

Persistent outbreak of the HIV-1 CRF19_cpx variant in treatment-naïve MSM patients in Malaga area (Spain)

Viciano I^{1,2}, González-Domenech CM^{3*}, Mayorga M⁴, de la Torre J⁵, Gómez-Ayerbe C^{1,2}, Castaño M⁴, Del Arco A⁵, Palacios R^{1,2}, Santos J^{1,2}

¹Institute of Biomedical Investigation of Malaga (IBIMA); ²Hospital Virgen de la Victoria, UGC Infectious Diseases and Microbiology, Malaga, Spain; ³Department of Microbiology, University of Granada; ⁴Hospital Regional Carlos Haya, UGC Infectious Diseases and Microbiology, Malaga, Spain; ⁵Infectious Diseases Unit Hospital Marbella, Spain; *Email: iadomenech@gmail.com

Background

During the period 2011-2016, the HIV-1 CRF19_cpx variant emerged as an outbreak in newly HIV diagnoses (NDVIH) in southern Spain [1]. Our aim was to determine the current status of this outbreak, analyzing the new cases of this variant in our area and their epidemiological relationship with the previous ones.

Results

N=523

n=12 (2.3%)

Table 1. Characteristics of the new cases of the CRF19_cpx variant as well as comparison of them within the overall cohort of this subtype in our area.

Characteristics		New cases	General Cohort
Number of patients		12	69
Age (years)		35.7±11.3	36.5±9.5
Age at diagnosis (years)		35.1±11.2	33.6±9.3
Risk behaviour	MSM	12(100.0)	64(92.8)
	HTX	0(0.0)	1 (1.4)
	Others/ unknown	0(0.0)	3 (4.3)
Education	No studies/ primary school	2(16.7)	7 (10.1)
	Under-graduate	7(58.3)	31 (44.9)
	University	2(16.7)	17 (24.6)
	Unknown	1(8.3)	13(18.8)
Origin	Spain	11(91.6)	64 (92.8)
	Argentina	0(0.0)	2 (2.9)
	France	0(0.0)	1(1.4)
	Italy	1(8.3)	1(1.4)
Seroconversion time (months)		31.7±23.8	17.4 (11.1-43.6)
Initial viral load		4.6±0.6	4.8±0.7
Initial lymphocyte CD4 count		444±272	397±208
Initial lymphocyte CD8 count		871±372	1013±527
Lymphocyte CD4 nadir		394±280	346(221-445)
Zenith viral load		4.1±1.1	4.8±0.9
Final lymphocyte CD4 count		593±281	716±296
Final lymphocyte CD8 count		1086±560	1029(757-1303)
Viral suppression**		10(90.9)	61(91.0)
AIDS cases*		0(0.0)	5(7.2)
Death		0(0.0)	1(1.4)
G190A Mutation		0(0.0)	29(42.0)

*Two cases of Kaposi Sarcoma, one oesophageal candidiasis and two *Pneumocystis jirovecii* pneumonia.
**Patients receiving antiretroviral therapy: 10 out of 11 new cases, and 67 out of 69 patients in total.

Viral load is expressed in log copies/mL and the CD4 count in cells/μL.
The quantitative variables are expressed as median and IQR or mean and standard deviation (abnormal or normal distribution, respectively), and the qualitative variables as n (%).
MSM: Men sex with men; HTX: heterosexual transmission.

Conclusions

- All the new cases of the CRF19_cpx variant emerged in our area during 2017 and half this year are phylogenetically clustered with the previous outbreak, pointing out its active status.
- The NDVIH infected with this variant possess similar epidemiological, clinical and immunovirological characteristics to those already included in the outbreak.
- None of the new sequences of this subtype showed the G190A mutation.
- The active transmission of the CRF19_cpx variant in our area should warn us about the necessity of intense epidemiological surveillance programs.

