Genotypic assessment of the viability of second-generation NNRTIs as an alternative therapy for ART-experienced individuals with multi-class HIV drug resistance in Botswana

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Background

- An increase in multi-class drug resistant (MDR) HIV variants substantially limits future antiretroviral therapy (ART) options
- There is constant need to monitor the emergence and spread of drug resistance to avoid selection of ineffective regimens
- The study investigated the prevalence of MDR HIV-1 strains within ART experienced individuals in Botswana, and evaluated the susceptibility of these strains to second-generation non-nucleoside reverse transcriptase inhibitors (NNRTIs), doravirine (DOR), etravirine (ETR), and rilpivirine (RPV).

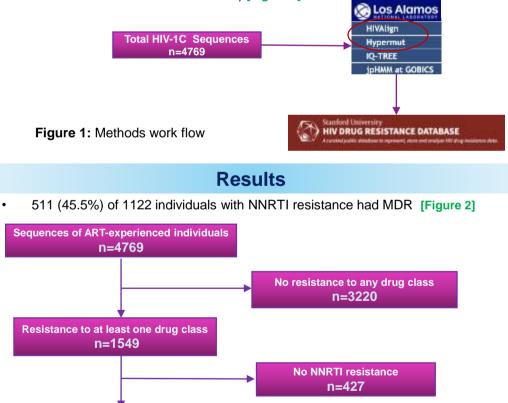
Methods

Study Population

This study included **4769** plasma derived HIV sequences from ART experienced individuals who had enrolled for the Botswana Combination Prevention Project (BCPP), 2013-2018, (n = 4747) and the Bosele study, 2015-2018, (n = 22)

Methods

- Sequences were aligned using the Los Alamos HIVAlign tool and adjusted for hypermutations according to the Hypermut tool
- Major HIV drug resistance mutations (DRMs) were analysed according to the Stanford HIV drug-resistance database.
- Participants harbouring MDR (resistance to ≥2 ARV classes), with at-least NNRTI resistance, were further evaluated for resistance to DOR, ETR, and RPV.
- The Stanford "DRM penalty scores" were utilised to predict resistance levels and interpretation (individuals with low-level, intermediate-level and high-level resistance were considered to have resistance) [Figure 1]



Results

- Majority of participants had low-level DOR (78.1%) and ETR (80.4%) resistance
- Mutations M230I (64.4%) and E138K (12.2%) both associated with high level RPV resistance were the most predominant [Table 1]
- MDR individuals failing second-generation NNRTIs had a high prevalence of ٠ resistance to NRTIs (399/495; 80.6%) and PIs (255/495; 51.5%) [Figure 3]

Table 1: Resistance to DOR, ETR and RPV, and prevalence of RAMs

	DOR (%)	ETR (%)	RPV (%)
	n=398	n=382	n=477
Overall (n=495)	80.4	77.2	96.4
Level of resistance			
Low Level	78.1	80.4	14.9
Intermediate	9	15.4	65
High Level	12.8	4.2	20.1
Specific Mutations			
A98G	-	-	3.6 ^a
L100I	0.8ª	0.8 ^b	0.6 ^c
K101E	3.5 ^a	3.7ª	2.9 ^b
K101P	-	0.3 ^c	0.2 ^c
V106A	0.5°	-	-
V106M	4.0 ^b	-	-
E138K	-	-	12.2 ^b
E138Q	-	-	0.8 ^a
Y181C	-	6.8 ^b	5.5 ^b
Y181I	-	0.3 ^c	0.2 ^c
Y188F	0.3 ^b	-	0.2 ^b
Y188L	1.5°	-	1.3 ^c
G190E	7.8°	8.1 ^b	6.5 ^c
G190S	0.5 ^b	-	-
H221Y	-	-	1.0 ^a
P225H	2.3 ^b	-	-
F227C	0.3 ^c	0.3 ^b	0.2 ^b
F227L	0.8 ^c	-	-
M230I	-	-	64.4 ^b
M230L	0.5°	0.5 ^b	0.4 ^c
Y318F	0.3 ^c	-	-

^a Mutation associated with intermediate resistance

- ^b Mutation associated with high-level resistance
- ^c Mutation associated with low-level resistance
- Mutation associated with susceptibility to the drug

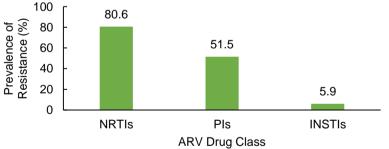


Figure 3 : Prevalence of resistance to NRTIs, PIs and INSTIs within MDR ART experienced individuals

Conclusion

We observed high proportion of resistance to second-generation NNRTIs among treatment-experienced individuals with MDR HIV variants who had no prior exposure to second-generation NNRTIs.

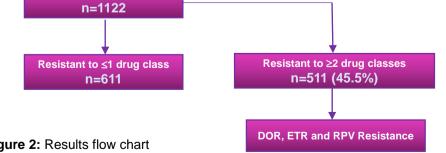


Figure 2: Results flow chart

DOR, ETR and RPV Resistance

NNRTI resistance

- Overall, 495/511 (96.9%; 95% CI: 95.1-98.2) had resistance to at least one second-generation NNRTI
- 99/511 (19.4%) had resistance to 1 second-generation NNRTI: either RPV (81.9%) or ETR (18.9%)
- 30/511 (5.9%) had resistance to 2 second-generation NNRTIs: either RPV and ETR (53.3%) or RPV and DOR (46.7%)
- 366/511 (71.6%) were resistant to all three ARVs DOR, ETR and RPV

- This limits their potential use as an alternative therapy for treatment experienced MDR individuals with MDR
- Our results strongly suggest genotypic resistance testing prior to ART use among treatment-experienced individuals.



Acknowledgments

References

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