BREACH

BELGIAN RESEARCH AIDS&HIV CONSORTIUM

Best Poster Contest

15 Posters

- 2 Basic Science
- 4 Clinical Science
- 9 Public Health

BREACH

BELGIAN RESEARCH AIDS&HIV CONSORTIUM

Long-read sequencing assay allows accurate characterization of the HIV-1 reservoir

Laurens Lambrechts[1,2], Rita Verstraeten[1,2], Noah Bonine[1,2], Ytse Noppe[1], Marion Pardons[1], Basiel Cole[1,*], Linos Vandekerckhove[1,*]

[1]HIV Cure Research Center, Ghent University, 9000 Ghent, Belgium

[2]These authors contributed equally.

BEST POSTER

Basic Science

"LONG-READ SEQUENCING ASSAY ALLOWS ACCURATE CHARACTERIZATION OF THE HIV-1 RESERVOIR"

Laurens Lambrechts, Rita Verstraeten, Noah Bonine, Ytse Noppe, Marion Pardons, Basiel Cole, Linos Vandekerckhove

Introduction

The advent of near full-length (NFL) [illegible] sequencing greatly expanded our understanding of the qualitative [illegible] revealing that 2-5% of the [illegible] can be considered genome-intact in ART-treated [illegible]. However, these assays are labor-intensive and based on [illegible] principles of [illegible] PCRs at limiting dilution, limiting their scalability. We developed a [illegible] sequencing assay to characterize many [illegible] from bulk DNA.

Methods

The long-read sequencing assay was performed on 15 chronic ART-suppressed individuals using a fixed input of 500 ng DNA extracted from peripheral blood CD4 T cells (reservoir sizes ranging from 321 to 6581 total HIV-1 DNA cp/Mio CD4 T cells). Individual proviruses were tagged with a different unique molecular identifier (UMI) at each end during a single reaction, followed by NFL PCR amplification and long-read sequencing on an Oxford Nanopore MinION (Figure 1B). UMI-based [illegible] allowed for the construction of highly accurate consensus [illegible] excluding aberrant chimeric PCR artefacts. In addition, [illegible] Individual Provirus Sequencing (FLIPS) was performed on 2 individuals (Figure 1A). Data from both assays were compared through phylogenetic analyses.

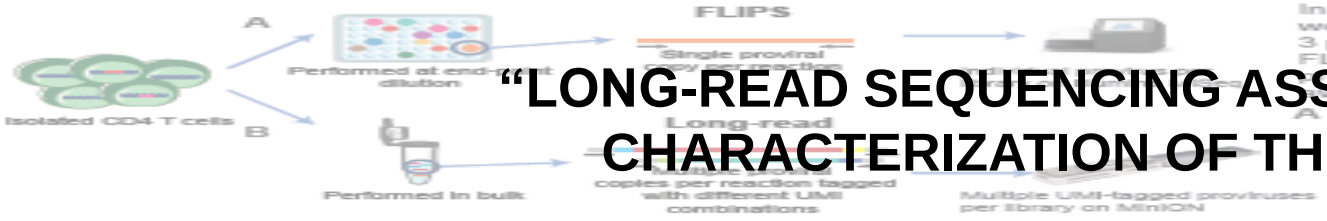


Figure 1: Schematic overview of the used assays. In A) the workflow of the gold standard full-length individual proviral sequencing (FLIPS) assay relying on limiting dilution is depicted while B) shows the long-read assay relying on unique molecular identifiers (UMI).

Results

Assay can be used on diverse reservoir sizes

The long-read assay could successfully be applied on our cohort and yielded an average of 14 distinct HIV-1 proviruses per participant (range: 3-42). Note that some participants (eg. 1 and 11), despite having a large reservoir, yielded only 3 different proviruses which could be due to the presence of large infected cell clones sharing the same provirus.

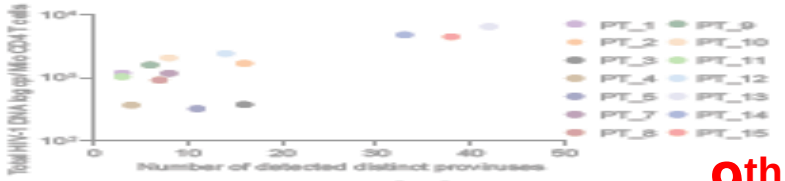


Figure 2: Reservoir size and number of distinct proviruses recovered [illegible] long-read assay for each participant.

Allows for HIV-1 genome classification

Across all participants, 213 distinct proviruses were retrieved of which 8% [illegible] considered as putatively intact.

