

Can we use sequential regimens in lieu of HIV drug resistance testing?

The SECOND-LINE resistance substudy

MA Boyd MD, FRACP The Kirby Institute University of New South Wales, Sydney, Australia

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Boyd et al. Lancet HIV E-pub 20 Jan 2015.



Disclosures

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Background

- ART failure is associated with drug resistance
- WHO recommends using a boosted-PI + 2N(t)RTIs after 1st line NNRTI+2N(t)RTI failure
- There is interest in implementing wider access to genotypic testing to optimise N(t)RTI selection



SECOND-LINE main study

Adults ≥16 years old Confirmed virological failure of NNRTI+2N(t)RTIs (pVL >500 copies/mL) No prior PI or InSTI exposure 48 weeks 96 weeks primary analysis final analysis V LPV/r 400/100mg bid + 2-3 N(t)RTIs* (n=271) *selected by either GART or algorithm

LPV/r 400/100mg bid + raltegravir 400mg bid (n=270) Stratified by site and baseline pVL >100,000 c/mL

Primary objective

 compare proportions with plasma viral load <200 copies/mL at week 48



SECOND-LINE main study

96 week results

	RAL arm	Control arm		Difference (RAL-Control)
	n/N (%)	n/N (%)		% (95%CI) p-value
Plasma viral load <200 copie	es/mL			
Intention to treat	217/270 (80.4)	206/271 (76.0)	↓	4.4 (-2.6, 11.3) 0.22
≤100000 copies/mL*	177/210 (84.3)	176/219 (80.4)		3.9 (-3.3, 11.1) 0.30
>100000 copies/mL*	40/60 (66.7)	30/52 (57.7)	$ \longrightarrow $	9.0 (-8.9, 26.9) 0.33
Per protocol	200/232 (86.2)	194/232 (83.6)	· · · · · · · · · · · · · · · · · · ·	2.6 (-3.9, 9.1) 0.44
Non-completion=failure	198/270 (73.3)	193/271 (71.2)	·	2.1 (-5.4, 9.7) 0.58
Plasma viral load <50 copies	s/mL			
Intention to treat	189/270 (70.0)	183/271 (67.5)	• • • • • • • • • • • • • • • • • • • •	2.5 (-5.3, 10.3) 0.54
Per protocol	175/232 (75.4)	175/232 (75.4)	↓	0.0 (-7.8, 7.8) 1.00
Non-completion=failure	173/270 (64.1)	175/271 (64.6)	• • • • • • • • • • • • • • • • • • •	-0.5 (-8.6, 7.6) 0.90
			i 	
			-14 -12 -10 -8 -6 -4 -2 0 2 4 6 8 10 12 14	
			Difference between arms (%)	
			Favours Control Favours RAL	

Virological response at week 96 by randomised arm, study population and baseline VL



Objectives

Examine the contribution of baseline N(t)RTIresistance as well as other potential predictive variables to virological failure (VF) in SECOND-LINE

- demographics, HIV history, ART history, ART adherence



Hypothesis

That the gGSS would predict an adequate response to therapy defined as a plasma viral load <200 copies per mL at week 96 in the N(t)RTI group

i.e.

- that the higher the score the more likely a patient in the N(t)RTI group would achieve and sustain a fully suppressed VL
- that baseline N(t)RTI resistance would have no association with outcome in the N(t)RTI-sparing arm



SECOND-LINE resistance

Methods Analysis population

Modified intention to treat (mITT)

Virological failure (VF)

- plasma viral load (pVL) ≥200 copies/ml
- central laboratory

Genotypic antiretroviral testing (GART)

• Viroseq HIV-1 type genotyping system for RT/PI and InSTI

Adherence

• Validated 7 day recall instrument

- 'all ART taken' versus 'most, half, very few or no ART taken'

– conducted at week 4 and week 48



SECOND-LINE resistance

Methods

Global Genotypic Sensitivity Score (gGSS)*

- combined GSS for lamivudine/emtricitabine, abacavir, zidovudine, stavudine, didanosine, and tenofovir for each viral isolate (max score = 6)
 - scores for each N(t)RTI = 0, 0.25, 0.50, 0.75, and 1 for high-level, intermediate, low-level, potential low-level resistance and susceptible respectively

Specific Genotypic Sensitivity Score (sGSS)*

- GSS for the N(t)RTIs used by each participant
- N(t)RTI arm only (max score = 2 or 3)

Multivariate logistic regression

• assess predictors of VF

*Stanford algorithm HIV database version 6.3.1 (http://hivdb.stanford.edu)



