High-Accuracy, Single-Base Resolution of Near-Full-Length HIV Genomes

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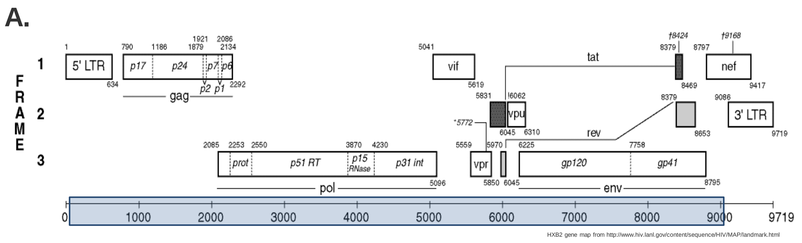
Introduction

The HIV-1 proviral reservoir is incredibly stable, even while undergoing anti-retroviral therapy, and is seen as the major barrier to HIV-1 eradication. Identifying and comprehensively characterizing this reservoir will be critical to achieving an HIV cure. Historically, this has been a tedious and labor intensive process, requiring high-replicate single-genome amplification reactions and reconstruction into full-length genomes by algorithmic imputation. Novel deep methods allow, for the first time, near-full-length HIV genomes.

Objectives

To develop single-molecule sequencing and analysis methods to determine the exact identity and relative abundances of near-full-length HIV genomes from samples containing mixtures of genomes without shearing or complex bioinformatic reconstruction.

Measuring the Diversity of Viral Infection



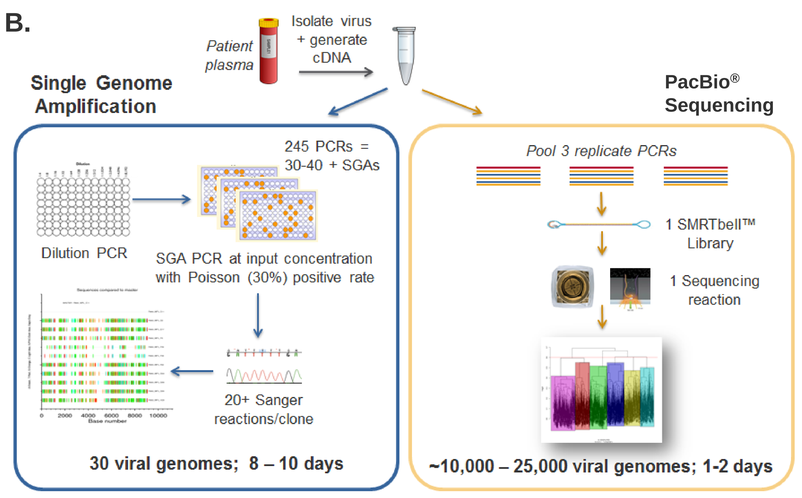


Figure 1. A) Clonal near-full-length amplicons were derived from single genome amplification (SGA) of primary proviral isolates or well-documented control strains. **B)** Viral genome SGAs have been analyzed via limiting dilution and overlapping Sanger sequencing, which then required complex bioinformatic reconstruction; PacBio® sequencing allows for pooling and sequencing of thousands of near-full-length HIV SGA genomes in one reaction.

PacBio® Sequencing of Intact HIV Genomes

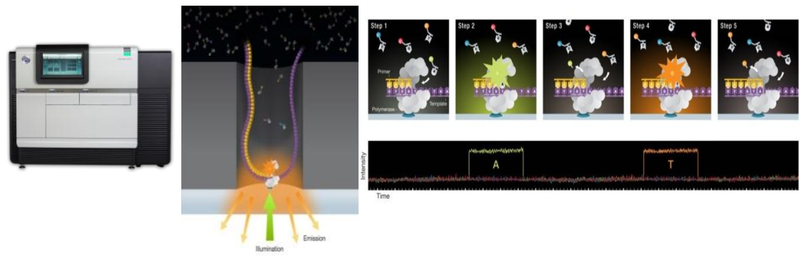
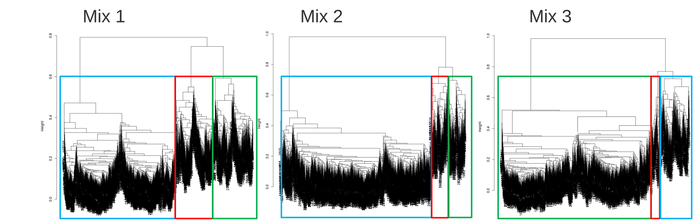


Figure 2. Clonal SMRTbell™ libraries were mixed at various abundances and sequenced as near-full-length (~9 kb) amplicons without shearing on the PacBio® RS II using P4-C2 chemistry and standard protocols.