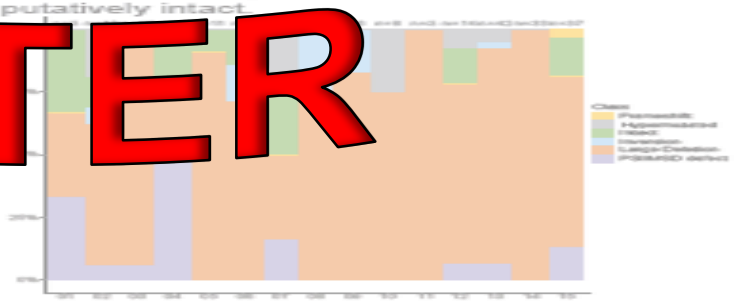


Figure 3: Classification of the HIV-1 genomes acquired with the long-read assay.

Overall agreement on observed proviral reservoir

In Participant 14, who displayed limited clonality (2/35 FLIPS genomes were clonal), only 1 overlapping provirus was found. While an overlap of 3 proviruses was observed in Participant 15 with higher clonality (33 of 36 FLIPS genomes were clonal). Comparing the 4 overlapping consensus [illegible] FLIPS counterparts showed an

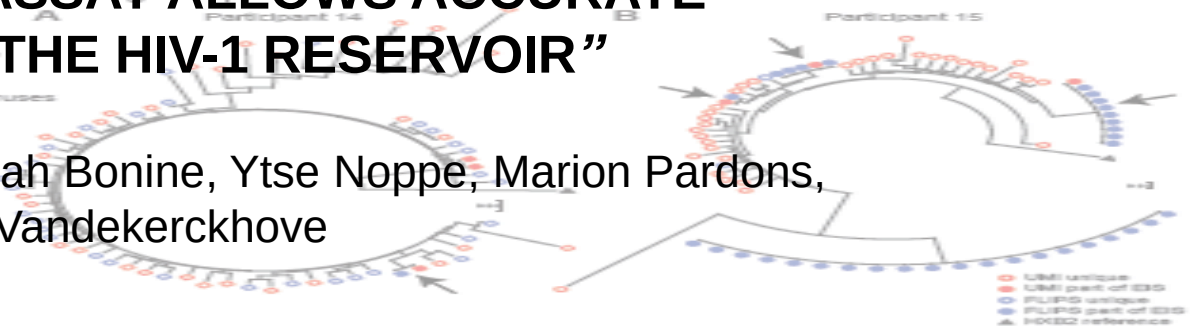


Figure 4: Phylogenetic analysis by Maximum Likelihood Trees. Trees included for Participant 14 and Participant 15. Genomes part of an expansion of identical sequences (EIS) are represented by filled circles. Arrows indicate matches of identical proviruses between the FLIPS and long-read assays.

Conclusions

The long-read assay offers a new NFL sequencing method which enables an accurate characterization of the proviral landscape in a more efficient way than current widely used NFL techniques.

9th BREACH SYMPOSIUM

November 30th, 2021, Dolce

HIV Cure Research Center
laurens.lambrechts@ugent.be

CHU Saint-Pierre

BREACH

BELGIAN RESEARCH AIDS&HIV CONSORTIUM

INFECTIOUS DISEASES DEPARTMENT
HIV REFERENCE CENTRE

UNIVERSITÉ LIBRE DE BRUXELLES

AS-EACS-20221-00346

Evolution of severe obesity and associated-comorbidities in HIV-positive patients with and without bariatric surgery: a case-control study

Victoria De Wit, Marc Delforge, Guy-Bernard Cadière, Stephane De Wit and Deborah Konopnicki

BEST POSTER

Clinical Science

- **Purpose**: Obesity and related-comorbidities are increasing in patients living with HIV (PLWH). Bariatric surgery (BS) is a safe and effective procedure in general population but small case series are available in PLWH. This study compares the evolution of severe obesity and associated comorbidities in PLWH with or without BS.
- **Methods** : Retrospective case-control study in PLWH and followed at Saint-Pierre University Hospital, with body mass index (BMI) ≥ 40 or ≥35 kg/m² with at least one comorbidity (diabetes, hypertension, sleep apnea syndrome, dyslipidemia); cases (n=27) underwent BS between 2006-2019; Controls (n=73) were PLWH matched (1 case/3 controls) on age, gender, ethnicity and BMI. Clinical and biological parameters were collected at 1, 2, 5 and 10 years follow up (FU) after BS.
- **Results** :

♀ ♂ HIV+ → BMI ≥ 40 or BMI ≥ 35 + comorbidity(ies)

- Surgery: 27 cases
  - 13 gastric bypass (GB)
  - 13 sleeve gastrectomy (SG)
  - 1 gastric banding
- Non-surgery: 73 controls

