

Principles of HIV drug resistance testing and interpretation

Dr Leon Levin
Right to Care



Learning outcomes

Upon completion of this module, you should be able to:

- Summarize the mechanisms of HIV drug resistance development
- Explain the basic nomenclature of HIV drug resistance mutations
- Describe the key principles of genotypic resistance testing and resistance interpretation algorithms
- Recognize the limitations of genotypic resistance testing

What does the viral load tell us?

- Where does the virus live?
- In the Blood?
- No
- In the liver
- Yes
- Spleen?
- Yes
- Lymph nodes?
- Yes
- So what does it mean if we find it in the blood?



Is the problem coming from this womans lounge?



So what does the viral load tell us?

- **It tells us that the HIV virus is making.....**



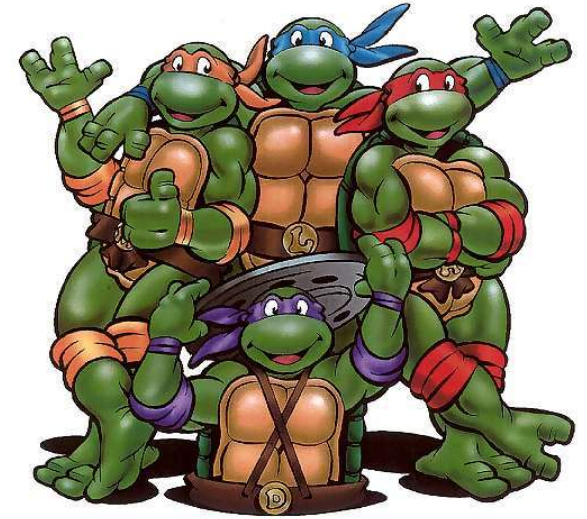


MUTATIONS

- **HIV virus produces 10 Billion new viruses per day**
- **It also makes mistakes when it reproduces itself**
- **One mistake occurs for every cycle of replication**
- **The reverse transcriptase enzyme has no prrooof reading mechanism and cant correct the mistakes**
- **These mistakes are called mutations**
- **Millions of mutations are formed daily**



MUTATIONS



- **If there is no antiretroviral drug around, the mutations quickly disappear**
- **If a mutation causes resistance to a drug, then that quasi species will continue to multiply while the other quasi species are suppressed by that ARV drug.**
- **This will lead to outgrowth of a resistant HIV strain**

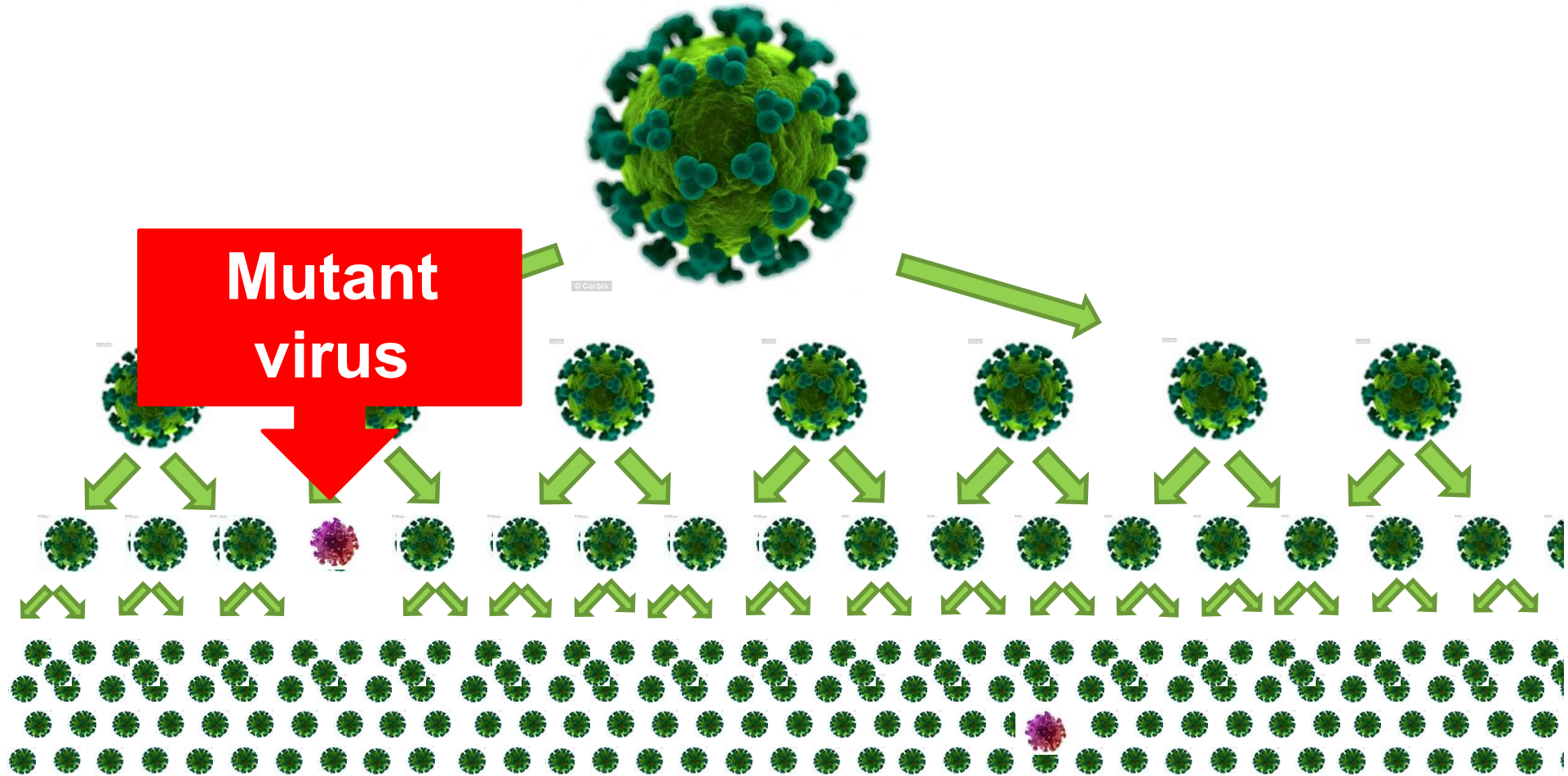


We need 2 things for resistance to develop

- **1) Viral multiplication (replication)**
- **2) Low levels of ARVs in the body**



