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The impact of migratory patterns in HIV profile: an analysis of genotype and resistance mutations of the migrant population in a tertiary hospital

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Background

The number of new diagnoses of HIV infection in the EU/EEA has increased significantly in the past years, due to war, the pandemic and natural disasters. The patterns of migration of people living with HIV throughout Europe accounted for 16.6% of the diagnosis made in 2022.[1,2] Depending on the country of origin, the HIV genotyping and resistance mutations may vary and limit the therapeutical options in this population.

Methods

We conducted a retrospective study of all the migrants that were followed in our HIV clinic between the years of 2021 to 2023. We retrieved data from their files namely country of origin, current ART, TCD4+ count, HIV viral load, genotyping and resistance testing.

Results

We evaluated 336 migrants in our HIV clinic, of which 142 had detectable viral load (>20 cp/mL), however, genotyping and resistance testing were performed only in 92 of these patients. The most common genotypes were unique recombinant forms (n=28), genotype C (n=20) and B (N=19). Genotype F1 (n=9) and genotype A1 (n=7) were also documented. Regarding resistance mutations, 2.68% had resistance to NRTI, 6.85% to NNRTI, 1.49% to PI and 3.5% to INSTI. Most of the patients did not have major mutations, 24 had only 1 class mutation, 9 had 2 class mutations and 3 had more than 3 class mutations. The majority of the mutations were found in patients from Latin America and Sub-Saharan Africa (Table 01). Among the migrants with mutations, only one did not have an INSTI based regimen. At the last consultation, 18 patients still had detectable viral load. However, from these 18, 4 were lost to follow-up and 1 returned to his country of origin.

Zone of Origin	NRTI	NNRTI	PI	INSTI
Latin America	M184MV, S68N, M41ML, K65R, S68G, M184I, S68SG, T215S	E138A, K103N, A106VI, V106VIM, E138G, V179E, V106VEIKL,V108VI, V118I, M230MI, E138EA, M230ML, L234LI	F53FL, Q58QEK, Q58E, N88ND, M46L, V82T, L90M, V82F	Q95K, Q146QK, D232DN, L74LIM, G18GRS, T66TS, S147SR, Q148QK, N155NK
Africa	K70N, M184V, M41L, E44ED, L74I, L210W, T215Y, Del67, T69G, K219E	K103N, V106I, V108VI, V106VI, E138G, G190AS, Y318YF, E138K, V79VD, H221Y, L100I, V106VI, E138A, M230L		D232DN, Y143YC, S147SG, Q146QK, G140GD, Q146QE
Asia		K103N		

Table 01. Resistance mutation pattern according to zone of origin.

Discussion

The prevalence of transmitted drug resistance in newly diagnosed HIV cases globally ranges from 10% to 17%, but in migrants the resistance rates are slightly higher, ranging between 15-20%, with some studies reporting values as high as 44%.[2,3,4] In our study, the rate of resistance is closer to the global prevalence rather than the migrant one. It is important to understand the continuous evolution of this population to adjust our prescription according to resistance patterns.

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