SECOND-LINE baseline characteristics

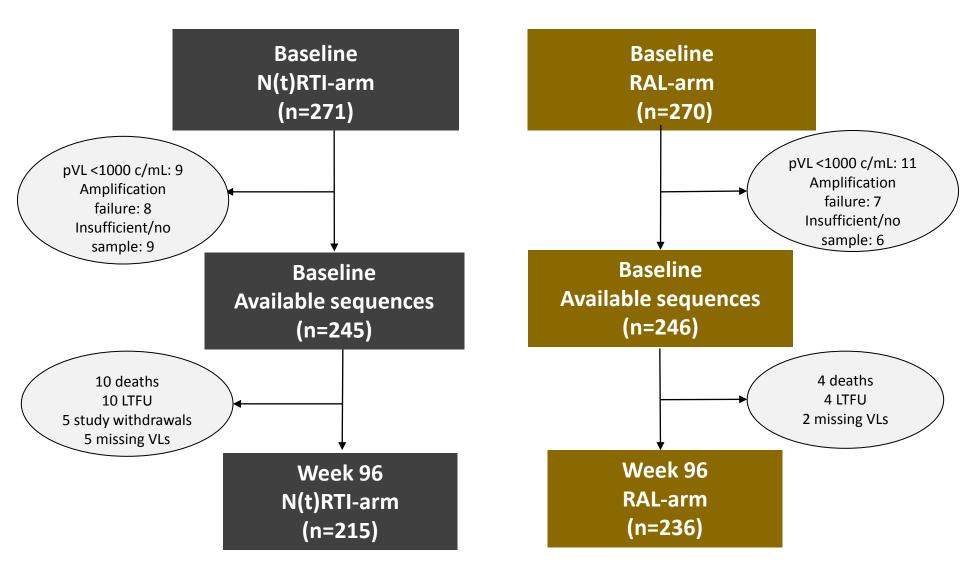
Characteristics		N(t)RTI-arm (n=271)	RAL-arm (n=270)
Median age (years)		38.5 (3-46)	38.4 (32-44)
Men		156 (57.6%)	142 (52.6%)
Population	Caucasian Asian Hispanic African	6.6% 43.2% 14% 36.2%	8.5% 41.5% 13.7% 35.9%
HIV disease stage	С	46.5%	47.4%
Median CD4+ T-cell	count (cells/μL)	189 (80-289)	190 (104-307)
Median Log ₁₀ plasma	a HIV RNA	4.3 (3-7-4.9)	4.2 (3.6-4.8)
Median duration of first-line ART (yrs)		3.3 (1.8-5.4)	3.5 (2.0-5.7)



SECOND-LINE N(t)RTI-arm drug selection

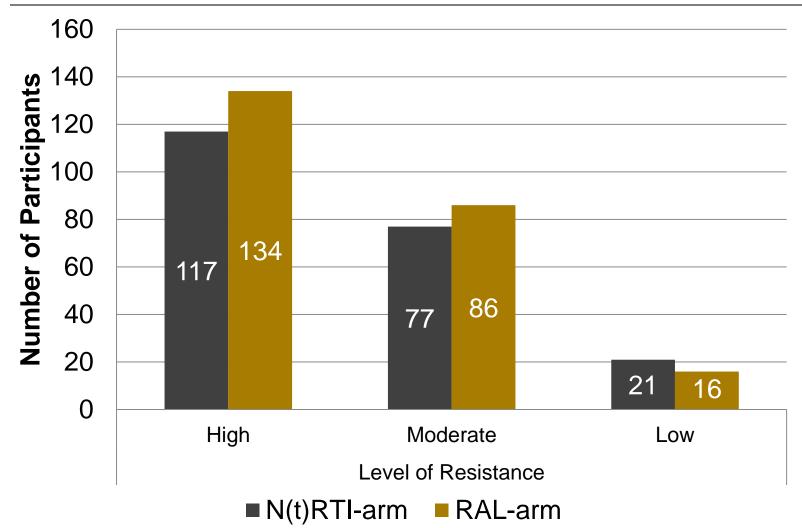
GART for N(t)RTI-selection	198 (73%)
Algorithm for N(t)RTI selection	73 (27%)
2N(t)RTIs in 2 nd line ART	208 (77%)
3N(t)RTIs in 2 nd line ART	63 (23%)
TDF in 2 nd line N(t)RTI-regimen	220 (81%)
3TC/FTC in 2 nd line N(t)RTI-regimen	236 (87%)
AZT in 2 nd line N(t)RTI-regimen	123 (45%)

