

A New Perspective On HCV Drug Resistance Multiple Paths To Sustained Virologic Response: Resistance Can Be Overcome



Slide set prepared by the
Forum for Collaborative HIV
Research and
Hepatitis C Virus Drug
Development Advisory Group



The Slide Deck

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Goals of the slide deck: Develop perspective on HCV viral resistance and what it means for future HCV therapy

The educational materials in this slide set:

- 1) Provide context for viral resistance in HCV
- 2) Address concerns around HCV resistance
- 3) Educate on prevention and how to overcome resistance to antiviral drugs

This educational material complements:

- 1) A primer of HCV viral lifecycle
- 2) A primer on how mutations are created and resistant variants are selected



Key points

1. HCV Is Curable

- a) Wild-type and resistant virus can be eliminated

2. Resistant Variants Occur Naturally

- a) Resistant variants to antiviral drugs exist before treatment
- b) Resistant variants can be selected/enriched during treatment
- c) Drug resistance may emerge during treatment with all (or any) antiviral drugs
- d) Resistance is a consequence of treatment failure, but is not always the cause

3. Maximize Response, Minimize Resistance

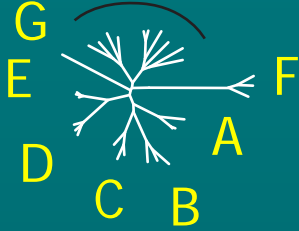
Many factors contribute to treatment response: virus, drug and patient

- a) The **genetic barrier** is related to the number and type of mutations required to overcome the clinical activity of a regimen. Mutations that decrease viral fitness (defined in slide #30) increase the resistance barrier.
- b) The **pharmacologic barrier** is increased by higher potency and higher drug levels
- c) **Tolerability** of a regimen and **patient adherence** are critical for treatment success

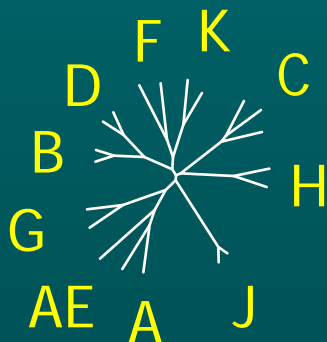


HCV sequences are more genetically diverse than HBV or HIV

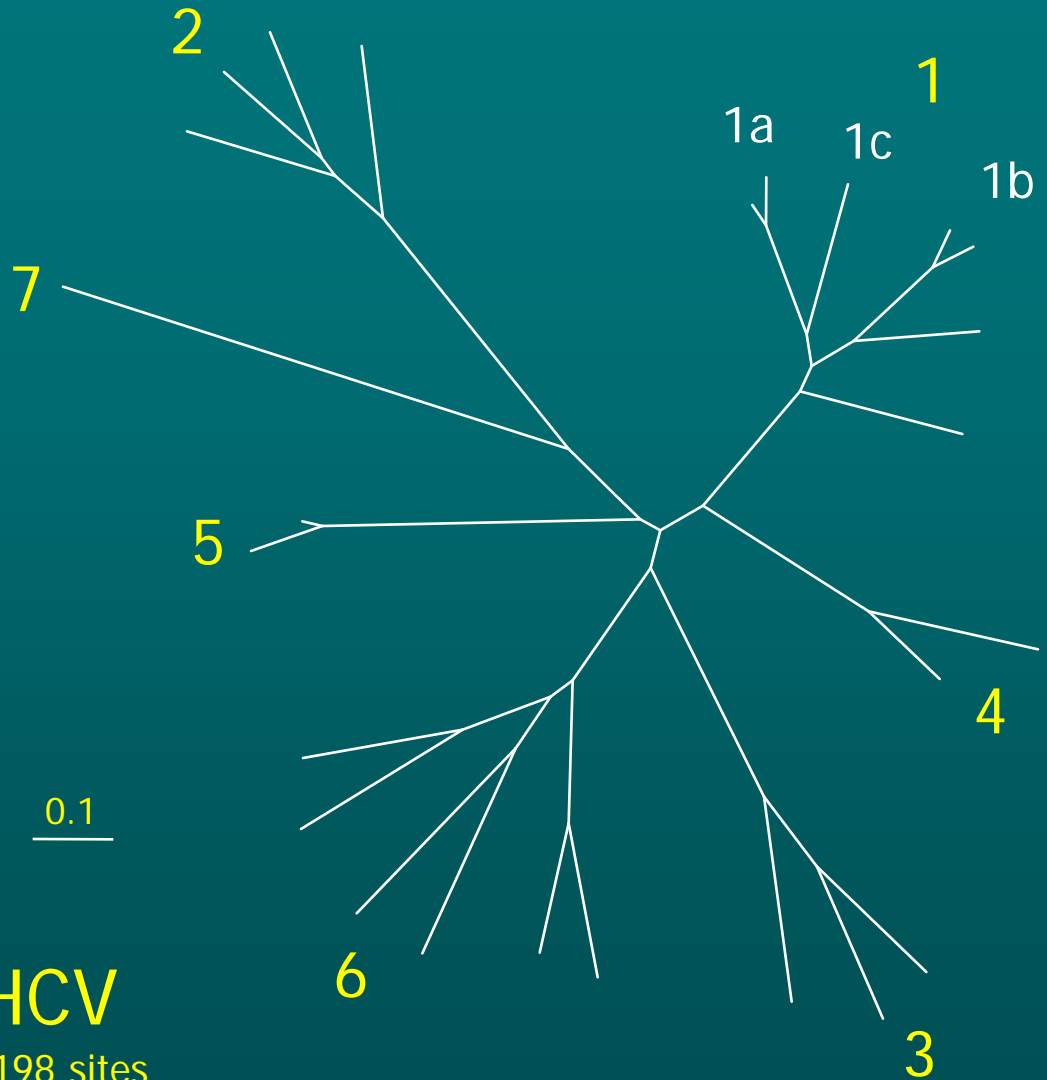
Non-human primate



HBV
3181 sites



HIV
8316 sites



HCV
9198 sites



Unlike HIV and HBV, HCV is curable

Virus	HIV	HBV	HCV
Genome	RNA	DNA	RNA
Mutation Rates	Very High	High	Very High
Virions Produced Daily	10^{10}	10^{13}	10^{12}
Viral Genetic Archiving	YES	YES	NO
Drug Targets	Multiple	One	Multiple
Cure With Current Therapy?	NO (Integrated viral DNA)	NO (cccDNA)	YES
Current Therapeutic Goal	Lifelong suppression	Lifelong suppression	Cure: clearance from plasma and liver



HBV, HIV and HCV have targeted drugs approved or in development

HIV

Protease **RT** (nucleoside) **RT** (non-nucleoside)
Co-receptor **Fusion** **Integrase**

HBV

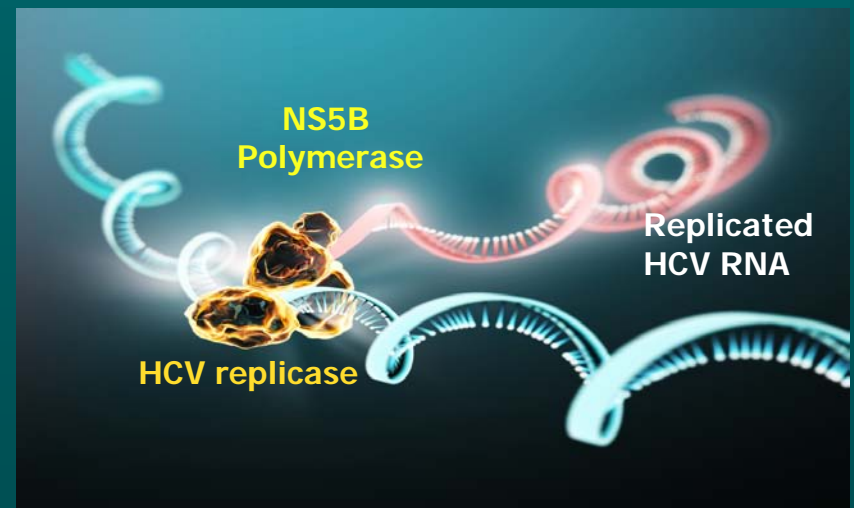
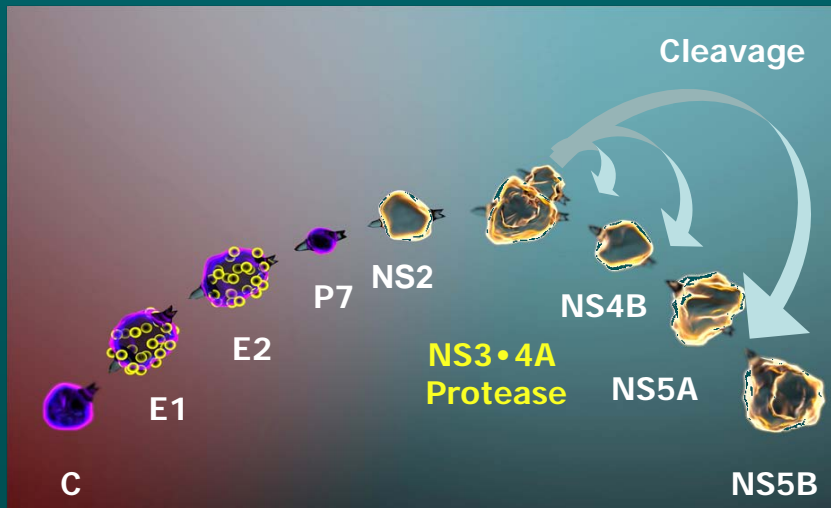
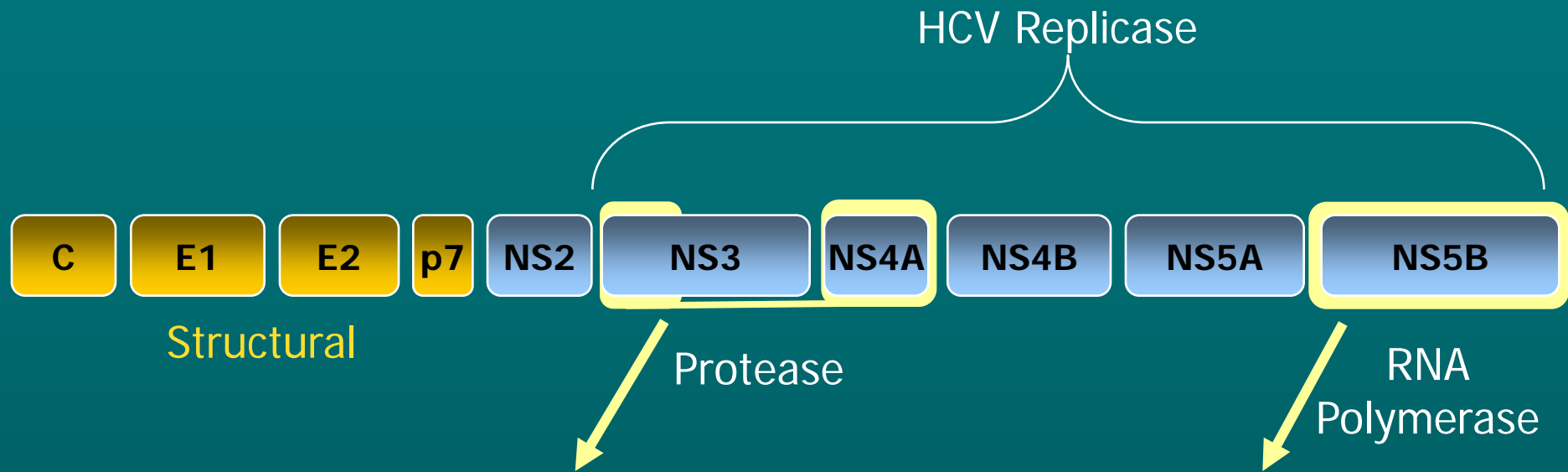
RT (nucleoside)

HCV

NS3 Protease* (Telaprevir, Boceprevir) **Polymerase** (nucleoside) **Polymerase** (non-nucleoside)
NS5A **NS4A** **NS4B** **P7**
Cyclophilin **Entry**

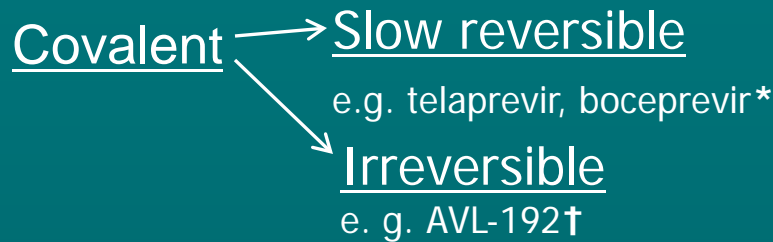


HCV enzymes provide good targets for drug development





HCV drug classification and development



Active site

GS 6620	IDX 184	INX 189
PSI 7977	PSI 938	RG 7128
TMC 649128		

**NS3
Protease**

NS5A

**NS5B
Polymerase**

Non-covalent
Linear

ACH 1625	ABT 450/R
Asunaprevir (BMS 650032)	
BI 201335	GS 9451

Macrocyclic

Danoprevir (RG7227/ITMN 191)
 GS 9256
 MK 5172
 TMC 435
 Vaniprevir (MK 7009)

ABT 267	ACH 2928
AZD 7295	BMS 790052
GS 5585	PPI 461

Palm

ABT 333
 ABT 072
 GS 9190
 Setrobuvir
 (ANA 598)

Thumb 1

BI 207127
 BMS 791325
 TMC 647055

Thumb 2

BMS 791325
 Filibuvir
 GS 9669
 VX 222

TLR-7

ANA 773

Cyclophilin

Debio 025
 SCY 635



Examples of HCV NS5B polymerase inhibitors and their binding sites

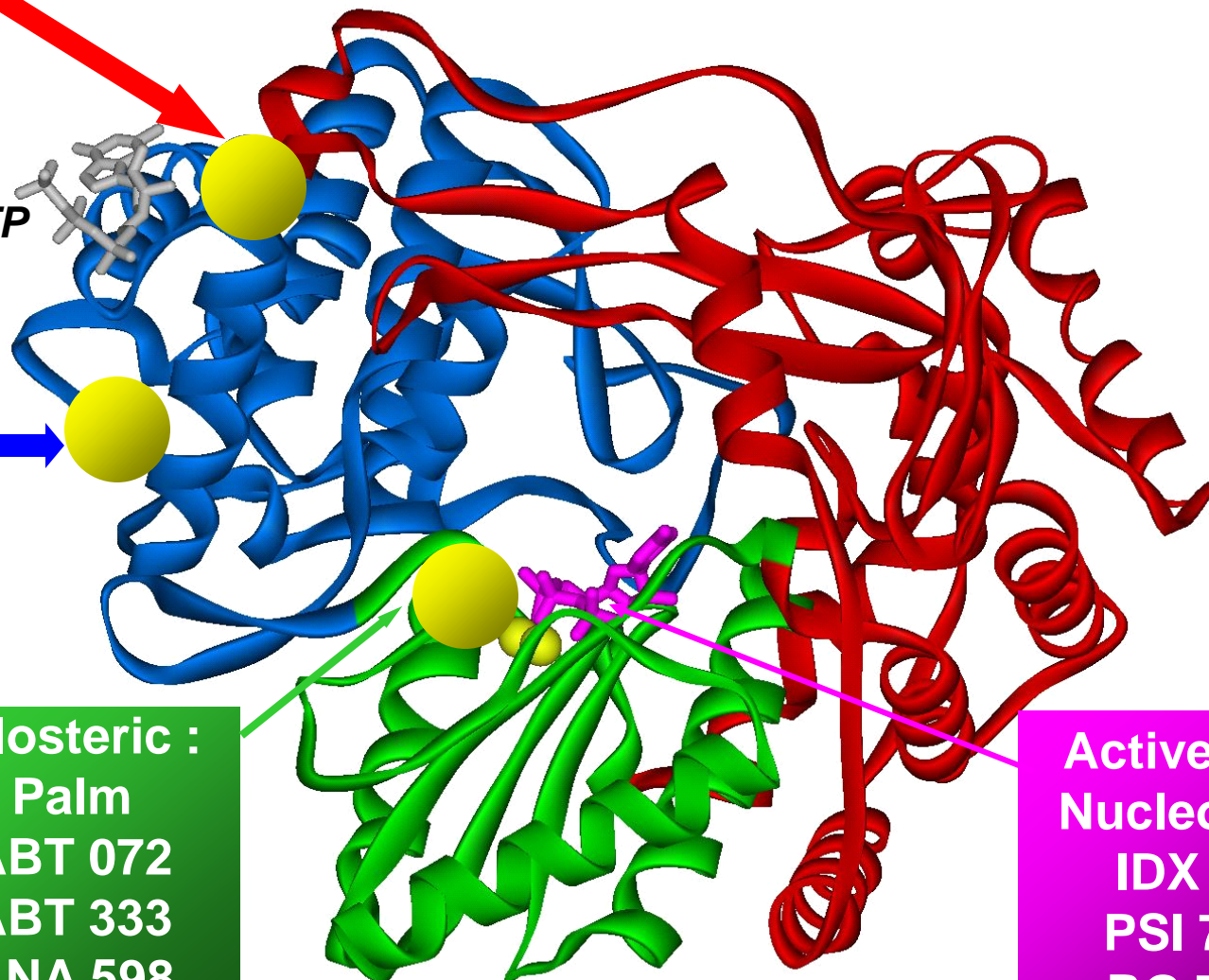
**Allosteric:
Thumb 1
BI 207127
TMC 647055**

