



# Dried Blood Spots and Other Sample Types for HIVDR Testing

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# Focus

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## SESSION ORGANIZER

Practical

Operational

Policy

## PROGRAM ORGANIZERS

Lessons from pMTCT

Seeding of HIV reservoirs with resistant virus

Next generation sequencing methods

# Practical

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## TOPIC 1

# Sample Types: Practicality

Liquid

Dried



Plasma



Whole Blood

# Dried Blood Spots (Advantages)

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Easy to collect

Easy to store

No pre-processing

RNA and DNA preserved for years with proper storage

Affords analysis on small blood volumes (50-250 $\mu$ L)

Cold chain not necessary for short-term storage (<2 weeks)

Noninfectious after drying

Easily shipped-nonhazardous material by regular mail or courier services

# Dried Blood Spots (Disadvantages)



## Reduced Sensitivity (12x-lower)

Limited by blood volume (50-75  $\mu\text{L}$  per spot); generally no more than 2 spots to maximize efficiency and minimize interfering substances

Nucleic acid degradation under poor storage conditions

## Specificity

contribution of cell-associated nucleic acid  
DNA and RNA at lower viral loads

## Accuracy

Concordance with plasma results

# Operational

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## TOPIC 2

# WHO/HIVResNet Global HIVDR Prevention and Assessment Strategy

## **Dried blood spots for HIV-1 Drug Resistance and Viral Load Testing: A Review of Current Knowledge and WHO Efforts for Global HIV Drug Resistance Surveillance**

*Silvia Bertagnolio<sup>1</sup>, Neil T. Parkin<sup>2</sup>, Michael Jordan<sup>1,3</sup>, James Brooks<sup>4</sup> and J. Gerardo García-Lerma<sup>5</sup>*

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50 representatives from different countries with HIVDR, laboratory, clinical, epidemiologic expertise

Role: Advise WHO on development of standardized tools, methodologies and training to evaluate emergence and transmission of HIVDR worldwide

Assist with development of early warning indicators to alert public health action related to HIV DR and ART programs



# WHO!MANUAL!FOR!HIV!DRUG!RESISTANCE!TESTING!

## USING!DRIED!BLOOD!SPOT!SPECIMENS!!

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**Table 1.** Overview of published studies investigating optimal DBS storage conditions

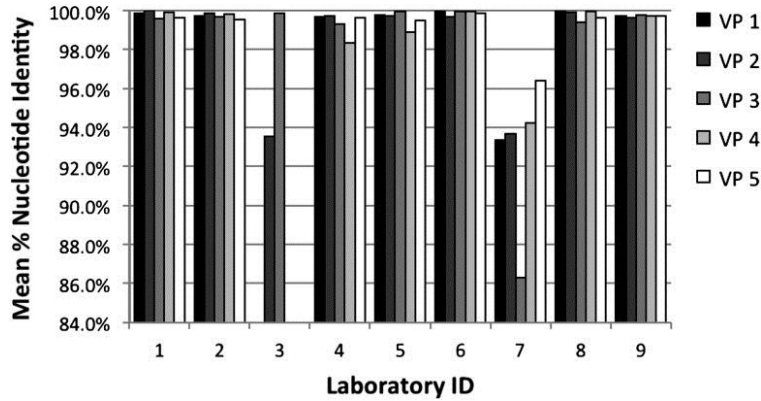
Storage conditions tested				
Study	Time	Temperature/Humidity	Desiccant	Outcomes
Garcia-Lerma <sup>15</sup>	1 to 16 weeks	37°C/high humidity, -20°C	Yes	DBS stable at 37°C only for 1-2 weeks. -20°C recommended for long-term storage. -20°C superior for short <u>and</u> long term.
Buckton <sup>4</sup>	3 months	-20°C, 4°C, 20°C		HIV DNA PCR only. No observed degradation in HIV DNA during 3 month study period.
Bertagnolio <sup>3</sup>	3 months	37°C/85% humidity	Yes	Good amplification rate (90%)
McNulty <sup>8</sup>	6 years 5 years 2-3 years	-30°C Ambient temperature and -70°C -20°C		Complete degradation at ambient temperature; stable at -30°C and -70°C; -20°C recommended for long-term storage
Nelson <sup>14</sup>	3 to 6 years	Ambient temperature	Yes	Moderately successful amplification rate (69%); 1 log drop in viral load.

