

## Dettaglio abstract

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**Title:** Impact of COVID-19 pandemic on retention in care of native and migrant PLWH in the ICONA cohort

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### Session/Topic

Prevention, access and engagement

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### Abstract

**Background:** COVID-19 pandemic had a negative impact on all HIV epidemic goals. However, little is known about the impact of the pandemic on HIV retention in care in Italy and whether the disruption of health service may have had a more profound effect in the migrant population.

**Methods:** All PLWH enrolled in Icona Foundation Cohort with active follow up (FU, defined as at least one among HIV-RNA, CD4 cells count, visit, clinical event except for death) were included in the study: those in FU from 01/09/2019 to 29/02/2020 constituted the pandemic period population, those in FU from 01/03/2018 to 31/08/2018 the historical period population (Figure 1a). Primary outcome was temporary LTFU, defined as no laboratory exams, ART modification, clinical visit or clinical event for  $\geq 1$  year. Logistic regression analysis was performed with LTFU as binary outcome and migrant status as the main exposure of interest. The model was controlled for gender, age, geographical location of site, AIDS diagnosis, maximum level of education and employment. Difference in difference (DID) analysis approach was also used, to estimate the potential impact of the pandemic to exacerbate the difference in risk of LTFU between migrants and natives. A sensitivity analysis restricted to centres with electronic data import was performed, to minimise potential bias due to delays in data reporting.

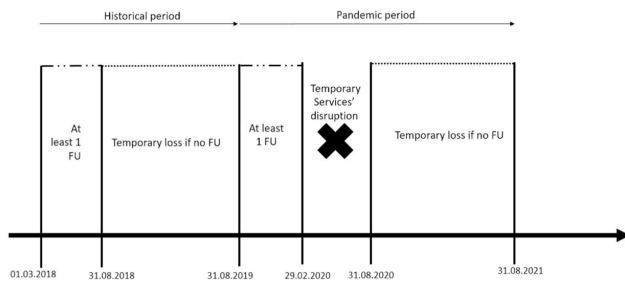
**Results:** A total of 8,847 and 8,135 PLWH were included in the pandemic and in the historical period population, with migrants accounting for 17% in both populations. In the unadjusted Cox regression model, during the pandemic period a higher risk of LTFU was observed for migrants when compared to native PLWH (odds ratio, OR, 1.96, 95%CI 1.70, 2.26,  $p < 0.001$ ), confirmed after adjustment for potential confounders (aOR, 1.78, 95%CI 1.49, 2.12,  $p < 0.001$ ) and partially even in the sensitivity analysis (aOR 1.54, 95%CI 0.97, 2.42,  $p = 0.07$ ).

DID analysis was performed in 6,659 PLWH who contributed to both periods (population characteristics, Figure 1b). In historical period (2018-2020), proportion of PLWH with LTFU was 1.2% (95%CI 0.9, 1.5) in natives vs 2.2% (95% CI, 1.3, 3.1) in migrants. In pandemic period, proportion of PLWH with LTFU was 10.9% (95% CI, 10.1, 11.7) in natives vs 19.2% (95% CI, 16.8, 21.7) in migrants, with a resulting DID of 7.4% (95% CI, 4.6; 10.1,  $p < 0.0001$ ). In the sensitivity analysis, lower risk of LTFU was detected for all groups, with migrants in pandemic period retaining the highest proportion of LTFU (7.2%, 95% CI, 4.3, 10) and a DID of 1.6 % (95% CI, -1.7, 4.9,  $p = 0.36$ ).

**Conclusion:** A higher proportion of LTFU in migrants compared to native PLWH was detected both in historical period and in pandemic period, although some of this effect appeared to be due to a delay in data reporting. Dedicated interventions to minimize LTFU of migrants are needed as the COVID-19

pandemic seemed to have exacerbated their risk of discharge from care even after one year from the first wave hit.

Figure 1A



1B: Main characteristics by nationality of PLWH contributing to both periods

Characteristics	Nationality		P-value*	Total
	Migrants N= 1013	Natives N= 5646		
Gender, n(%)			<.001	N= 6659
Female	391 (38.6%)	989 (17.5%)		1380 (20.7%)
Mode of HIV Transmission, n(%)			<.001	
IDU	32 (3.2%)	626 (11.1%)		658 (9.9%)
Homosexual contacts	355 (35.0%)	2665 (47.2%)		3020 (45.4%)
Heterosexual contacts	577 (57.0%)	2058 (36.5%)		2635 (39.6%)
Other/Unknown	49 (4.8%)	297 (5.3%)		346 (5.2%)
Nationality, n(%)			<.001	
Not Italian	1013 (100.0%)	0 (0.0%)		1013 (15.2%)
AIDS diagnosis, n(%)			0.009	
Yes	168 (16.6%)	762 (13.5%)		930 (14.0%)
CVD diagnosis, n(%)			<.001	
Yes	4 (0.4%)	109 (1.9%)		113 (1.7%)
HBsAg, n(%)			0.140	
Negative	920 (90.8%)	5009 (88.7%)		5929 (89.0%)
Positive	14 (1.4%)	102 (1.8%)		116 (1.7%)
Not tested	79 (7.8%)	535 (9.5%)		614 (9.2%)
HCVAb, n(%)			<.001	
Negative	899 (88.7%)	4499 (79.7%)		5398 (81.1%)
Positive	54 (5.3%)	763 (13.5%)		817 (12.3%)
Not tested	60 (5.9%)	384 (6.8%)		444 (6.7%)
Calendar year of baseline**			1.000	
Median (IQR)	2018 (2018, 2018)	2018 (2018, 2018)		2018 (2018, 2018)
Age, years			<.001	
Median (IQR)	40 (33, 48)	48 (40, 56)		47 (38, 55)
CD4 count, cells/mmc			<.001	
Median (IQR)	615 (402, 844)	695 (505, 916)		684 (485, 908)
<=200 cells/mmc	58 (5.7%)	224 (4.0%)	0.010	282 (4.2%)
CD4 count nadir, cells/mmc			0.180	
Median (IQR)	286 (130, 444)	293 (157, 429)		292 (151, 430)
CD8 count, cells/mmc			0.175	
Median (IQR)	844 (619, 1157)	833 (610, 1108)		834 (611, 1115)
Viral load, log10 copies/mL			<.001	
Median (IQR)	1.28 (0.00, 1.57)	0.30 (0.00, 1.57)		0.78 (0.00, 1.57)
>500,000 copies/mL, n(%)	10 (1.0%)	37 (0.7%)	0.103	47 (0.7%)
>100,000 copies/mL, n(%)	26 (2.6%)	102 (1.8%)	0.243	128 (1.9%)
<=50 copies/mL, n(%)	880 (87.1%)	5120 (90.8%)	<.001	6000 (90.2%)