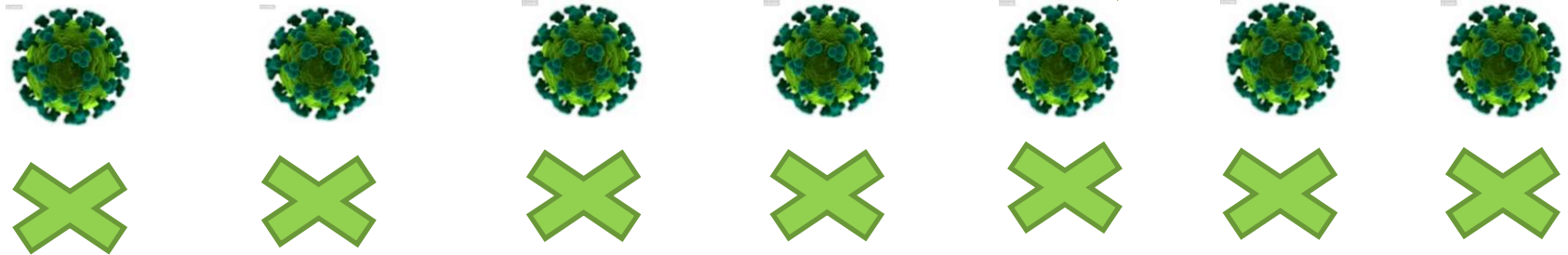
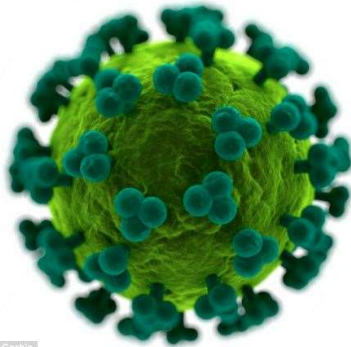
NO ARVS



NO RESISTANCE

Animation sequence courtesy of Dr Julia Turner

SUFFICIENT LEVELS OF ARVS

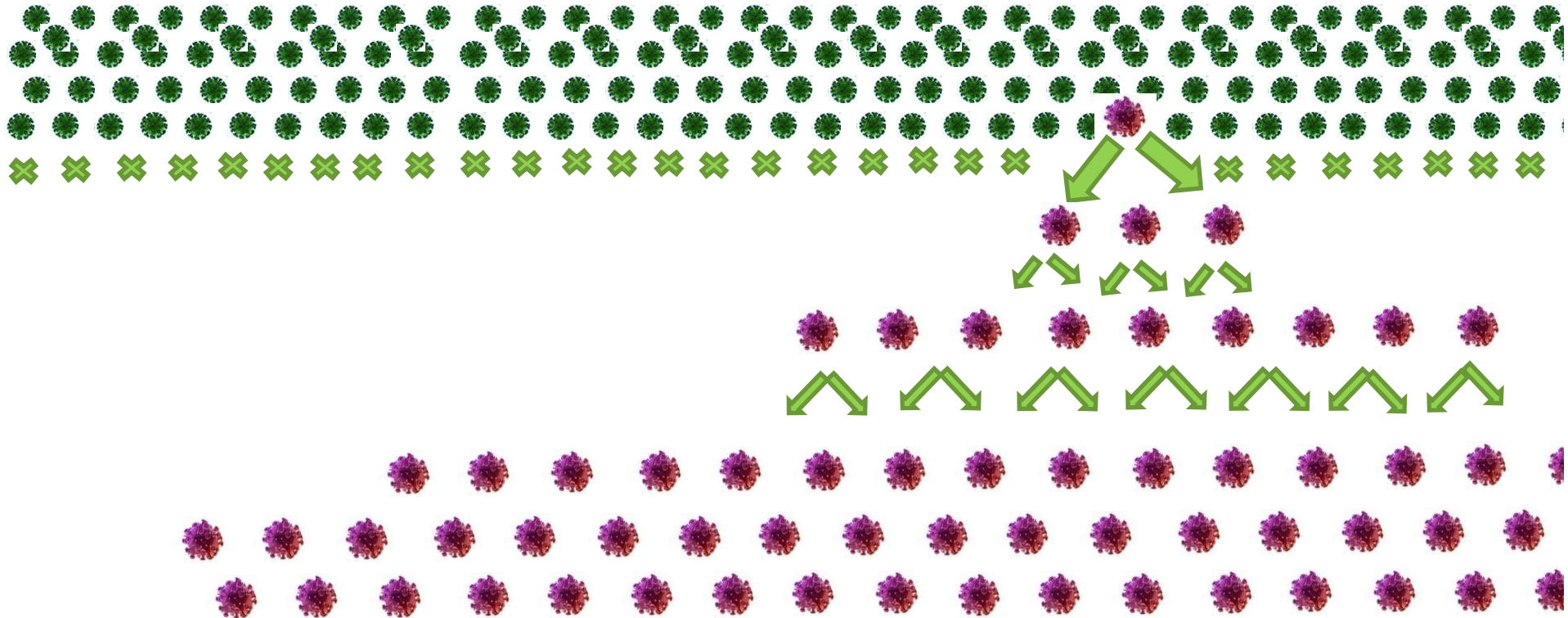


NO REPLICATION
NO RESISTANCE

Animation sequence courtesy of Dr Julia Turner



LOW LEVELS OF ARVS PRESENT



**REPLICATION + LOW LEVELS
OF ARVs=RESISTANCE**

Animation sequence courtesy of Dr Julia Turner

Poll 2

- You do a resistance test on a female patient taking AZT/3TC/LPV/r. It comes back susceptible to all the ARVs.
- 1. What does this mean? (Multiple Choice)
 - A) There is no resistance so she can continue on the same regimen
 - B) She has been non-adherent
 - C) This is Wild Type virus
- 2. Could there still be viral resistance? (Single Choice)
 - D) Yes
 - E) No
 - F) Not sure