Allosteric GTP

**Allosteric:
Thumb 2
Thiophene
Filibuvir
GS 9669
VX 222**

**Allosteric :
Palm
ABT 072
ABT 333
ANA 598**

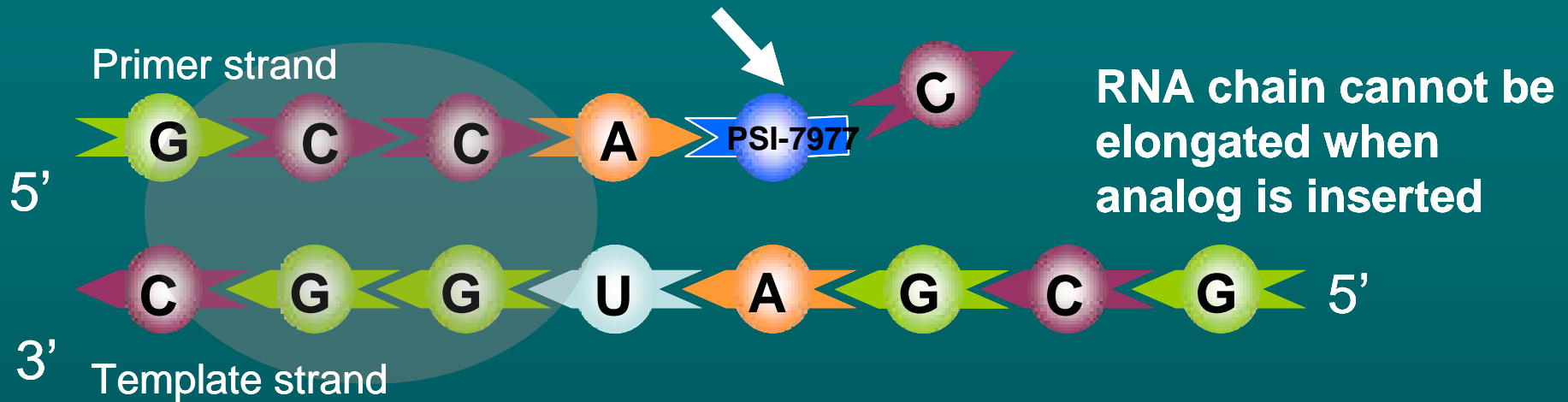
**Active Site :
Nucleosides
IDX 184
PSI 7977
RG 7128**





Nucleotide analogs are chain-terminators

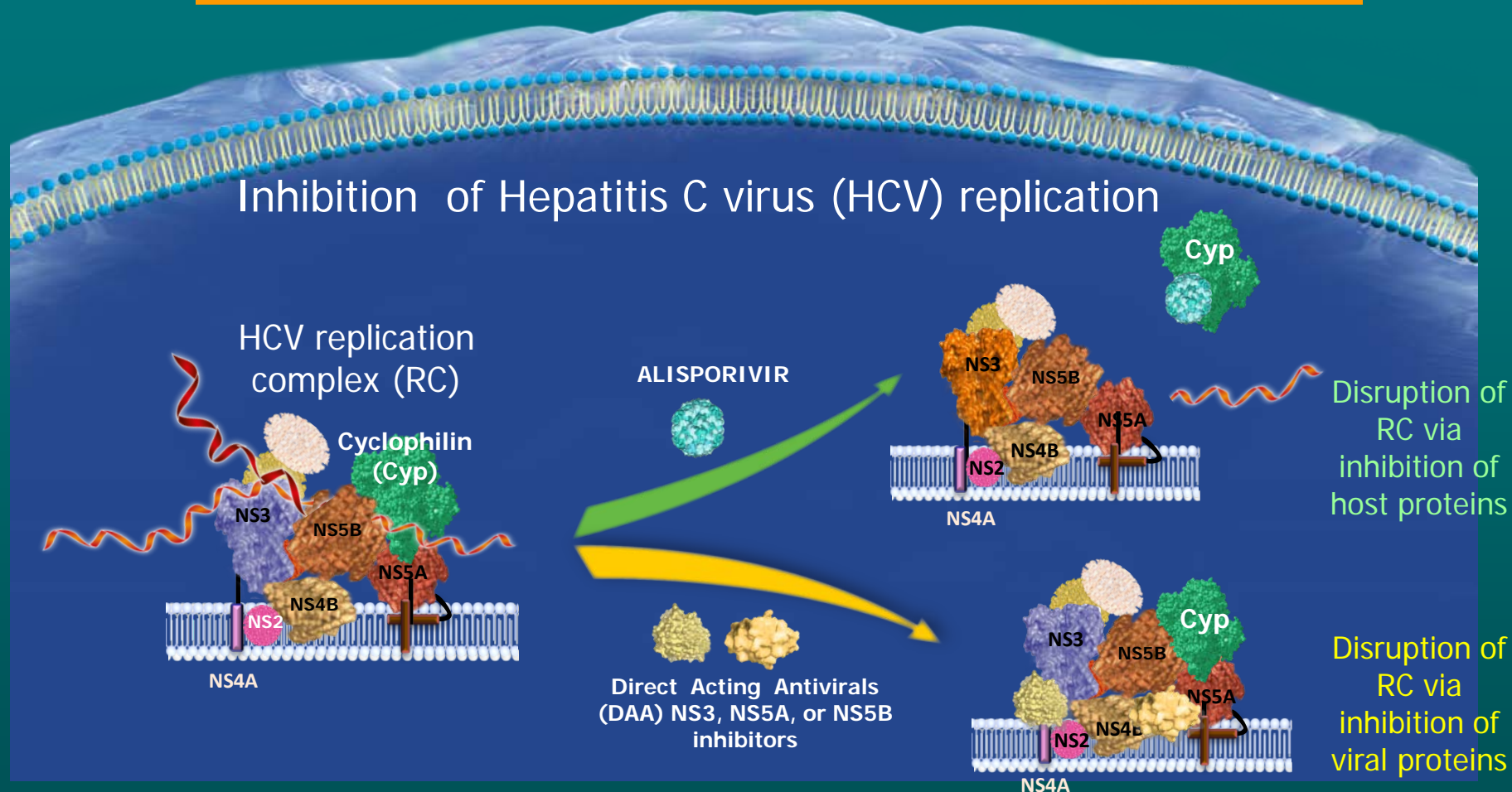
Nucleotide Chain-terminator (e.g., PSI-7977)



- Mechanism of action, e.g., chain termination, does not rely on enzyme homology across HCV genotypes
- Both pyrimidine and purine analogs can inhibit activity
- Antiviral activity of nucleotides is conserved against PI-resistant or non-nuc polymerase inhibitor resistant virus



Mechanism of action and key attributes of cyclophilin inhibitor, alisporivir



Key attributes of host-targeting antiviral (HTA), alisporivir

- Mechanism of action different from direct acting antivirals (DAA)
- High barrier for HCV resistance
- Compelling efficacy with pan-genotypic coverage



Mechanism of action of NS5A replication complex inhibitors

- Role of NS5A in HCV replication remains elusive
- Precise mechanism of action in HCV replication currently under investigation
- NS5A inhibitor, BMS-790052 and similar chemotypes:
 - Bind to HCV NS5A protein in cell culture¹
 - Interact with the NS5A N-terminus of Domain 1²
 - Block both cis- and trans-acting functions of NS5A³
 - Alter the subcellular localization of NS5A into functional replication complexes therefore suppressing HCV RNA replication⁴

1. Gao, M. *Nature*, 2010; **465**: 96-100

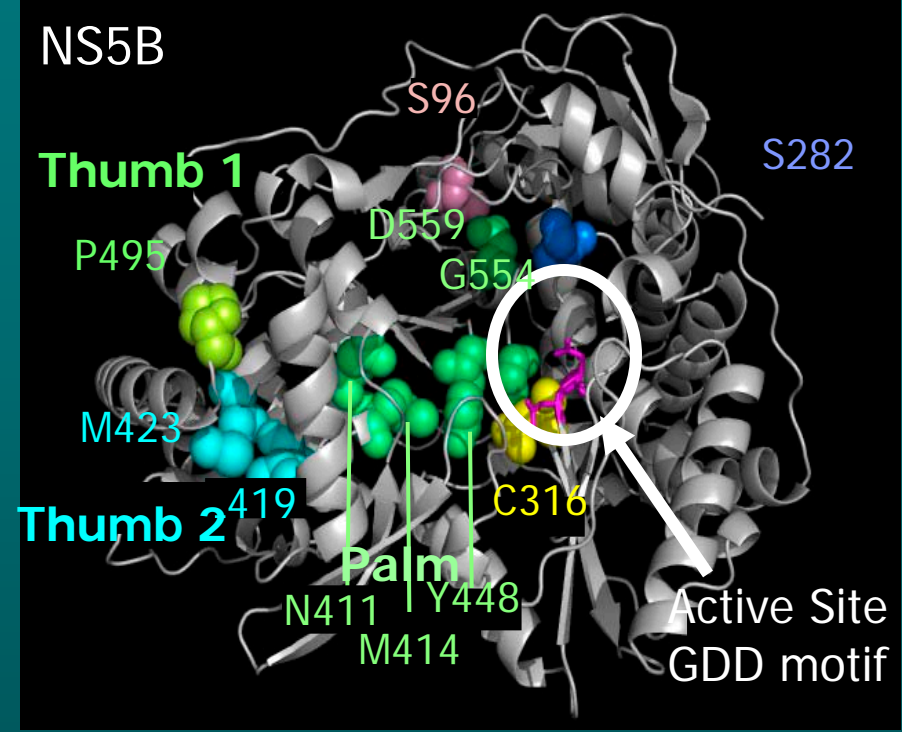
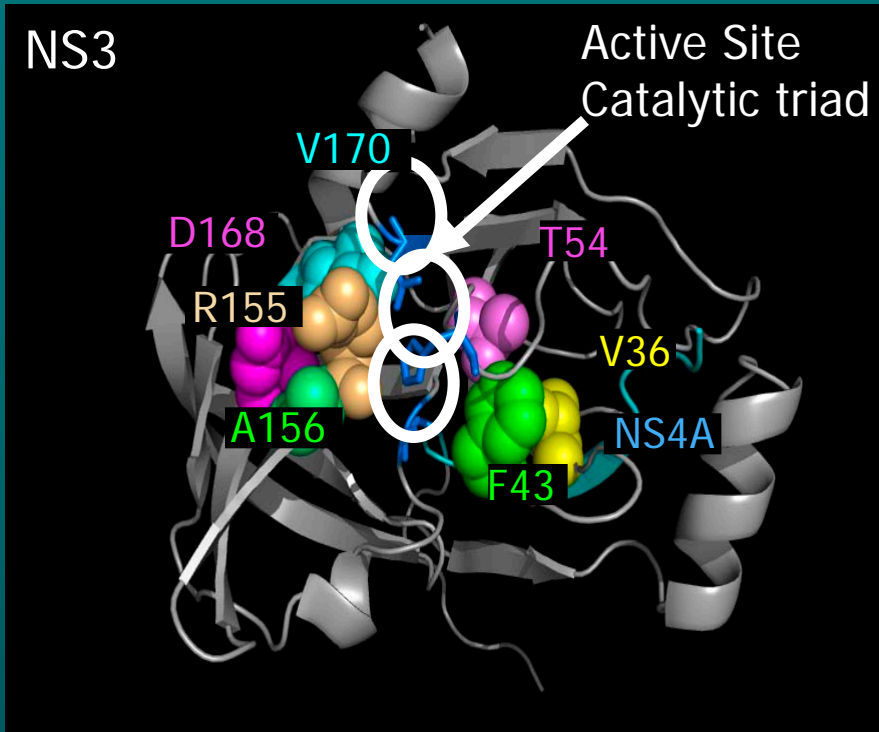
2. Lemm, J.A. *J Virol*, 2010; 84 (1): 482-491

3. Fridell, R.A. *J Virol* 2011; 85(14): 7312-20

4. Lee, C. *Virology* 2011; 414(1):10-8



All antiviral drugs can select resistant variants



NS3

Amino acid changes conferring resistance to NS3 protease and NS5B polymerase inhibitors

NS5B



Nucleotide changes result in codon changes that can confer resistance to a drug

Example: Codon 155 of the HCV Protease



G → **A**

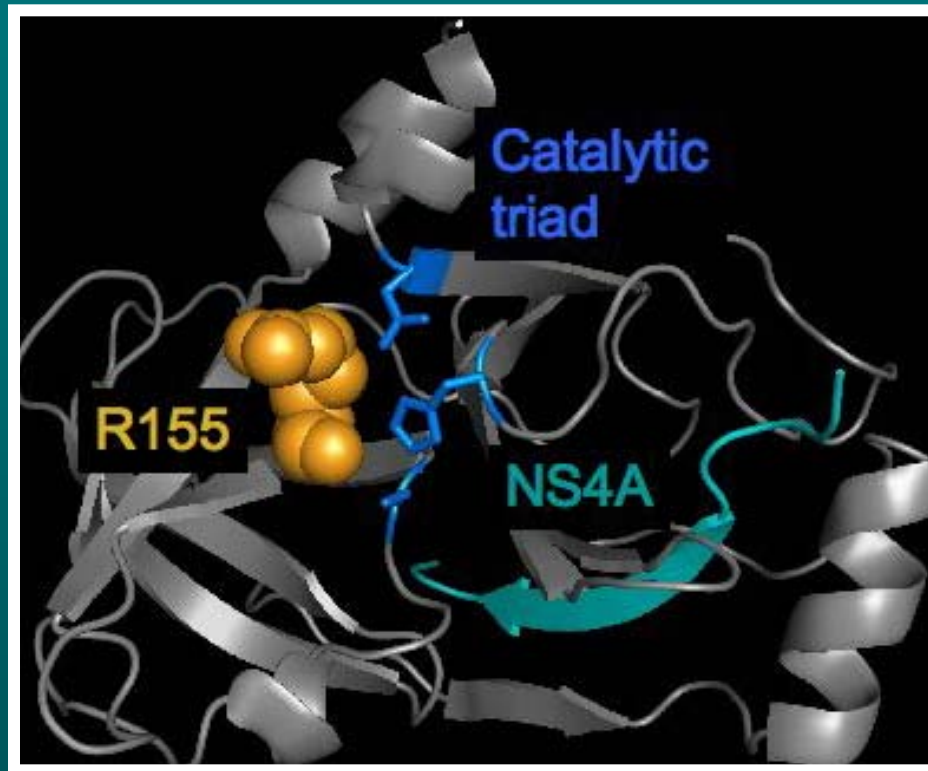


Consensus "wild type"
amino acid

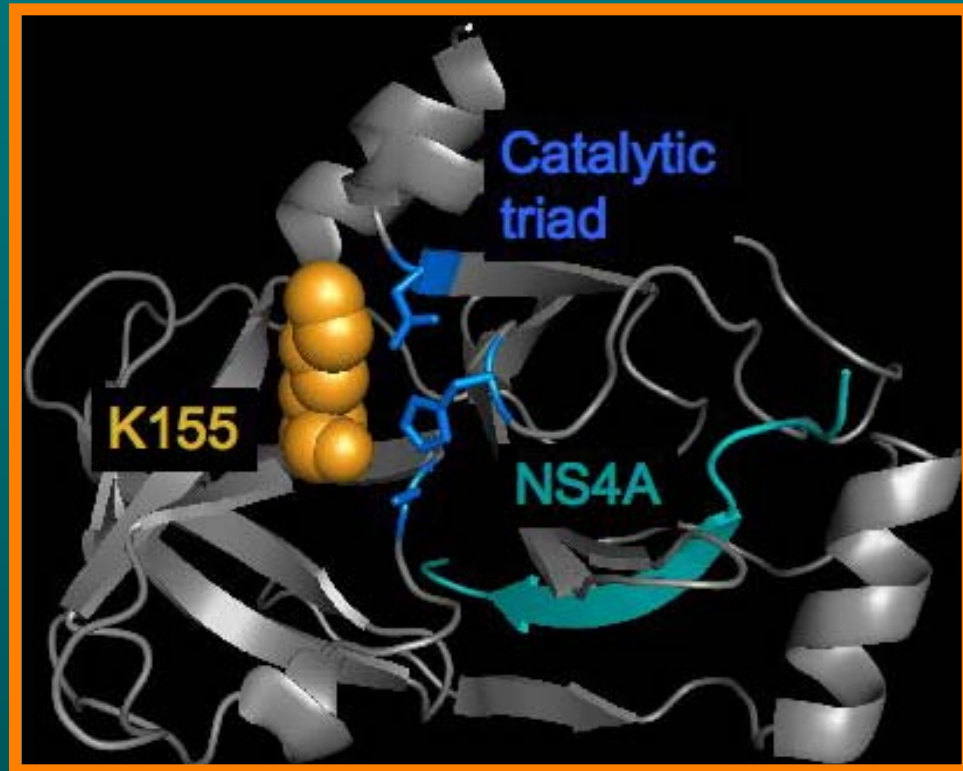
Resistant variant amino acid



Codon changes may result in amino acid changes, which can change the interaction with a drug