**Table 3.** Overview of alternative published HIV DBS genotyping methods

Study	Genotyping method(s)	Amplicon size	Storage conditions	Sample characteristics	Number of samples tested	Viral load of tested samples (copies/mL)	Amplification success rate*	Sequence concordance vs. plasma†
Masciotra 2007 <sup>7</sup>	Viroseq	1.8 kb	-20°C, 18 to 26 weeks	Mostly treatment experienced, subtype B	60	78 to 676,694 (median: 9135)	Overall: 83% VL>2000: 100% VL <2000: 54%	98.8%
Youngpairoj 2008 <sup>11</sup>	Viroseq or in-house nested RT-PCR	1.8 kb or 1 kb	4°C, 1 year	Treatment experienced, subtype B	40	518 to 676,694 (median: 13,680)	Viroseq: 57.5% In-house: 95%	94.5% (drug resistance mutations, DBS/in house vs. plasma/ViroSeq)
McNulty 2007 <sup>8</sup>	In-house nested RT-PCR	1 kb	-20°C, 2-3 years	Untreated, subtypes from Cameroon, subtypes A, CRF02	40	665 to 645,256 (median: 23,715)	Overall: 92% VL>10,000: 100% VL <10,000: 73%	98.5%
Ziemniak 2006 <sup>12</sup>	In-house nested RT-PCR	RT: 663 bp	Ambient, 0-5 months	Treated and untreated patients from the US, subtype B	9	<50 to 94,600 (median: 17,792)	Overall: 94% VL≥193: 100%	Not assessed
Bertagnolio <sup>3</sup>	In house nested RT-PCR	RT: 700 bp	37°C, 85% humidity, 3 months	Untreated subjects from Mexico, subtype B	103	Not all tested	90.1% either PR or RT region; 78.2% for both regions	99.9% (in samples with resistance mutations)
Hallack <sup>6</sup>	Trugene	1.3 kb	-20°C	Treated and untreated patients from the US, subtype B	33	1178 to 414,212 (median: 11,666)	Overall: 78.8% VL >6000: 90.5% VL <6000: 58.3%	99.3%
Garrido <sup>5</sup>	In-house nested RT-PCR: RT and gp41 fragments	RT: 726 bp	4°C, <i>no desiccant</i>	Treated patients from Angola; many subtypes	77	1000 to 850,000	RT: 30% gp41: 43%	Not assessed
Steege <sup>10</sup>	In-house nested RT-PCR	PR: 458 bp RT: 646 bp	-20°C	Treated and untreated patients from Kenya; subtypes A, C, D, CRF16	29	55 to >100,000	96.6% either PR or RT region; 89.7% for both regions; VL > 100: 100%	Not assessed
Buckton <sup>4</sup>	In-house nested RT-PCR	PR: 758 bp RT: 805 bp	-20°C	Clinic patients from the UK; subtypes A, B, C, CRF02	12	80 to 115,300 (median 10,950)	PR: 83% RT: 100%	Not assessed

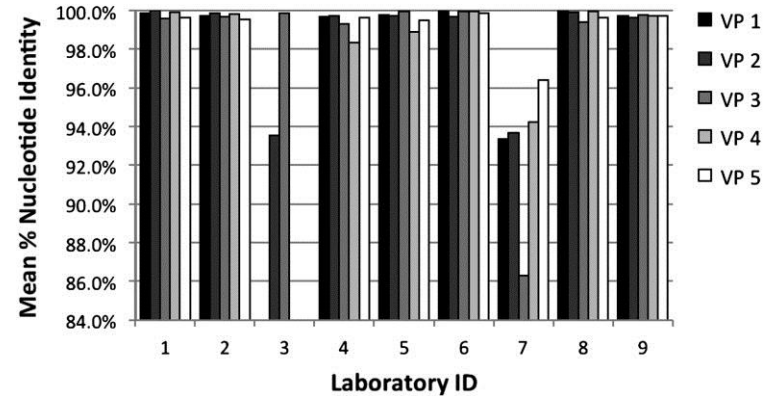
\*Note: it is likely that the quality of field-collected DBS is substantial inferior to that of lab-collected DBS (which are often used in comparison studies) and especially plasma, with respect to amplification success rates  
 † mean nucleotide sequence identity, unless otherwise noted

# In-House Genotyping Performance on DBS in the Global WHO Laboratory Network



Sequence Reproducibility

Mean sequence identity 96.7-100%



Sequence Accuracy

Mean percentage identity 98.4-100%



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Methods

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## A sensitive genotyping assay for detection of drug resistance mutations in reverse transcriptase of HIV-1 subtypes B and C in samples stored as dried blood spots or frozen RNA extracts

Carrie Ziemniak<sup>a</sup>, Allison George-Agwu<sup>a</sup>, William J. Moss<sup>b</sup>,  
Stuart C. Ray<sup>c</sup>, Deborah Persaud<sup>a,\*</sup>

