

# Prevalence and factors associated to the detection (population and next generation sequencing) of archived 3TC resistance mutations in aviremic HIV-infected adults (GEN-PRO)

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## PURPOSE

- To evaluate in aviraemic patients the frequency of re-detection of M184V/I and K65R/E/N mutations in proviral DNA (pDNA) by population sequencing (PS) and next generation sequencing (NGS), the concordance between both techniques and predictive factors for clearance of M184V/I-K65R/E/N.

## METHODS

- Observational, cross-sectional study.



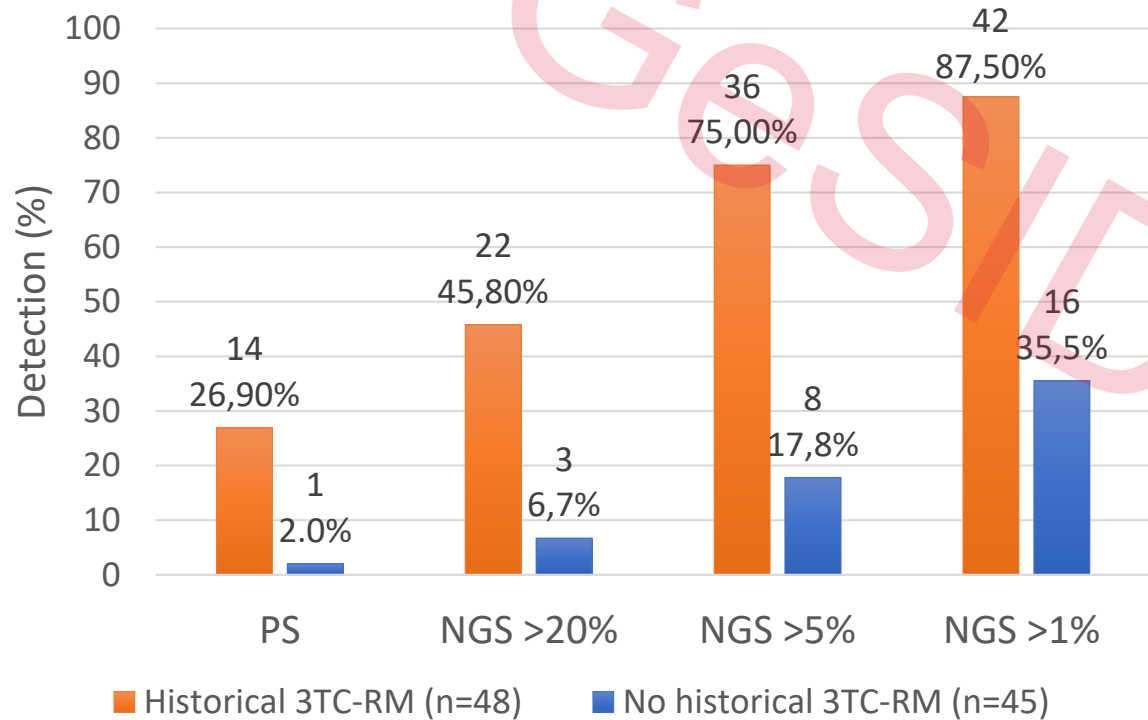
- Resistance mutations (RM) were identified and quantified using PAsEq system (IrsiCaixa).

# PARTICIPANTS CHARACTERISTICS

<b>N=102</b>	<b>Historical M184V/I and/or K65R/E/N (n=52)</b>	<b>No historical M184V/I and/or K65R/E/N (n=50)</b>	<b>p value</b>
Male sex, n (%)	36 (69.2)	41 (82.0)	NS
Age (years), median (IQR)	52.2 (49.0–58.4)	47.6 (41.8–54.2)	<b>0.017</b>
Intravenous drug user, n (%)	17 (32.7)	7 (14.0)	<b>0.028</b>
Years since HIV diagnosis, median (IQR)	21.9 (17.5–24.7)	12.7 (6.7–20.3)	<b>&lt;0.001</b>
Time on ART (years), median (IQR)	19.3 (17.0–22.6)	9.7 (5.9–16.1)	<b>&lt;0.001</b>
Current ART, n (%)			
- 2 NRTI + (1 NNRTI or 1 PI or 1 II)	21 (40.4)	35 (70.0)	<b>0.001</b>
- PI-based dual therapy	15 (28.8)	12 (24.0)	
- PI-based monotherapy	16 (30.8)	3 (6.0)	
Current ART including 3TC/FTC, n(%)	24 (46.2)	47 (94.0)	<b>&lt;0.001</b>
Time on current ART (years), median (IQR)	4.5 (3.0–7.1)	3.5 (2.2–6.5)	NS
Years of HIV-RNA suppression, median (IQR)	8.8 (5.7–12.3)	6.3 (4.2–10.9)	NS