Wild type NS3



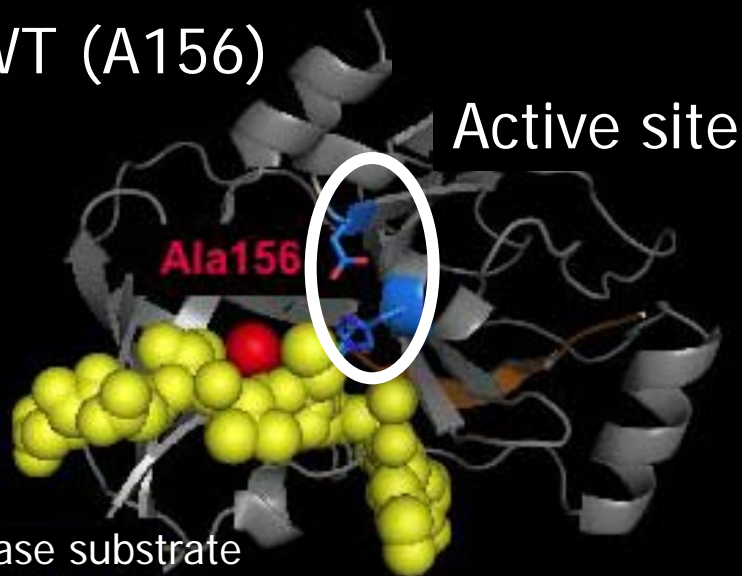
R155K variant NS3

- Decreased binding of a drug results in decreased inhibition of viral replication
- Decreased binding to the natural ligand results in decreased viral replication

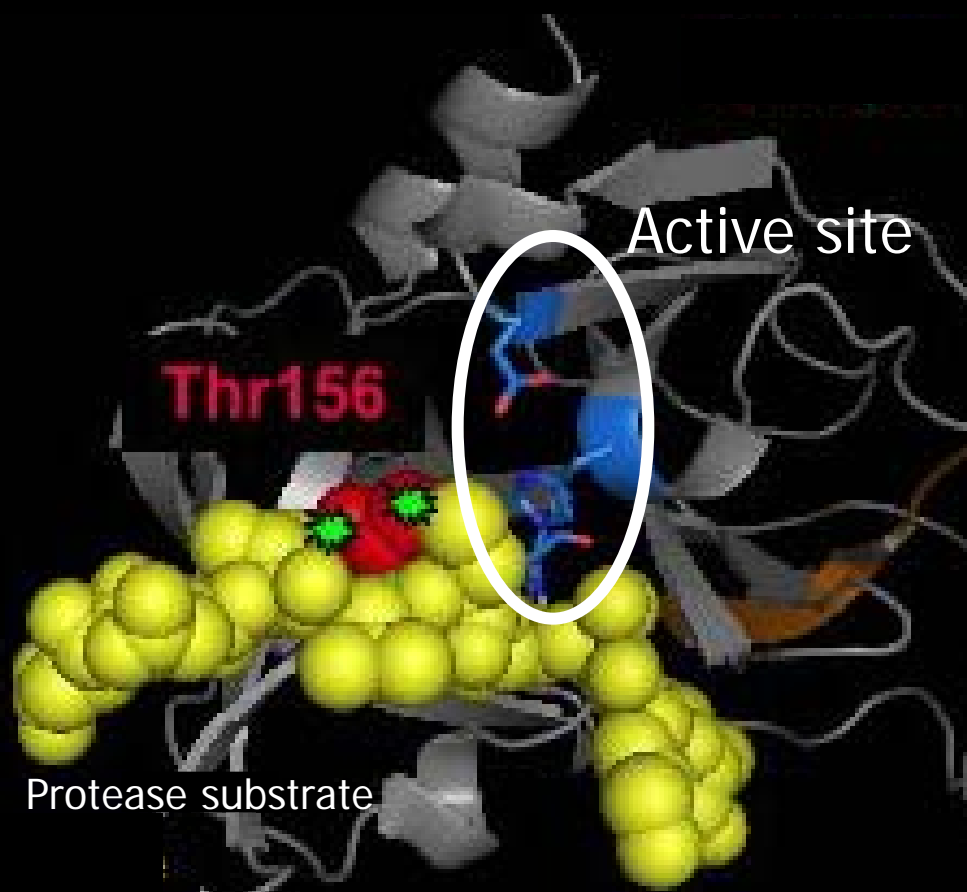


Resistance often results in reduced viral fitness

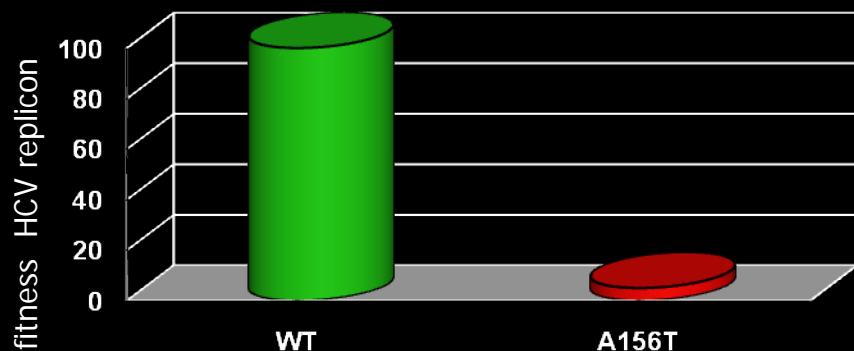
WT (A156)



Resistant Variant (A156T)



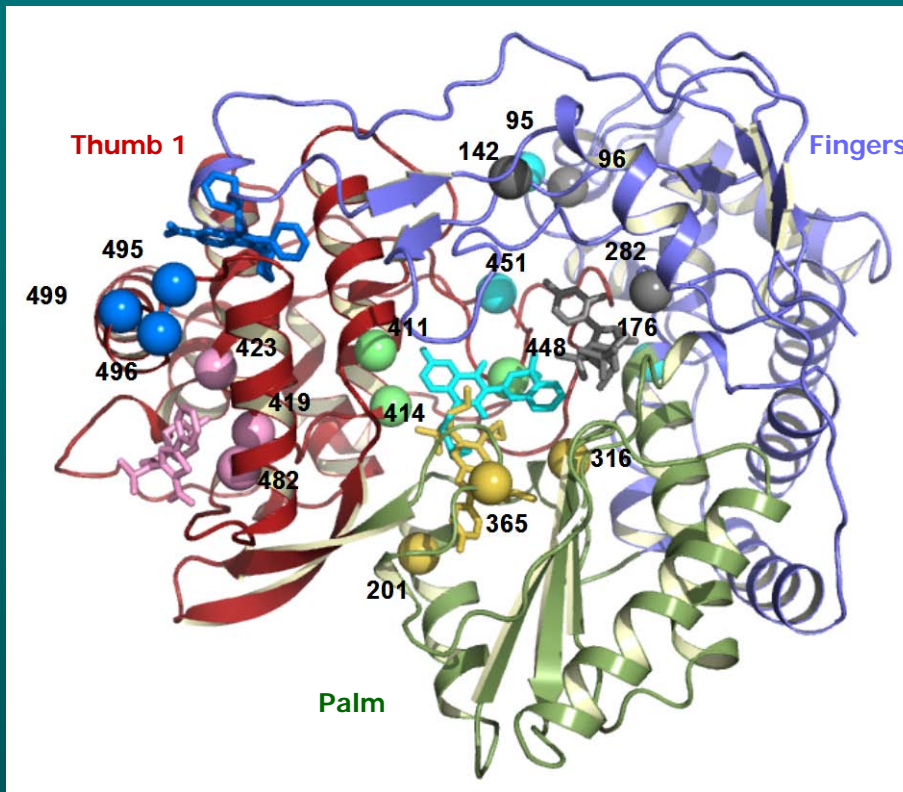
The A156T variant is less fit than WT



Steric hindrance prevents the substrate from efficiently binding to the mutant protease active site



Resistance mutations associated with NS5B polymerase nucleoside and non-nucleoside inhibitors



Nucleoside Inhibitors

- R1626: S96T (*in vitro*)
- R7128: S282T (*in vitro*)

Non-Nucleoside Inhibitors

- Filibuvir: M423T (in patients)
- VCH-759 and VCH-916: M423T/V/I, L419V/M, I482L/V/T, V494A/I (in patients)
- HCV796: C316Y/N, S365T/A (in patients)
- ABT333: S556G (in patients); C316Y, Y448C (*in vitro*)

- Though *in vitro* studies with **nucleoside analogs** have demonstrated the selection of resistant variants, they have not been observed in patients with HCV infection.
- Wide range in frequency of resistance mutations associated with **non-nucleoside analogs**. While many are only observed *in vitro*, some are also associated with viral breakthrough in clinical trials.



Changes in drug susceptibility: Detection of resistance

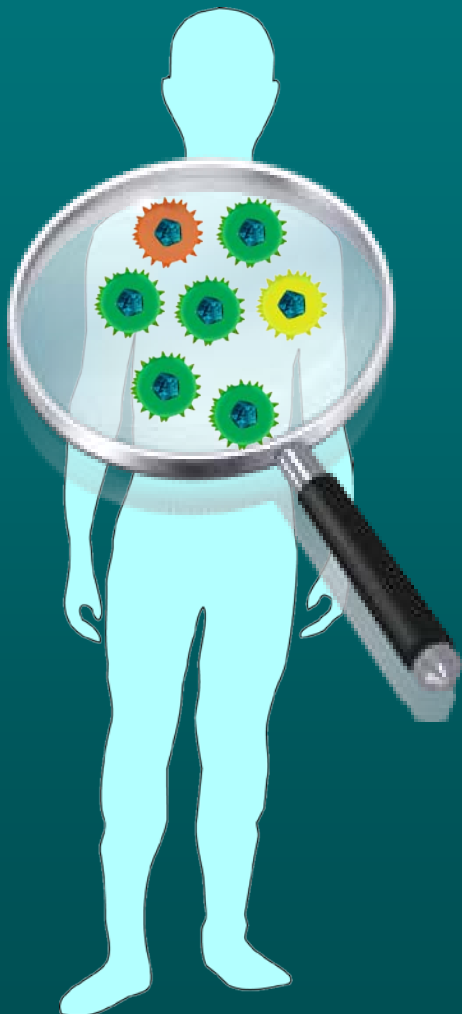
- Sequence analysis and phenotype analysis are used in combination to identify/discover resistance pathways
- **Sequence Analysis:** Detects specific amino acid substitutions relative to a pre-treatment or standard reference sequence that are known to decrease susceptibility to antiviral agents.
 - Can identify substitutions known to impact drug susceptibility
 - Can identify novel drug resistance pathways associated with treatment failure
- **Phenotypic Analysis:** Determines drug concentrations needed to inhibit viral replication.
 - Effective concentration (EC): drug concentration required to inhibit viral replication by 50% or 90% (EC₅₀ or EC₉₀)
 - Less susceptible (resistant) viruses will require *more* drug to be inhibited, thus an *increase* in EC₅₀ or EC₉₀



Resistant Variants Occur Naturally



Resistant variants are present before treatment

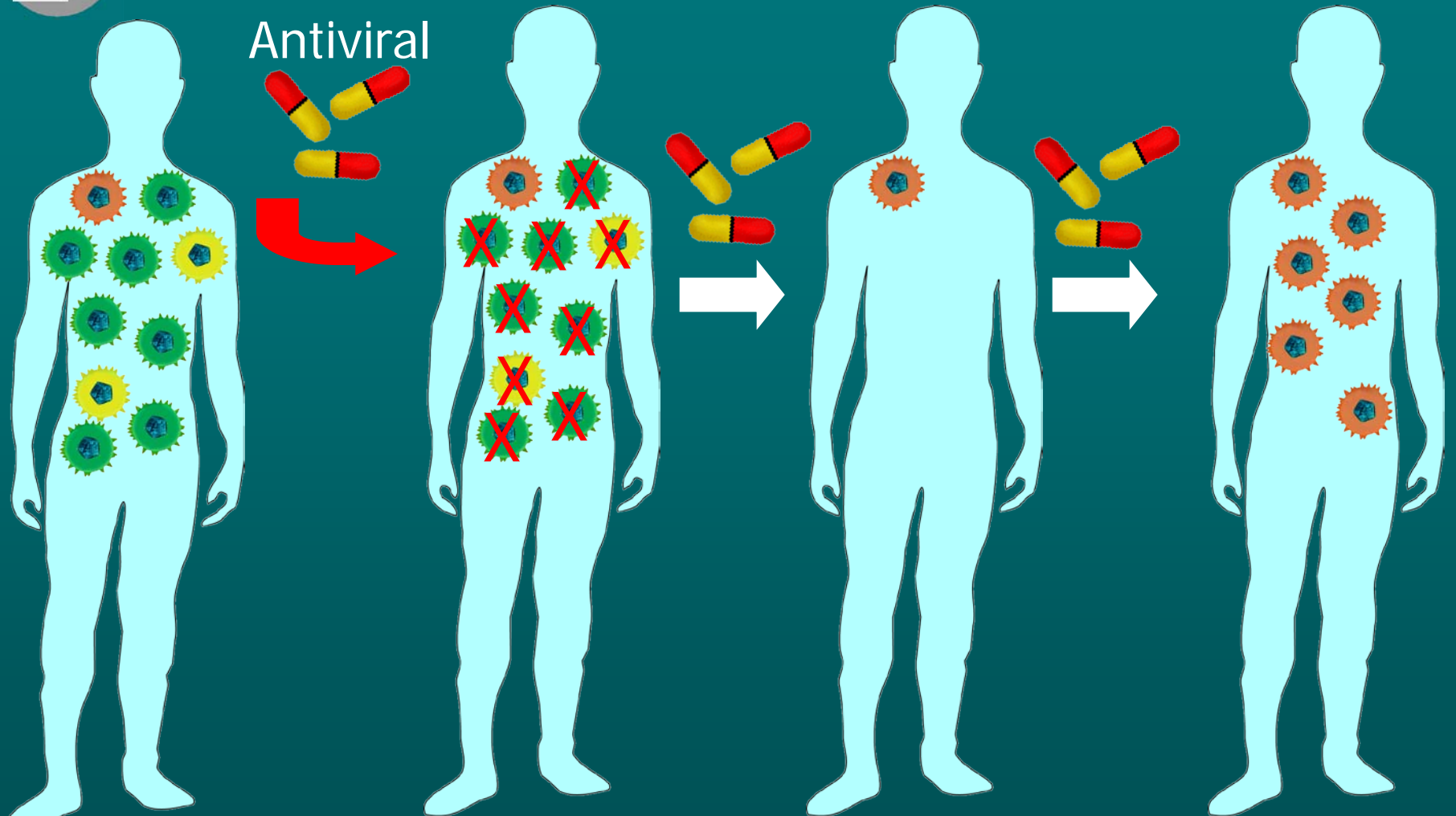


- HCV exists as a mixture of populations of genetically distinct, but closely related, virions in every patient¹
 - $\sim 10^{12}$ viruses produced per day
 - ~ 1 nucleotide mutation per virus produced
 - All possible single nucleotide-mutant viruses, and all combinations of double nucleotide-mutant viruses, are thought to preexist before treatment in most patients²
- Most resistant variants are relatively unfit and are undetectable prior to therapy with current technology^{3,4}

1. Pawlotsky JM. *Clin Liver Dis*, 2003; 7:45-66
2. Rong L. *Sci Transl Med*, 2010; 2 (30):30ra32
3. Kuntzen. *Hepatology*, 2008; 48(6):1769-78
4. Bartels DJ. *J Infect Dis*, 2008; 198: 797-9



Resistant variants can be selected during treatment



Antiviral

Potent antiviral therapy eliminates sensitive variants

Resistant variants are uncovered which can then expand



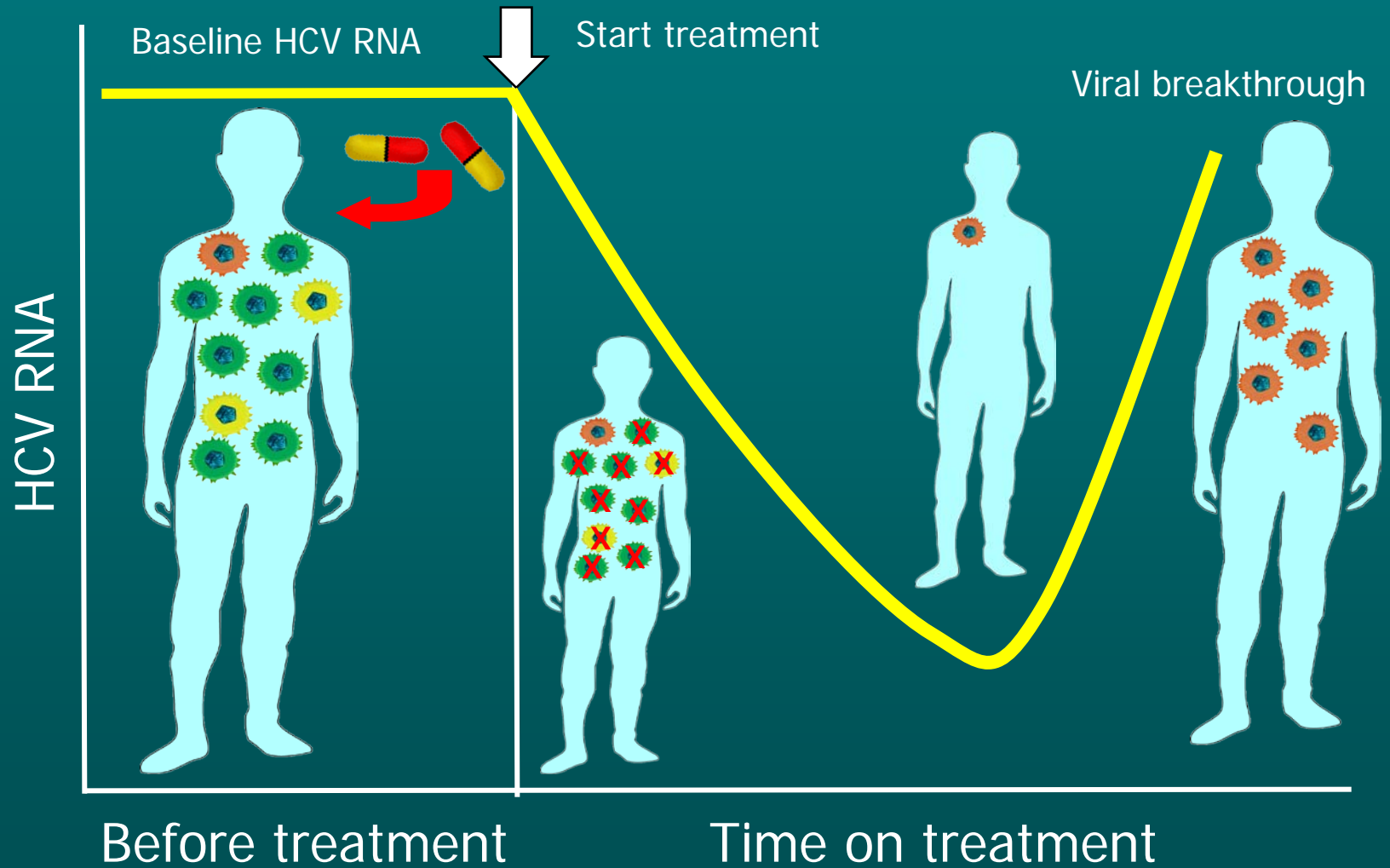
Resistant virus



Sensitive virus



Frequent monitoring of HCV RNA levels can detect treatment failure and resistance



