

Association of new HIV diagnoses within long-lived transmission clusters from Malaga area (Spain)

Viciano I^{1,2}, González-Domenech CM^{3*}, Sena Corrales, G²; Gómez Ayerbe, C^{2,3}; Villalobos, M²; Ojeda, G²; Nuño, E²; Clavijo, E²; Palacios Muñoz, R^{2,3}; Santos, J^{2,3}

¹Institute of Biomedical Investigation of Malaga (IBIMA), Spain; ²Hospital Virgen de la Victoria, UGC Infectious Diseases and Microbiology, Malaga, Spain; ³Department of Microbiology, University of Granada; *Email: iadomenech@gmail.com

Background

The early HIV diagnoses (NDHIV) and the decrease of the hidden infections rate are the goals of a proactive contact study (CS) among them, performing at Virgen de la Victoria Hospital (southern Spain) from September of 2017. Our aim was the molecular epidemiological determination of the transmission clusters (TC) comprising these NDHIV, clarifying if they are expanding previous TCs in our area or, on the contrary, they are actively arising new TCs.

Results

59 NDHIV

n_{CS}=41 (69.5%)

n_{TC}=30 (73.2%)

Table 1. Subtyping of NDHIV included in our contact study.

Subtype	Number of sequences
Pure subtypes:	
A1	1(2.4)
B	24(58.5)
Circulating Recombinant Forms (CRFs):	
CRF 01_AE	1(2.4)
CRF 02_AG	1(2.4)
CRF 12_BF	2(4.8)
CRF 19_cpx	7(17.0)
CRF 20_BG	1(2.4)
CRF 47_BF	1(2.4)
Undetermined	3(7.3)

Material and Methods

- We considered all the HIV-1 genotype resistance tests performed in NDHIV and participating in the contacts study in our hospital, from January-2017 to June-2018.
- Drug resistance mutations were determined with Viroseq HIV@ system and the partial sequence of HIV-1 *pol* gene provided phylogenetically compared to a cohort of 451 naïve patients diagnosed between 2004 and 2015 and clustered in 86 TCs previously described.
- The belonging to a prior TC was based on a phylogenetic criterion as well as using the mean pairwise distance.
- Therefore, a NDHIV was phylogenetically considered within any cluster if the branch-support measure (SH-like aLRT test) is $\geq 90\%$.
- The alignment was done by ClustalX and the phylogenetic reconstruction inferred by maximum likelihood method (FastTree program).
- Regarding pairwise distances, they were estimated directly from the sequence alignment (MEGA-X software package) and the difference of 0.015 substitution/site with any sequence included in a particular TC, as maximum threshold of belonging to such TC.

Fig.2. Topology of the new transmission cluster (TC) emerged within our cohort and exclusively composed by three NDHIV. It is also depicted an already TC (TC=17) integrating two NDHIV.