Study disposition



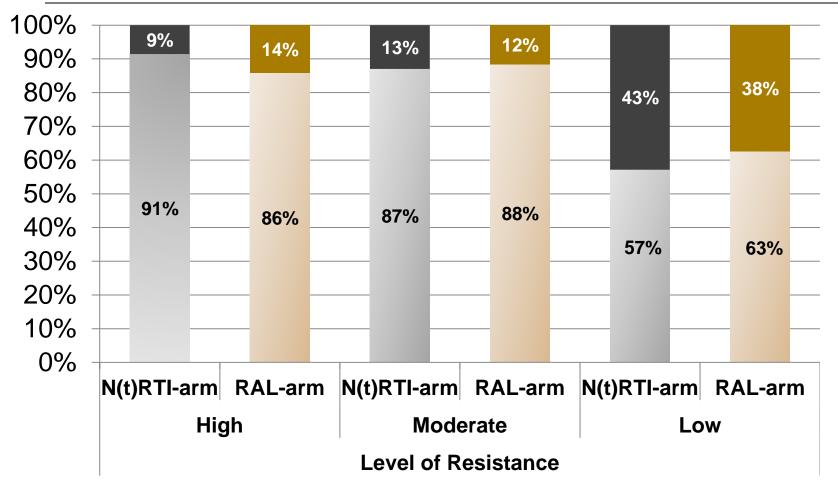


Distribution of baseline global GSS by treatment arm



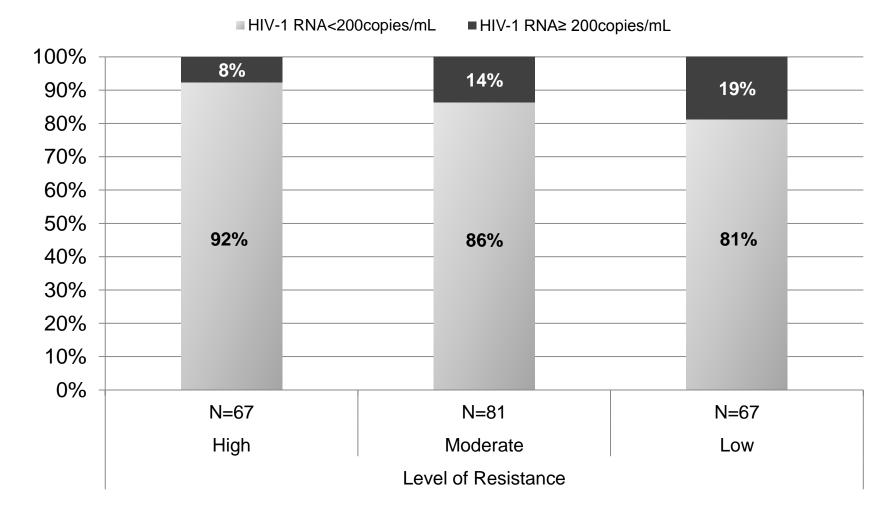


VF at W96 by gGSS at baseline by treatment arm





VF at W96 by sGSS at baseline in the N(t)RTI-arm





Predictors of VF over 96 weeks

Predictors	Multivariate OR	95% CI	p-value overall
Population			
Asian (n=212, VF=19)	1		
Caucasian (n=34, n=4)	2.28	0.65, 8.02	
Hispanic (n=66, VF=13)	3.13	1.21, 9.13	
African (n=182, VF=31)	3.49	1.68, 7.28	0.007
Baseline VL			
≤100,000 c/mL (n=399, VF=45)	1		
>100,000 c/mL (n=96, VF=23)	3.43	1.70, 6.94	<0.001



Predictors of VF over 96 weeks

Predictors	MVA OR	95% CI	p-value
Adherence at W4			
All ART in last 7 d (n=419, VF=50)	1		
<all 7="" art="" d<br="" in="" last="">(n=70, VF=18)</all>	2.18	1.07, 4.47	0.032
Adherence at W48			
All ART in last 7 d (n=434, VF=51)	1	0.65, 8.02	
<all 7="" art="" d<br="" in="" last="">(n=45, VF=13)</all>	3.43	1.09, 5.69	0.03
gGSS			
High resistance (n=251, VF=29)	1		
Moderate resistance (n=163, VF=20)	1.03	0.52, 2.03	
Low resistance (n=37, VF=15)	4.73	1.04, 11.46	0.002

ACTG 5273 (SELECT): impact of baseline resistance on risk of virological failure

Baseline NRTI Resistance	HR for VF in Both Arms (95% CI)	p-value
K65R, ≥ 3 TAMs, Q151M or 69 ins/del ■ yes vs no (ref)	0.49 (0.31-0.76)	.001
IAS NRTI mutations $\ge 3 \text{ vs} < 3 \text{ (ref)}$	0.45 (0.30-0.70)	< .001
 K65R and/or M184V/I No K65R but M184V/I vs no M184V/1 (ref) K65R and M184V/I vs no M184V/1 (ref) 	0.41 (0.25-0.67) 0.19 (0.08-0.44)	< .001

La Rosa AM, et al. Lancet E-pub 18 April 2016.



