BEYOND FAST-TRACK CITIES: DYNAMIC OF HIV CLUSTERS IN A FRENCH REGION NEAR PARIS

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BACKGROUND

The Loire Valley region is a low-density demographic and medical region with the second most elevated rate of positive HIV testing in France (1.4/1000 screening) after Paris, despite a low testing rate (60/1000 inhabitants). Among new HIV diagnoses, 40% are men having sex with men (MSM) and 43% are heterosexuals (HET) born abroad. We investigated the role and characteristics of transmission clusters in the HIV dynamics in this region close to the fast-track city of Paris, for appropriate local response.

METHODS

- 1305 HIV *pol* gene sequences collected in Loire Valley region over a decade (2010-2020), from adults (>15y/o) living with HIV, combined with epidemiological data.
- Putative transmission clusters were inferred using HIV TRACE methodologies (≤0.015 substitutions/site, Tamura Nei 93 substitution model).
- Risk factors of being part of a cluster were studied using an uni- and multi-variate logistic regression model.

RESULTS

Of the 1,305 participants **(Figure 1 and Table 1)**

- **38%** (N = 494) women
- **53%** (N = 694) heterosexuals
- 44% (N = 579) born out of France and 36% from Sub-Saharan Africa
  ↳ migrants had **less CD4** (296 vs 443 if born in France, $p < 0,01$), and were predominantly **women** (62%)

- **86 clusters inferred** (N = 276 sequences, clusterisation rate 21%)

Including: **33 clusters of N ≥ 3**, 170 individuals (3-16/cluster)
14 expanding clusters since 2017 despite PrEP introduction in 2016.

Risk factors of clustering (Figure 2)

- MSM born in France (OR 2.57, p <0.01)
- Higher viral load at diagnosis (OR 1.36, p <0.01)
- Residency in a specific subdivision (OR 3.65, p <0.01)
- On the contrary, heterosexuals born abroad **were less at risk of clustering** (OR 0.01, p <0.01)

Large clusters (N ≥ 7) (Figure 3)

- Virological control was reached for a median of 75% (IQR 74-87) of subjects *versus* 84% for the total cohort
- Clade CRF06_cpx was involved in a persistently expanding cluster

HIV phylogenetic analysis in a French region near the fast track city of Paris suggest **a two-faceted dynamic** regarding key population requiring **targeted prevention approaches**:

French-born MSM in *local transmission networks* and **HET migrants**, with *delayed diagnosis* or *infection before settlement*

CONCLUSIONS

In the Loire Valley region, we found that French-born MSM were part of local transmission networks but not HET migrants, suggesting a two-faceted HIV dynamic. Delayed diagnosis or infection before settling in the region could lead to under-representation of migrants in the cluster analysis. Locally, epidemic control would require further implementation of PrEP and TASP in MSM to slow the dynamics of HIV clusters and generalized access to HIV screening for migrants. The same actions are promoted by the Paris Sans SIDA initiative and should be extended to neighboring territories.

	Total (N = 1305)
Sexe (F/M/T)	494 (38) / 810 (62) / 1
Age at diagnosis	
16-25	269 (21)
26-35	472 (36)
36-49	391 (30)
≥ 50	173 (13)
Division of residency	
Indre-et-Loire	560 (43)
Loiret	358 (27)
Loir-et-Cher	142 (11)
Cher	148 (11)
Indre	30 (2)
Others	67 (5)
Contamination	
MSM	433 (33)
Heterosexual	694 (53)
PWID	67 (5)
Others	35 (3)
Unknown	76 (6)
Birth Country	
Metropolitan France	715 (55)
Migrants	579 (44)
French overseas	20 (2)
Europe	31 (2)
Sub-Saharan Africa	468 (36)
North Africa	27 (2)
Others	33 (3)
Unknown	11 (1)
Acute infection	97 (7)
CDC category	
A	1038 (80)
B	35 (3)
C	232 (18)
CD4 (cell count/mm³) median (± IQR)	371 (192-576)
Viral load (copies/ml) median (± IQR)	15,000 (141-110,000)
Virological control	
Viral suppression	1094 (84)
Never undetectable	39 (3)
Insufficient control	124 (10)
No follow up	48 (4)
Clade	
B	611 (47)
02_AG	285 (22)
06_cpx	21 (2)
ART resistance	348 (27)
Coinfection	
HBV	65 (5)
HCV	124 (10)
STI	139 (11)

Table 1. Population characteristics.
N (%) except if stated otherwise. CD4 and viral load are values at diagnosis. Virological control was defined as: « *undetectable at last visit or ≥ 90% of undetectable viral load since first undetectability* ». PWID = people who inject drugs.

