HIV Drug Resistance in Ireland, 2019

Key Points

- Of 529 HIV diagnoses in 2019, 40% (n=210) were ART-experienced, 38% (n=202) were ART-naïve and 22% (n=117) were ART status unknown.
- HIV drug resistance testing could be carried out for 43% (n=230) of those diagnosed with HIV-1 in Ireland in 2019 and could not be carried out for 57% (n=299).
- Of those who were ART-naïve, 80% (n=162/202) could be tested for HIV drug resistance.

Transmitted HIV drug resistance (TDR):

Of those who were ART-naïve and were tested for HIV drug resistance:

- Fourteen individuals had surveillance drug resistance mutations (SDRMs), categorised using the World Health Organization (WHO) SDRM 2009 list, and the integrase strand transfer inhibitor (InSTI) SDRM 2019 list.
- Prevalence of TDR was 8.6% (95% CI 5.2% -14.0%), representing a decrease compared to the prevalence in 2018 (10.8%; 95% CI 7.2% - 16.0%), although not statistically significant.
- By drug class, prevalence of TDR was 6.2% for non-nucleoside-analogue reverse transcriptase inhibitors (NNRTIs), 1.9% for protease inhibitors (PIs), 1.2% for nucleoside-analogue reverse transcriptase inhibitors (NRTIs), and 0.6% for InSTIs.
- By HIV-1 subtype, the majority of TDR cases was subtype B (50%), followed by subtype C (21.3%), and subtype CRF01_AE (14.3%).
- By region of origin, prevalence of TDR was 12.5% among people born in Latin America, 11.7% among people born in Ireland, and 7.9% among people born in sub-Saharan Africa.
- By probable route of transmission, prevalence of TDR was 11.8% among gay, bisexual and other men who have sex with men (gbMSM), and 8.3% among heterosexual females.

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Explanation of terms

HIV drug resistance category

The World Health Organization (WHO) commonly classifies HIV drug resistance into three main categories (1):

ADR	Acquired drug resistance (ADR) develops because of viral replication in the presence of antiretroviral drugs.
TDR	Transmitted drug resistance (TDR) is detected among antiretroviral drug-naïve people with no history of antiretroviral drug exposure. TDR occurs when previously uninfected individuals are infected with virus that has drug resistance mutations.
PDR	Pre-treatment HIV drug resistance (PDR) refers to resistance that is detected among people initiating first-line treatment for the first time, or among people reinitiating first-line treatment following a previous exposure. Examples of previous exposure include antiretroviral drugs for preventing mother-to-child transmission of HIV, pre-exposure prophylaxis (PrEP), and first-line antiretroviral therapy that was followed by a period of treatment interruption. PDR can be either transmitted or acquired.

HIV drug class and current treatment guidelines

HIV antiretroviral drugs are categorised by drug class based on how they interfere with the HIV life cycle. The four main drug classes are as follows:

NRTI	Nucleoside-analogue reverse transcriptase inhibitors (NRTIs) were the first antiretroviral class for HIV treatment. They work by blocking reverse transcriptase, an enzyme that HIV needs to replicate itself. Examples of NRTIs include emtricitabine and tenofovir, both of which are used in the formulation of HIV pre-exposure prophylaxis (PrEP).
NNRTI	Non-nucleoside analogue reverse transcriptase inhibitors (NNRTIs) also prevent HIV replication by blocking reverse transcriptase. NNRTIs have played an important role in the management of HIV-1 infections in resource-limited countries.
PI	Protease inhibitors (PIs) prevent HIV replication by selectively binding to viral proteases and inhibiting maturation of the virus.
InSTI	Integrase strand transfer inhibitors (InSTIs) are the newest antiretroviral class in HIV treatment. They work by blocking HIV integrase, which is used by HIV to insert its viral RNA (in cDNA form) into the DNA of the host CD4 cell.

In Ireland, guidelines from the British HIV Association (BHIVA), the European AIDS Clinical Society (EACS), the US Department of Health and Human Services (DHHS), and the WHO are used to make decisions regarding first line therapy (2). Triple-drug therapy, consisting of two NRTIs plus a third agent from one of the other three drug classes (the choice of which depends on a number of factors including risk of poor adherence), is recommended for antiretroviral

treatment of (ART)-naïve people living with HIV. The WHO recommends the use of an unboosted InSTI with a high genetic barrier (e.g. dolutegravir) as a preferred third agent (3).