Material and Methods

- We considered all the HIV-1 genotype resistance tests performed in NDVIH at Virgen de la Victoria Hospital, reference center in southern Spain, 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 submitted to REGA v3.0 for subtyping.
- Sequences assigned as CRF19_cpx subtype were phylogenetically compared to the 254 reference sequences of the same variant retrieved from the LANL, as well as to the 55 ones comprising the already described CRF19_cpx variant outbreak.
- The alignment was done by ClustalX and the phylogenetic reconstruction inferred by maximum likelihood method (PhyML v3.0 program). The cluster reliability was supported on the value of SH-like aLRT test.
- The resistance mutations were predicted using Stanford algorithm v7.1.1.
- We also collected demographic, clinical and immunovirological data.

Cases of CRF 19_cpx variant , 2011-2018

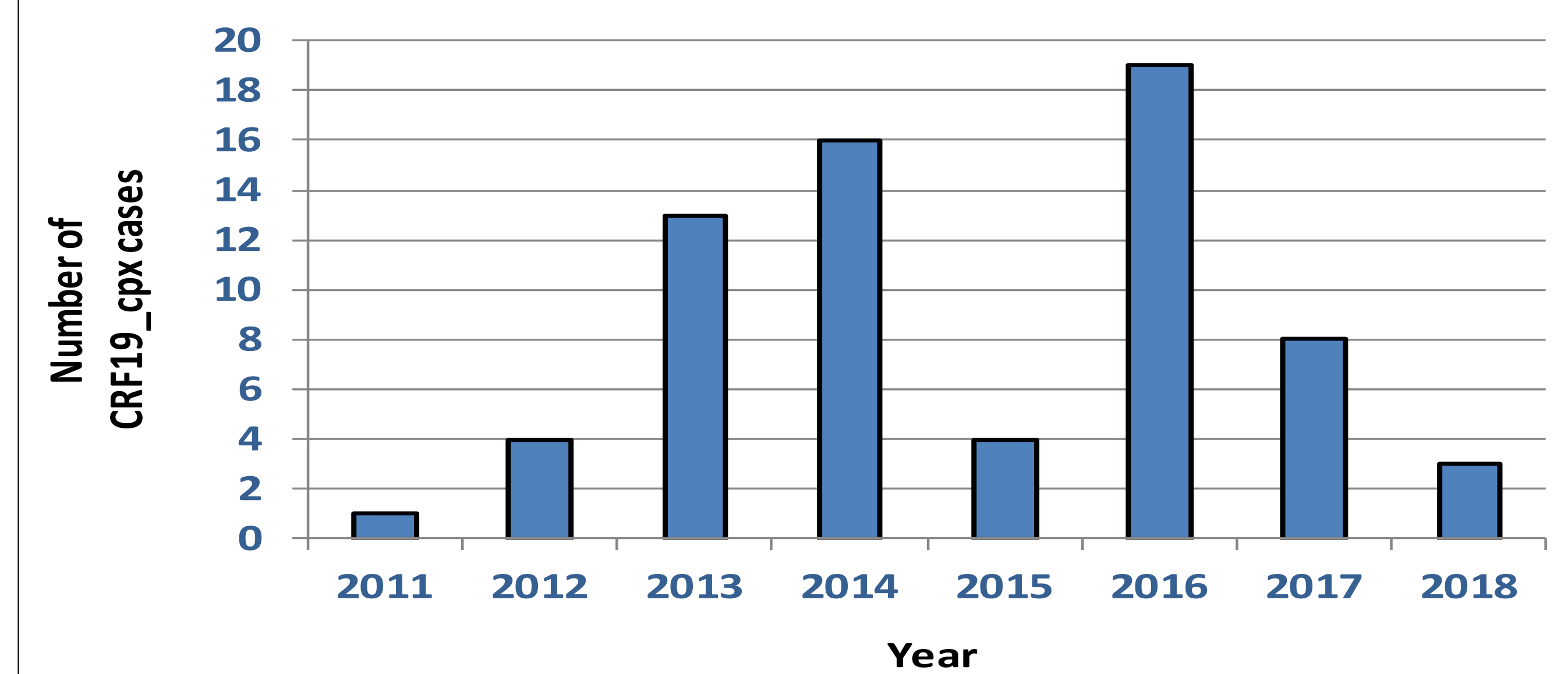


Fig.1. Cases of CRF 19_cpx variants in our area over time.