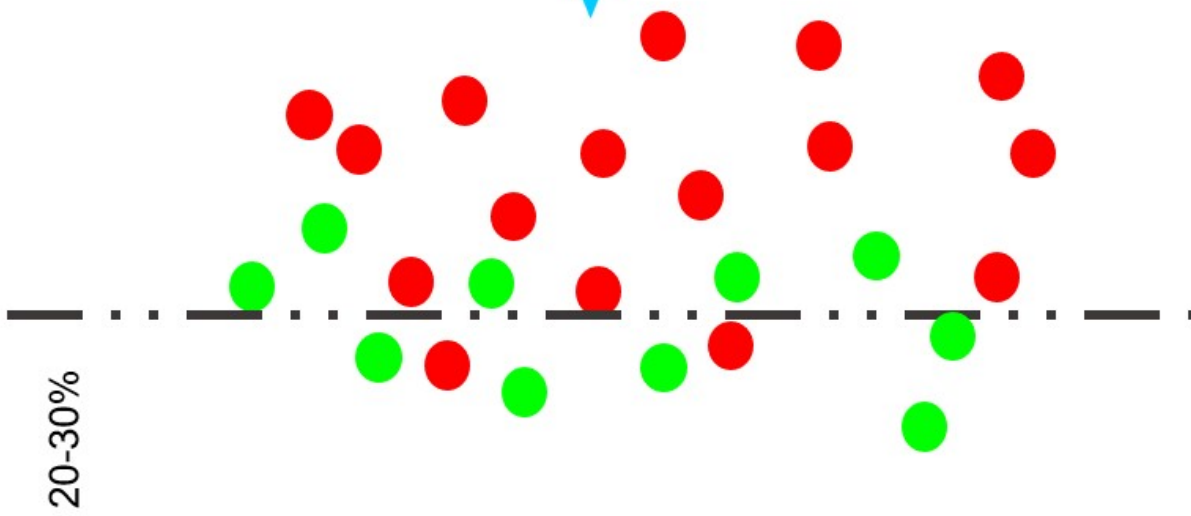
Class	Drug	STAN v6.2.0 29/05/2012
NRTI	Zidovudine	S
	Didanosine	S
	Stavudine	S
	Lamivudine	S
	Emtricitabine	S
	Abacavir	S
	Tenofovir	S
NNRTI	Nevirapine	S
	Efavirenz	S
	Etravirine	S
	Rilpivirine	S
PI/Boosted PI	Indinavir	S
	Saquinavir	S
	Nelfinavir	S
	Fosamprenavir	S
	Lopinavir	S
	Atazanavir	S
	Tipranavir	S
Darunavir	S	

The battle of the HIV Viruses



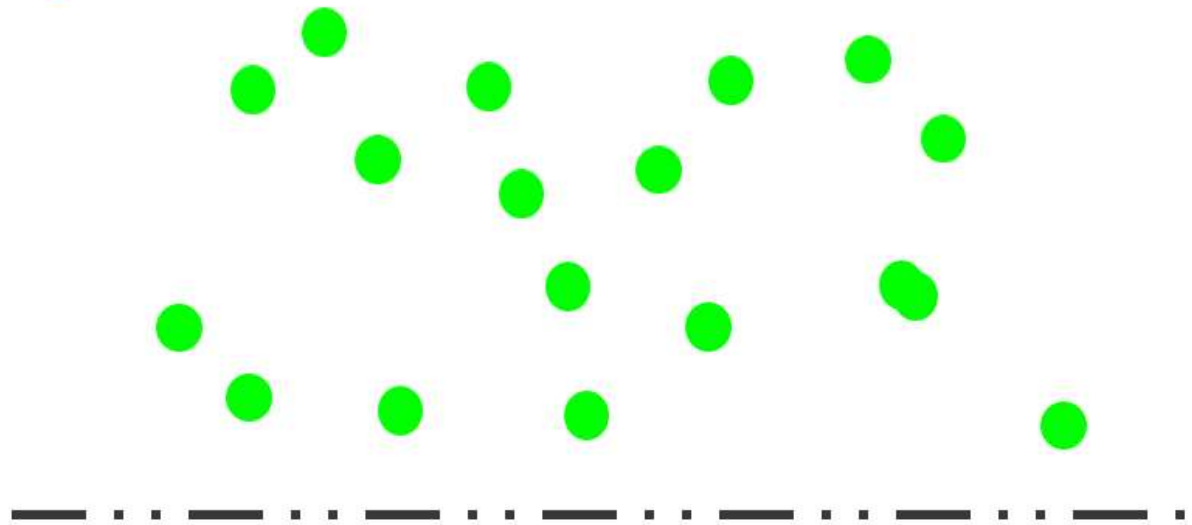
- Resistant virus
- Wild-type virus

Slide courtesy of Dr Anna Maria Geretti



- Resistant virus
- Wild-type virus

Slide courtesy of Dr Anna Maria Geretti



20-30%



How to do resistance testing

- **Therefore make certain that patient is adherent before doing resistance testing**
- **Maintain patient on current antiretroviral therapy - resistance testing must be performed whilst the patient is taking the antiretroviral therapy regimen they are failing**
- **Ask patient to take ARVs regularly for 1 month and then do resistance testing**



Poll 3

- **High Viral Loads**



Question?

If you see 2 patients with the following viral loads, which one do you think is more likely to have resistance?

- VL: 2 000
- VL: 200 000

Resistance mutations generally weaken the HIV virus and reduce its replicability



MUTATION NOTATION

M184V

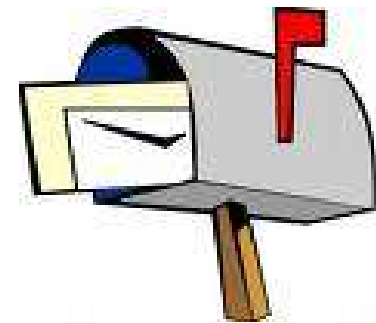


MUTATIONS

M184V



Address of the mutation on
the viral Gene



MUTATIONS

M184V



What should be there
in wild type
(Methionine)



MUTATIONS

M 1 8 4 V



What should be there
in wild type
(Methionine)



What is there
instead (Valine)



Genetic barrier to resistance

- **Some drugs have a low genetic barrier to resistance**
- **Some drugs have a high genetic barrier to resistance**