Background

HIV drug resistance (HIVDR) is the ability of HIV to replicate and evolve in the presence of antiretroviral drugs (1). The WHO reports that currently all HIV antiretroviral drugs are at risk of becoming ineffective, as therapies become more widely used around the globe and the potential for HIVDR increases. Consequences include treatment failure, implications for first line treatment options and national treatment guidelines, and onward transmission of HIVDR (4).

HIVDR can be either acquired (ADR) or transmitted (TDR). Population surveillance of TDR is recommended to preserve treatment options and to control future HIV epidemics (4).

HIV became a notifiable disease in Ireland under the Infectious Disease Regulations in 2011. Since 2012, all diagnoses of HIV are reported using the national Computerised Infectious Disease Reporting system (CIDR). Since 2017, HIV epidemiological data from CIDR are linked to HIVDR data provided by the National Virus Reference Laboratory (NVRL), in order to produce national TDR prevalence rates.

Methods

Criteria for inclusion in surveillance

The criteria for inclusion in HIVDR surveillance are: a person aged ≥18 years, who has been tested prior to commencing their first antiretroviral treatment (ART) regimen in Ireland for susceptibility to any of the available antiretroviral (ARV) drugs in the four main drug classes: NRTIs, NNRTIs, PIs, and InSTIs.

Persons are identified as having TDR using HIVDR data from NVRL in combination with information on prior exposure to ART from CIDR.

Prior exposure to antiretroviral treatment

Of all individuals diagnosed with HIV in Ireland in 2019 (5), a high proportion (43%, n=226/529) was previously diagnosed with HIV abroad and had been previously exposed to ART (87%, n=198/226). Information on prior ART is recorded on HIV enhanced surveillance forms, which are completed by the practice or clinic where HIV is diagnosed (or the referral clinic) and provided to Departments of Public Health who enter data onto CIDR. Data for this report were extracted from CIDR on 14th December 2021. ART refers to treatment of HIV infection and does not include pre-exposure prophylaxis (PrEP) or post-exposure prophylaxis (PEP).

Genotypic antiretroviral resistance testing (GART)

The NVRL undertakes all genotypic antiretroviral resistance testing (GART) in Ireland. GART was performed using Sanger sequencing: drug resistance mutations (DRMs) were identified using Stanford University software (HIVdb algorithm versions 8.7 - 8.9-1) (6).

Sequencing was performed for 43% (n=230) of the total HIV diagnoses in 2019 (n=529). For the remaining 57% (n=299), sequencing was not performed due to either low viral load (n=240) suggestive of being already on treatment at the time of the first diagnosis in Ireland, or because there was no suitable sample for analysis (n=59).

Of the 230 HIV diagnoses that underwent GART, complete HIV-1 protease, reverse-transcriptase, and integrase mutation profile could be generated for 226 persons. Due to technical reasons, partial sequence data only were generated for four persons.

Genotypic definition of transmitted HIV-1 drug resistance

To compare TDR rates across geographic regions and times, WHO recommended in 2009 the adoption of a consensus genotypic definition of transmitted HIV-1 drug resistance, comprising a list of 93 RT/PR surveillance drug resistance mutations (SDRMs) (7). In 2019 a list of 24 non-polymorphic InSTI-selected mutations for quantifying InSTI-related TDR was published for the first time (8). In this study, TDR was defined as the presence in ART-naïve individuals of one or more mutations from the WHO 2009 SDRM list or the 2019 InSTI SDRM list.

TDR can be both underestimated and overestimated when using the WHO 2009 surveillance list to categorise drug resistance. Underestimation of TDR may arise due to the omission of relevant PI/NRTI/NNRTI mutations identified since 2009. Overestimation may arise from the inclusion of mutations that confer resistance to some drugs no longer recommended for first line therapy.