Evolution of BMI at 1, 2, 5, 10 years (cases) and 4,1 years (controls)

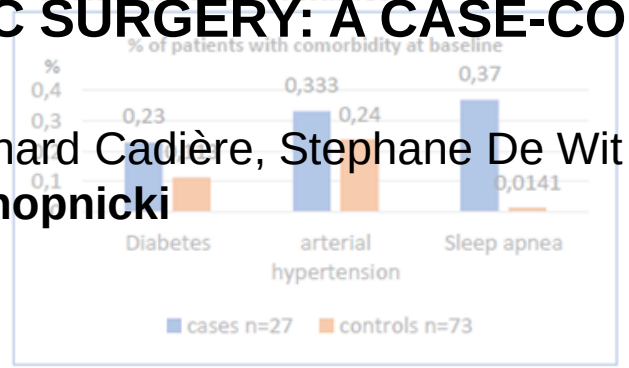
Although controls had lower baseline BMI and both cases and controls received the same dietary advices, weight loss was statistically significantly greater in cases. All cases reached BMI ≤30 at all FU times while controls remained >35 kg/m².

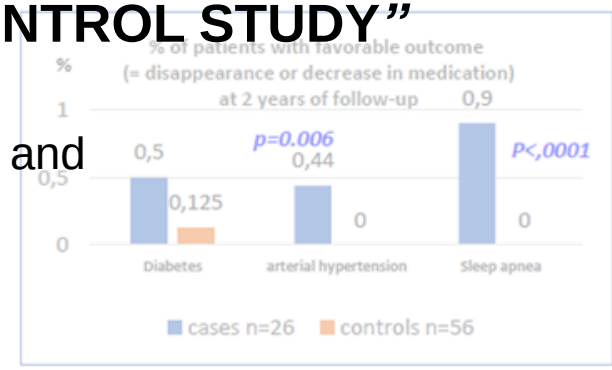
"EVOLUTION OF SEVERE OBESITY AND ASSOCIATED-COMORBIDITIES IN HIV-POSITIVE PATIENTS WITH AND WITHOUT BARIATRIC SURGERY: A CASE-CONTROL STUDY"

Victoria De Wit, Marc Delforge, Guy-Bernard Cadière, Stephane De Wit and **Deborah Konopnicki**

Baseline characteristics	Controls (n=73)	Bariatric surgery (n=73)	p
Median age (years)	42.2	44.4	NA (not applicable)
Female sex	85.2%	83.6%	NA
Sub Saharan African origine	77.8%	75%	NA
HIV heterosexually acquired	77.8%	85%	NA
HIV median CD4 count (IQR) (cells/µL)	646 (455-862)	704 (460.5-900.5)	ns
Under cART (%)	92.6%	91%	ns
Cumulative time with HIVRNA<50 cp/ml (IQR) (years)	6.7 (3.8-11.1)	5.7 (2.7-10.3)	ns
Weight (IQR) (kg)	112 (100-135)	100 (96-114)	0.0042
BMI (IQR) kg/m²	41.1 (37.8-45.4)	37.3 (36.4-39)	0.0017
BMI ≥40 kg/m² (%)	63%	19.2%	0.0004

Evolution of comorbidities:





- Major Surgery complications rate was 11% and 2 cases needed a second BS because of weight regain, similarly to what is described in the literature in the general population.
- GB led to greater loss of excess weight than SG at 2 years (respectively 89.3% vs 60.8%, p=0.0

- HIVRNA suppression was maintained in all but 1 patient with transient dysphagia after SG; after switching cART for a smaller pill, HIVRNA became undetectable again
- Exposure to different cART that could have impact on weight (Tenofovir disoproxil or alafenamide/Integrase Inhibitors/Rilpivirine) was similar in cases and controls both at baseline and during follow up .

Conclusion: Bariatric surgery among PLWH is safe and effective both on severe obesity and related comorbidities with no impact on viral suppression.

9th BREACH SYMPOSIUM

November 30th, 2021, Dolce

EACS European AIDS Clinical Society

18th [illegible] Kingdom

BEST POSTER

Public Health

"ROLES AND OPPORTUNITIES FOR THE FAMILY PHYSICIAN IN PROVIDING PREP – AN ONLINE QUALITATIVE STUDY IN FLANDERS, BELGIUM"

Jef Vanhamel, Thijs Reyniers, Edwin Wouters, Christiana Nöstlinger, Josefien van Olmen, Thibaut Vanbaelen, Heleen Van Mieghem, Ella Van Landeghem, Anke Rotsaert, Marie Laga and Bea Vuylsteke

9th BREACH SYMPOSIUM
November 30th, 2021, Dolce

Contact and information: Jef Vanhamel (jvanhamel@itg.be)