MOLECULAR ANALYSIS SUGGESTS LOW ONWARD HIV-1 TRANSMISSION AMONG MIGRANTS IN GREECE

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BACKGROUND

- Forty-four per cent of those diagnosed in the EU/EEA in 2020 were migrants (defined as people originating from outside of the country in which they were diagnosed) [1].
- In Greece, the number of new HIV-1 diagnoses in migrants increased during 2016-2019 [2].
- Considering that there is a gap in our knowledge related to the geographic origin of HIV-1 acquisition that could impact public health policies, our aim was to trace the geographic origin of HIV-1 subtype C and CRF02_AG infections, the most prevalent non-A1 and non-B clades in Greece, using molecular epidemiology methods.

METHODS

- Our study sample consisted of 146 HIV-1 subtype C and 139 CRF02_AG *pol* gene sequences of people living with HIV (PLWHIV) diagnosed during 1999 - 2015 in Greece.
- HIV-1 subtyping was carried out by automated subtyping tools (COMET, REGA).
- We analyzed phylogenetically the subtype C (N=78) and CRF02_AG (N=61) sequences from migrants along with all the available subtype C and CRF02_AG sequences from non-migrants. We also included a random set of globally sampled sequences (subtype C: 972; CRF02_AG: 858), and the most closely related sequences identified using the BLAST tool (subtype C: 50; CRF02_AG: 33), as references. Phylogenetic trees were estimated by the maximum likelihood method (RAxML v8.0.20, FastTree v2.1).
- Molecular transmission clusters (MTCs) were phylogenetic clusters including sequences from Greece at proportions >70%, receiving bootstrap value >75% and SH-support >0.9. Robustness of MTCs was confirmed by ML transfer bootstrap observation (TBE).
- The putative origin of HIV-1 acquisition was traced by using a combination of the clustering pattern for each sequence (within or outside a MTC) and an estimation of this parameter provided by phylogeographic analysis (ancestral character reconstruction using the criterion of parsimony; Mesquite v3.5).
- Statistical analysis was based on multivariable logistic regression models for the investigation of parameters associated with clustering (STATA 13-StataCorp LP).

Molecular epidemiology study showing that migrants did not impact the HIV epidemic in Greece.

RESULTS

- Phylogenetic analysis revealed that 27 (34.6%) and 21 (34.4%) sequences from subtype C and CRF02_AG infected migrants clustered within MTCs (Figure 1). The size of MTCs ranged between 2 and 12 sequences for subtype C (21 MTCs in total) and 2 and 49 sequences for CRF02_AG (16 MTCs in total) (Figure 1).

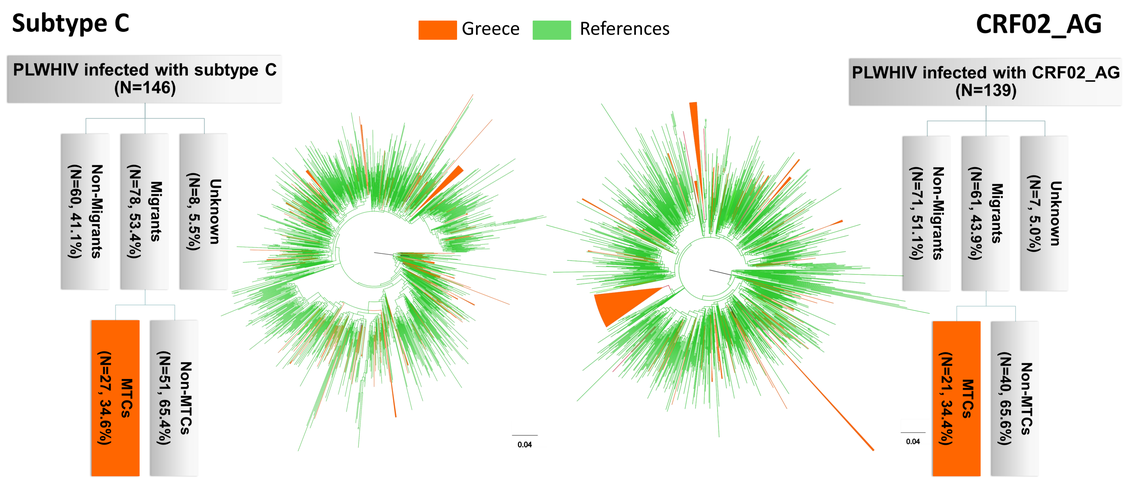

Figure 1 *Study population graphics. The highlighted boxes correspond to migrants diagnosed in Greece infected with HIV-1 subtype C and CRF02_AG within molecular transmission clusters (MTCs); Unrooted phylogenetic trees estimated by RAxML v8.0.20 of HIV-1 subtype C and CRF02_AG sequences sampled in Greece and a global reference dataset. MTCs are indicated as triangles.*

RESULTS (Cont.)

- Multivariable logistic regression analysis showed that parameters associated with clustering were the year of sampling for subtype C (OR: 1.25, 95% CI: 1.13-1.38) and Greek origin for subtype C (non-migrants vs migrants OR: 3.95, 95% CI: 1.65-9.48) and CRF02_AG (non-migrants vs migrants OR: 38.11, 95% CI: 8.09-79.44).
- Phylogeographic analysis showed that 23.3% of subtype C and 23.8% of CRF02_AG HIV-1 transmissions within migrants occurred in Greece.

CONCLUSIONS

- ✓ Only 35% of subtype C and 34% of CRF02_AG infections within migrants were found in local networks in Greece. Moreover, for both clades Greek origin was associated with infections within MTCs.
- ✓ Only a small proportion of subtype C (23%) and CRF02_AG (24%) HIV-1 transmissions within migrants originated in Greece.
- ✓ Our findings provide evidence that HIV-1 infections among migrants were not associated with onward transmission, thus suggesting that migrants did not impact the HIV epidemic in Greece.

ADDITIONAL KEY INFORMATION

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References:

[1] European Centre for Disease Prevention and Control/WHO Regional Office for Europe. HIV/AIDS surveillance in Europe 2021 - 2020 data. Stockholm: ECDC; 2021.

[2] National Public Health Organization, https://eody.gov.gr/en/