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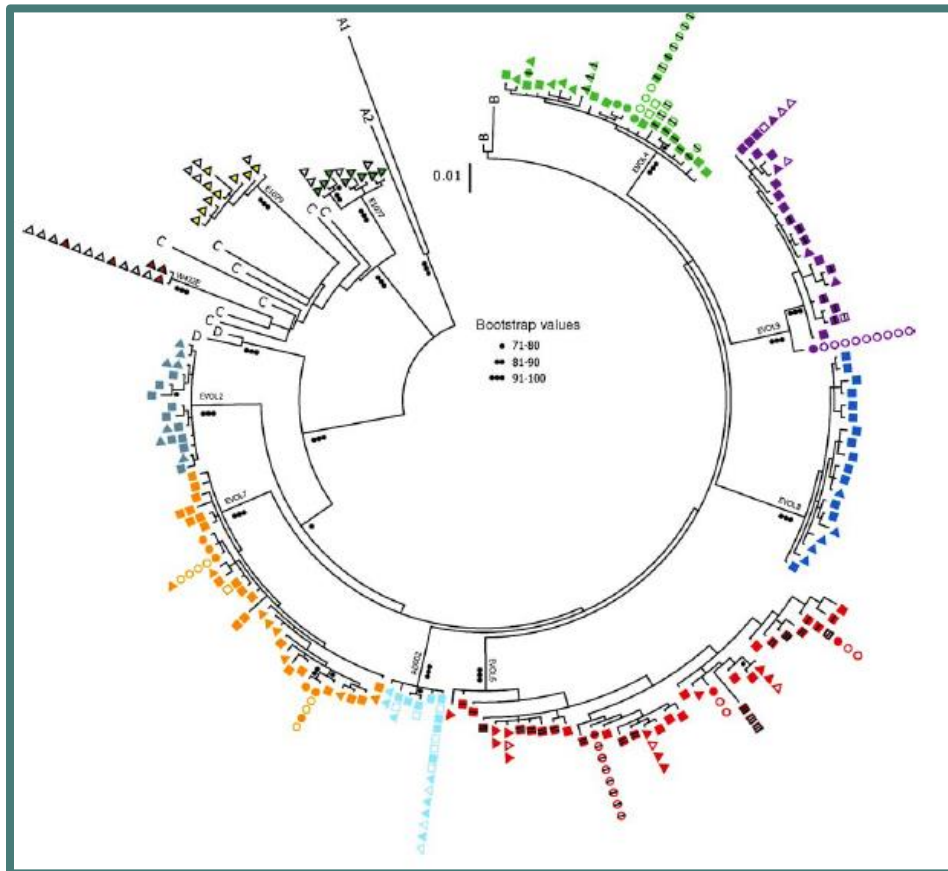
<sup>b</sup> Department of Epidemiology, Johns Hopkins University Bloomberg School of Public Health, Baltimore, MD, United States

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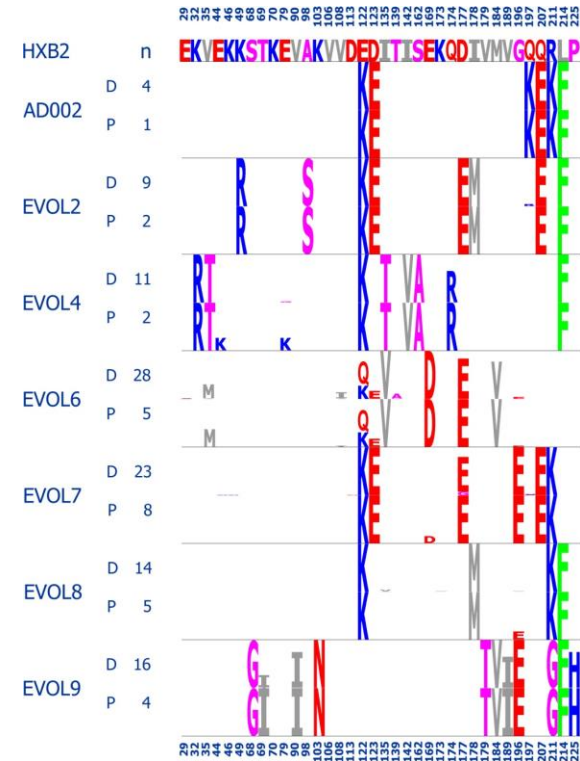
Received 3 March 2006; received in revised form 16 May 2006; accepted 25 May 2006