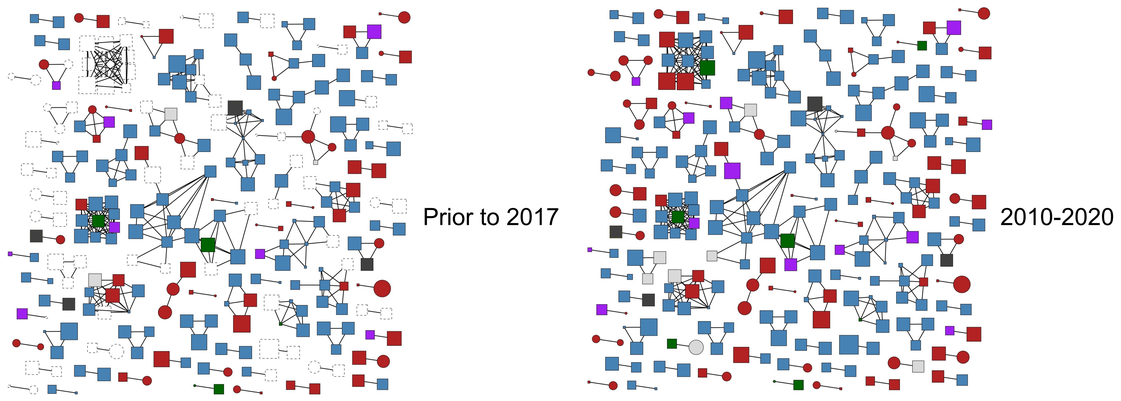


Figure 1. HIV transmission networks in Centre-Val de Loire region between 2010 and 2020.
Each person is represented individually; square = man and circle = woman ; color = risk group (*see legend*) and empty = undiagnosed people on the indicated period (before 2017) ; each size is proportional to viral load at diagnosis. Lines represent pairwise distance between 2 individuals. A genetic distance threshold of 1.5% was applied to define clusters. New identification after 2017 are posterior to PrEP introduction in France.

Figure 2. Risk factors of clustering.
Forrest plot (multivariate logistic regression model)

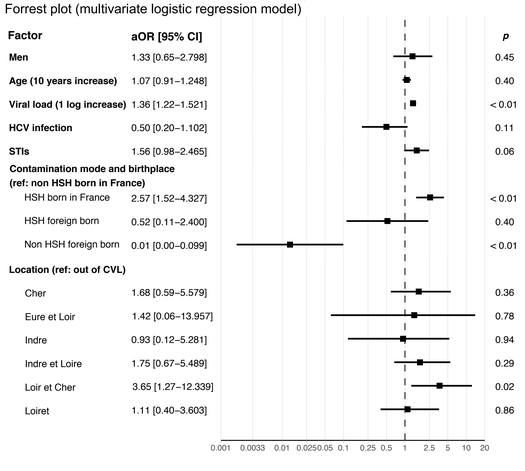
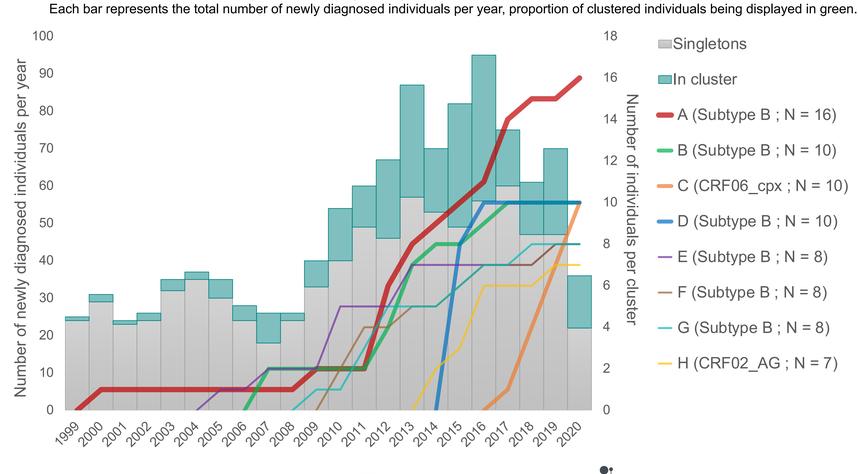


Figure 3. Growth of large clusters (N ≥ 7) according to the year of diagnosis
Each bar represents the total number of newly diagnosed individuals per year, proportion of clustered individuals being displayed in green.



ADDITIONAL KEY INFORMATION Contact karl.stefic@univ-tours.fr

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