Summary

Virological failure in the SECOND-LINE trial was associated with:

- self-reported non-adherence
- higher baseline gGSS
- baseline pVL >100,000 copies/mL
- study population



Conclusions

For HIV treatment and care programs the results support:

- greater investment in understanding and implementing effective adherence support and interventions
- greater emphasis on a reliable drug supply
- the use of sequential ART regimens in lieu of HIVDR



Acknowledgements

Writing Committee: Boyd MA, Moore CL, Molina J-M, Wood R, Madero JS, Wolff M, Ruxrungtham K, Losso M, Renjifo B, Teppler H, Kelleher A, Amin J, Emery S, Cooper DA. Project Team: Amin J, Arriaga M, Berthon-Jones N, Boyd MA, Cooper DA, Courtney-Vega K, Emery S, Espinosa N, Haskelberg H, Hough S, Humphries A, Lee W, Moore CL, Taylor J, Valdovinos M, Pussadee K.

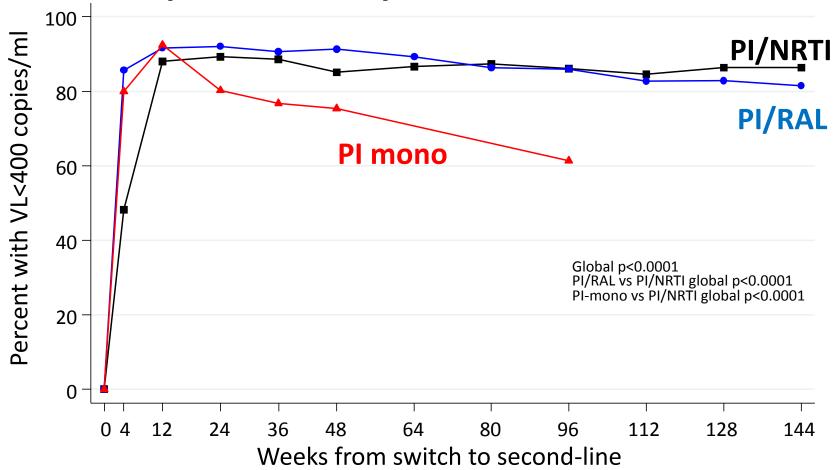
Site Investigators: Belloso W, Bittar, V, Cabello R, Casiro A, Chetchotisakd P, Contarelli J, Foulkes S, Gotuzzo E, Gazzard B, Kamarulzaman A, Lupo S, Madero JS, Garcia Messina O, Mohapi L, Molina JM, Nwizu C, Perez C, Phanuphak P, Salazar R, Sanchez J, Soo CT, Supparatpinyo K, Smith D, Villanueva JA, Wood R, Wolff M.

Site Staff: Angel EB, Arumboro R, Balazar JV, Borja SR, Cabello R, Clarke A, Copertari G, David DO, Delfino M, Echeveria J, Ferret S, Khotphuwieng T, Lee A, Kumar S, La Rosa A, Loh AL, Man S, Mootsikapun P, Kim LK, Northland RG, Omar SFS, Poongulali S, Pussadee K, Salami D, Sarangapany J, Sugandhavesa P, Kaplan R, Maor C, Higgs C, Tan M, Trape L, Chung W-Y, Aploon J, Lourens R, Lai Fong C, Valdovinos M, Viloria G, Wongvoranet C, HIV Immunovirology (Biobank) Laboratory staff, St. Vincent's Hospital Centre for Applied Medical Research. Study Partners: Merck, AbbVie, amfAR, NHMRC.