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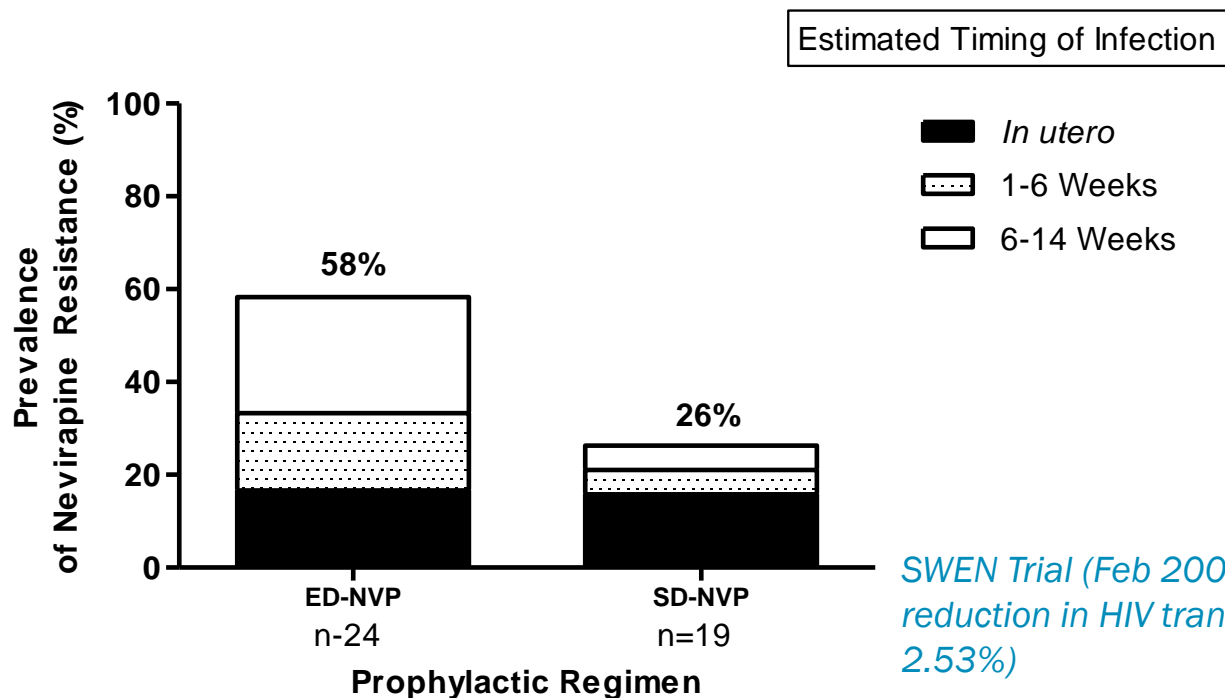
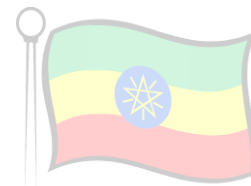
# Concordance between Plasma and DBS Genotypes



663 bp HIV RT

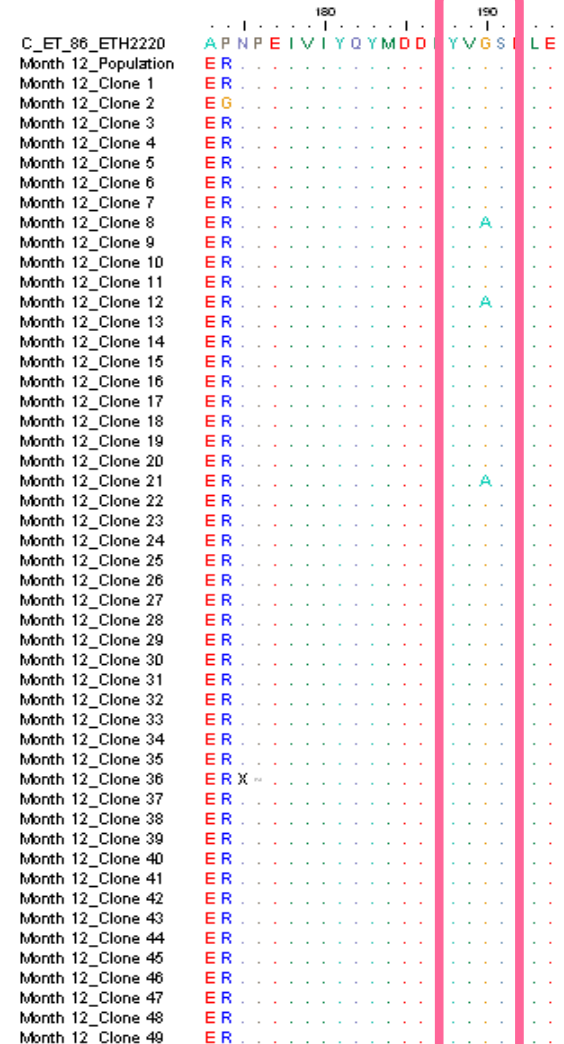
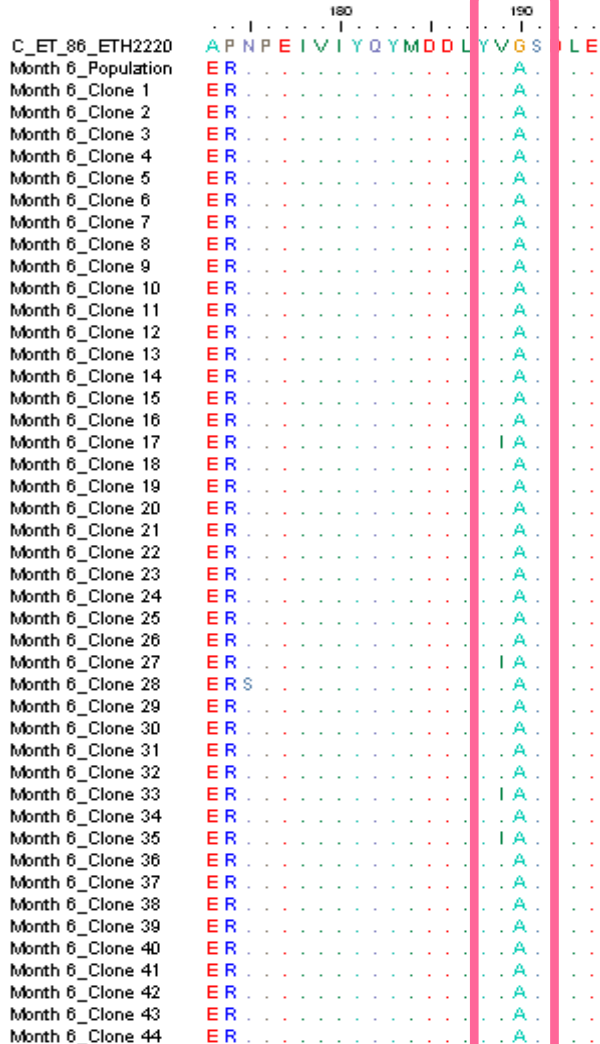