Patients have viral variants with different levels of resistance to a drug



Resistant virus



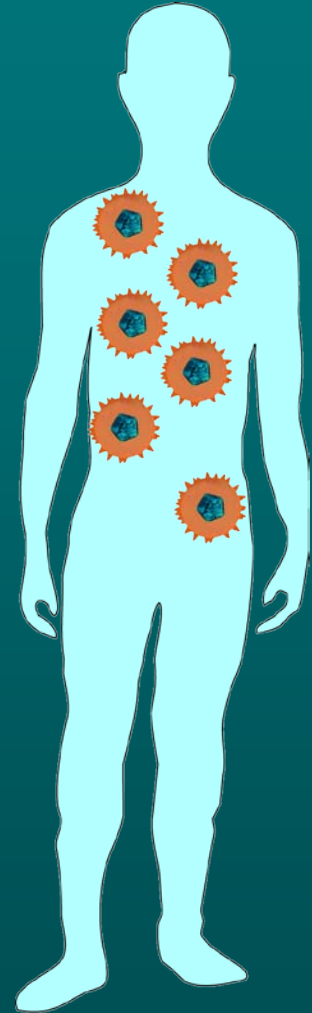
Sensitive virus



Say "NO" to **CRAP** therapy

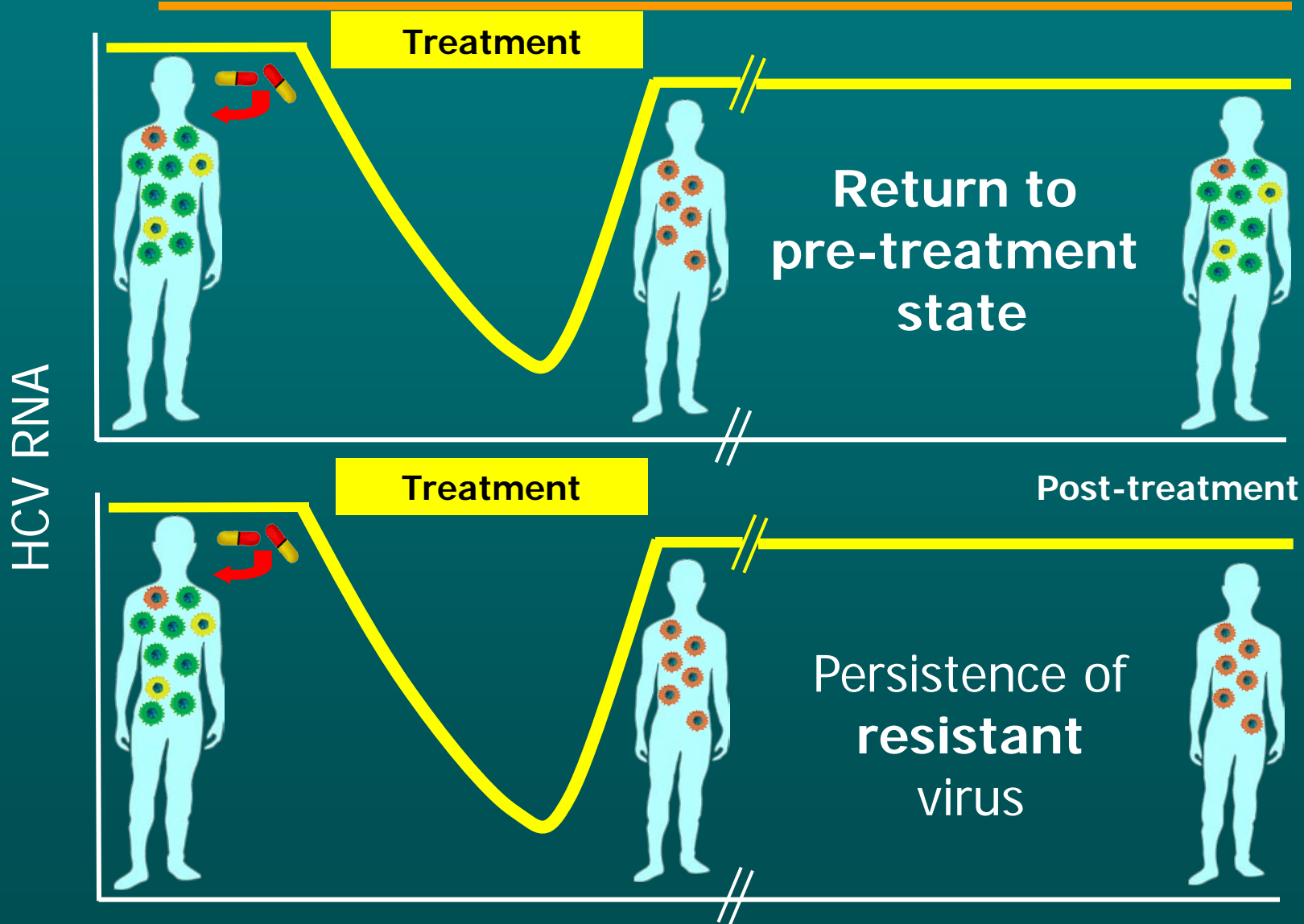
Continued **R**eplication under **A**ntiviral **P**ressure

- Continued replication in the presence of drug will likely lead to further evolution of the viral population.
- In theory, further evolution can result in a more fit, drug-resistant viral population that may remain enriched in the patient, even in the absence of drug pressure.
- This should be prevented by discontinuing the direct acting antiviral if a patient has a confirmed increase in HCV RNA levels while adhering to therapy.





Potential fate of resistant variants after treatment



Resistant virus

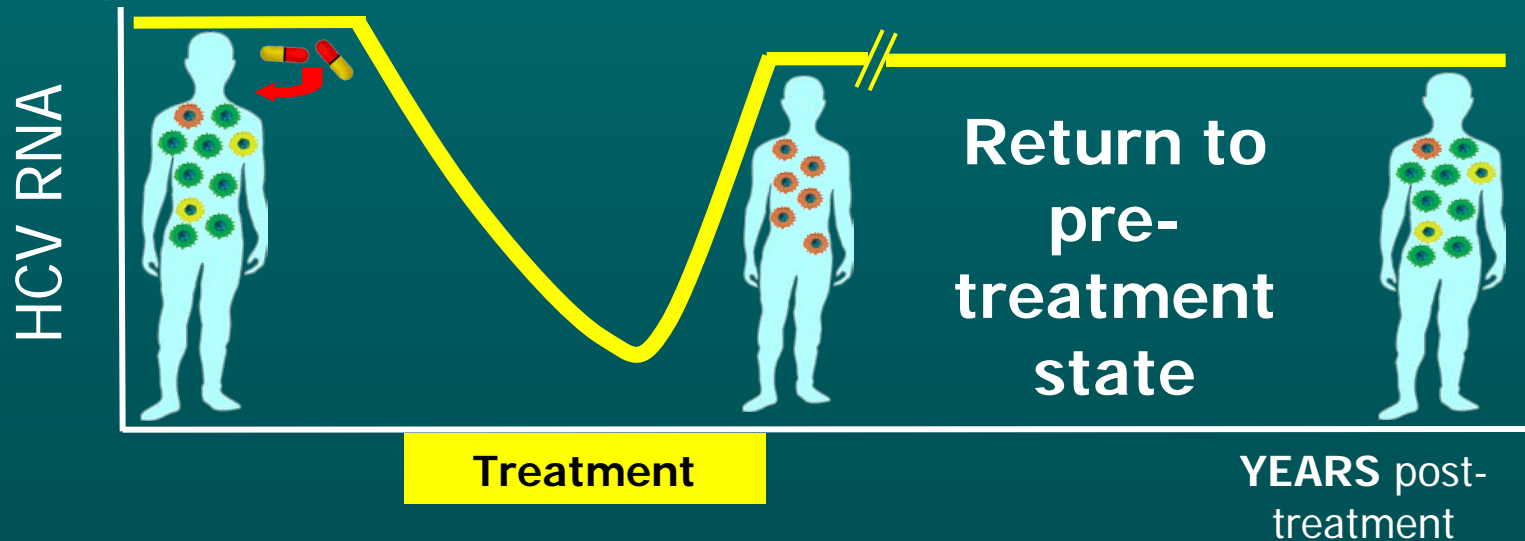


Sensitive virus



Long-term follow-up of patients with resistant variants after failing treatment

- Population and clonal amino acid analyses of HCV from patients with protease inhibitor resistance indicate that drug-resistant patient viral populations *may* return to pre-treatment levels over time in many patients



Resistant virus



Sensitive virus

Kieffer T., et al. *AASLD*, 2010, Abstract # LB11

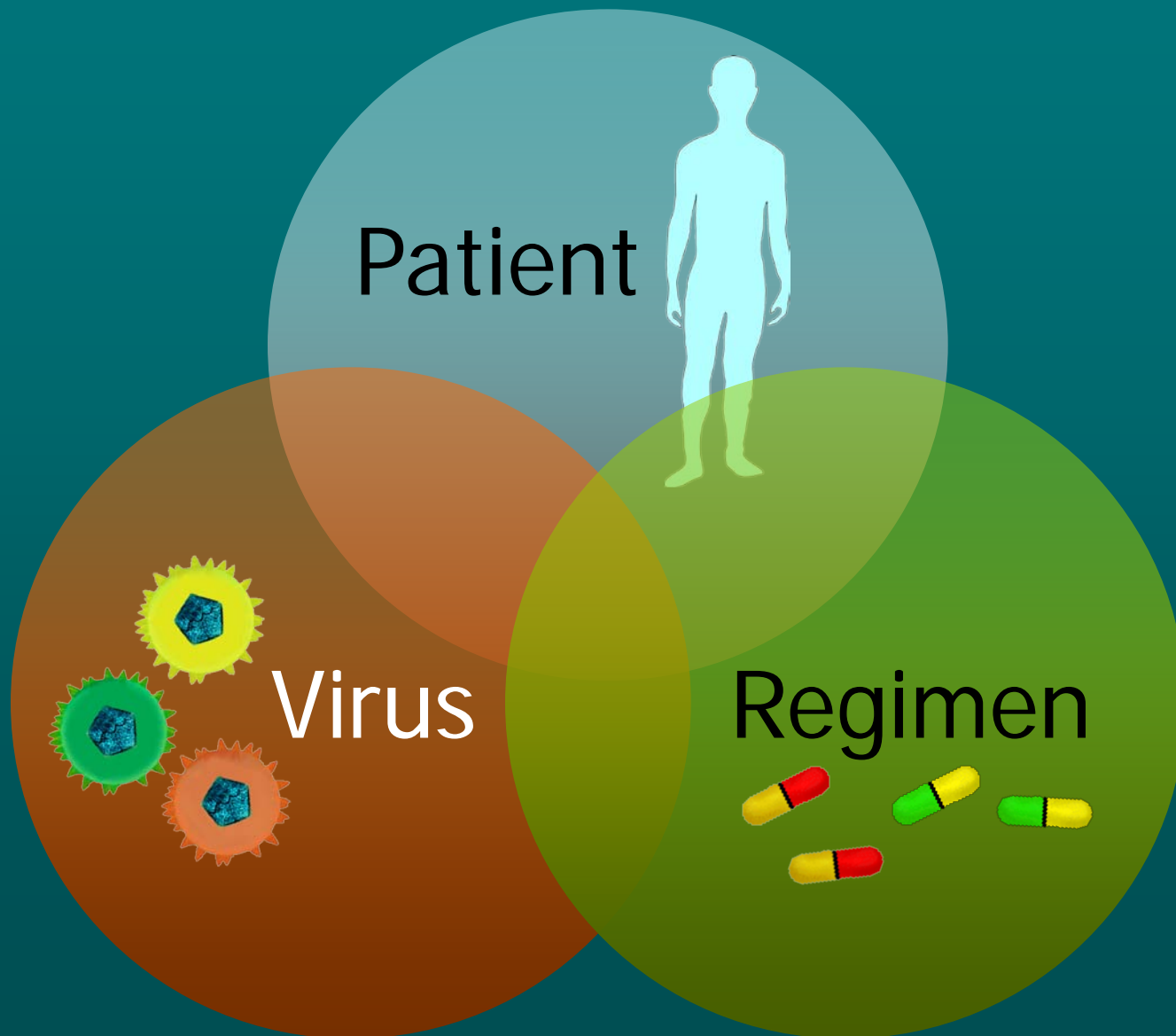


Patient viral populations may return to pre-treatment state over time

- For protease inhibitors (telaprevir or boceprevir), 59-89% of patients no longer had detectable resistant variants after a median follow-up time of 25-29 months
- Understanding the clinical significance of treatment-acquired resistance requires studies in which patients who experienced virologic failure while on a direct acting antiviral (DAA), are re-treated with a DAA regimen



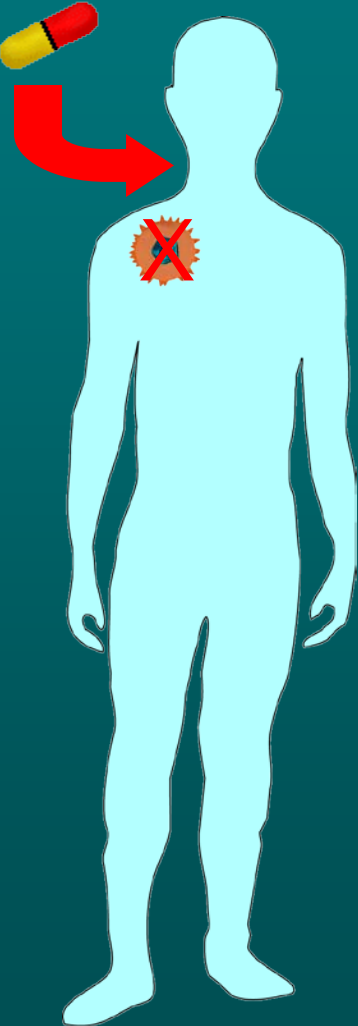
Many factors contribute to response



Virologic barriers to resistance



Antiviral



Genetic barrier

- Number and type of nucleotide changes required for a virus to acquire clinical resistance to an antiviral regimen¹