De-convolute Mixture of HIV-1 Genomes

- Sequenced three samples containing synthetic mixtures of HIV-1 clones at different abundances



EXP (%):	60	20	20	80	10	10	80	5 15
OBS (%):	59	21	20	81	10	9	80	5 15

RESULT: Three genomes estimated in each sample with 100% consensus accuracies across the entire ~9 kb genomes and within 1% of expected abundances.

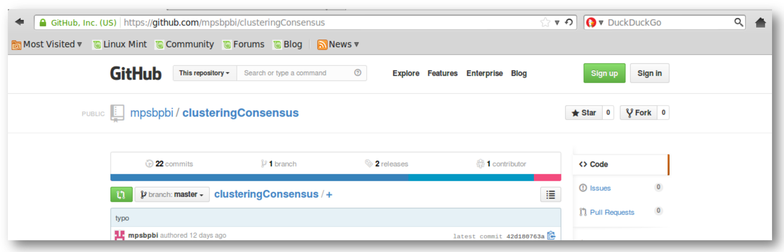
CluCon Strong Clustering Technique

- Consensus Sequence Clustering Under Binomial Bounds:
  - Generate alignment to run-specific consensus
  - Identify minor variant column regions
  - If no minor variants, return consensus
  - If divergence between read pairs is larger than expected by noise, then separate out as sub-cluster.
  - Recursively work on sub-clusters
- Clones in mixtures at ~5% divergence (or 500 positions)
- High statistical confidence in cluster consensus calls at this degree of genetic divergence.

CluCon Software

- CluCon software and data available:

  https://gibhub.com/mpsbpbi/clusteringConsensus



Single Base Resolution of Mixed Genomes

- Performed SMRT Sequencing on a synthetic mixture of 5 HIV clones that differed by only one or two nucleotides.
- Analyzed using CluCon software
- 5 strains differed by 1-2 bases (highlighted by color below)
  - Two genomes differ by one base (1, 3)
  - Two genomes differ by two bases (0, 4)
  - Single genome had no differences (2)

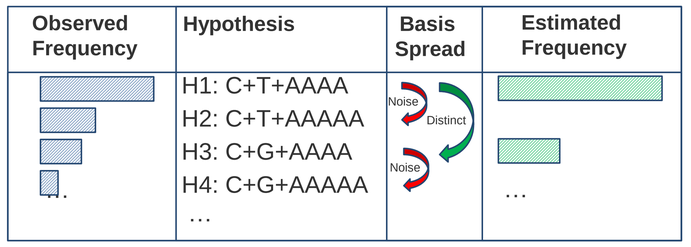
Estimated Genome Haplotypes and Relative Abundances:

```
0 'AAAT+AAAAAAG+GT+GCA+ATTTACC+ACCC+' 25.2%
1 'AATT+AAAAAAG+AT+GGA+ATTTACC+ACCC+' 21.6%
2 'AAAT+AAAAAAG+AT+GGA+ATTTACC+ACCC+' 21.0%
3 'AAAT+AGAAAAG+AT+GGA+ATTTACC+ACCC+' 19.6%
4 'AAAT+AAAAAAG+AT+GGA+ATTTTACC+ACCC+' 12.6%
```

RESULT: 100% accurate near-full-length HIV-1 genomes.

CluCon Fine Clustering Technique

- Consensus Linear System Basis Function De-convolution
- Modified CluCon Strong: call when the number of minor variant column regions is too small for binomial bounds to have power
- Tally read identities at the variant sites; putative haplotypes count
- Estimate true haplotypes from observed reads by discounting noisy haplotypes using basis functions representing sequencing noise



Conclusions

Complete characterization of near-full-length HIV-1 genomes with Single Molecule, Real-Time Sequencing

- Sanger-quality, fully phased across entire genome
- *De novo* clustering technique is reference agnostic
- Single run yields 1,000s of distinct HIV genomes
- Deconvolute samples containing complex mixtures of genomes with single base resolution
- Provides unique capacity to identify and characterize integrated, intact proviral HIV genomes

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