# Genotyping from DBS to Assess Clinical Trial Outcomes (Ethiopian Infants)



Genotyping successful from 93% of 46 infants with DBS collected at age 6 months  
 Stored for a median of 3.2 years (IQR 1.6-4.1 yrs)  
 Relevant clinical findings: Higher prevalence of nevirapine resistance at 6 months in ED-NVP compared with SD-NVP exposed infants  
 56% still with NVP resistance detectable at one year

# Preservation of Low-frequency Nevirapine Resistance Mutations in DBS



**Month 6**  
G190 A Clonal Frequency (n=44) = 100%

**Month 12**  
G190 A Clonal Frequency (n=49) = 6.1%

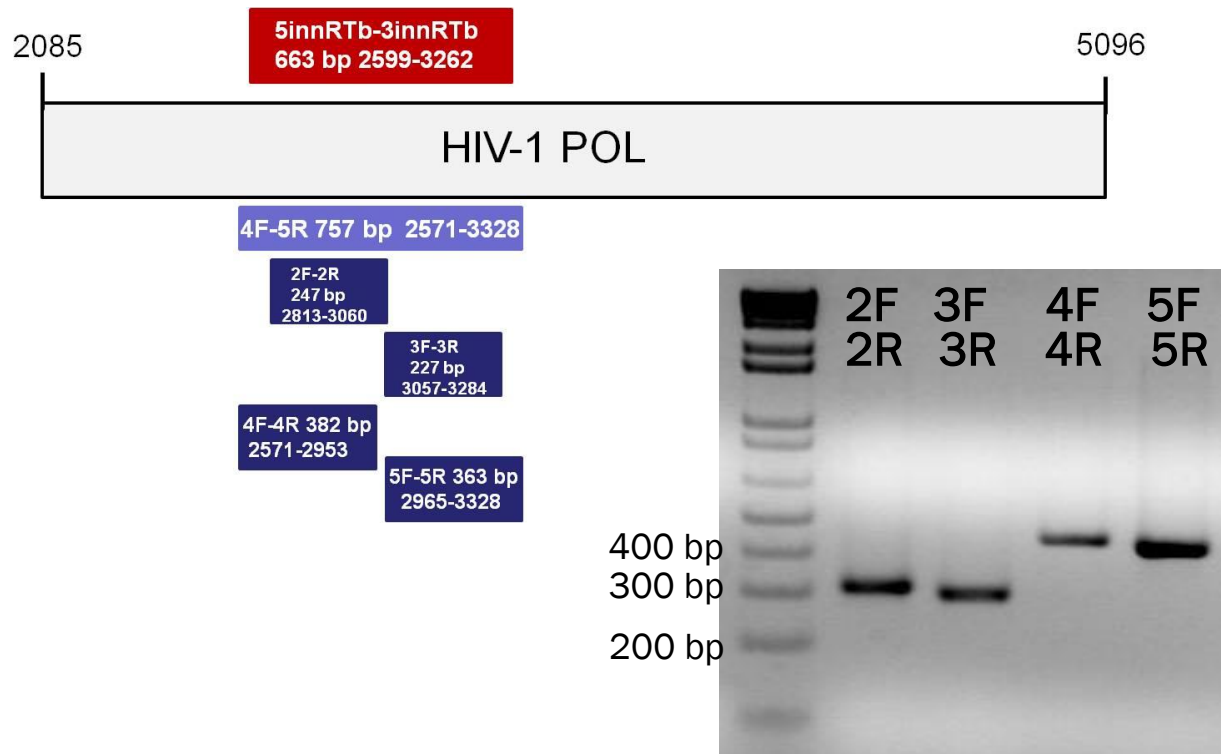
# Conclusion

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**FEASIBILITY OF GENOTYPING FROM DBS COLLECTED DURING A CLINICAL TRIAL IN A RESOURCE-CONSTRAINED SETTING AND DESPITE YEARS OF STORAGE**

