# ENTRY KINETICS OF GLOBALLY REPRESENTATIVE AND VERTICALLY TRANSMITTED HIV Nicholas E. Webb, Nicole Tobin, Grace M. Aldrovandi 1131Department of Pediatrics, David Geffen School of Medicine, University of California, Los Angeles.

INTRODUCTION

- HIV entry is an organized process that depends on transient states
- Transiently exposed regions in the fusion protein gp41 are highly conserved, attractive vaccine targets
- ▶ MPER is targeted by bnAbs with wide breadth (e.g. 2F5, 4E10, 10E8)
- ► HR1 is targeted by T20 (Fuzeon)

Understanding the kinetics of transient states may shed light on new transmission associated phenotypes and lead to new avenues of vaccine development

### BACKGROUND

- ► A variety of techniques are available for measuring kinetics<sup>[1-6]</sup>
- Time of addition allows multiple stages to be measured with a single, standardized protocol
- Previous kinetic studies are limited to only a few isolates
- Breadth of kinetics among circulating isolates is not well characterized

### GOAL

Our goal is to characterize the breadth of HIV-1 entry kinetics among circulating HIV Envelope (Env) isolates and isolates associated with transmission

### APPROACH

- Time of addition kinetics assay, optimized for reproducibility
- Measure kinetics of six helix bundle formation using T20
- Measure kinetics of co-receptor (CoR) engagement using CCR5 inhibitor maraviroc (MVC)
- Structurally diverse and transmission-associated isolates (255 HIV Env isolates characterized)
  - Standard R5-using M and T-tropic isolates (JR-CSF, BaL)
  - 10 isolates from globally representative neutralization panel<sup>[7]</sup>
  - 14 acute T/F Envs (clade B)<sup>[8]</sup>
  - 107 early/longitudinal isolates from 5 adult transmission pairs (clade C) • 14 mother-to-child (MTCT) transmitted Envs (Clade C, D, A, with BG505)<sup>[10</sup>
  - 108 Zambian Maternal and Infant MTCT isolates associated with breast milk (BMT) and in utero (IUT) transmission (ZEBS, clade C)<sup>[11]</sup>

## **RESULTS & SIGNIFICANCE**

- Very well confined window of average T20 delay (4-16 min). This is only a small part of natural range (<1 min, >40 min).
- Extreme kinetics are rare members of quasispecies.
- Infant BMT isolates had some of the slowest extremes
- Prehairpin is exposed during co-receptor engagement. Kinetic component of T20 sensitivy linked to co-receptor kinetics.
- Only a few amino acids lie between average and extreme kinetics. Kinetic extremes might be part of a normal phenotypic landscape

**HIV-1** exhibits a broad and dynamic landscape of kinetic phenotypes that link co-receptor binding to gp41 exposure and sensitivity to gp41targeting inhibitors.

### references

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Delay is how long it takes to go from CD4-bound to either the co-receptor bound maraviroc (MVC) resistant state or the T20-resistant six helix bundle.

PRIMARY HIV-1 ISOLATES EXHIBIT BROADLY DIVERSE KINETICS T20 delay classes: 255 primary HIV Env isolates extremely early ≤2 min Well-formed distribution of T20 delays centered about 2-4 min early 4-16 minutes with broad range of extremes 4-16 min average from as early as <30 seconds to as late as >32 minutes. late 16-32 min extremly late ≥32 min 1 2 3 4 5 6 Breadkdown of T20 kinetics by panel and patient



![](_page_0_Figure_42.jpeg)

Rare frequency of early extremes when we have only one isolate from each patient.

Early and late extremes are most commonly obseved as rare members of a patient's quasispecies.

![](_page_0_Figure_45.jpeg)

**DIVERSE KINETICS LINKED TO BREAST MILK TRANSMISSION** Stacked histogram, ZEBS isolates in-utero (IUT) breast milk (BMT) Maternal Infant Kinetic diversity primarily linked to Infant Envs associated with breast milk transmission Both maternal and infant BMT Envs can have extremely late T20 delay. 1 Maternal Maternal Infant BMT Envs have the latest extremes. -2 -1 0 1 2 3 4 5 6 7 4 5 6 7 -2 -1 0 1 2 3 4 5 6 log<sub>2</sub>(T20 delay (min)) -log<sub>2</sub>(T20 delay (min)) -Similar, diverse range of T20 Envs associated with transmission kinetics for maternal and in utero have very narrow range of kinetics. infant ZEBS isolates.

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(n=255 Envs)

-2 -1 0

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Lognormal distribution provides a highly accurate description of infection over time

![](_page_0_Figure_57.jpeg)

![](_page_0_Figure_59.jpeg)

![](_page_0_Figure_65.jpeg)

Genotypic features associated with extreme slow kinetics primarily map to gp120 and not gp41. Supports the role of co-receptor binding in prehairpin exposure kinetics.

⊢**−**+ -2 -1 0 1 2 3 4 5 6 log<sub>2</sub> (T20 delay (min))

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![](_page_0_Picture_72.jpeg)