

## OUTBREAK OF HIV AMONG PEOPLE WHO INJECT DRUGS (PWID) DISCOVERED THROUGH PHYLOGENETIC ANALYSIS: ARE WE SEEING JUST THE TOP OF THE ICEBERG?

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### Background:

Although reduced by harm reduction interventions, isolated and outbreak HIV transmission still occurs in PWID. Identification of clusters could foster public health measures to stop the chain of transmission.

### Methods:

Available sequences from people living with HIV (PLWH) attending an outpatient clinic in Lombardy since 2015 were included in a phylogenetic analysis based on Maximum Likelihood (ML) method to confirm subtype and define transmission clusters (ref. HIV-1 subtype B HXB2, bootstrap >90%). Epidemiological investigation included interviews and consultation of medical records.

### Results:

Among 794 PLWH followed up between 01/01/2015 and 31/12/2022, 167 had at least one pol sequence available while viraemic; ML tree based on these B-subtype sequences identified a single cluster of 20 subjects (bootstrap 98%), of whom 19 (95%) harboured the V106I mutation, *versus* 2/147 (1.36%) unlinked to the cluster ( $p=0.0001$ ).

Of these 20 "cluster members", 4 (20%) women, median (range) age 32 (21-57) years, 4 (20%) were diagnosed in prison, 3 (15%) in addiction centres, 6 (30%) as outpatients, 6 (30%) as inpatients, 1 (5%) in street mobile unit. All cases were HCVAb positive. All patients had a known history of injecting drug use and most had the same drug use network. The first case was diagnosed in 2006, the second, in 2015, had a datable primary HIV infection.

We hypothesize a founder effect of the first case during a period of low adherence to efavirenz-containing antiretroviral therapy, possibly selecting for V106I mutation. The subsequent spread of HIV over the following 7 years is likely due to sharing of injecting equipment in a close group of epidemiologically linked individuals.

### Conclusion:

HIV transmission through injecting drug use includes the risk of spreading drug resistance. Phylogenetic analysis, by identifying transmission clusters, could serve as innovative strategy for real-time monitoring of HIV clustering, thereby favouring targeted outbreak response interventions.

### Disclosure of Interest Statement:

*The conference collaborators recognise the considerable contribution that industry partners make to professional and research activities. We also recognise the need for transparency of disclosure of potential conflicts of interest by acknowledging these relationships in publications and presentations.*

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