# Use of Dried-Blood-Spot Samples and In-House Assays To Identify Antiretroviral Drug Resistance in HIV-Infected Children in Resource-Constrained Settings<sup>▽</sup>

Carrie Ziemniak,<sup>1</sup> Yohannes Mengistu,<sup>2</sup> Andrea Ruff,<sup>3</sup> Ya-Hui Chen,<sup>1</sup> Leila Khaki,<sup>4</sup> Abubaker Bedri,<sup>2</sup> Birgitte B. Simen,<sup>5</sup> Paul Palumbo,<sup>6</sup> Susan H. Eshleman,<sup>4</sup> and Deborah Persaud<sup>1\*</sup>





# Storage Conditions and Yield of Genotyping Clinical Trial #2 (IMPAACT P1060)

	<b>Initial Yield</b>  (No. Positive/ No. Tested) [%]	<b>Negative Samples Tested with Shorter Amplicons</b>  (No. Positive/ No. Tested) [%]	<b>Overall Yield with complete coverage of HIV- RT</b>  (No. Positive/ No. Tested) [%]
Overall	38/49 [78%]	3/11 [27%]	41/49 [84%]
Optimally Stored	29/33 [88%]	1/4 [25%]	30/33* [91%]
Sub-optimally Stored	9/16 [56%]	2/7 [43%]	11/16 [69%]

Stored for 0.3 to 1.8 years

Yield increased with optimal storage and with shorter amplicons



# Conclusion

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**EQUIVALENCY OF DBS GENOTYPING WITH  
PLASMA BY POPULATION SEQUENCING**

**FEASIBLE FOR MONITORING CLINICAL TRIALS  
AND ART OUTCOMES IN RESOURCE-  
CONSTRAINED SETTINGS**

# Next Generation Sequencing Methods

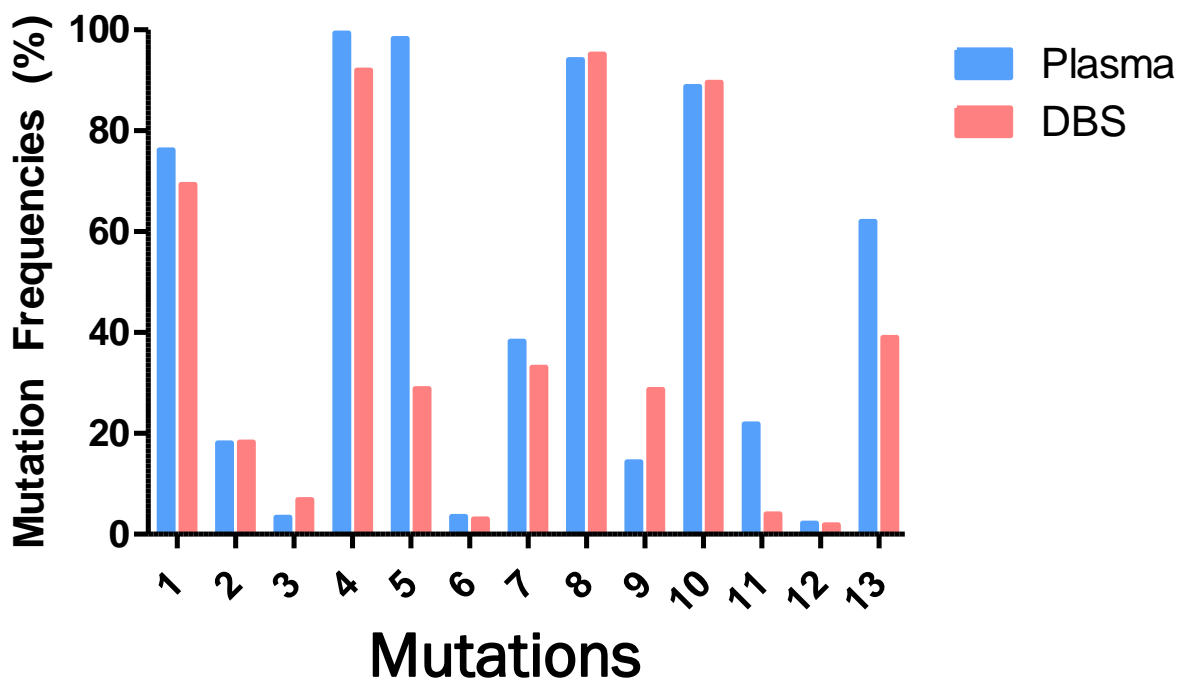
## Pyrosequencing Dried Blood Spots Reveals Differences in HIV Drug Resistance between Treatment Naïve and Experienced Patients