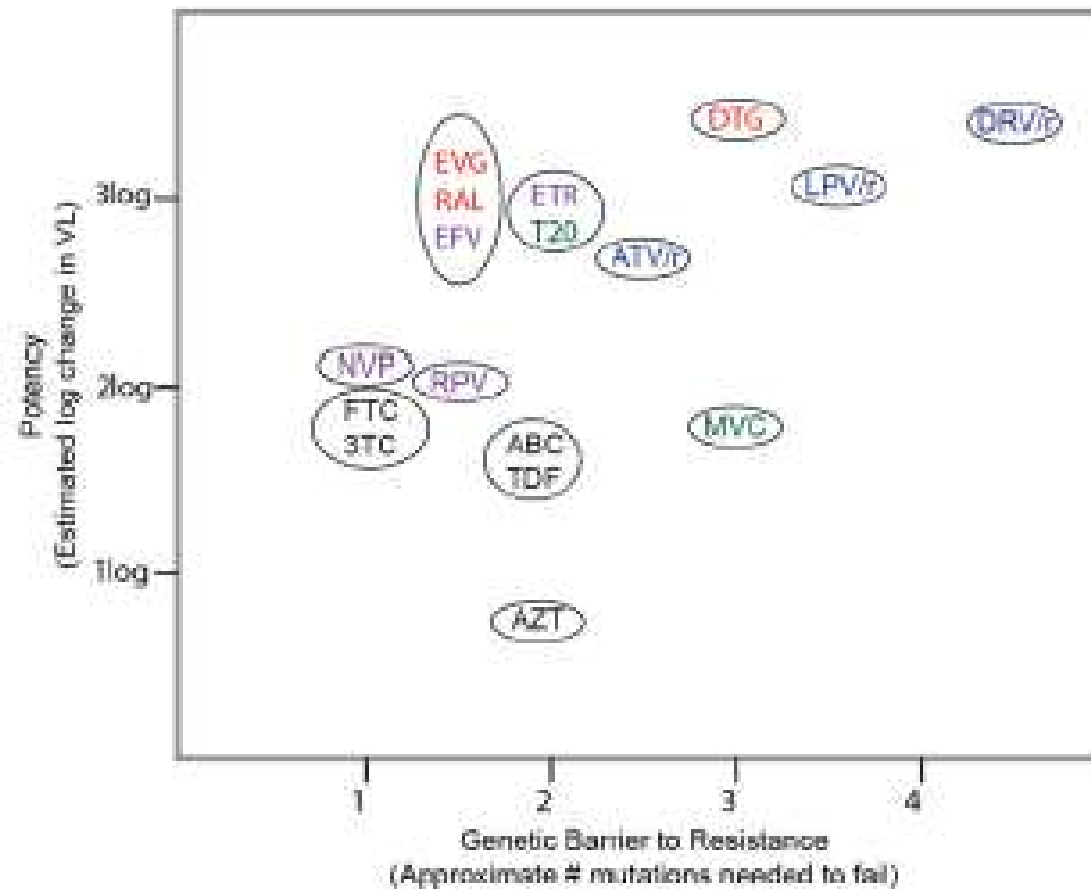


Fig. 1. ARV potency versus genetic barrier to resistance. Abbreviations: ARV; antiretroviral; VL; viral load; ABC; abacavir; ATV/r; boosted atazanavir; DRV/r; boosted darunavir; DTG; dolutegravir; EFV; efavirenz; FTC; emtricitabine; EVG; elvitegravir; T20; enfuvirtide; ETR; etravirine; 3TC; lamivudine; LPV/r; boosted lopinavir; MVC; maraviroc; NVP; nevirapine; RAL; raltegravir; RPV; rilpivirine; and TDF; tenofovir. ARVs in black font are nucleoside or nucleotide reverse transcriptase inhibitors (NRTIs), those in purple font are non-NRTIs (NNRTIs), those in blue font are protease inhibitors (PIs), those in red font are integrase strand transfer inhibitors (INSTIs), and those in green font are entry inhibitors. ARVs appearing together in the same ellipse should be considered to have roughly equivalent potencies and genetic barriers to resistance.

Genetic barrier to resistance

- Lamivudine – single mutation (M184V) confers high-level resistance to lamivudine (**low genetic barrier**)
- Efavirenz – single mutation (e.g. K103N) confers high-level resistance and cross-class resistance (**low genetic barrier**)
- Lopinavir/ritonavir – requires several mutations to confer resistance (**high genetic barrier**)
- Dolutegravir-**high genetic barrier**



HIV drug resistance testing

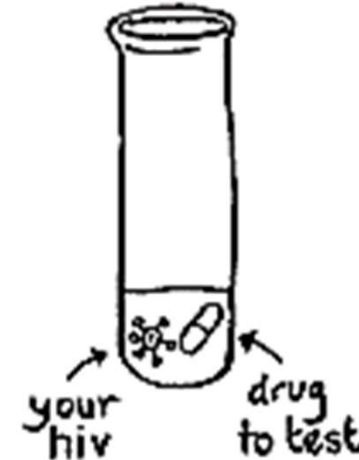
1. genotype

Genotype tests look to see how the structure of a sample of your HIV may have changed.



2. phenotype

Phenotype tests see whether HIV drugs still work to control your type of HIV.



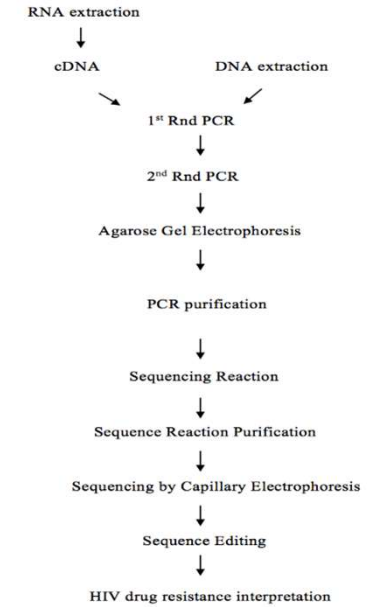
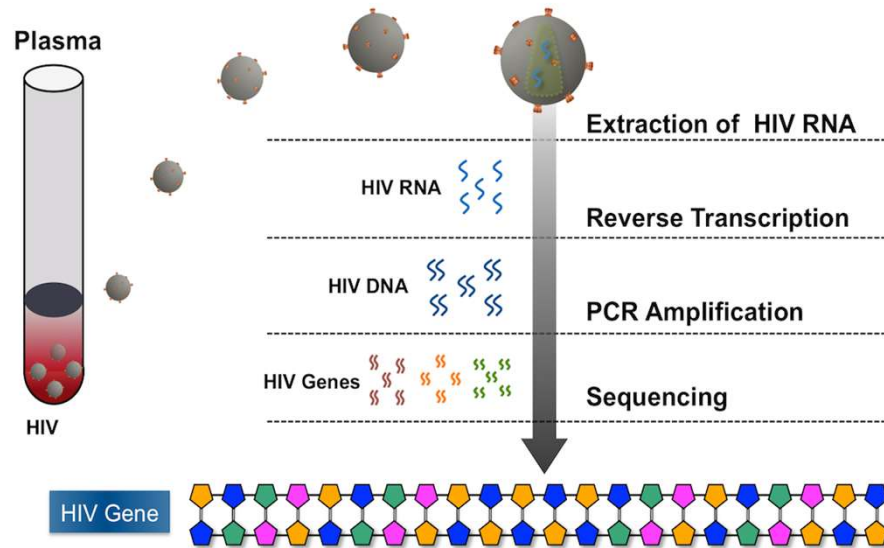
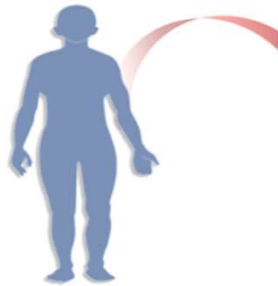
Genotyping