Statistical analysis

Ninety-five percent confidence intervals (CI) were computed using the Wilson score interval for binomial proportions, with STATA v16 software (StataCorp LLC, Texas, USA). CIs for TDR prevalence during the period 2004-2008 were computed using data from a separate study on documented prevalence of HIV type 1 antiretroviral TDR in Ireland from 2004 to 2008, CIs for 2015, 2016, 2017, and 2018 were calculated using data from annual reports (5,9-12).

Results

Prior exposure to antiretroviral treatment

Of 529 HIV diagnoses in 2019, information on exposure to ART was available for 78% (n=412): 40% (n=210) were ART-experienced with history of prior exposure to antiretroviral treatment, 38% (n=202) were ART-naïve with no previous history of exposure to ART, and 22% (n=117) were ART-unknown as no data on previous exposure to ART was available.
Completeness of information on prior exposure to ART by suitability for sequencing is presented in Appendix 1.

Transmitted HIV drug resistance

Sequencing was performed for 80% (n=162/202) of ART-naïve individuals diagnosed in 2019. Of those, 14 had one or more mutations from the 2009 surveillance list or the 2019 InSTI surveillance list, representing a TDR prevalence of 8.6% (CI 5.2% – 14.0%). Thirteen people had resistance to one drug class and one had resistance to three drug classes (Table 1). By drug class, resistance to NNRTIs (6.2%; CI 3.4% – 11.1%) was the highest, followed by resistance to PIs (1.9%; CI 0.6% – 5.3%), NRTIs (1.2%; CI 0.3% – 4.4%), and InSTIs (0.6% CI; 0.1% – 3.4%).

Table 1 Number of individuals with drug resistance mutations (WHO 2009 surveillance list or 2019 InSTI surveillance list), by drug class and history of prior exposure to ART, Ireland, 2019

Number of individuals with GART data	All (n=230)	ART-experienced (n= 18)	ART-naïve (n=162)	ART-unknown (n=50)
PI	4	0	3	1
NRTI	2	1	1	0
NNRTI	15	3	9	3
NRTI+NNRTI	1	1	0	0
NRTI+InSTI	2	1	0	1
NRTI+NNRTI+InSTI	1	0	1	0
Total	25	6	14	5

Figure 1 presents the categorisation of TDR cases. A list of surveillance drug resistance mutations (SDRMs) by HIV subtype is presented in Appendix 2.

