VRI collected between January 2012 and December 2014 were included. RNA was extracted from DSS and sequences (888-bp, *env* gene), when amplified, were used for the phylogenetic analyses. Subtype or CRF assignments were achieved using the neighbor-joining method and checked by BLAST. Bayesian coalescent-based methods were used to explore the temporal and spatial dynamics of the identified clusters. A multivariate analysis using logistic regression was performed to identify factors associated with clustering.

Results: Of 17,010 DSS collected during the 3-year period, 1,868 corresponded to a VRI (11.0%) of which 723 *env* fragments (38.7%) were amplified and sequenced. The analyses correspond to 549 (75.9%) cases for which the sociodemographic data were available. 493 (89.8%) were men, and 315 were identified as MSM. Non-B T/F viruses were found in 196 cases (35.7%), belonging to 6 subtypes (A,C,D,F,G,H) and 7 CRFs. CRF02_AG was the most prevalent non-B clade (96 cases). 43 dyads/clusters were identified (range 2-11 cases), including 107 individuals (19.5%) among whom 70 MSM. Within 8 clusters involving ≥ 3 individuals, 96% were MSM. The largest cluster involved MSM infected by a CRF02_AG variant. The other clusters were B (5), D (1) and G (1). The only factor associated with clustering was being MSM (OR=5.5, 95CI= [2.1-14.1], p=0.0004).

Conclusions: The study shows the feasibility of the surveillance of the HIV epidemic at a country level using DSS and combining an assay for VRI to phylogenetic analysis of T/F viruses and

sociodemographic data. MSM represent the main driving force of the current French epidemic. The observation of actively growing spatiotemporal clusters, particularly of non-B strains, allows identification of specific sexual networks that may be targets for intervention.