Abstract citation ID: ckae144.2069

Molecular transmission clusters in newly HIV-1 diagnosed migrants in Portugal from 2014 to 2019

Marta Pingarilho

M Pingarilho[1], A Videira[1], M Miranda[1], C Sebastião[1,2,3], BH BEST-HOPE study group[1], S Seabra[1], MR Oliveira Martins[1], P Gomes[4,5], V Pimentel[1], A Barroso Abecasis[1]
[1]Saúde Pública Global, NOVA-IHMT, Lisbon, Portugal
[2]Saúde Pública, Centro de Investigação em Saúde de Angola, Caxito, Angola
[3]Saúde Pública, Instituto Nacional de Investigação em Saúde, Luanda, Angola
[4]Doenças Infeciosas, Laboratório de Biologia Molecular, LMCBM, SPC, CHLO-HEM, Lisbon, Portugal
[5]Egas Moniz School, Egas Moniz Center for Interdisciplinary Research, Almada, Portugal
Contact: martapingarilho@ihmt.unl.pt

Background: Portugal has an important HIV burden with a total of 804 diagnosed cases in 2022. Migrants remain a significant source of HIV infections, with 45% of newly reported cases. We aimed to evaluate the characteristics of HIV-1 molecular transmission clusters (MTCs) among migrants followed in Portugal, diagnosed between 2014 and 2019.

Methods: 265 migrants, newly HIV-1 diagnosed were included in the BESTHOPE project with clinical, socio-behavioral and genomic data. Pol nucleotide-based phylogenetic analyses were used to infer HIV-1 MTC. Those were constructed using ClusterPickerGUI_1.2.3 considering SH-aLRT higher than 90 of branch support and a pairwise genetic distance of ≤ 4.5. Logistic regression analyses were used to examine the relationship between the sociodemographic and clinical data associated with HIV-1 clustering.

Results: 66.8% of the migrants included in the study were males with a median age at diagnosis of 36.0 years old (IQR:29-45). Most migrants were from African countries (50.6%) followed by Brazil (39.6%). Sixty-eight (33%) of the migrants were included in clusters. Being in cluster was significantly associated with region of origin, with individuals from South America more likely to be in cluster (OR = 14.85, 95%CI:1.52-144.79), compared to individuals from Africa; with transmission route, with men who have sex with men (MSM) more likely to be in cluster (OR = 23.52, 95%CI:2.35-235.10), compared to the heterosexuals and with subtype, with subtypes B less likely to be in cluster (OR = 0,017, 95%CI:0,001-0,254) compared with subtype non-B.

Conclusions: Migrants HIV transmission clusters in Portugal are associated with specific health determinants, such as region of origin, transmission route and subtype. Targeted prevention health strategies are needed to mitigate transmission of HIV within this population. Funded by FCT to GHTM - UID/04413/2020 and LA-REAL - LA/P/0117/2020; BESTHOPE (HIVERA:249697); and MARVEL (PTDC/SAU-PUB/4018/2021).

Key messages:

- HIV transmission clusters in migrant are associated with their region of origin, transmission route and subtype.
- Targeted prevention health strategies are needed for the migrant population.