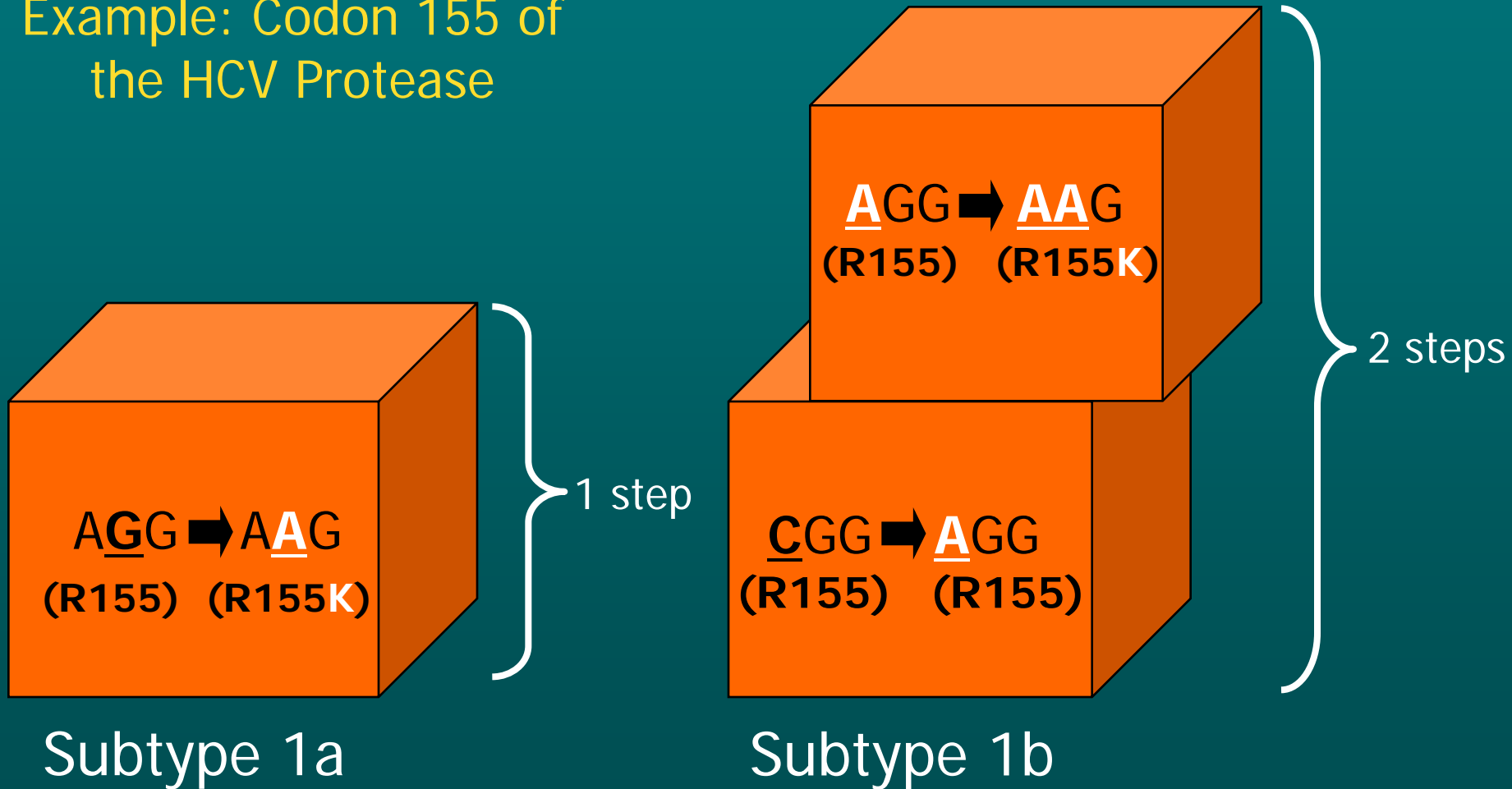
Viral fitness

- Relative capacity of a viral variant to replicate in a given environment
- Resistance mutations frequently compromise viral function and thus reduce viral fitness compared to wild-type in a drug-free environment



Multiple nucleotide changes maybe required to create a single amino acid change

Example: Codon 155 of the HCV Protease

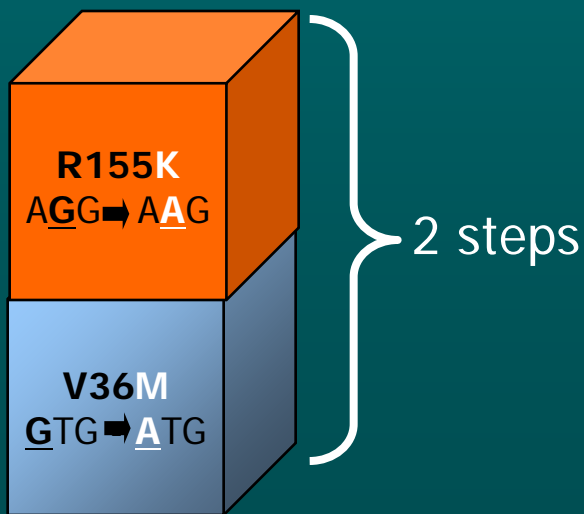




Clinical implications of genetic barrier to resistance – acquisition of protease inhibitor resistant variant V36M+R155K

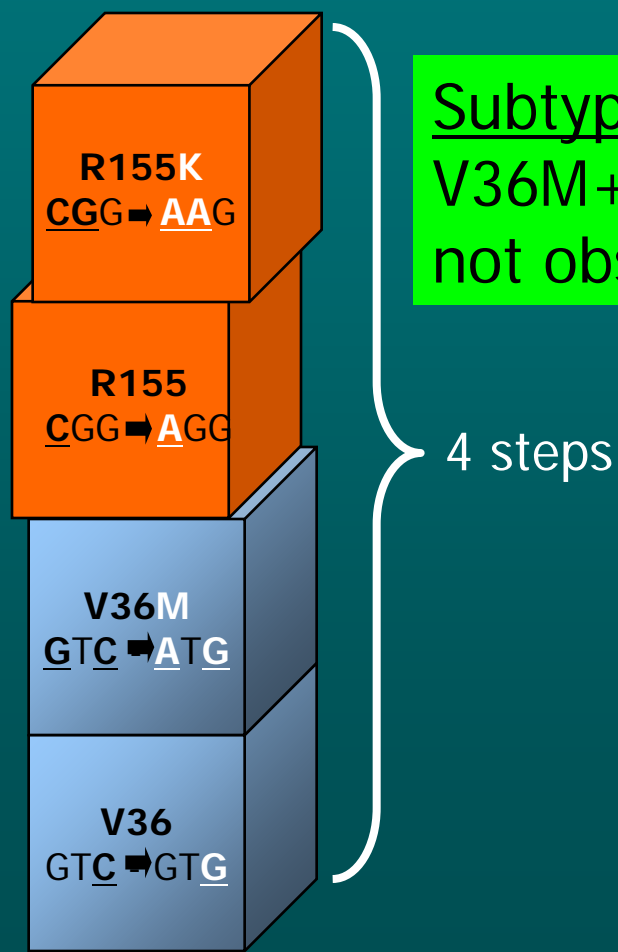
Subtype 1a

V36M+R155K variant
observed clinically^{1,2}



Subtype 1b

V36M+R155K variant
not observed clinically





Resistant profiles in non-SVR patients

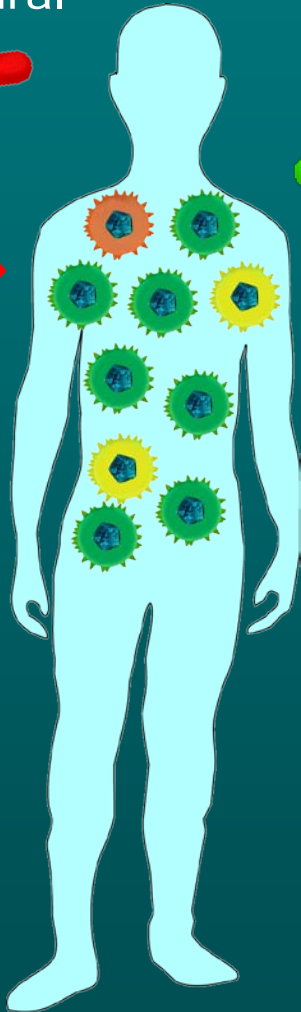
Variant	% of sequenced patients	
	Subtype 1a	Subtype 1b
WT	16%	46%
V36M	10%	3%
R155K	20%	0%
V36M+R155K	46%	0%
V36A	3%	16%
T54A	<1%	22%
A156S/T	3%	13%

Note: : Information from a subset of patients in trials. Not a complete list of treatment-emergent substitutions observed in clinical trials. See drug Prescribing Information for a complete list.

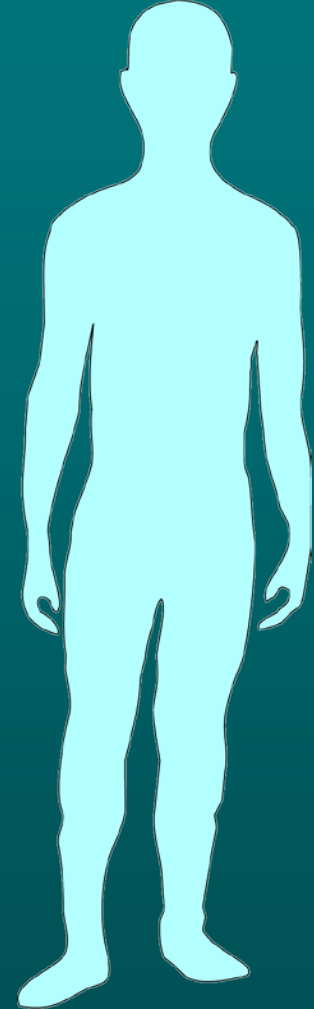
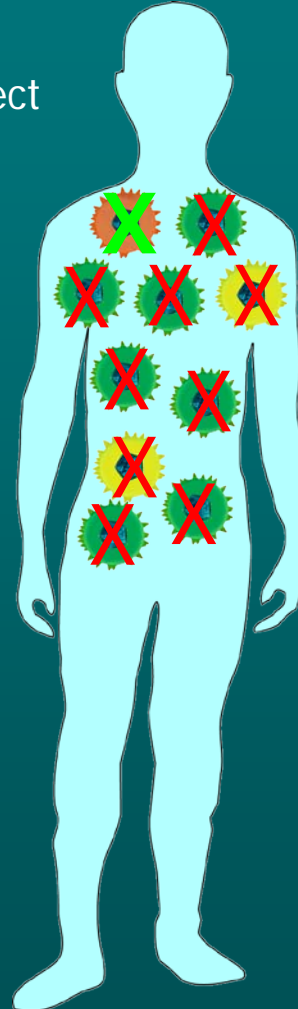
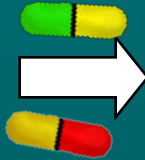


Combination drug regimens increase the genetic barrier to resistance

Antiviral



Peg-IFNa/RBV
&/or additional direct acting antivirals
DAA(s)



Eliminate variants with addition of Peg-IFNa/RBV or DAA (s) with non-overlapping resistance



Resistant virus



Sensitive virus



Lack of cross-resistance between Peg-IFN α /RBV &/or a combination of antiviral agents may provide an opportunity for elimination of resistant variants

Target	Variant	NS3 Covalent: Slow Reversible	NS3 Non-covalent: Linear and Macrocylic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg-IFN	RBV
NS3 Protease	V36M	R	S	S	S	S	S	S	S	S
	T54A	R	S	S	S	S	S	S	S	S
	R155K	R	R	S	S	S	S	S	S	S
	A156T	R	R	S	S	S	S	S	S	S
	D168V	S	R	S	S	S	S	S	S	S
NS5A	L31V	S	S	R	S	S	S	S	S	S
	Y93H	S	S	R	S	S	S	S	S	S
NS5B	S282T	S	S	S	R	S	S	S	S	S
	C316Y	S	S	S	S	R	S	S	S	S
	M414T	S	S	S	S	R	S	S	S	S
	R422K	S	S	S	S	S	S	R	S	S
	M423T	S	S	S	S	S	S	R	S	S
	P495S	S	S	S	S	S	R	S	S	S

Note this is not a comprehensive list of known HCV direct acting antivirals (DAA) resistance pathways. 4 fold shift represents arbitrary cutoffs for illustrative purposes only

S = Susceptible
(< 4 fold shift in HCV replicon EC50)

R = Resistant
(>4 fold increase in EC50)



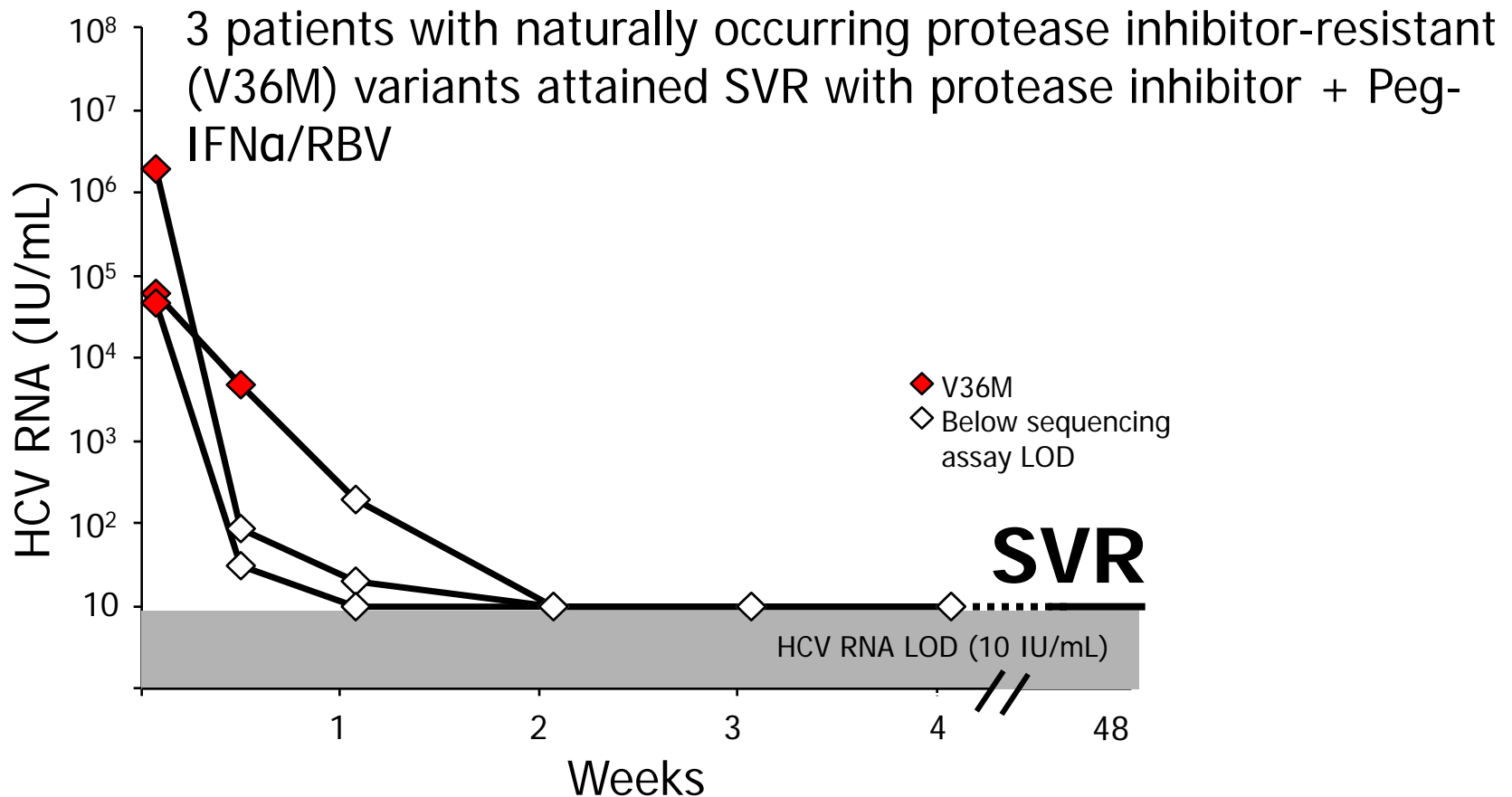
Terms used to guide treatment response in HCV infection

- **HCV RNA undetectable:** HCV RNA level below the limit of detection of a particular assay (not necessarily to be interpreted as HCV RNA “negative” or having cleared HCV for patients on treatment)
- **RVR (Rapid virologic response):** Undetectable HCV RNA at week 4 of therapy
- **eRVR (Extended RVR):** Undetectable HCV RNA at weeks 4 and 12 of therapy
- **EVR (Early virologic response):** $>2\log_{10}$ decline in HCV RNA at week 12 of therapy (also known as partial EVR, pEVR)
- **cEVR (Complete EVR):** Undetectable HCV RNA at week 12 of therapy
- **SVR (Sustained virologic response):** Undetectable HCV RNA 24 weeks after treatment cessation
- **Null responder:** $< 2\log_{10}$ IU/mL decline in HCV RNA at week 12 of therapy
- **Failure of HCV therapy:** Persistence of HCV RNA in serum after therapy

Resistant variants can be eliminated with a combination drug regimen



Target	Variant	NS3 Covalent: Slow Reversible	NS3 Non-covalent: Linear and Macrocytic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg- IFN	RBV
NS3	V36M	R	S	S	S	S	S	S	S	S

