

# HIV-1 drug resistance among recently infected individuals in Krasnodar region, Russia, 2021

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## Background

HIV incidence refers to the estimated number of new HIV infections during a certain period (e.g., per year), which is different from the number of people diagnosed with HIV in this year. For this reason, determining the time after infection is

### Materials & Methods

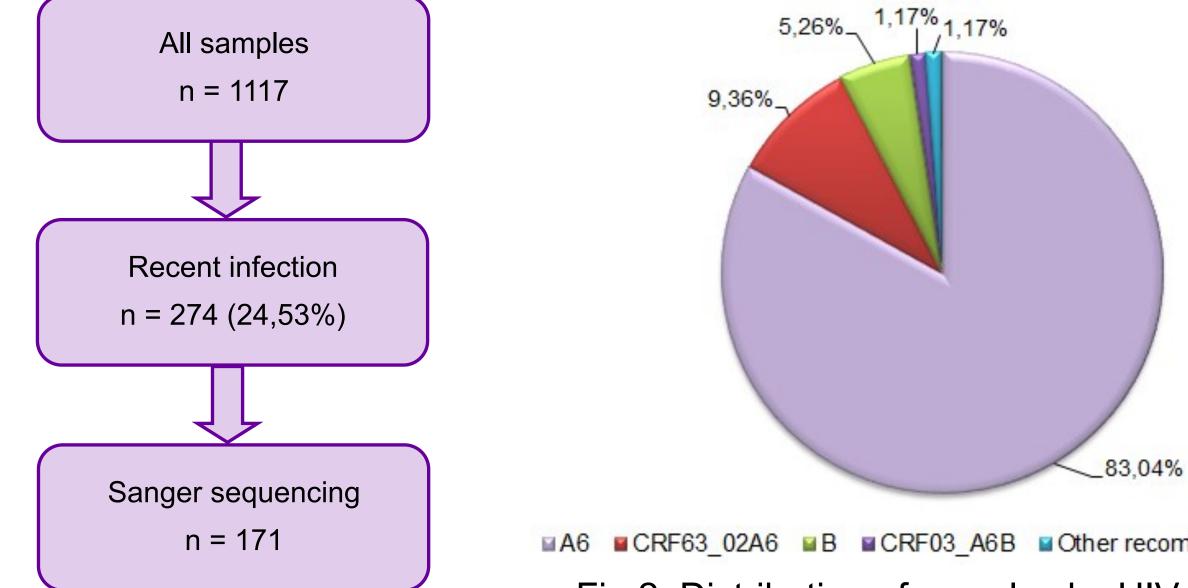
The prevalence of SDRMs was studied among individuals infected with HIV up to 9 months (identified by DS-EIA-HIV-Ab-TERM kit (Diagnostic Systems, Russia)). Nucleotide sequences of *pol* region including protease gene and fragment of re-

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a very important epidemiological and prognostic parameter. Recent Infection Testing Algorithm (RITA) is an approach based on laboratory methods that allow to discriminate recent (up to 12 months or less after infection) and established HIV infection.

The roll-out of antiretroviral therapy (ART) has been a major breakthrough in the global response to the HIV epidemic. Unfortunately, the success of ART is frequently limited by the onset of HIV drug resistance (DR), included DR among people who are treatment naïve as a result of the transmission of DR-variants of the virus.

The aim of the study was to analyze the prevalence of surveillance drug resistance mutations (SDRMs) among people who are treatment naïve and received the status «recent infection» in one-step RITA.



verse transcriptase gene (2253–3369 bp according to the HXB2, GenBank accession number K03455) were obtained using AmpliSens HIV-Resist-Seq kit (CRIE, Russia) by Sanger sequencing. Alignment and nucleotide analysis was carried out in BioEdit v7.2.5. Subtyping was carried out by the Stanford HIVdb Program and subsequently confirmed by HIV BLAST tool (http://www.hiv.lanl.gov/). The Stanford HIV DR Database (CPR Tool) was used to describe and interpret SDRMs.

#### Results

This study was conducted to determine the duration of HIV infection in newly diagnosed people living with HIV in Krasnodar region. Plasma samples were obtained from individuals with the first positive immune blot test during 2021 (n=1117) (fig. 1). All samples were tested using DS-EIA-HIV-Ab-TERM kit, and 274 (24.53%) samples had a "recent HIV infection" result: the mean age of individuals was 38.02 and 165 (60.22%) of them were male.

One hundred seventy-one samples were sequenced from this group and passed sequence quality control. Subtyping results showed that the predominant subtype was sub-subtype A6 (83.04%, 142/171). CRF63 02A6 was detected for 9.36% (16/171), subtype B – for 5.26% (9/171). The other 2.34% (4/171) were circulating and unique recombinant forms (fig. 2).

■A6 ■CRF63 02A6 ■B ■CRF03 A6B ■Other recombinants (URFs) Fig.2. Distribution of samples by HIV subtype.

Fig.1. Samples testing process.

Sample ID	Gender	NRTI SDRMs	NNRTI SDRMs	PI SDRMs
2	male		<b>K103N</b> , G190S	
18	male		K103N	
223	male		K103N	
225	male	L74V		
273	male			M46I
306	male			M46I
538	male			185V
561	female			M46I
565	male			M46L
638	male			M46I
664	male	M41L		
735	female		K103N	
751	male		K103N	
785	female		K101E	
802	male		K101E	
845	male			M46I
903	male		K103N	
919	male		<i>K103N</i> , P225H	
933	male	D67G		
939	female		K103N	
975	male		K103N	
1016	male		K103N	

SDRMs were detected in 14.04% of individuals (24/171) (table 1): the mean age was 35.0 and 19 (79.2%) of them were male. These individuals harbored SDRMs NNRTIS 8.19% (14/171), NRTIS 1.75% (3/171), and PIS 4.09% (7/171). The to mutations were: NNRTI – K101E (2/171, 1.17%), K103N (11/171, 6.4%), G190S (1/171, 0.6%), P225H (2/171, 1.17%); NRTI – M41L, D67G, L74V (1/171, 0.6% of each mutation); and PI – M46I/L (6/171,3.5%) and I85V (1/171, 0.6%). Each individual was infected with HIV-1 resistant only to one drug class.

## Conclusions

It should be noted that we analyzed the prevalence of SDRMs only among recent individuals; this group most accurately reflects the current HIV epidemic. A 14.04% prevalence in this group exceeds 10%-threshold mentioned in the WHO guidelines, which recommended as the threshold to trigger clinical baseline resistance testing. Therefore, it is necessary to continue studies in this field of identification and analysis of newly HIV cases.

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