Study Participants



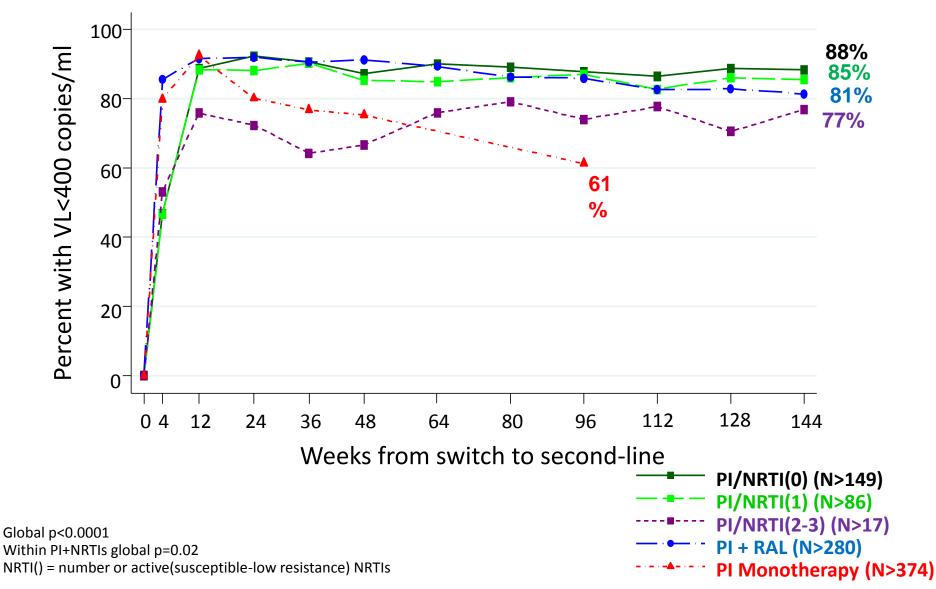
EARNEST VL responses by randomized arm



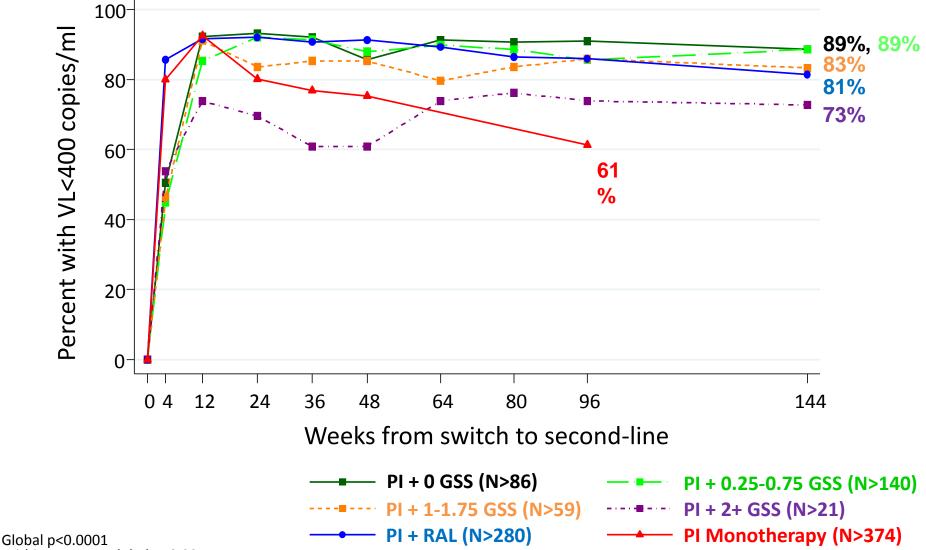
Week 96 outcomes: Paton, NEJM 2014; 371; 234-47; Week 144 outcomes: Hakim, Poster 552, CROI 2015

EARNEST

VL response by no. of active NRTIs in the regimen



EARNEST VL response by GSS of NRTIs in the regimen



Within PI+NRTIs global p=0.007



Emergent N(t)RTI Mutations, n, (%)

	NtRTI-arm	RAL-arm
Total number with amplifiable sequence	64	65
Number of participants with mutations	8 (12.5)	2 (3.1)
Major mutations	8 (12.5)	2 (3.1)
Number of major mutations	8	2
M184V	1	0
D69N	3	1*
T69NT	2	0
K219KN	0	1
T215NSTY	1	0
K70G	1	0

*participant switched to TDF/FTC prior to VF



Emergent PI Mutations, n (%)

	NtRTI-arm	RAL-arm
Total number with amplifiable sequence	64	65
Number of participants with mutations	2 (3.1)	0
Major mutations	1 (1.6)	0
Minor mutations	1 (1.6)	1 (1.6)
Number of major mutations	2	0
M46I	1	0
V82AV	1	0
Number of minor mutations	1	1
A71V	1	0
L90F	0	1





Emergent InSTI Mutations, n(%)

	NtRTI-arm	RAL-arm
Total number with amplifiable sequence	72	79
Number of participants with mutations	1 (1.4)	20 (25.3)
Major mutations	0	16 (20.3)
Minor mutations	1 (1.4)	4 (5.1)
Number of major mutations	0	19
N155HN	0	14
Q148QR	0	2
T66AST	0	2
Y143SY	0	1
Number of minor mutations	1	5
L74ILM	1	2
T97AT	0	2

Study Flow