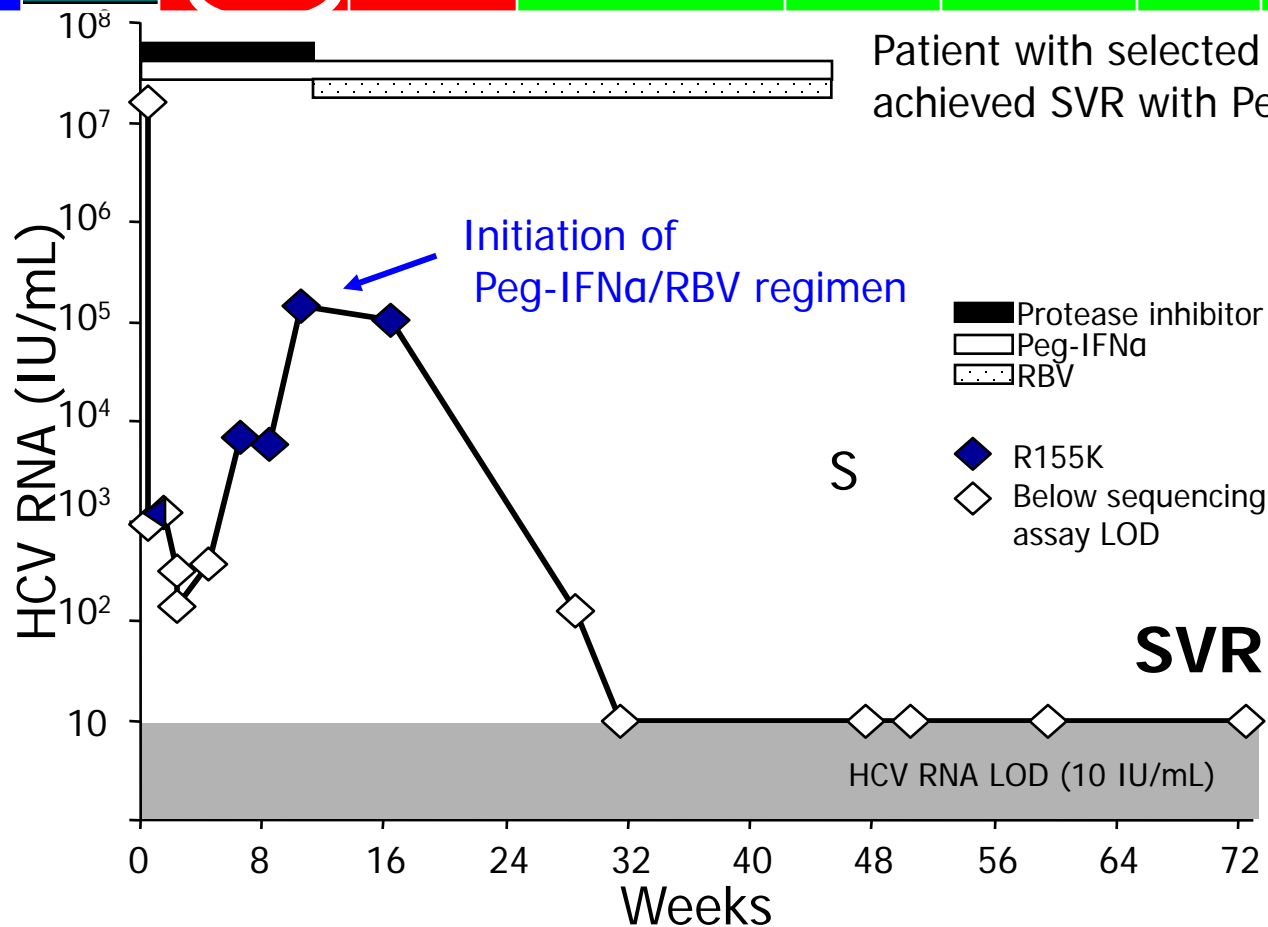




Patients with protease inhibitor-resistant variants can respond to Peg-IFNa/RBV

Target	Variant	NS3 Covalent Slow Reversible	NS3 Non-covalent: Linear	NS3 Non-covalent: Macrocylic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg-IFN	RBV
NS3	R155K	R	R	S	S	S	S	S	S	S	S

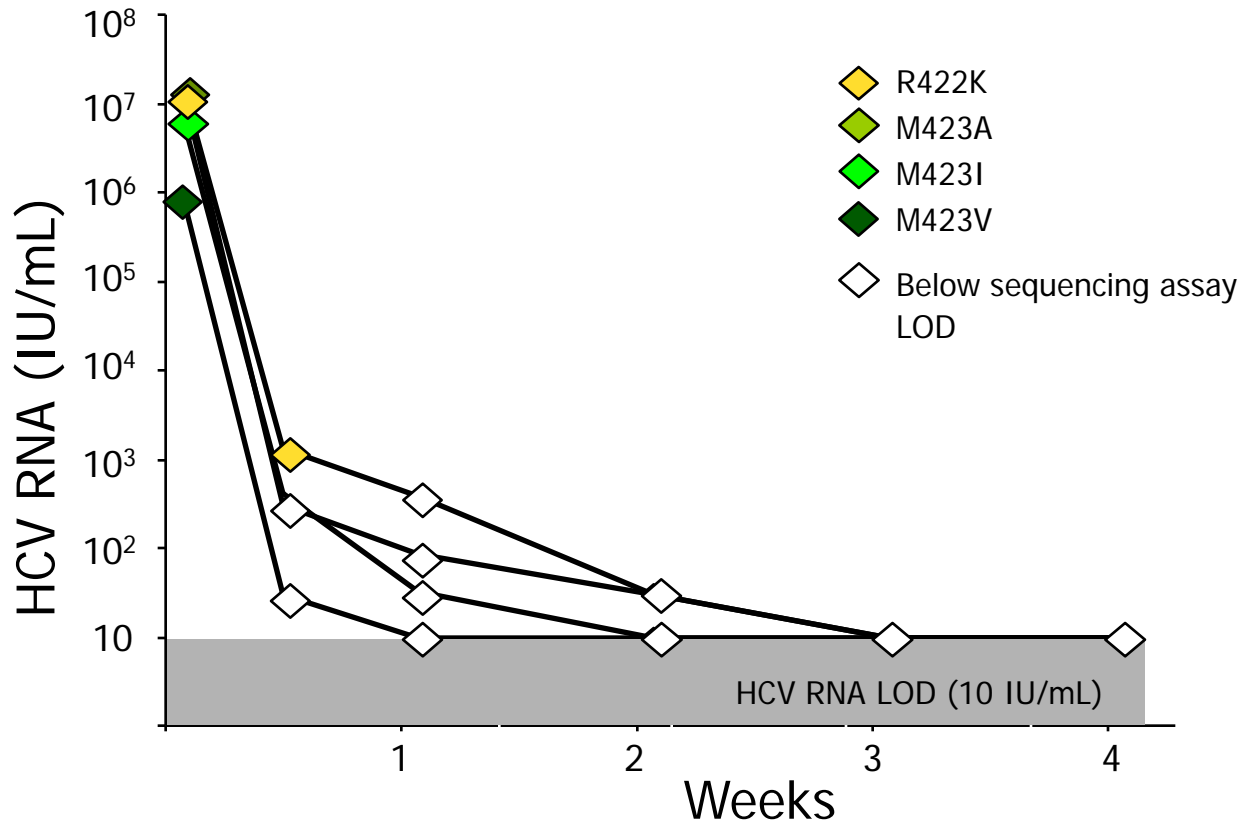
Patient with selected NS3 R155K variant achieved SVR with Peg-IFNa/RBV





Patients with naturally occurring polymerase inhibitor-resistant variants can respond to protease inhibitor + Peg-IFN α /RBV

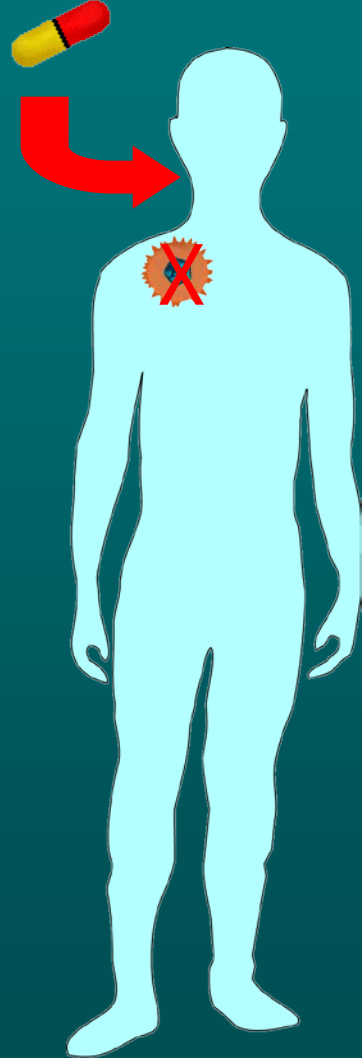
Target	Variant	NS3 Covalent: Slow Reversible	NS3 Non-covalent: Linear and Macrocylic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg- IFN	RBV
NS5B	R422K	S	S	S	S	S	S	R	S	S
	M423T	S	S	S	S	S	S	R	S	S



Pharmacological barriers to resistance



Antiviral



Higher potency

- Create/use drugs with stronger binding affinity

Higher drug levels

- Create/use drugs with longer half-life
- Increase target organ exposure
- Take recommended dosage at recommended dosing intervals
- Follow recommended food intake requirements

Improved tolerability and adherence

- Create/use drugs with minimal drug/drug interactions
- Create drugs with favorable safety profiles and convenient dosing schedules
- Develop better side effect management protocols

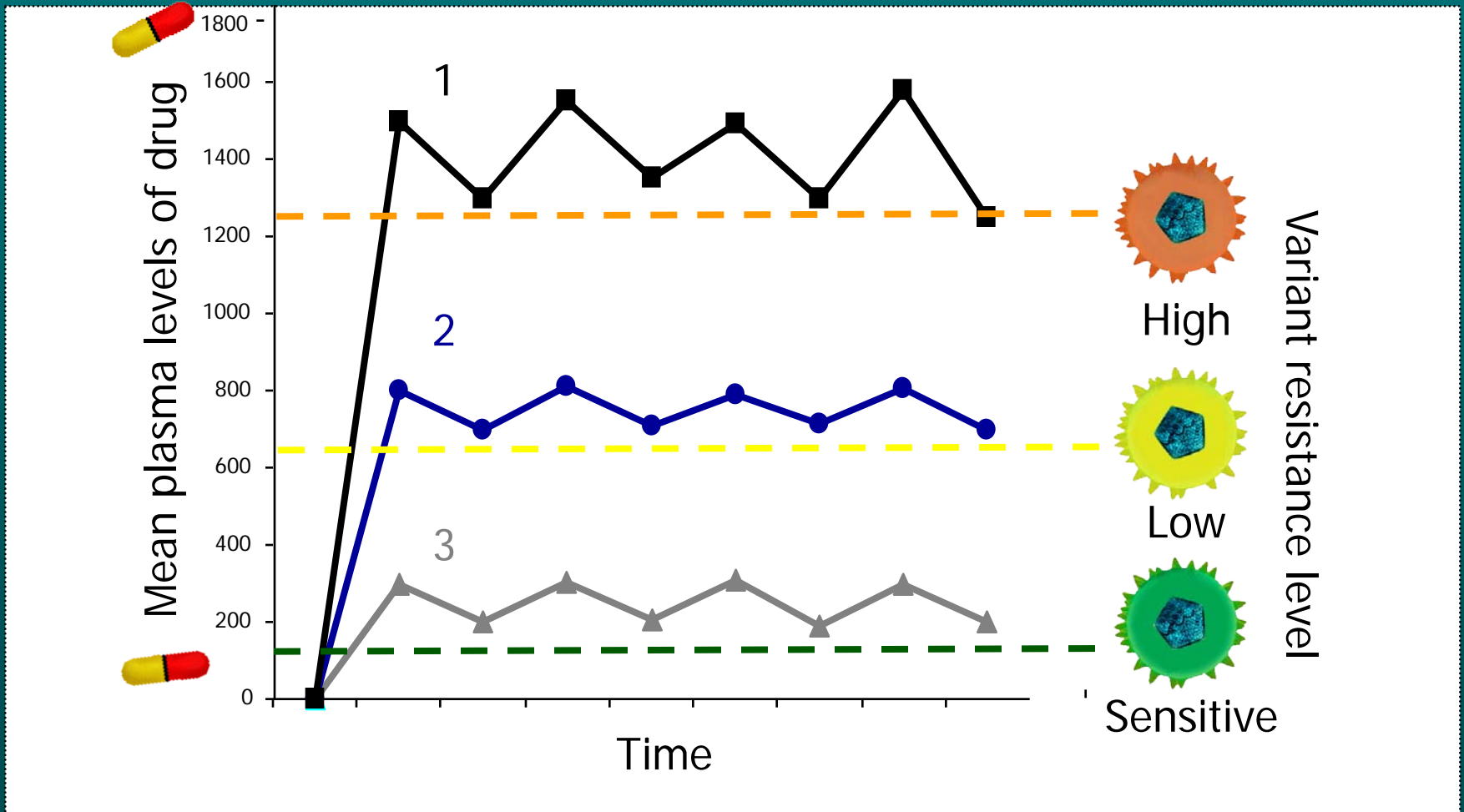
Combination drug regimens

- Develop potent regimen of direct-acting antiviral drugs with or without Peg-IFNa/RBV



Resistance is not an all or none phenomenon

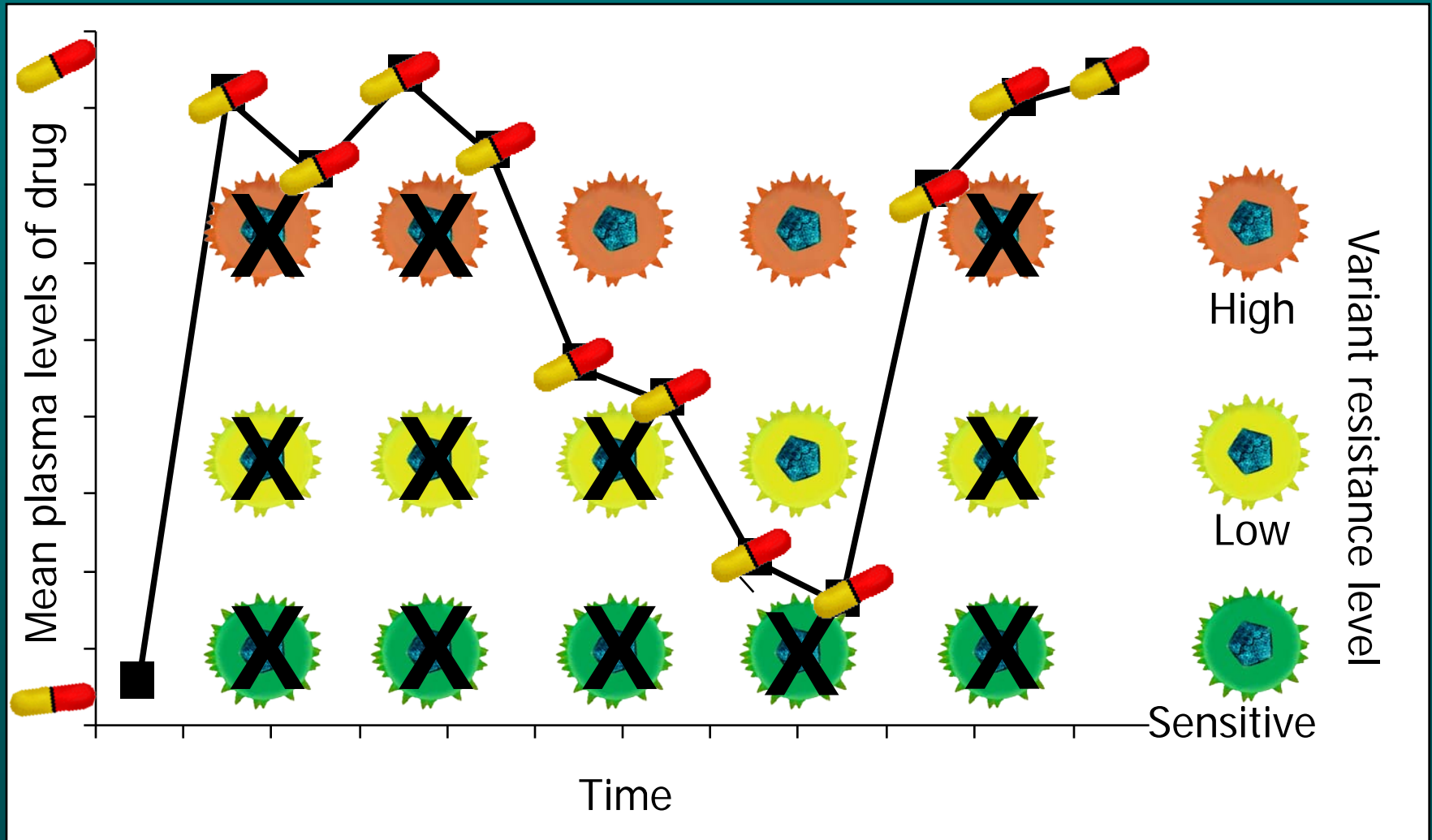
- Clinical resistance occurs if drug levels are not sufficient to inhibit viral replication
- Highly resistant viruses need very high drug levels (may not be achievable) to inhibit their replication