Sequencing of the HIV-1 gene to detect resistance-associated amino acid substitutions (i.e. mutations)

Phenotyping

Measures the ability of a virus to replicate in cell culture in serial dilutions of ARV drugs, thereby directly quantifying the concentration of drug required to inhibit viral replication

How is genotypic drug resistance testing done?



Sanger sequencing



Polymerase chain reaction



Output File

>Sequence1

```
GTAAACTAAAGCCAGGAATGGATGGCCCAAAGATTAACAATGGCCATTGAC
AGAAGAGAAAATAAAAGCATTAAACAGAAATTTGTAACGAAATGGAGAAGGAAGG
AAAAATTACAAAATTGGGCCTGAAAATCCATATAACACTCCAATATTTGCCATA
AAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTCAAT
AAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACATCCAGCAGGG
TTAAAAAAGAAAAAATCAGTGACAGTACTGGATGTGGGGGGATGCATATTTTTCA
GTTCCTTTAGATGAAGACTTCAGGAAATATACTGCATTTACCATACCTAGTATAA
ACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTTCCACAGGGATGGA
AAGGATCACCAGCAATATTCCAAAGTAGCATGATAAAAATCTTAGAGCCCTTTA
GAACAAAAAATCCAGAAATAGTCATCTATCAATATATGGATGATCTGTATGTAG
GATCTGACTTAGAAATAGGGCAACATAGAGCAAAAATAGAGGAGTTAAGAGCA
CATCTATTAAGTGGGGATTTACCACACCAGACAAGAAACATCAGAAGGAACC
CCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAGC
CTATACAGCTGCCAAAAAAGGATAGCTGGACTGTCAATGATATACAGAAGTTAG
TGGGAAAACATAACTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAA
CTTTGTAAACTCCTTAGGGGGGCTAAAGCACTAACAGACATAGTACCACTAACT
GAAGAAGCAGAATTAGAATTAGCAGAGAACAAGGAAATACTAAAAGA
```





Stanford University

HIV DRUG RESISTANCE DATABASE

A curated public database to represent, store and analyze HIV drug resistance data.

[HOME](#)

[GENOTYPE-RX](#)

[GENOTYPE-PHENO](#)

[GENOTYPE-CLINICAL](#)

[HIVdb PROGRAM](#)

[ABOUT HIVdb](#)

SIERRA 2.0 Web Service

- ▶ Access to the new HIVdb features
- ▶ Customizable results using GraphQL
- ▶ Open source Python client
- ▶ Additional clients are pending

[LEARN MORE](#)

CPR Calibrated Population Resistance

INTERACTIVE MAP

[Surveillance Mutations](#)

[Point-of-Care / Essential Mutations](#)

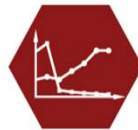
Query Pages



Genotype-treatment

Retrieve sequences (and/or mutations) from persons receiving selected HIV drugs

Retrieve sequences and treatments from viruses with specific mutations



Genotype-clinical

Summaries of genotype-clinical outcome studies

Genotype-clinical outcome datasets (download)



Genotype-phenotype

Retrieve drug susceptibility data for isolates with selected mutations

Download genotype-phenotype research datasets



References

Published drug resistance studies in HIVDB

Published studies by Stanford database group

New Submissions

[View All](#)

[HIVdb Program](#)

Drug Resistance Summaries (Download PDF)

[PIs](#) [NRTIs](#) [NNRTIs](#) [INSTIs](#)

[HIVseq Program](#)

[HIValg Program](#)

[HIV-1 Genetic Variability for Drug Resistance](#)

<https://hivdb.stanford.edu>

HIVdb Program

Genotypic Resistance Interpretation Algorithm

HIVdb version 8.3 (last updated 2017-03-02)

HIVdb accepts user-submitted protease, RT, and integrase sequences or mutations and returns inferred levels of resistance to the most commonly used protease, nucleoside, non-nucleoside, and integrase inhibitors. Its purpose is educational and as such it provides extensive comments and a highly transparent scoring system that is hyperlinked to data in the HIV Drug Resistance Database. A detailed description of the program as well as all updates is in the [Release Notes](#). A [web service](#) has been created to allow users to access HIVdb programmatically.

Sequences can be entered as plain text if just one sequence is entered. Sequences must be entered using the FASTA format if multiple sequences are entered. Sequences can be pasted in the text box or uploaded using the File Upload option. The upper limit is currently 1000 sequences containing 3000 nucleotides per sequence.

By default the program output will contain an HTML page with a navigation sidebar linking to the results for each sequence. Users selecting the spreadsheet output options, will obtain links to tab-delimited files containing tabular sequence summary data, tabular resistance summary data, and a formatted amino acid sequence alignment. Detailed descriptions of the HTML and spreadsheet output are explained in the [Release Notes](#).