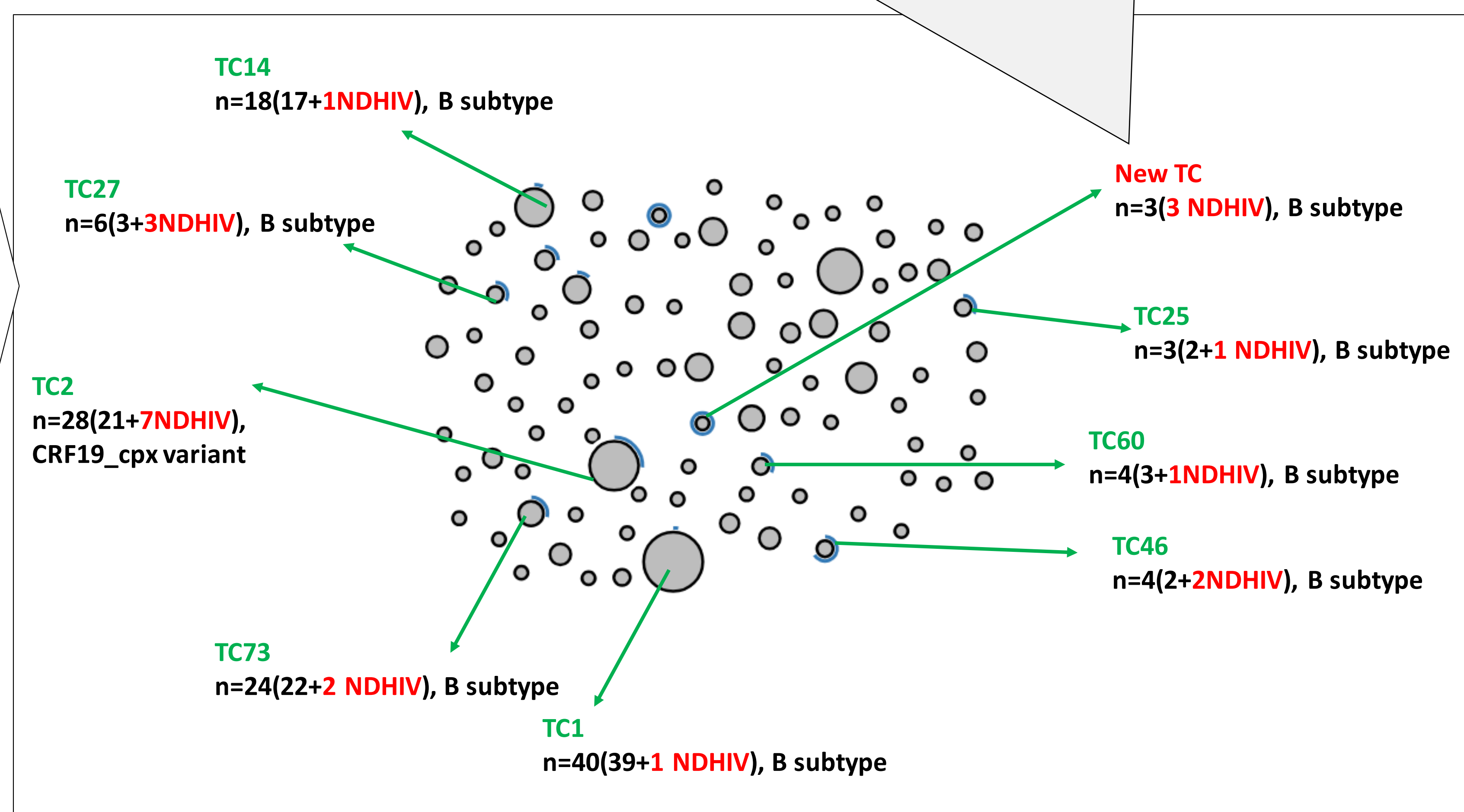