Hezhao Ji<sup>1</sup>, Yang Li<sup>1</sup>, Binhua Liang<sup>2,3</sup>, Richard Pilon<sup>1</sup>, Paul MacPherson<sup>4</sup>, Michèle Bergeron<sup>1</sup>, John Kim<sup>1</sup>, Morag Graham<sup>3,5</sup>, Gary Van Domselaar<sup>2</sup>, Paul Sandstrom<sup>1</sup>, James Brooks<sup>1\*</sup>

	Average Sequence Concordance Rates		
Plasma viral load (c/ml)	DBS vs. Plasma	DBS vs. PBMC	Plasma vs. PBMC
504-50,192	82.9 ± 11.9%	78.9 ± 10.9%	75.3 ± 14.7%
<5000	72%	75.3%	65.7%
≥5000	88.8%	80.9%	80.6%

Plasma/DBS concordance highest at VL≥5000 copies/ml and with no ART exposure

# Next Generation Sequencing from DBS Clinical Trial #2 (IMPAACT P1060)

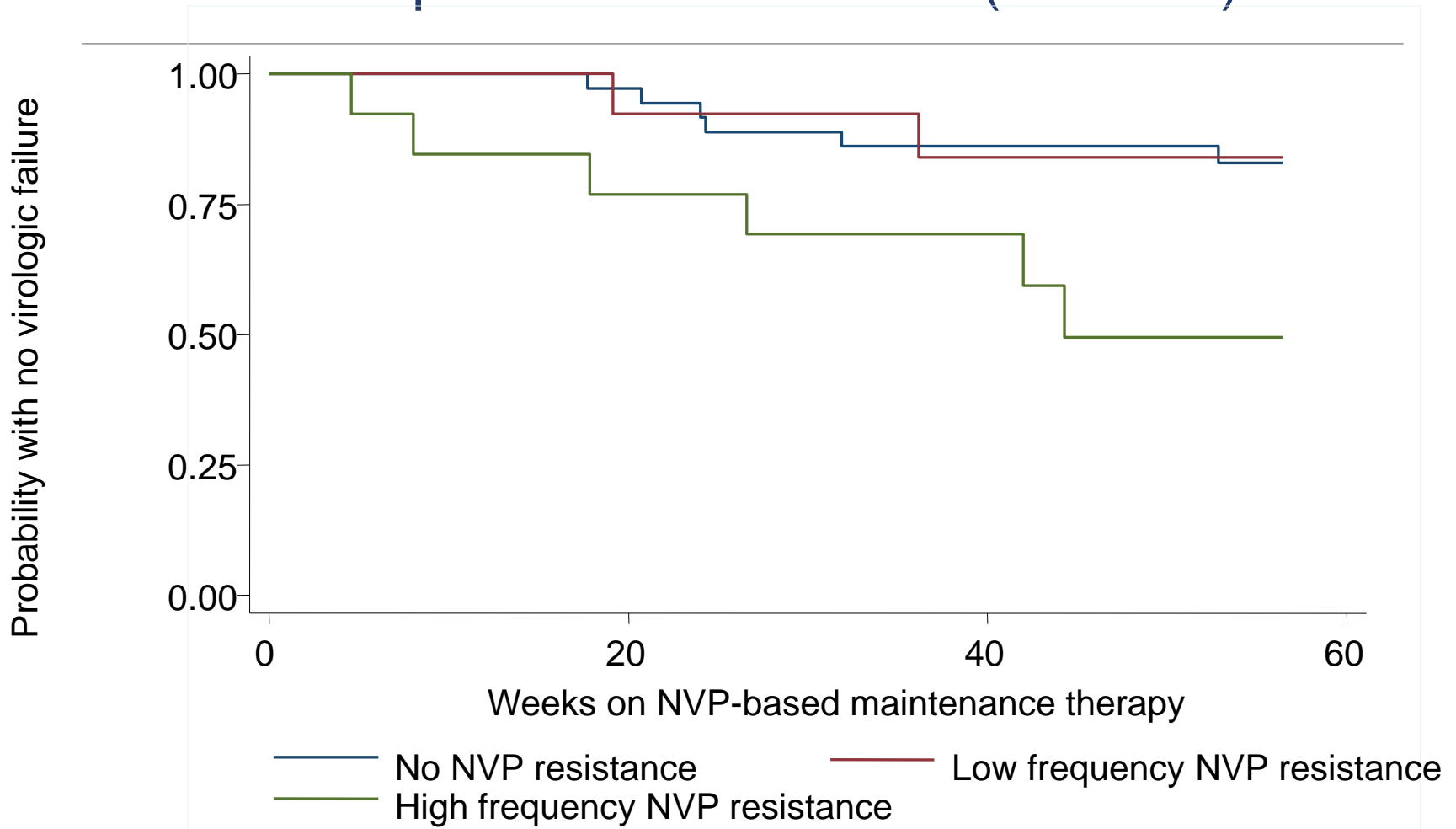


97.1% concordance between DRMs in plasma and DBS

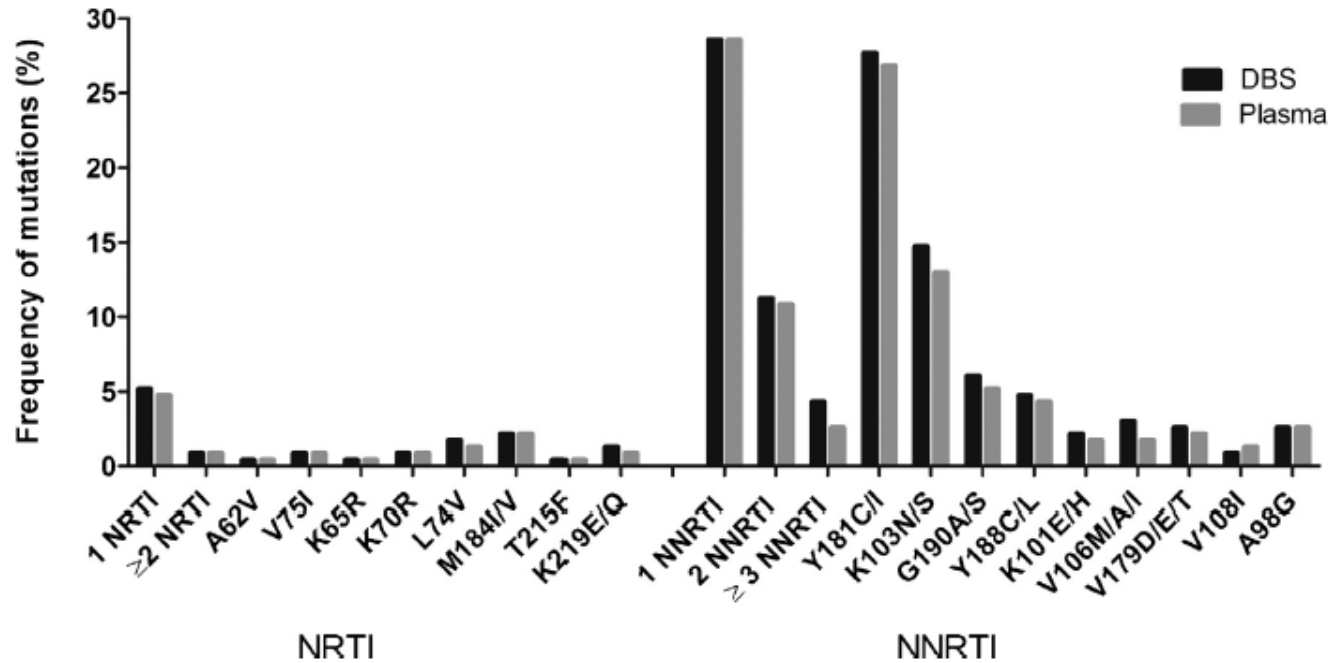
Median mutant frequencies DBS 3.4% (IQR 1.6-30.0%) vs. 3.5% (IQR 1.4-38.3%) in plasma