Drug display options

By default, results will be shown for checked ARVs. Use checkboxes for additional ARVs. ([select all ARVs](#), [revert to default](#))

NRTI: ABC AZT FTC 3TC TDF D4T DDI

NNRTI: EFV ETR NVP RPV

INSTI: DTG EVG RAL

PI: ATV/r DRV/r LPV/r FPV/r IDV/r NFV SQV/r TPV/r

Input mutations

Input sequences

Header: (optional)

Upload text file: No file chosen

```
>Sequence1
CCTCAAATCACTCTTTGGCAACGACCCCTTTGTCACAATAAAAGTAGGGGGCCAGACAAGAGAGGCTCTCCTAGACACAGGGGAGATGATACAGTATTAGAAGAAATAAATTTGCCAGGAAATGGAAACAAAAATAAGGAGGAATTGGAGGTTTTGT
CAGAGTAAACAGCATGATGATGTAACATAGACATTTGCGGAAAAAGGTTACAGGTACAGTGGTGGTAGGGCTACACCTGCCAACATAATTGGAAGAACATGATGACTCAGCTTGGATGCACACTAAATTTCCAATTAGCCCCATTAACTGTACC
AGTAAACTGAAGCCAGGAATGGATGGCCAAAGGTTAAACAATGGCCATTGACAGAAGAAAAATAAAGCATTAAACAGAAATCTGTGAAGAAATGGAGAAGGAAAGAAAAATACAAAAATTTGGCCTGACAATCCATATAACACTCCAATATTTGCCAT
AAAAAAGAAGGACAGTACTAAGTGGAGAAAAGTAGTAGACTTCAGGGAGCTTAATAAAGAAGCAAGACTTTTGGGAGGTTCAATTAGGAATACCCACCCAGCAGGGTTAAAAAGAGCAATCAGTGACAGTGCTAGATGTGGGAGATGCATATTTTT
CAGTTCCTTTAGATGAAGACTTAGGAAGTACTGCATTCACCATACCCAGTGTGAACAATGAGACACCAGGGATTAGATATCAATATAATGTGCTTCCACAGGGATGGAAGGATCACCAGCAATATCCAAAGTAGCATGACAAAAATTTAGAACCTT
TTAGAGCAAGAAATCCAGAAATGGTCATCTATCAATATGTGGATGACTTGTATGAGGATCTGATTTAGAAATAGGGCAACATAGAAAAAAGATAGAAGAGTTAAGAGAACATCTATTAGCTGGGGACTTACCACCCAGATAAGAAACATCAGAAAGAAC
```

Output options

HTML Printable HTML Spreadsheets (TSV) XML

Reset

Analyze

Drug Resistance Interpretation: PR

PI Major Resistance Mutations: M46I, I54V, L76V, V82A, L90M
 PI Accessory Resistance Mutations: L10F
 Other Mutations: I15V, L19T, K20R, M36I, R41K, K55R, R57K, Q61D, I62V, L63T, E65D, H69K, A71V, I72T, L89M, I93L

Protease Inhibitors

atazanavir/r (ATV/r) High-Level Resistance
darunavir/r (DRV/r) Low-Level Resistance
lopinavir/r (LPV/r) High-Level Resistance

PR Comments

PI Major

- M46I/L are relatively non-polymorphic PI-selected mutations. In combination with other PI-resistance mutations, they are associated with reduced susceptibility to each of the PIs except DRV.
- I54V is a non-polymorphic PI-selected mutation that contributes reduced susceptibility to each of the PIs except DRV.
- L76V is a non-polymorphic mutation selected by IDV, LPV and DRV. It reduces susceptibility to these PIs and to FPV and NFV. It increases susceptibility to ATV, SQV and TPV. L76V is included in the Tibotec DRV genotypic susceptibility score.
- V82A is a non-polymorphic mutation selected primarily by IDV and LPV. It reduces susceptibility to these PIs and contributes cross-resistance to each of the remaining PIs except DRV and TPV.
- L90M is a non-polymorphic PI-selected mutation that reduces susceptibility to each of the PIs except TPV and DRV.

PI Accessory

- L10F is a common non-polymorphic, PI-selected accessory mutation associated with reduced susceptibility to DRV, FPV, IDV, LPV, and NFV.

Other

- K20R is a highly polymorphic PI-selected accessory mutation.
- A71V/T are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Dosage Considerations

- There is evidence for low-level DRV resistance. If DRV is administered it should be used twice daily.

Mutation Scoring: PR

PI	ATV/r	DRV/r	LPV/r
M46I	10	0	10
I54V	15	0	15
V82A	15	0	30
L90M	25	0	15
M46I + V82A	10	0	10
M46I + L90M	10	0	0
I54V + V82A	10	0	10
I54V + L90M	10	0	5
V82A + L90M	10	0	5
L10F	0	5	5
L76V	0	20	30
M46I + L76V	0	0	10
Total	115	25	145

Drug Resistance Interpretation: RT

NRTI Resistance Mutations: L74V, M184V
 NNRTI Resistance Mutations: K103S
 Other Mutations: E6N, V35T, T39E, S48T, E53D, V60I, K122E, I135V, K173A, Q174R, D177E, I178M, T200K, Q207E, R211A, F214L, V245K, A272P, L283I, T286A, E291D, V292I, I293V

Nucleoside Reverse Transcriptase Inhibitors

abacavir (ABC) High-Level Resistance
zidovudine (AZT) Susceptible
emtricitabine (FTC) High-Level Resistance
lamivudine (3TC) High-Level Resistance
tenofovir (TDF) Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors

efavirenz (EFV) Intermediate Resistance
etravirine (ETR) Susceptible
nevirapine (NVP) High-Level Resistance
rilpivirine (RPV) Susceptible

RT Comments

NRTI

- M184V/I cause high-level in vitro resistance to 3TC and FTC and low-level resistance to ddi and ABC. However, M184V/I are not contraindications to continued treatment with 3TC or FTC because they increase susceptibility to AZT, TDF and d4T and are associated with clinically significant reductions in HIV-1 replication.
- L74V/I cause high-level resistance to ddi and intermediate resistance to ABC.

NNRTI

- K103S is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. Because K103S is a 2-bp change from the wildtype K and a 1-bp change from K103N, patients with K103S may be likely to have once had K103N.