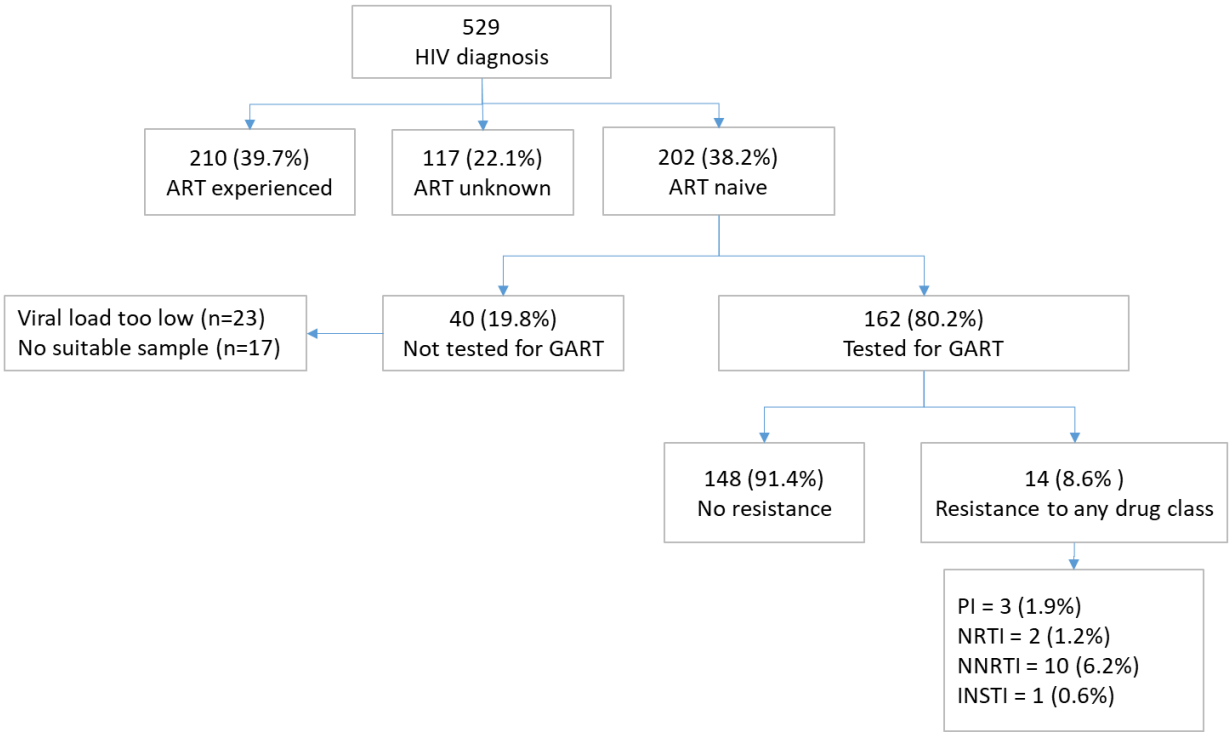

Figure 1 Categorisation of transmitted HIV drug resistance (TDR), Ireland, 2019 (TDR defined as ≥1 mutation from WHO 2009 surveillance list or 2019 InSTI surveillance list).

Demographic characteristics

Table 2 presents the demographic characteristics of ART-naïve people tested and of those with TDR (any drug class) in 2019. Data should be interpreted with caution due to wide confidence intervals caused by the small sample size for some subgroups. By region of origin, TDR prevalence was 12.5% among people born in Latin America, 11.7% among people born in Ireland and 7.9% among people born in sub-Saharan Africa. By probable route of transmission, TDR prevalence was 12.5% among people who inject drugs (PWID), 11.8% among gay, bisexual and other men who have sex with men (gbMSM), and 8.3% among heterosexual females.

Table 2 Demographic characteristics of ART-naïve population tested, and of those with transmitted HIV drug resistance (TDR), Ireland, 2019. (TDR defined as ≥1 mutation from WHO 2009 surveillance list or 2019 InSTI surveillance list)

		Total ART-naïve population tested	**Individuals with SDRMs**	**Prevalence of TDR**	**95% CI**	
		N	N	%		
Total		162	14	8.6	5.2	14.0
Sex	Male	122	11	9.0	5.1	15.4
	Female	40	3	7.5	2.6	19.9
Age group (years)	15-24	16	1	6.3	1.1	28.3
	25-34	74	7	9.5	4.7	18.3
	35-44	39	4	10.3	4.1	23.6
	45+	33	2	6.1	1.7	19.6
Region of origin	Ireland	60	7	11.7	5.8	22.2
	Sub-Saharan Africa	38	3	7.9	2.7	20.8
	Latin America	32	4	12.5	5.0	28.1
	Europe	21	0	0.0	-	-
	Other /Unknown	11	0	0.0	-	-
Probable route of transmission	gbMSM	85	10	11.8	6.5	20.3
	Heterosexual male	23	0	0.0	-	-
	Heterosexual female	36	3	8.3	2.9	21.8
	PWID	8	1	12.5	2.2	47.1
	Other /Unknown	10	0	0.0	-	-
Median CD4 count* (range)		374 (0-1,512)	346 (9-846)			
Subtype	B	71	7	9.9	4.9	19.0
	C	47	3	6.4	2.2	17.2
	A	14	0	0.0	-	-
	CRF01_AE	11	2	18.2	5.1	47.7
	F	6	1	16.7	3.0	56.4
	CRF02_AG	6	0	0.0	-	-
	G	4	1	25.0	4.6	69.9
	Other**	3	0	0.0	-	-

*CD4 count was unknown for 30 (18%) ART-naïve people tested, and for three (21%) people with TDR.
**Subtypes CRF12_BF (n=2) and J (n=1).

Table 3 presents the demographic characteristics of people with TDR by drug class. Combined TDR resistance to NRTI, NNRTI and InSTI was detected in a single case of a heterosexual female born in Sub-Saharan Africa.