Discordance more likely when present at low frequencies (median 1.5%; IQR 1.2-3.2)

# Associations between Nevirapine Resistance Frequencies and Virologic Failure with Nevirapine-based HAART ( P1060)

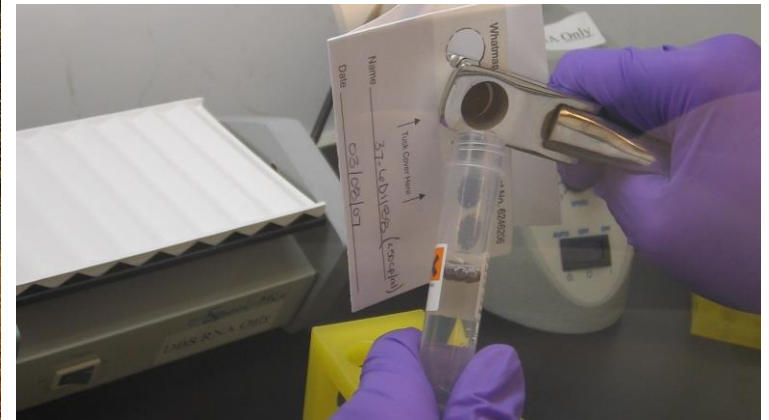


# High Sensitivity and Concordance of DBS and Plasma Genotypes



Location	Population (N=238)	Approach	Findings
South Africa (5 sites)	Median age 27 wks [IQR 13-51 wks]	Paired plasma and DBS immediately stored at -80	Yield: 97.9% plasma 98.7% DBS  92% concordance 99.5% mean nucleotide identity

# DBS facilitates Drug Resistance Monitoring in Resource-Constrained Settings





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IMPAACT Network (P1060 Team)

(Paul Palumbo, M.D. and Sue Eshleman, M.D.)

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