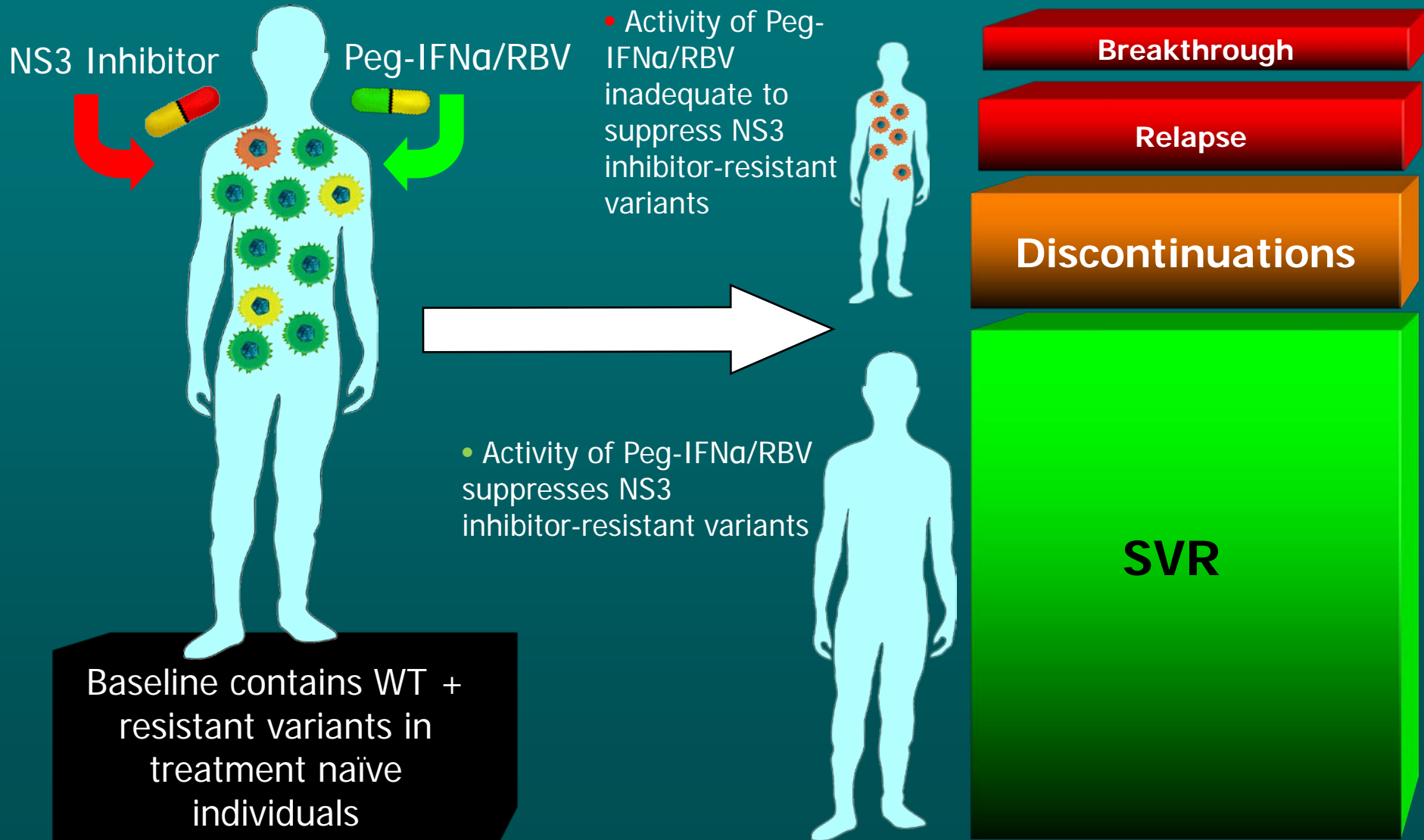
Importance of drug levels over time

Drug trough levels must be sufficient to suppress viral replication





Resistance emerges as a result of treatment failure



McHutchison JG. , et al. *N Engl J Med*, 2009; 360(18): 1827-183

Sarrazin, C. & Zeuzem, S. *Gastro*, 2010;138:447-62

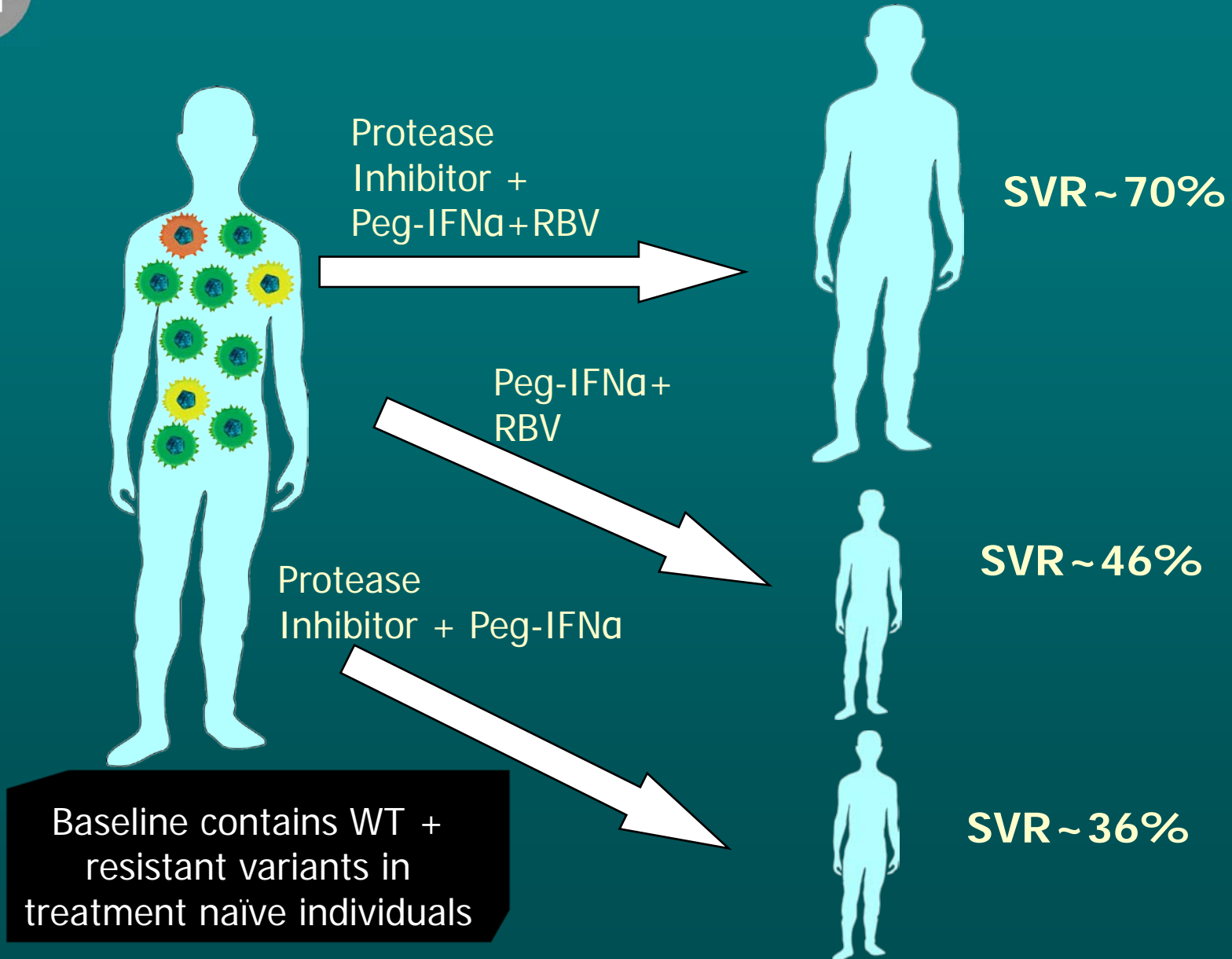
Hezode C. , et al. *N Engl J Med*, 2009; 360(18): 1839-1850

Kwo PY., et al *Hepatology*, 2008;48:1027A

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Contribution of Peg-IFNa/RBV to SVR



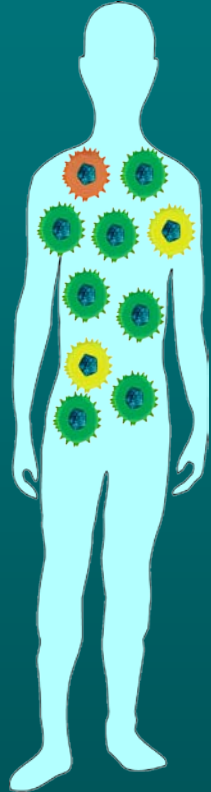
McHutchison J.G., et al. *N Engl J Med*, 2009; 360(18): 1827-1838

Hezode C., et al. *N Engl J Med*, 2009; 360(18): 1839-1850

Kwo PY., et al. *Hepatology*, 2008;48:1027A

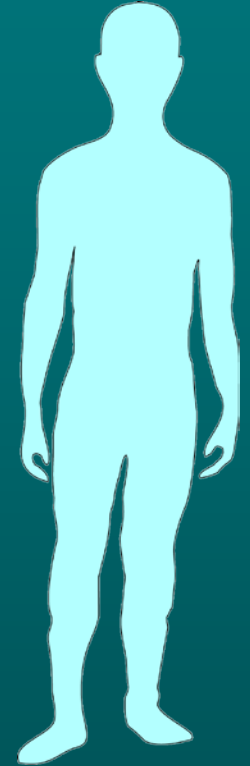


Peg-IFNa/RBV (PR) treatment experienced patients can be re-treated



**Peg-IFNa/RBV
treatment experienced**

Prior PR response	Retreatment SVR rate (approximate)	
	PR	PR + Protease Inhibitor
Relapse	22%	86%
Partial	15%	60%
Null	5%	32%



SVR



Definitions

Prior relapser: Achieved undetectable HCV RNA at end of treatment, but failed to achieve SVR

Prior partial responder: Achieved ≥ 2 log drop in HCV RNA at week 12 of prior therapy, but never became undetectable while on treatment

Prior null responder: Achieved < 2 log drop in HCV RNA at week 12 of prior therapy



IL28B genotype: Is there a role in the era of direct acting antivirals (DAAs)?

- Certain single nucleotide polymorphisms (SNPs) upstream of *IL28B* gene are associated with the rate of SVR in patients treated with **Peg-IFN α /RBV**:
 - SNP rs12979860: favorable allele=C, unfavorable allele=T
 - SNP rs8099917: favorable allele=T, unfavorable allele=G
- IL28B genotype can have an impact on the efficacy of a Peg-IFN α /RBV/DAA regimen
- IL28B genotype has also recently been shown to affect the activity of an interferon-free IFN-free, combination DAA regimen, although its impact is likely dependent on the anti-HCV potency and durability of the regimen



IL28B genotype effect on SVR in genotype-1 treatment-naïve patients

- Certain single nucleotide polymorphisms (SNPs) upstream of *IL28B* gene are associated with SVR in patients treated with Peg-IFNα/RBV (PR)¹⁻³:
 - SNP rs12979860: favorable allele=C, unfavorable allele=T

IL28B SNP rs12979860	PR (Ideal)		Telaprevir ⁵ (ADVANCE)		Boceprevir ⁶ (SPRINT-2)	
	ITT ⁴ Population	Adherent ³ Population	TVR/PR	PR control	BOC/PR*	PR control
CC	69%	~79%	90%	64%	80-82%	78%
CT	33%	~38%	71%	25%	65-71%	28%
TT	27%	~26%	73%	23%	55-59%	27%

* Includes BOC/RGT and BOC/PR48 arms, mITT

1 Tanaka Y., et al. *Nature Genetics*, 2009; 41:1105-1109

2 Suppiah V., et al. *Nature Genetics*, 2009; 41: 1100-1104

3 Ge D., et al. *Nature*, 2009; 461:399-401

4 Thompson A.J., et al. *Gastro*, 2010; 139: 120-129

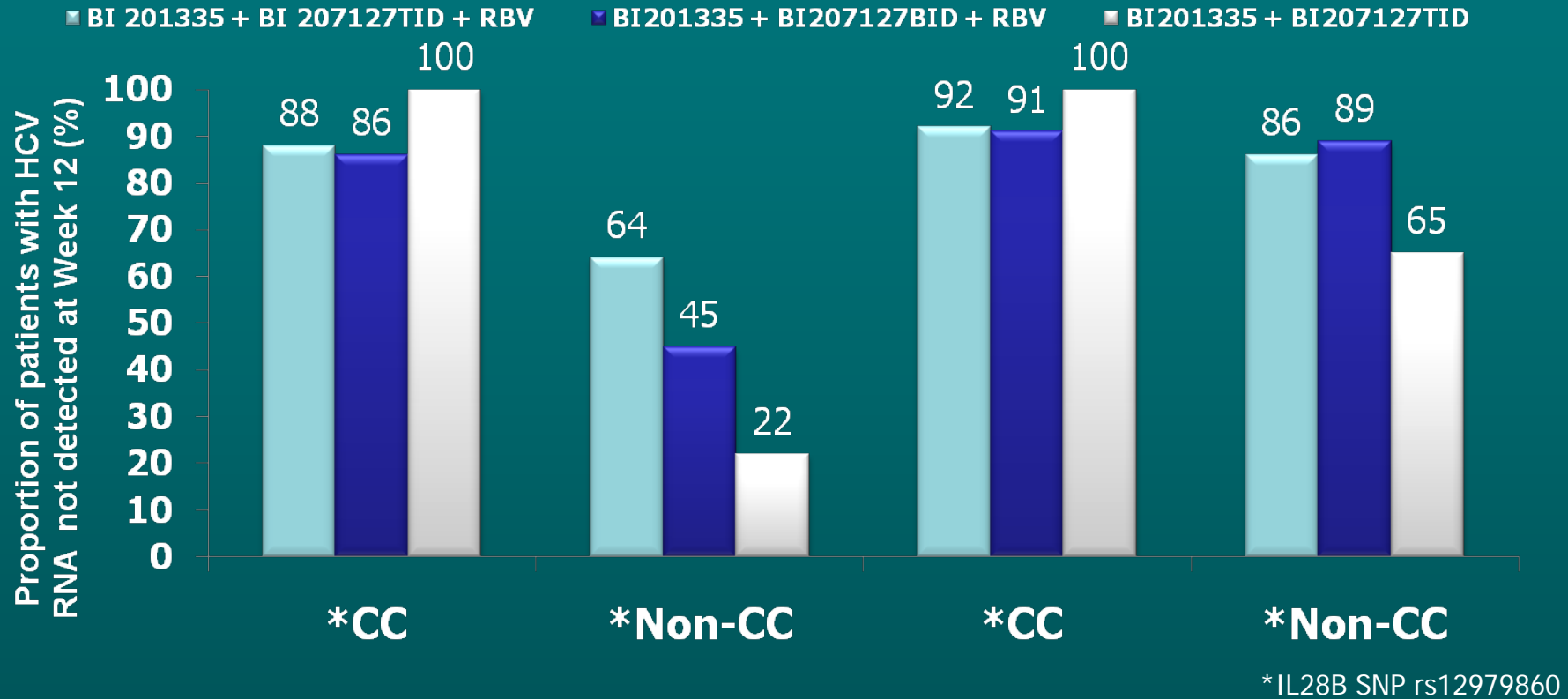
5 INCIVEK™ [package insert]. Cambridge, Mass: Vertex Pharmaceuticals Inc; 2011

6 VICTRELIS™ [package insert]. Whitehouse Station, NJ: Merck & Co, Inc; 2011

Footnotes: 1) Data from ADVANCE and SPRINT-2 based only on subjects who consented to IL28B genotype analysis; 2) Results are confounded by variable treatment durations in active and control arms



IL28B Genotype Can Influence Activity of an IFN-free Regimen: Proportion of GT1 patients with HCV RNA Not Detected at Treatment week 12 by IL28B Genotype and Subtype (per protocol analysis)



GT-1a

GT-1b

BI201335 + BI207127 _{TID} + RBV	22/25	39/61	24/26	79/92
BI201335 + BI207127 _{BID} + RBV	6/7	10/22	10/11	32/36
BI201335 + BI207127 _{TID} , no RBV	3/3	2/9	7/7	13/20

BI 201335: Protease Inhibitor

BI 207127: Polymerase Inhibitor



Interferon-free, combination direct acting antiviral (DAA) regimens: Progress and challenges

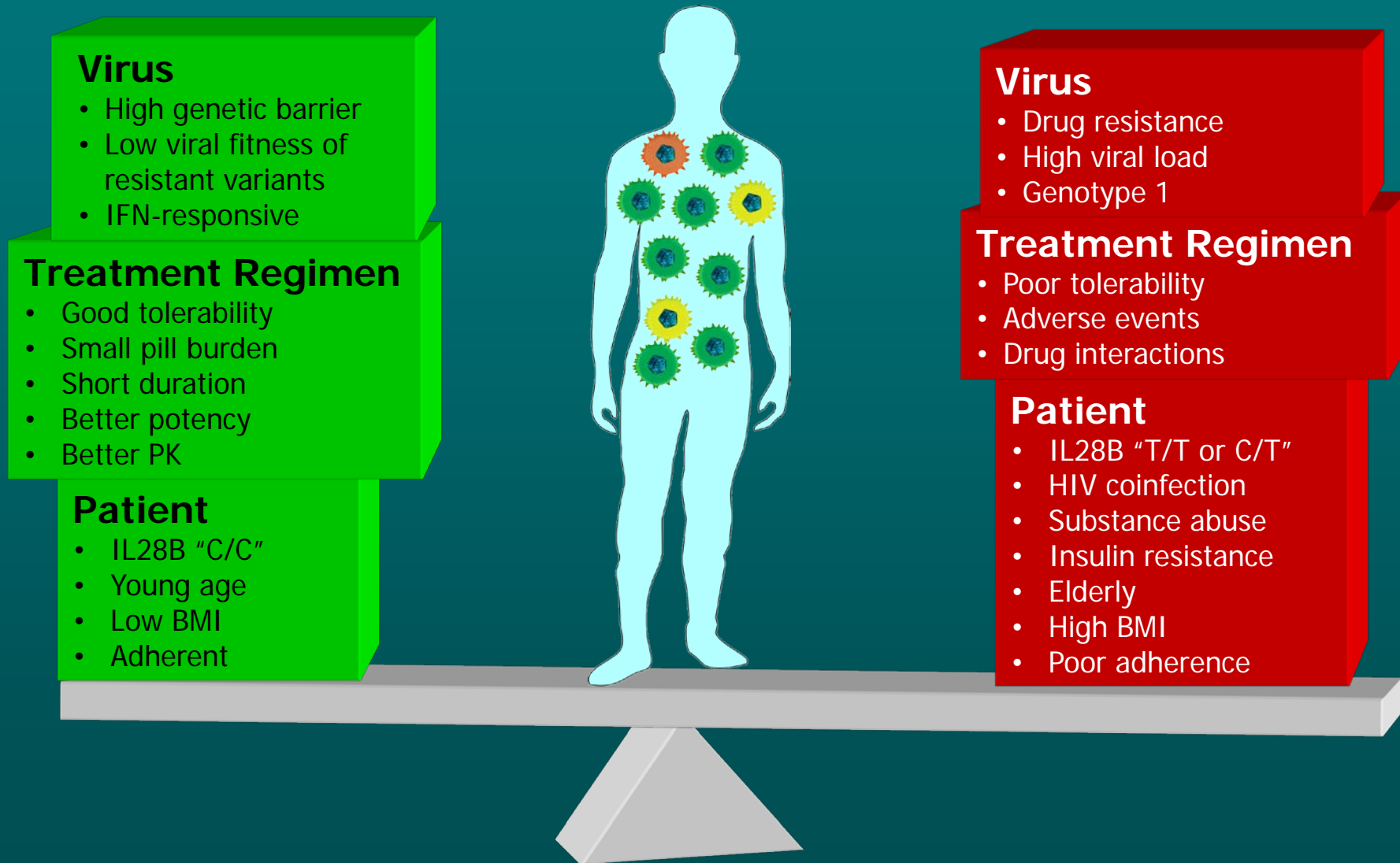
- There is an urgent need for safe and effective treatment regimens that do not include Peg-IFN α and/or RBV.
- In a Peg-IFN α /RBV/DAA regimen, Peg-IFN α /RBV enhance DAA antiviral durability by suppressing DAA-resistant variants
- Numerous clinical trials investigating the efficacy of combination DAA regimens to replace Peg-IFN α and/or RBV have been conducted or are in progress.
- Challenge: **Anti-HCV potency without durability \neq SVR**
- Lessons learned from trials conducted to date:
 - Two potent, low resistance barrier DAAs are most likely not adequate to achieve SVR for a majority of patients
 - Virologic breakthrough with a combination DAA regimen can occur early (few days) or late (2-3 months); only SVR proves efficacy
 - HCV genotype/subtype can have a major impact
 - Inclusion of RBV may have a role in combination DAA therapy