Table 3 Transmitted HIV drug resistance (TDR) by demographic characteristics and drug class, Ireland, 2019 (TDR defined as ≥1 mutation from WHO 2009 surveillance list or 2019 InSTI surveillance list).

n=14

		PI	NRTI	NNRTI	NRTI+NNRTI+InSTI
Age group (years)	15-24	1	0	0	0
	25-34	1	1	4	1
	35-44	1	0	3	0
	45+	0	0	2	0
Region of origin	Ireland	2	0	5	0
	Latin America	1	1	2	0
	Sub-Saharan Africa	0	0	2	1
Probable mode of transmission	MSM/bisexual	3	1	6	0
	PWID	0	0	1	0
	Heterosexual	0	0	2	1

Trends

The available data on trends in TDR in Ireland are shown in Figure 2. Trends should be interpreted with caution due to the different methods used over time to define TDR and history of prior exposure to ART (5, 9-12) and the differing completeness of data over time.

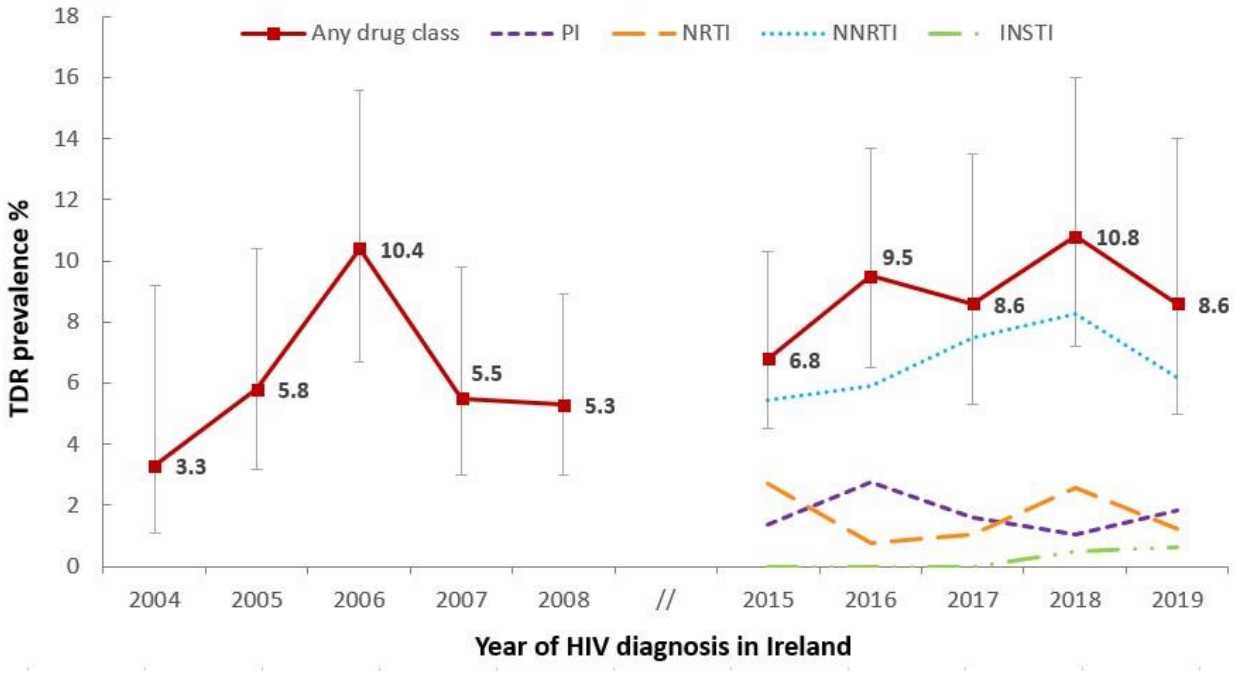

Figure 2 Prevalence (%) and 95% confidence intervals of transmitted HIV drug resistance (TDR) in Ireland, 2004-2008 and 2015-2019. Prevalence for 2004 to 2016 was calculated using different methods and may not be compared reliably with 2017-2019 data.

