STUDY ON THE FREQUENCY OF DUAL INFECTIONS IN NEW HIV-1 DIAGNOSES IN SPAIN

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BACKGROUND

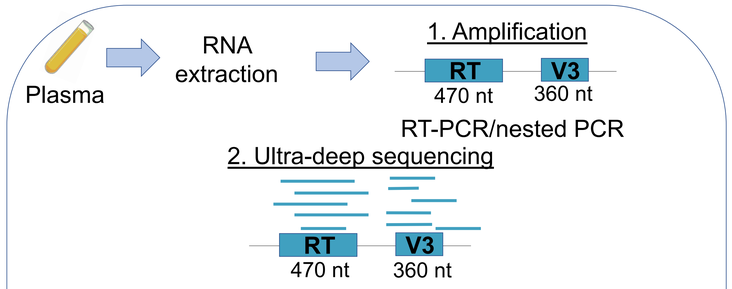
- HIV-1 dual infection (DI) occurs when an HIV-1 infected patient is infected simultaneously (coinfection) or sequentially (superinfection) with a new viral variant. Subsequently, both variants can recombine generating a new recombinant virus. If this new recombinant virus is transmitted, it can become a new circulating recombinant form.
- It has been reported that dual infections may be associated with increase in viral loads and decrease with CD4⁺ T-cell counts.
- A previous study in Spain reported an 8.6% frequency of dual infections in 81 MSM patients in Madrid (Casado et al., 2020*).
- Objectives of our study: estimation of HIV-1 DI frequency in a larger cohort comprising individuals from different Spanish regions, antiretroviral drug-naïve and newly diagnosed in recent years, with examination of associations with clinical, epidemiological and virological variables.

*Casado et al. (2020). AIDS Res Hum Retroviruses; 36: 896-904. doi: 10.1089/AID.2020.0068.

Among 498 **HIV-1 infections newly diagnosed in Spain** in 2017-2020, 23 (**4.6%**) **dual infections** were detected by UDS of two genome fragments.

Dual infections were significantly **associated with** membership in **transmission clusters** and **non-subtype B** infections.

METHODS



RESULTS

DIs were detected in 23 (4.6%) of 498 patients from 6 Spanish regions. 10 were intrasubtype (9 B, 1 CRF02_AG) and 13 were intersubtype (all B+non-B). 14 DIs were detected in RT, 5 in V3, and 4 in both fragments

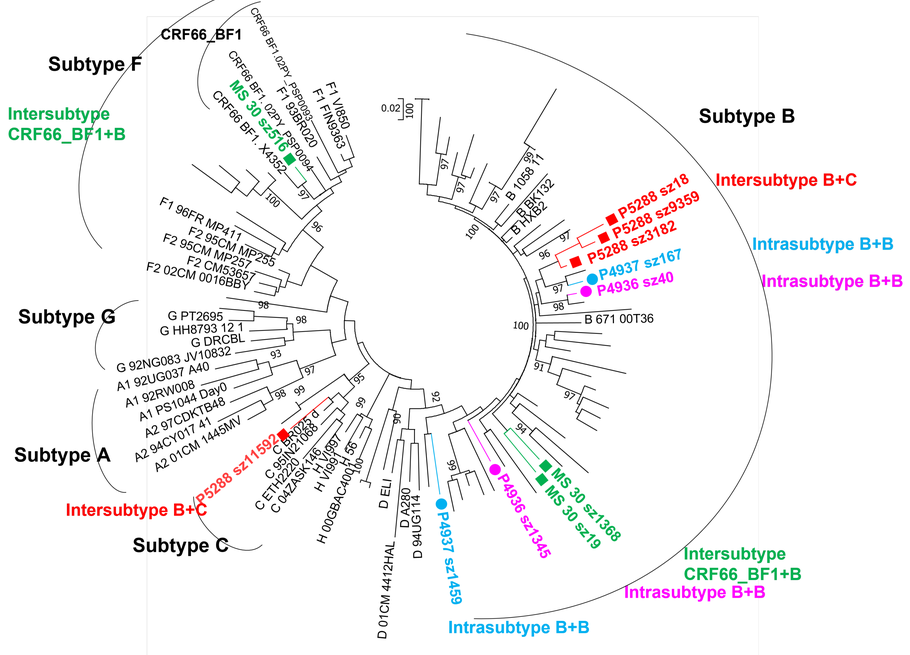
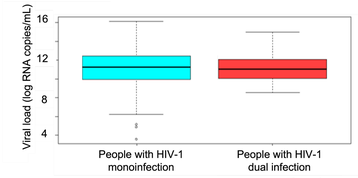


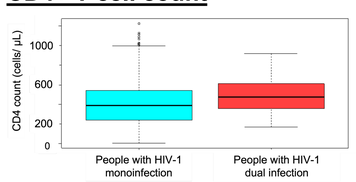
Fig. 1. Maximum likelihood phylogenetic tree of OTUs of the RT fragment of 4 DIs. OTUs of 2 intrasubtype (B+B) and 2 intersubtype (B+C, B+CRF66_BF1) dual infections are highlighted with the names of the viruses in color. For each OTU, the number of sequences represented by it is indicated.

Viral load



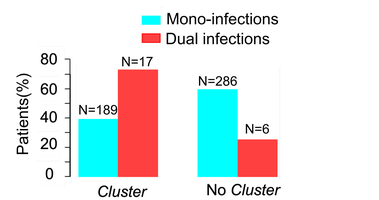
P-value = 0.612

CD4+ T-cell count



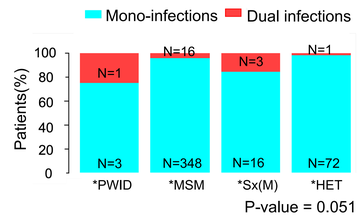
P-value = 0.03

Transmission cluster membership



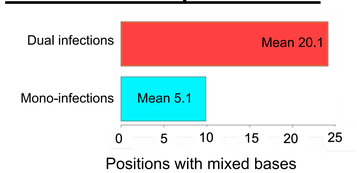
P-value = 0.0015

Transmission route



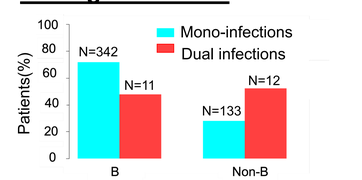
P-value = 0.051

Mixed bases in protease-RT



P-value = 0.044

HIV-1 genetic form



P-value = 0.013

Fig. 2. Infections belonging to a transmission cluster of ≥4 individuals were significantly associated with DIs. CD4⁺ T-cell count was slightly significantly higher in DIs. Age, gender, and viral load were not significantly associated with DIs. There was a marginally non-statistically significant tendency for more frequent DIs in MSM and persons who inject drugs. Infection with a non-subtype B virus was significantly associated with DI. Mixed bases in protease-RT previously identified in Sanger sequencing were significantly more numerous in DIs.
*PWID: People who inject drugs; MSM: Men who have sex with men; Sx(M): Men with nonspecified sexual transmission; HET: Heterosexual

CONCLUSIONS

- DIs were detected in 4.6% of new HIV-1 diagnoses in Spain.
- DIs were more frequent among infections with non-subtype B viruses and among infections belonging to transmission clusters.
- Largest study of DIs based on UDS.

ADDITIONAL KEY INFORMATION

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