Maximize Response, Minimize Resistance



A balance of multiple factors contribute to SVR

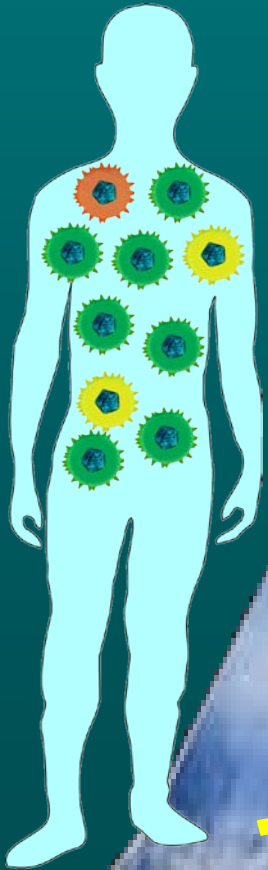




Regimen characteristics that increase likelihood of achieving SVR



SVR



-
- Shorter regimen
 - Adherence-friendly regimen
 - Minimal drug-drug interactions
 - Good tolerability
 - Potent viral suppression
 - Overcome virologic resistance
 - Combination regimens



Patient factors can provide obstacles to achieving SVR



SVR

**M
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E**

Unmanaged Depression

Non-adherence

Fatty Liver

Insulin resistance

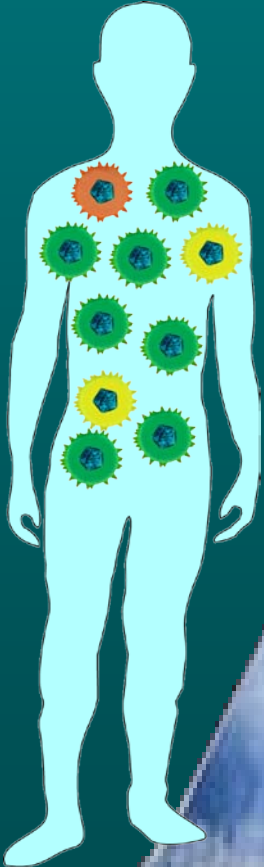
UNMODIFIABLE FACTORS

**Genetics
IL28B TT/CT**

Male

African American

Age >50yrs

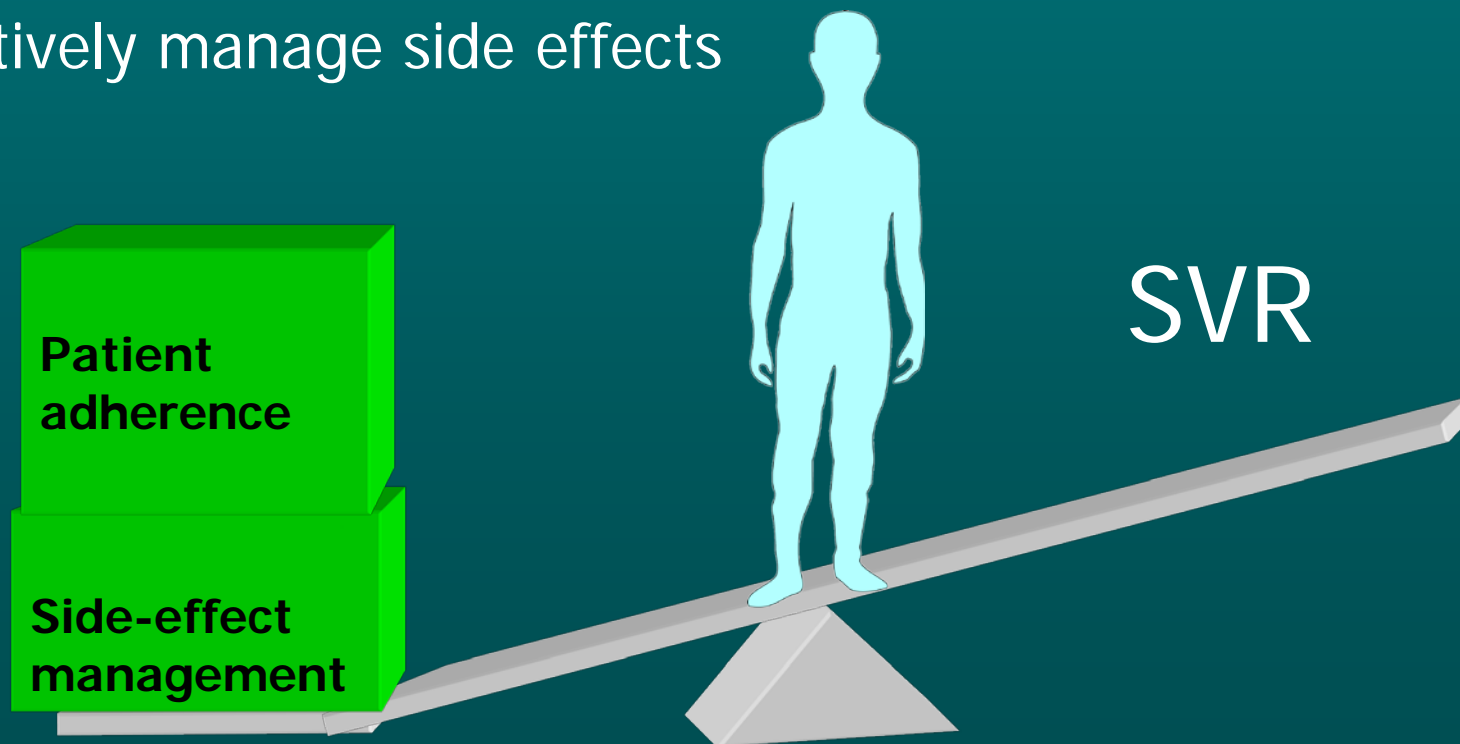




Adherence shifts the balance for SVR

Doctors and patients can maximize response:

- ✓ Right dose of drug
- ✓ At the right time
- ✓ Follow dietary recommendations
- ✓ Actively manage side effects





Future drug regimens could improve SVR rates

Industry, academia, regulators and community can work together to improve the quality of drugs available for HCV infected patients

Improved Regimen

- Improved tolerability
- More convenient dosing
- Smaller pill burden
- Shorter duration



SVR



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Doug Richman
Christoph Sarrazin
Chip Schooley
Scott Seiwert
Debra Sieminski
Mark Sulkowski
Tracy Swan
Theresa Turcotte
David Wyles



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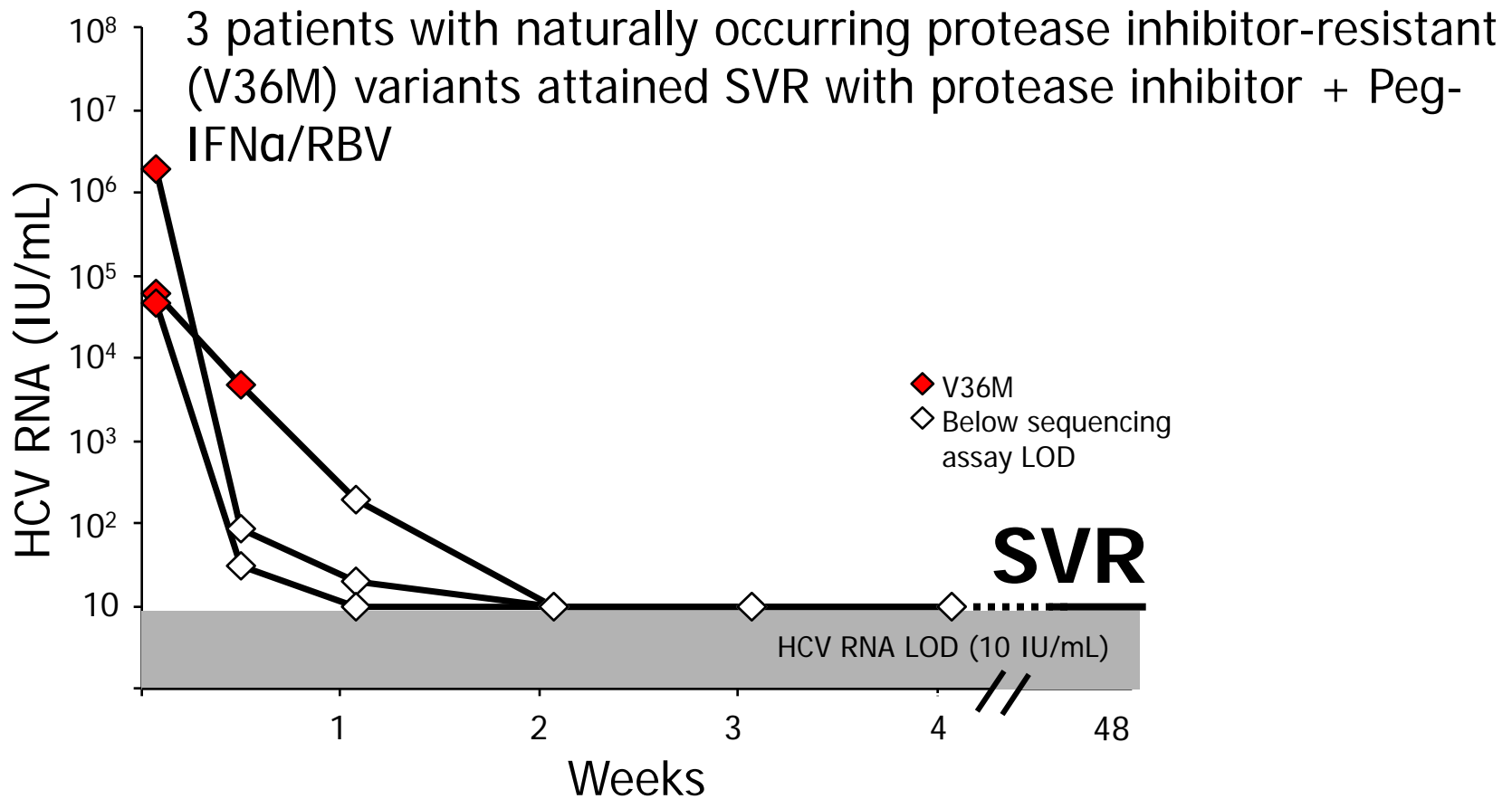
Nina Mani, FCHR

nmani@hivforum.org

Resistant variants can be eliminated with a combination drug regimen



Target	Variant	NS3 Covalent: Slow Reversible	NS3 Non-covalent: Linear and Macrocytic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg- IFN	RBV
NS3	V36M	R	S	S	S	S	S	S	S	S

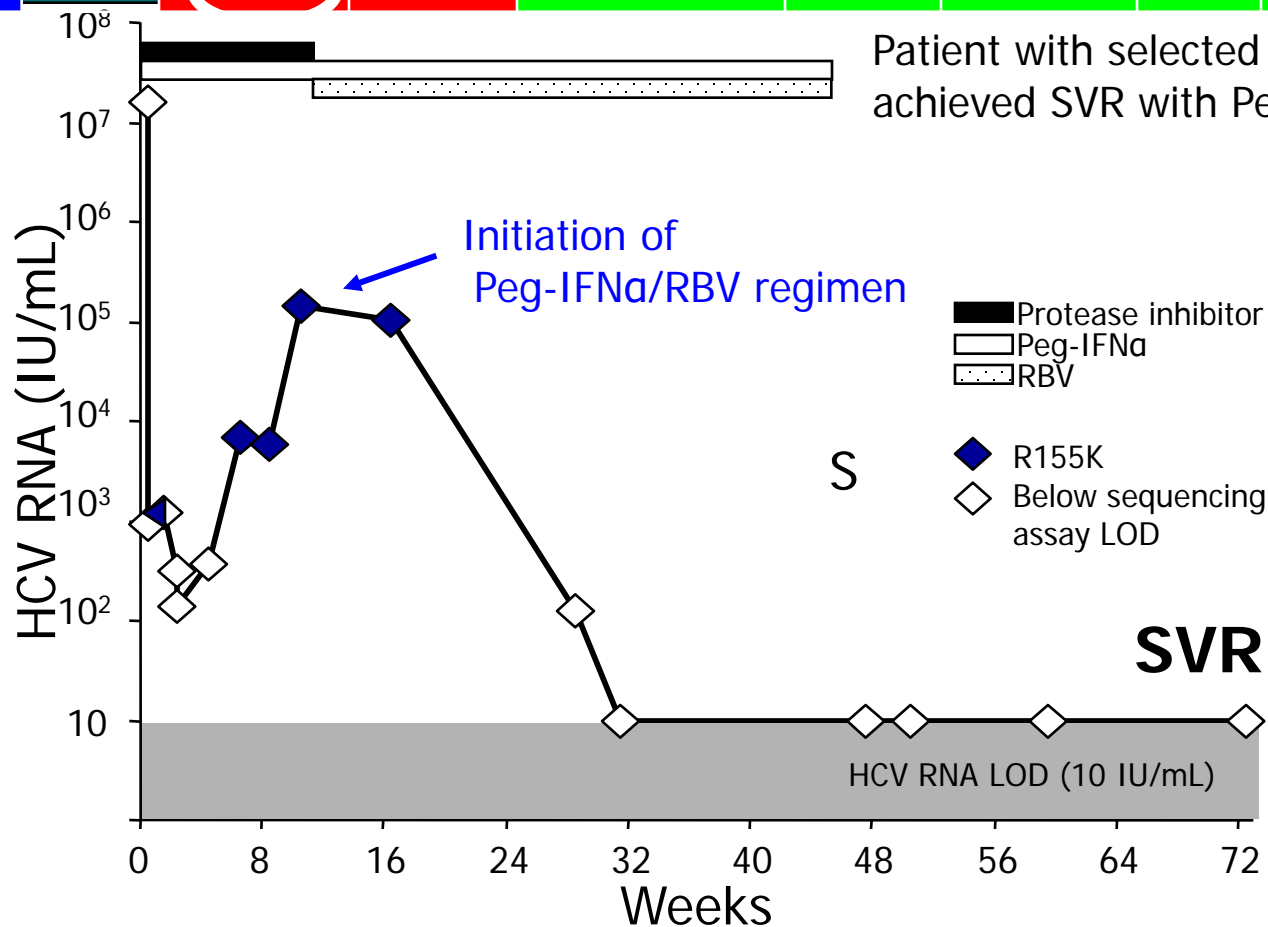




Patients with protease inhibitor-resistant variants can respond to Peg-IFNa/RBV

Target	Variant	NS3 Covalent Slow Reversible	NS3 Non-covalent: Linear	NS3 Non-covalent: Macrocylic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg-IFN	RBV
NS3	R155K	R	R	S	S	S	S	S	S	S	S

Patient with selected NS3 R155K variant achieved SVR with Peg-IFNa/RBV





Patients with naturally occurring polymerase inhibitor-resistant variants can respond to protease inhibitor + Peg-IFN α /RBV

Target	Variant	NS3 Covalent: Slow Reversible	NS3 Non-covalent: Linear and Macrocylic	NS5A inhibitor	NS5B nucleoside	NS5B Palm	NS5B Thumb 1	NS5B Thumb 2	Peg- IFN	RBV
NS5B	R422K	S	S	S	S	S	S	R	S	S
	M423T	S	S	S	S	S	S	R	S	S