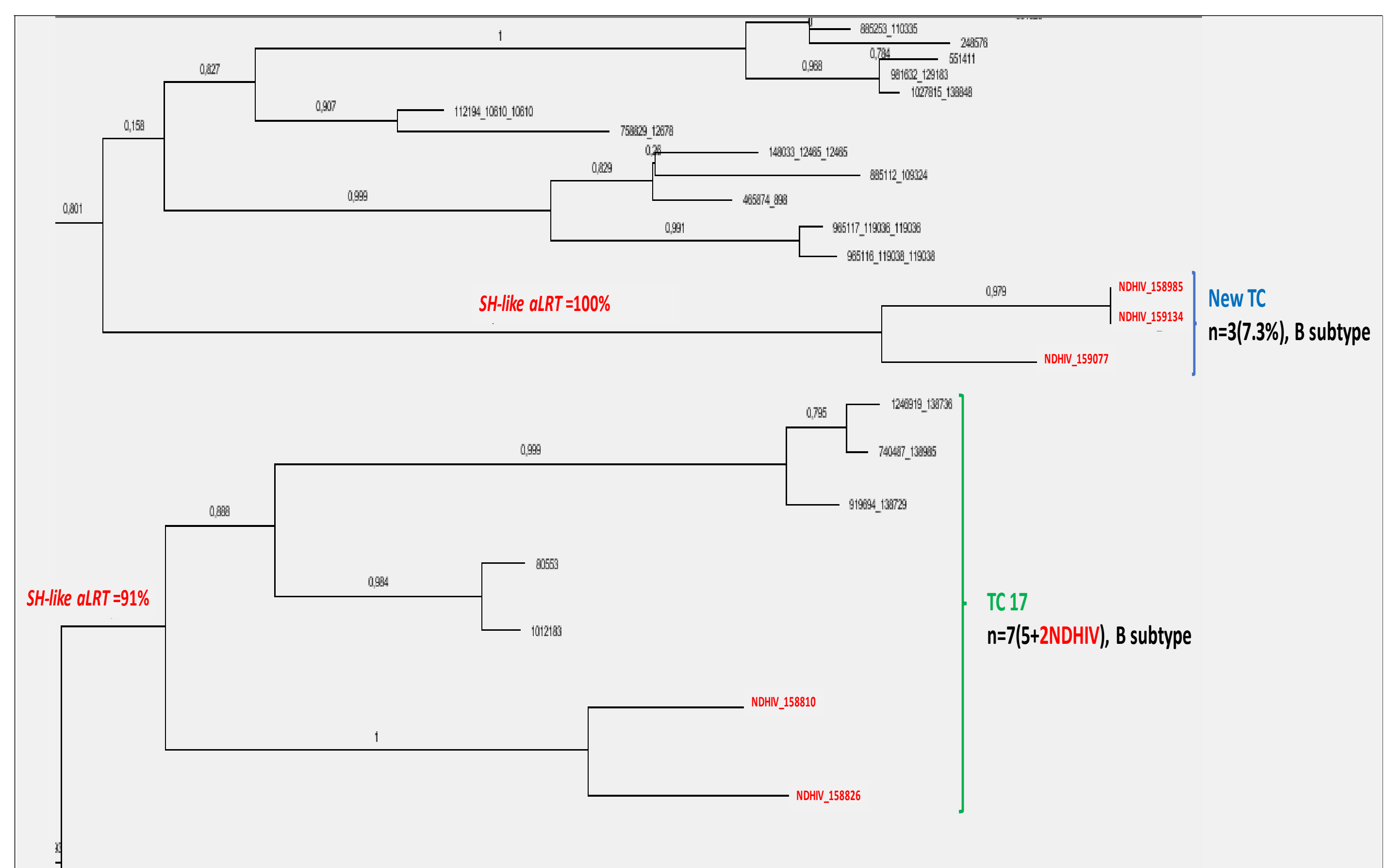