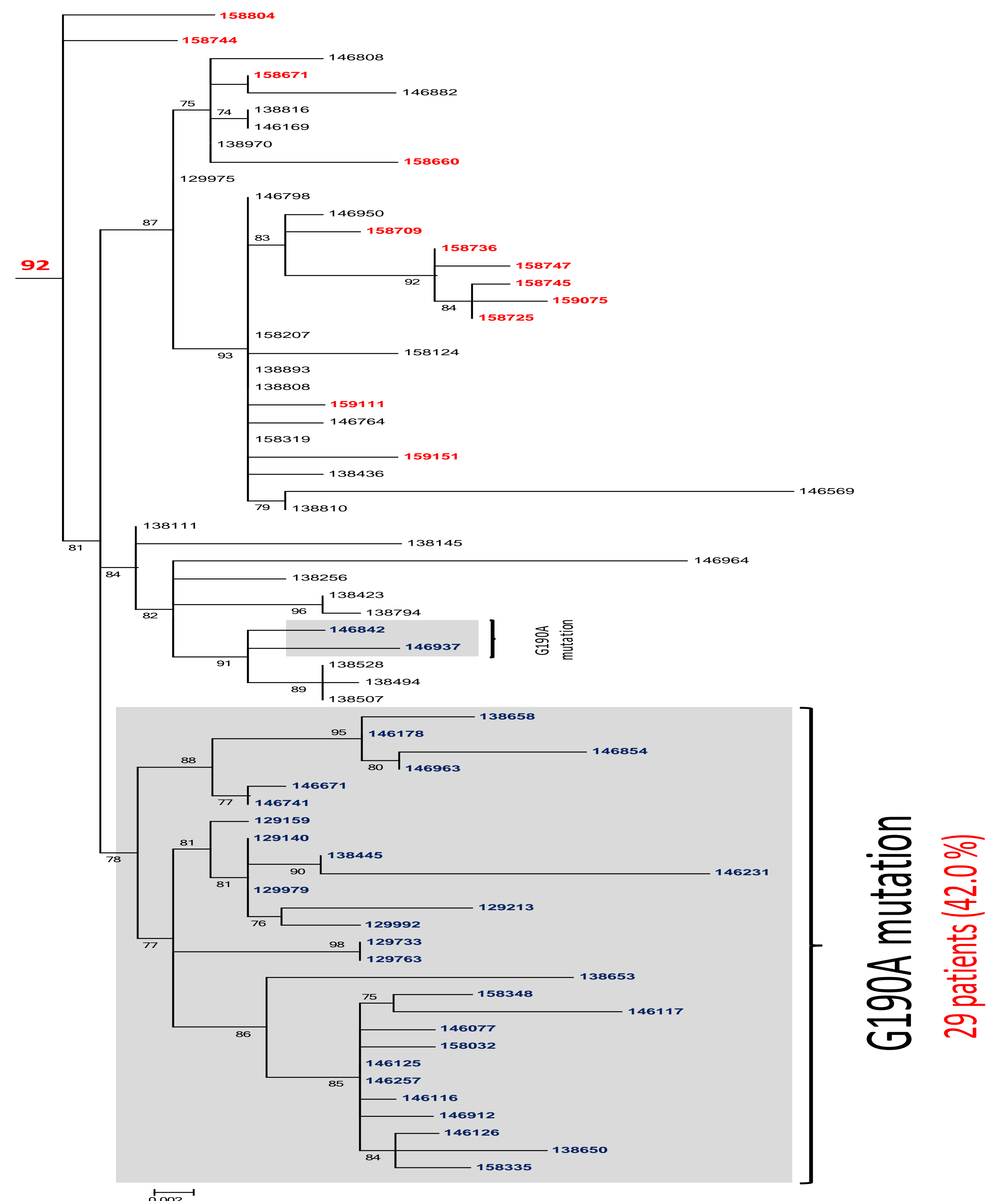


Fig.2. Subtree showing the phylogenetic relationship among the new cases (in red) of CRF19_cpx variant and those already described as an outbreak [1]. Sequences with G190A mutation in the RT are depicted in blue and grey shaded.

References

- Emergence as an outbreak of the HIV-1 CRF19_cpx variant in treatment-naïve patients in southern Spain. PLoS ONE. 2018.