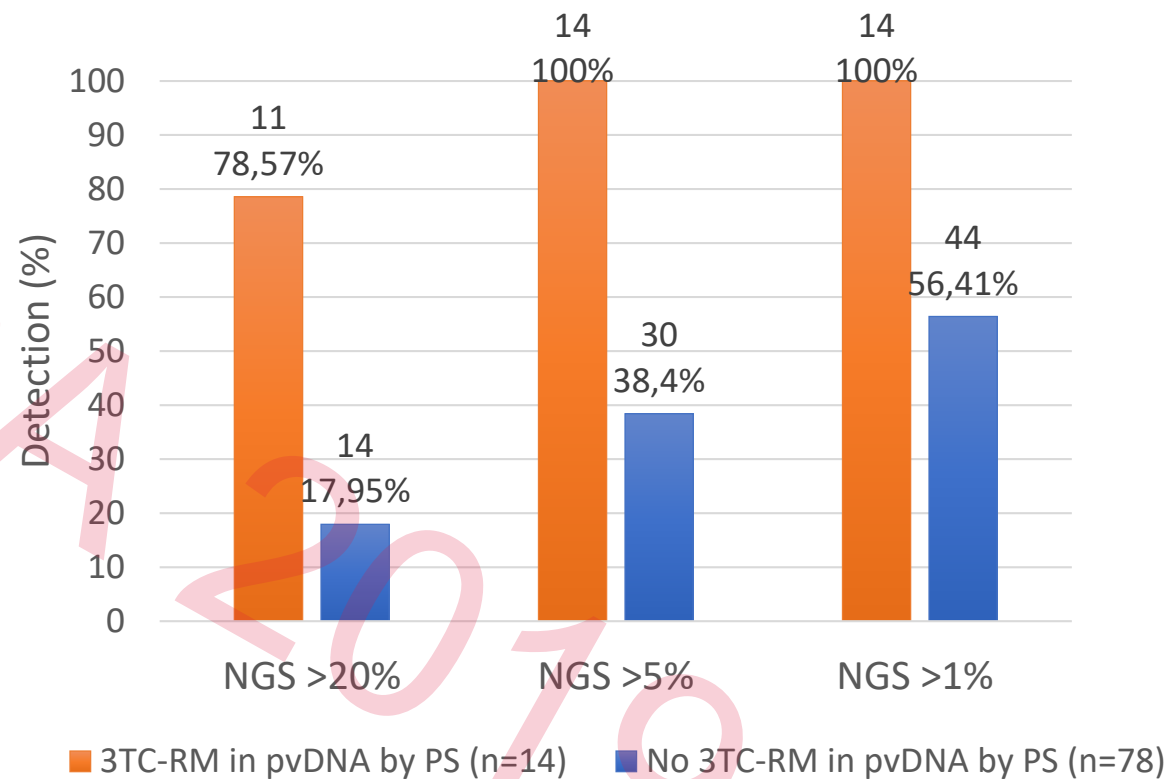
No differences regarding race, CD4 nadir, current CD4 count and CDC stage

### Detection of 3TC-RM by PS and NGS according to prior history of mutations\*



\*PS did amplify 1 sample from one participant without historical mutations.  
 NSG did not amplify samples from 9 participants (4 with historical mutations)

### Comparison of detection of 3TC-RM by NGS at different thresholds in participants with and without detection of mutations by PS\*



\* All comparisons p<0.001, except NGS>1% comparison in pvDNA p=0.002

# Univariate analysis for factors associated to detection of 3TC-resistance mutation in pvDNA in those participants with historical 3TC-resistance mutations

	OR for M184V/I and/or K65R/E/N detection by PS (n=52)	OR for M184V/I and/or K65R/E/N detection by NSG>20% (n=48)	OR for M184V/I and/or K65R/E/N detection by NSG>5% (n=48)	OR for M184V/I and/or K65R/E/N detection by NSG>1% (n=48)
Male sex	0.48 (0.13–1.71)	0.43 (0.12-1.51)	0.35 (0.07–1.87)	0.40 (0.04–3.76)
Age >50 years old	1.69 (0.40–7.20)	1.41 (0.41-4.87)	0.67 (0.15–2.93)	0.40 (0.04–3.76)
HIV acquisition by IDU	1.15 (0.24–5.39)	1.6 (0.36-7.07)	<b>12.86 (1.29–128.14)*</b>	-
Years since HIV infection diagnosis	1.06 (0.96–1.16)	<b>1.1 (0.99-1.22)**</b>	<b>1.16 (1.02–1.32)*</b>	1.06 (0.93–1.22)
Years with suppressed HIV-RNA	1.05 (0.90–1.23)	1.06 (0.92-1.23)	0.99 (0.83–1.16)	0.99 (0.80–1.23)
Years on ART	<b>1.14 (0.99–1.33)**</b>	1.11 (0.97-1.27)	1.08 (0.94–1.24)	1.06 (0.89–1.26)
Years on current ART	1.15 (0.90–1.47)	1.02 (0.81-1.27)	1.01 (0.78–1.31)	0.95 (0.68–1.32)
3TC in current ART	<b>0.22 (0.05–0.92)*</b>	<b>0.34 (0.1-1.12)**</b>	0.51 (0.14–1.92)	0.83 (0.15–4.58)
3-drugs regimen	<b>0.14 (0.02–0.79)*</b>	<b>0.13 (0.03-0.6)*</b>	0.62 (0.14 – 2.73)	0.82 (0.12–5.67)

\*p<0.05, \*\*p<0.1

## CONCLUSIONS

- Proviral DNA population sequencing detects a minority of historical 3TC resistance mutations. **Next generation sequencing increases sensitivity**, but the 5% threshold still misses one quarter of historical 3TC resistance mutations.
- A **regimen including 3TC is associated with no-detection** of archived 3TC resistance mutations in proviral DNA by population sequencing

**P-110** Dolutegravir and Lamivudine for maintenance of HIV viral suppression in adults with and without historical resistance to lamivudine:48-week results of a pilot clinical trial (**ART-PRO**)

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