Mutation Scoring: RT

NRTI	ABC	AZT	FTC	3TC	TDF
<u>L74V</u>	30	0	0	0	0
<u>M184V</u>	15	-10	60	60	-10
<u>L74V + M184V</u>	15	0	0	0	0
Total	60	-10	60	60	-10

NNRTI	EFV	ETR	NVP	RPV
<u>K103S</u>	45	0	60	0
Total	45	0	60	0

Input mutations

Input sequences

Reverse Transcriptase

D67N x K70KR x L74LV x L100IL x K103KN x

M184V x T215FIST x K219EK x

Input mutation(s)

Select mutations:

40	41	44	62
---	---	---	---
65	67	68	69
---	---	---	---
70	74	75	77
---	---	---	---
90	98	100	101
---	---	---	---
103	106	108	115
---	---	---	---
116	118	138	151
---	---	---	---

Protease

M46I x I54V x L76V x V82A x

Input mutation(s)

Select mutations:

10	11	13	20
---	---	---	---
23	24	30	32
---	---	---	---
33	35	36	43
---	---	---	---
46	47	48	50
---	---	---	---
53	54	58	63
---	---	---	---
71	73	74	76
---	---	---	---

Drug Resistance Interpretation: PR

PI Major Resistance Mutations:	M46I, I54V, L76V, V82A
PI Accessory Resistance Mutations:	None
Other Mutations:	None

Protease Inhibitors

atazanavir/r (ATV/r)	High-Level Resistance
darunavir/r (DRV/r)	Low-Level Resistance
lopinavir/r (LPV/r)	High-Level Resistance

PR Comments

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- **V82A** is a non-polymorphic mutation selected primarily by IDV and LPV. It reduces susceptibility to PIs except DRV and TPV.

Drug resistance interpretation algorithms

- At the heart of most genotype interpretation algorithms are simple scoring systems, based on the presence of specific mutations.
- Each mutation is associated with a penalty score for each drug, so predicted susceptibility to each drug is based on sum of penalty scores from all mutations
- Once the total score is calculated the estimated level of resistance is summarized as follows:
 - Hypersusceptible: total score < 0
 - Susceptible: total score 0 to 9
 - Potential low-level resistance: total score 10 to 14
 - Low-level resistance: total score 15 to 29
 - Intermediate resistance: total score 30 to 59
 - High-level resistance: total score ≥ 60



Pros and cons of genotypic resistance testing

Pros

- Genotypic testing can be used to detect mutations that are causing resistance on a current regimen
- It can also help to conserve treatment options by showing the ineffective drug within a particular regimen

Cons

- Generally requires minimum viral load of at least 1000 copies/mL to ensure adequate viral amplification
- Cannot detect low-frequency mutations (minority variants) at $\leq 20\%$ - 30% of the viral population
- Will only detect currently circulating strains, with no information on archived mutations
- It is better at determining which drugs won't work than which drugs will work



Indications for Resistance testing in 2023 NDoH Guidelines



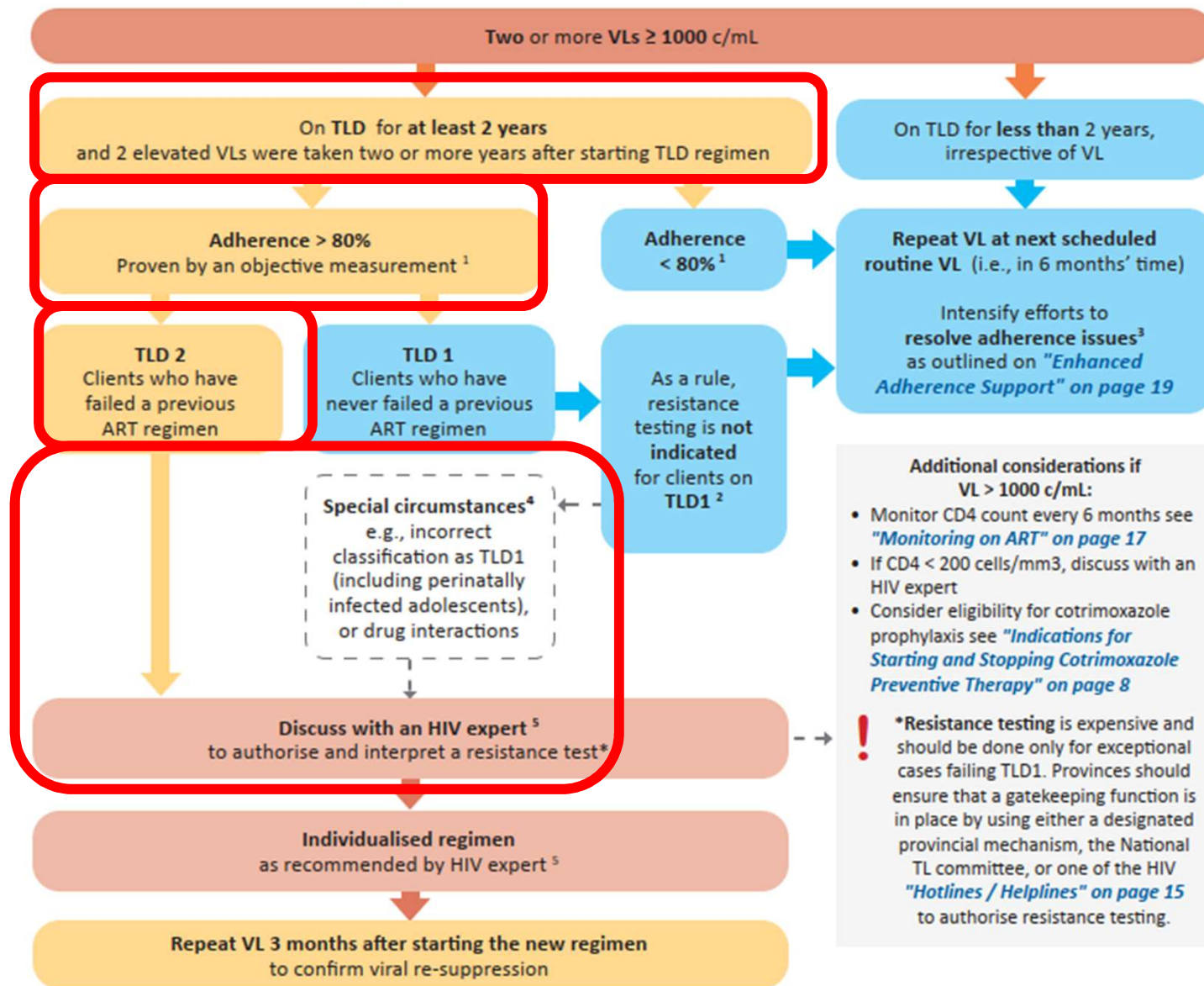
Switching Existing Clients to DTG-containing Regimens

(Adults, adolescents or children who have never used a DTG-containing regimen in the past)