Fig.3. Transmission network showing the clusters (TCs) in our cohort according to a genetic distance criterion (0.015 substitutions/site). We indicated the already established TCs including new cases (NDHIV) and which are also supported by a phylogenetic criterion. Image provided by HIV-TRACE analysis through <http://datamonkey.org> [2,3].

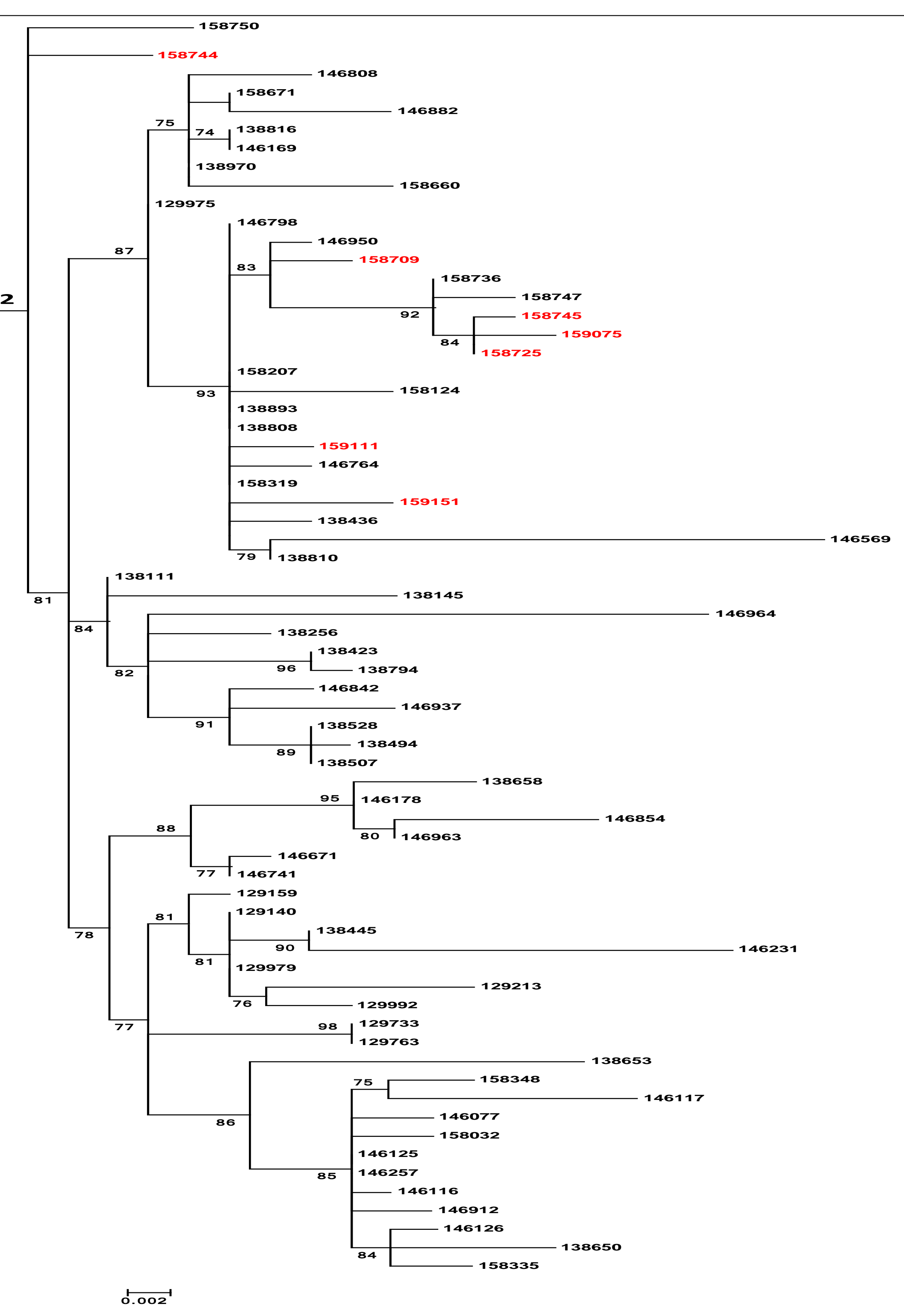


Fig.1. Subtree showing the phylogenetic relationship among the new cases (in red) of CRF19_cpx variant and those already described as an outbreak [1].

Conclusiones

- Almost three out of four NDHIV included in this study expand previous TC, already defined in our area.
- The incidence of new TCs is relatively low.
- The molecular epidemiology of the contacts study points out to networks including already diagnosed and under follow-up patients.

References

- Emergence as an outbreak of the HIV-1 CRF19_cpx variant in treatment-naïve patients in southern Spain. *PLoS ONE*. 2018.
- Datamonkey 2.0: a modern web application for characterizing selective and other evolutionary processes. *Mol. Biol. Evol.* 2018.
- HyPhy: hypothesis testing using phylogenies. *Bioinformatics*. 2005.