Discussion

The prevalence of TDR in Ireland in 2019 was 8.6%, a decrease from 10.8% in 2018 and a shift back to the prevalence estimated in 2017. Even though fluctuations in TDR have been observed over the years in Ireland, these differences are not statistically significant and TDR prevalence has remained steady overall.

By drug class, the prevalence of NNRTI-related TDR remained the highest (6.2%), even though it represented a decrease compared to 2018 (8.2%). In contrast, PI-related TDR prevalence was 1.9% in 2019, an increase from 1% in 2018. NRTI-related TDR prevalence decreased from 2.6% in 2018 to 1.2% in 2019, and InSTI-related TDR was found in a single case in 2019, similar to 2018 (0.6% and 0.5%, respectively). Of note, this was the first time in Ireland, since national surveillance of TDR began in 2017, that resistance to InSTI has been found simultaneously in combination with NRTI and NNRTI resistance.

Latest data gathered in the United Kingdom on HIV drug resistance (2002-2016) showed a TDR prevalence of 10% (any-drug class), based on the WHO 2009 SDRM categorisation (15). According to the most recent WHO report on HIV drug resistance (1), data from 2014 to 2020 show high levels (>10%) of NNRTI-related PDR (resistance to efavirenz and/or nevirapine) among adults initiating first-line ART in 21 of 30 low to middle income countries (LMICs). PDR was higher in specific subpopulations, such as females, and people reinitiating first-line ART following previous exposure. PDR is not currently monitored in Ireland as data on treatment interruption are not yet systematically collected.

By region of birth, prevalence of TDR was higher among some subgroups, including people born in Latin America (12.5%), and people born in Ireland (11.7%) but the differences among regions were not statistically significant. TDR in people born in Sub-Saharan Africa region decreased from 14.3% in 2018 to 7.9% in 2019. By probable route of transmission, TDR prevalence was highest among gbMSM (11.8%), an increase from 10.7% in 2018, but this increase was not statistically significant (12). Prevalence of TDR among heterosexual females was 8.3%, a decrease from 9.1% in 2018. In contrast to previous years, no cases of TDR were found in heterosexual males.

Some limitations should be considered regarding surveillance of HIV drug resistance in Ireland. For instance, completeness of data could be improved for certain variables like the history of exposure to ART as those without this information are excluded from analysis, which may result in underestimation of TDR. Furthermore, it is not possible to perform genotypic characterization of HIV drug resistance for all cases, as many samples contain low viral loads that suggest current viral suppression due to antiretroviral treatment. Limitations of demographic analyses include that testing biases may exist due to better testing access and uptake among some subgroups.

In this study, HIV drug resistance was categorised in accordance to the WHO 2009 SDRM list in combination with the 2019 InSTI SDRM list. Use of the WHO 2009 list can result in under estimation or in overestimation of TDR, due to reasons previously described. Other available methods to categorise HIV drug resistance include using the scoring system of Stanford HIVdb

algorithm. However, TDR prevalence can be largely overestimated using this method, as it includes mutations that are not relevant in the perspective of first-line ART management.

Early engagement in care and immediate initiation of effective ART are critical for clinical benefits to individuals and to prevent onward transmission of TDR. Therefore, data from this report and continuation of TDR surveillance in future, may be helpful to guide development of national treatment guidelines, or indeed preferred medicine strategies for the management of HIV. This study does not include TDR prevalence to individual drug level, but inclusion of this information may be considered for future reports.

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Appendices

Appendix 1 – History of exposure to antiretroviral treatment of new HIV diagnoses in Ireland- 2019 by GART suitability.

Previously exposed to antiretroviral treatment?	All		Tested for GART		Not tested for GART	
	n	%	n	%	n	%
Yes	210	39.7	18	8.6	192	91.4
No	202	38.2	162	80.2	40	19.8
Unknown	117	22.1	50	42.7	67	57.3

Appendix 2 – Surveillance drug resistance mutations among ART-naïve people tested for HIV drug resistance, by HIV-1 subtype, Ireland, 2019 (mutations from the WHO 2009 surveillance list and WHO 2019 InSTI surveillance list).

