

**Results:** We identified 38 transmission clusters with 104 MSM, which included 26.6% of the total 305 MSM from our database used for cluster analysis. The overall prevalence of TDR was 8.2%. Only subtype C was significantly associated with TDR. 10.5% of the clusters had at least 1 drug resistance mutation (K103N, L90M or N88S). There was no significant difference in the prevalence of TDR between MSM inside and outside clusters. 50% of the clusters were composed of portuguese native MSM only, whereas 16% had exclusively migrant MSMs. No significant difference was found in the proportion of portuguese and migrant MSM inside and outside clusters. Factors associated with HIV-1 transmission clusters were age at diagnosis, district of residence, unprotected anal or vaginal sex with a woman, HIV testing frequency, presenter status and subtype. 87% of men engaged in sexual activity only with other men, while 13% with both men and women.

**Conclusions:** Specific subgroups of MSM are contributing to HIV dissemination in Portugal. Direct and precise prevention measures based on molecular epidemiology should be developed.

**Key messages:**

- Specific subgroups of MSM are contributing to HIV dissemination in Portugal.
- Direct and precise prevention measures based on molecular epidemiology should be developed.

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**HIV-1 transmission clusters and drug resistance in men who have sex with men in Portugal**

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**Introduction:** In 2022, 45.8% of diagnoses in the EU/EEA with known route of transmission were in Men who have Sex with Men (MSM). We aim to characterise HIV transmission clusters and transmission of drug resistance (TDR), as well as its determinants, using integrated sociodemographic, behavioural, clinical, and viral genomic data of MSMs newly diagnosed in Portugal between 2014 and 2019.

**Methods:** This study included data from 340 MSM who were diagnosed with HIV-1 infection. These individuals were newly diagnosed at 17 hospitals in Portugal between September 2014 and December 2019. Phylogenies were constructed and transmission clusters were identified with branch support  $\geq 90\%$  and 1.5% genetic distance. Logistic regression models were computed to examine the factors associated with clusters of transmission and with the presence of TDR.