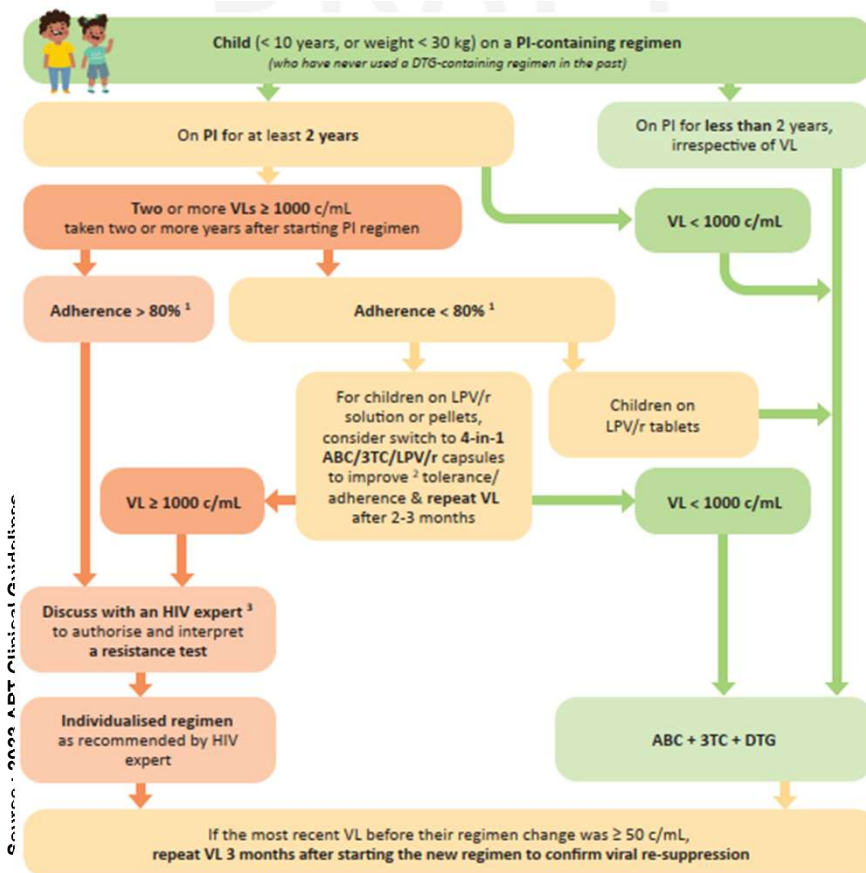
VL-dependent regimen switches			
Relevant to all clients who have been on PI-based regimens for more than two years: their VL result in the last 12 months will influence the decision of how and when to switch to a DTG-containing regimen			
VL considerations	Current Regimen	Criteria for switch	Regimen if change indicated
VL < 1000 c/mL	Any LPV/r or ATV/r regimen for more than 2 years	Switch all to a DTG-containing regimen If VL in last 12 months was ≥ 50 c/mL, continue to switch same day, but do ABCDE assessment, provide EAC if needed, and repeat the VL after 3 months as per "The VL non-suppression algorithm" on page 19	TLD provided no renal dysfunction and age ≥ 10 yrs and weight ≥ 30 kg If clients does not qualify for TDF ABC¹/3TC/DTG
² Two or more VLs ≥ 1000 c/mL taken two or more years after starting PI regimen	Adult or adolescent on any LPV/r or ATV/r regimen and adherence less than 80% ³	Switch all to a DTG-containing regimen Do not do a resistance test These clients are unlikely to have PI resistance mutations. Rather switch to a more tolerable once daily FDC regimen which is likely to support adherence. Manage as per "The VL non-suppression algorithm" on page 19	TLD provided no renal dysfunction and age ≥ 10 yrs and weight ≥ 30 kg If clients does not qualify for TDF ABC¹/3TC/DTG
	Adult or adolescent on any LPV/r or ATV/r regimen and adherence more than 80% ³	<p>Clients who meet the definition of confirmed virological failure and have confirmed adherence more than 80% may need a resistance test.</p> <p>These clients do not qualify for a same-day switch.</p> <p>Discuss with an HIV expert⁴ to authorise and interpret a resistance test.</p> <p>Provide individualised regimen as recommended by HIV expert. Repeat VL 3 months after the regimen change to confirm re-suppression, as per the "Management of Confirmed Virological Failure on TLD" on page 21</p>	
	Child < 10 years, or weight < 30 kg on any LPV/r or ATV/r regimen	These clients do not yet qualify for TLD and may require a resistance test. Refer to algorithm "Switching children on PI-containing regimens to DTG-containing regimens" on page 16	

Management of Confirmed Virological Failure on TLD

(also applicable to other DTG-containing regimens)



The NDoH recommends all children ≥ 4 weeks and ≥ 3 kg be transitioned to a DTG containing regimen



All children should be initiated on a DTG based regimen

refills or attendance of scheduled clinic visits in the previous 6-12 months of <math>< 80\%</math>, adherence difficulties in young children are often linked to poor tolerability of unpalatable formulations, particularly LPV/r solution. It is important to ask the caregiver about how the child tolerates the medication e.g., does the child refuse to swallow the medicine or spit out or vomit the medicine, and whether the caregiver has been able to overcome this. Considering these limitations, objective measures of good adherence could include one of the following:

- a) Pharmacy refills > 80% in the last 6-12 months (if this is known)
 - b) Attendance of > 80% of scheduled clinic visits in the last 6-12 months (if this is known)
 - c) Detection of current antiretroviral drug/s in the client's blood or urine, if available
2. If a switch to the 4-in1 capsules does not improve adherence, or is not available, continue to switch to ABC + 3TC + DTG as for non-adherent children on LPV/r tablets
 3. The following would qualify as HIV experts: the HIV Helplines, a paediatric infectious disease specialist or the paediatric Third line ART committee

Right to Care HELPLINE

For nurses, doctors, pharmacists and other health care workers needing expert advice on all paediatric, adolescent and adult HIV and TB management.

Call during office hours
"please call me", sms or whatsapps
may be sent and we can call you back.

HIV Helpline
(adult and paediatric)

082 352 6642

TB Helpline
063 698 6543



USAID
FROM THE AMERICAN PEOPLE



Right to care
Training Health & Humanity

References & additional resources

Clavel D, Hance AJ. HIV drug resistance. N Engl J Med 2004; 350:1023-1035. <https://doi.org/10.1056/NEJMra025195>

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