	All	B	C	CRF01_AE	F	G
Number of ART-naïve individuals tested PI *	160	70	46	11	6	4
Number of ART-naïve individuals tested NRTI/NNRTI	162	71	47	11	6	4
Number of ART-naïve individuals tested InSTI*	161	70	47	11	6	4
Number of ART-naïve individuals with SDRMs (any drug class)**	14	7	3	2	1	1
PI mutations (n=3)						
L90M	1	1				
M46L	1	1				
V82M	1					1
NRTI mutations (n=2)						
K70R	1	1				
M184V	1		1			
NNRTI mutations (n=11)						
K101E	1	1				
K103N	5	2	2		1	
L100I	1		1			
V106M	1		1			
Y181C	1			1		
Y188H	1	1				
Y188L	1			1		
InSTI mutations (n=1)						
N155H	1		1			
Total number of surveillance drug resistance mutations	17	7	6	2	1	1

*Two samples did not generate a sequence for the protease domain. In addition, one of these samples did not generate a sequence for the InSTI domain.

**Excludes HIV-1 subtypes A (n=14), CRF02_AG (n=6), CRF12_BF (n=2), and J (n=1), as there were no SDRMs detected among ART-naïve individuals with these subtypes.

Appendix 3 – European-Level Surveillance of HIV Drug Resistance

Even though official data at the European level are not yet available, a reporting system for the European-level surveillance of HIVDR was commenced by the European Centre for Disease Prevention and Control (ECDC) in 2019, for 2018 and historical data. The criteria for inclusion in surveillance was defined as any newly diagnosed treatment-naïve HIV patient tested prior to initiating HIV treatment for susceptibility to any of the antiretroviral drugs available at the time in the four main drug classes. HIVDR was defined as any mutation or combination of mutations that produces low, intermediate, or high-level resistance to any relevant NRTI, NNRTI, PI or InSTI (14).

The protocol used the Stanford HIVdb to categorise HIV drug resistance. The Stanford HIVdb is an online bioinformatics tool (https://hivdb.stanford.edu) that uses a clinical algorithm to analyse drug resistance data and is primarily used for individual patient management. It returns inferred levels of resistance to the most commonly used protease, nucleoside, non-nucleoside, and integrase inhibitors. Benefits of the algorithm include the fact that it is updated frequently and that it includes recently identified surveillance drug resistance mutations, unlike the WHO 2009 SDRM list. Drawbacks however include the fact that it also includes drug resistance mutations that do not meet the criteria for TDR surveillance, and that are not clinically relevant in terms of first line treatment options. Therefore, TDR prevalence can be overestimated.

Using the EU-level surveillance protocol to categorise drug resistance in Ireland in 2019, 27 ART-naïve individuals were identified with low, intermediate or high-level resistance to at least one drug class, a prevalence of 16.7% (CI 11.7% - 23.2%) and a decrease from 19% (14.2% - 25.2%) in 2018, even though not statistically significant. Table 3a presents the frequency of resistance by drug class and prior exposure to ART.

Of the 27 individuals who were ART-naïve, 26 had resistance to one drug class and one had resistance to three drug classes. Resistance to NNRTIs was highest (12.4%; CI 8.1% - 18.3%) and was significantly higher than resistance to PIs (2.5%; CI 1.0% - 6.2%), NRTIs (1.9%; CI 0.6% - 5.3%), and InSTIs (1.2%; CI 0.3% – 4.4%).

Table 3a – Number of individuals with low, intermediate or high-level HIV drug resistance mutations (from Stanford University HIVdb susceptibility algorithm), by drug class and prior exposure to ART, Ireland, 2019.

	All	ART-naïve	ART-experienced	ART-unknown
PI	7	4	1	2
NRTI	2	2	0	0
NNRTI	31	19	5	7
InSTI	1	1	0	0
NRTI+NNRTI	2	0	2	0
NRTI+InSTI	2	0	1	1
NRTI+NNRTI+InSTI	1	1	0	0
Total	46	27	9	10

Table 3b shows the list of drug resistance mutations detected in all individuals (regardless of prior exposure to ART), by HIV subtype. Table 3c shows the list of drug resistance mutations detected in people who were ART-naïve, by HIV subtype.

The median age among ART-naïve individuals with drug resistance mutations was 35 years (range 18-60 years); which remained unaltered when analysing males (range 18-60 years) and females (range 24-50 years).

By region of origin, prevalence of drug resistance mutations among ART-naïve persons was 23.3% (n=14/60) among persons born in Ireland, 21.9% (n=7/32) among persons born in sub-Saharan Africa, and 10.5% (n=4/38) among persons born in Latin America.

By probable route of transmission, prevalence of drug resistance mutations among ART-naïve persons was 19.4% (n=7/36) among heterosexual females, 17.4% (n=4/23) among heterosexual males, and 15.3% (n=13/85) among gbMSM.

Table 3b – Drug resistance mutations among all individuals tested for HIV drug resistance, by HIV-1 subtype, Ireland, 2019 (low, intermediate or high-level resistance as categorised by the Stanford University HIVdb susceptibility algorithm).

	All	B	C	F	G	J	CRF01_AE	CRF02_AG	CRF12_BF
Number of individuals tested PI*	227	88	77	10	5	1	12	10	3
Number of individuals tested NRTI/NNRTI*	229	89	79	10	5	1	12	10	3
Number of individuals tested InSTI*	228	88	78	10	5	1	12	10	3
Number of individuals with DRMs (any drug class)**	46	15	20	2	1	1	2	3	2
PI mutations (n=7)									
K20T	1					1			
M46L	2	2							
Q58E	2	1	1						
V82M	1				1				
L90M	1	1							
NRTI mutations (n=11)									
K65R	1	1							
D67N	1		1						
K70R	2	1	1						
M184V	5	1	3					1	
T215A	1	1							
T215I	1		1						
NNRTI mutations (n=38)									
A98G	1							1	
L100I	1		1						
K101E	2	1	1						
K103N	8	2	5	1					
V106M	2		2						
V108I	1		1						1
E138A	12	2	9	1					
E138G	1							1	
E138K	3	2	1						
Y181C	2		1				1		
Y188H	1	1							
Y188L	1						1		
G190A	1		1						
P225H	1		1						
F227L	1		1						
InSTI mutations (n=5)									
G140S	1	1							
Q148R	1	1							
N155H	1		1						
G163R	1								1
R263K	1							1	
Total number of drug resistance mutations	61	18	32	2	1	1	2	3	2

*Four samples had a partial mutation profile: three samples did not generate a sequence for the protease domain; two did not generate a sequence for the integrase domain, and one did not generate a sequence for the reverse transcriptase domain.

**Excludes HIV-1 subtypes A and CRF07_BG, as there were no DRMs detected among individuals with these subtypes.

Table 3c – Drug resistance mutations among ART-naïve individuals tested for HIV drug resistance, by HIV-1 subtype, Ireland, 2019 (low, intermediate or high-level resistance as categorised using the Stanford University HIVdb susceptibility algorithm).

	All	B	C	F	G	J	CRF01_AE	CRF02_AG	CRF12_BF
Number of individuals tested PI*	160	70	46	6	4	1	11	6	2
Number of individuals tested NRTI/NNRTI	162	71	47	6	4	1	11	6	2
Number of individuals tested InSTI*	161	69	47	6	4	1	11	6	2
Number of individuals with DRMs (any drug class)**	27	11	8	1	1	1	2	1	2
PI mutations (n=4)									
K20T	1					1			
M46L	1	1							
V82M	1				1				
L90M	1	1							
NRTI mutations (n=3)									
K70R	1	1							
M184V	1		1						
T215A	1	1							
NNRTI mutations (n=22)									
A98G	1							1	
L100I	1		1						
K101E	1		1						
K103N	5	2	2	1					
V106M	1		1						
V108I	1								1
E138A	5	1	4						
E138K	3	2	1						
Y181C	1						1		
Y188H	1	1							
Y188L	1						1		
F227L	1		1						
InSTI mutations (n=2)									
N155H	1		1						
G163R	1								1
Total number of drug resistance mutations	31	10	13	1	1	1	2	1	2

*Two samples did not generate a sequence for the protease domain. In addition, one of these samples did not generate a sequence for the integrase domain.

**Excludes HIV-1 subtype A (n=14) as there were no DRMs detected among ART-naïve individuals with this subtype.