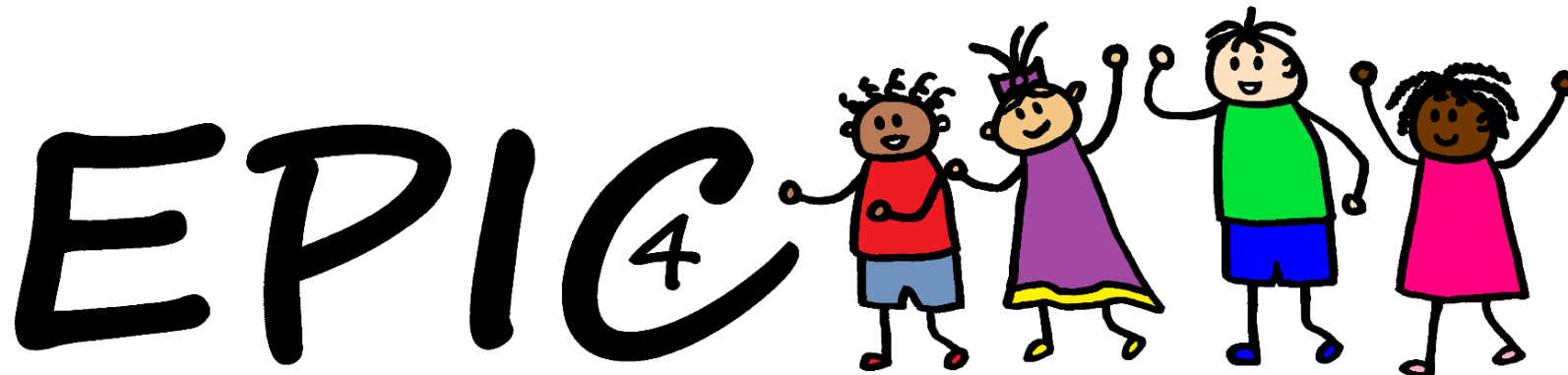


Genotyping of HIV-1 isolates infecting children and adolescents with undetectable viral load under antiretroviral therapy

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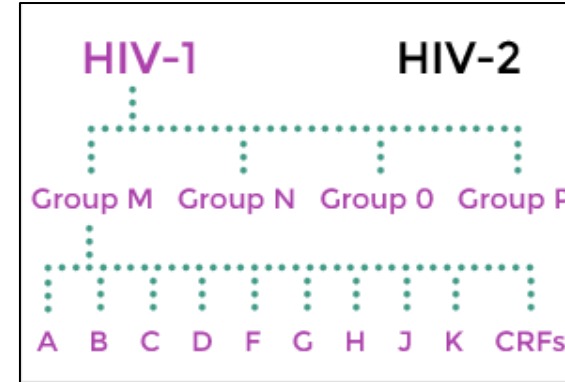
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I have no conflict of interest to disclose



INTRODUCTION

- ❖ The **genetic diversity** of HIV-1 is a **major obstacle** to prevention and cure.
- ❖ **Group M**, which is responsible for the **AIDS pandemic**, is subdivided into 9 subtypes and many more recombinant forms (CRF).



- ❖ The **Early Pediatric Initiation: Canada Child Cure Cohort (EPIC⁴)** regroups 228 children vertically infected by HIV-1 and under antiretroviral therapy (~70% of all vertically infected children in Canada).
- ❖ We studied (1) the size of the **viral reservoir** at different time points and in different cell subsets and (2) the presence and level of markers of immune activation, tissue inflammation, microbial translocation and endothelial dysfunction.



Knowledge of HIV clade is important as it may influence HIV outcomes such as levels of viremia, disease progression and antiretroviral drug resistance.

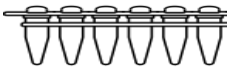
OBJECTIVE: Genotyping of HIV-1 isolates infecting 15 of the 73 participants of the EPIC⁴ study whose subtype remained unknown.

EXPERIMENTAL APPROACH

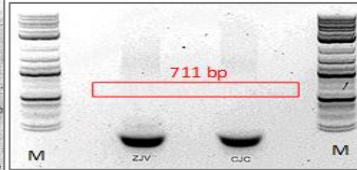
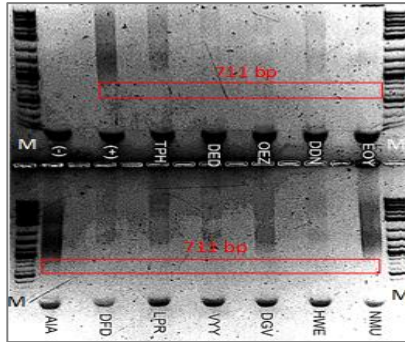
Gag gene amplification (nested PCR)

PBMCs of 15 participants

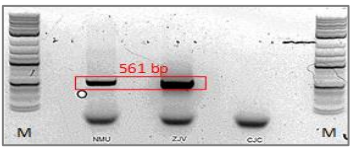
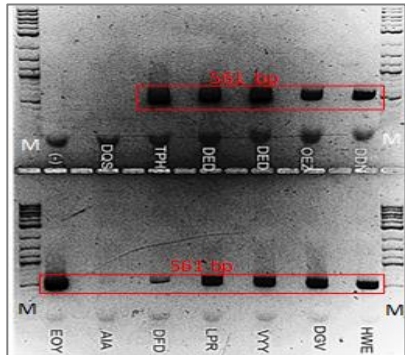
PK cell lysis



1st primers:
P17OUT1 and
P17OUT2



2nd primers:
P17IN1 and
P17IN2



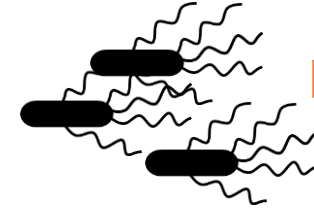
Cloning

Insert
amplicon



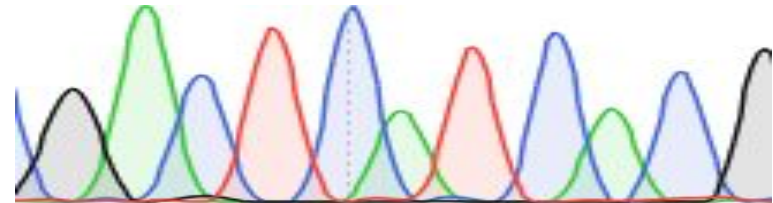
Transformation

Competent *E. Coli*

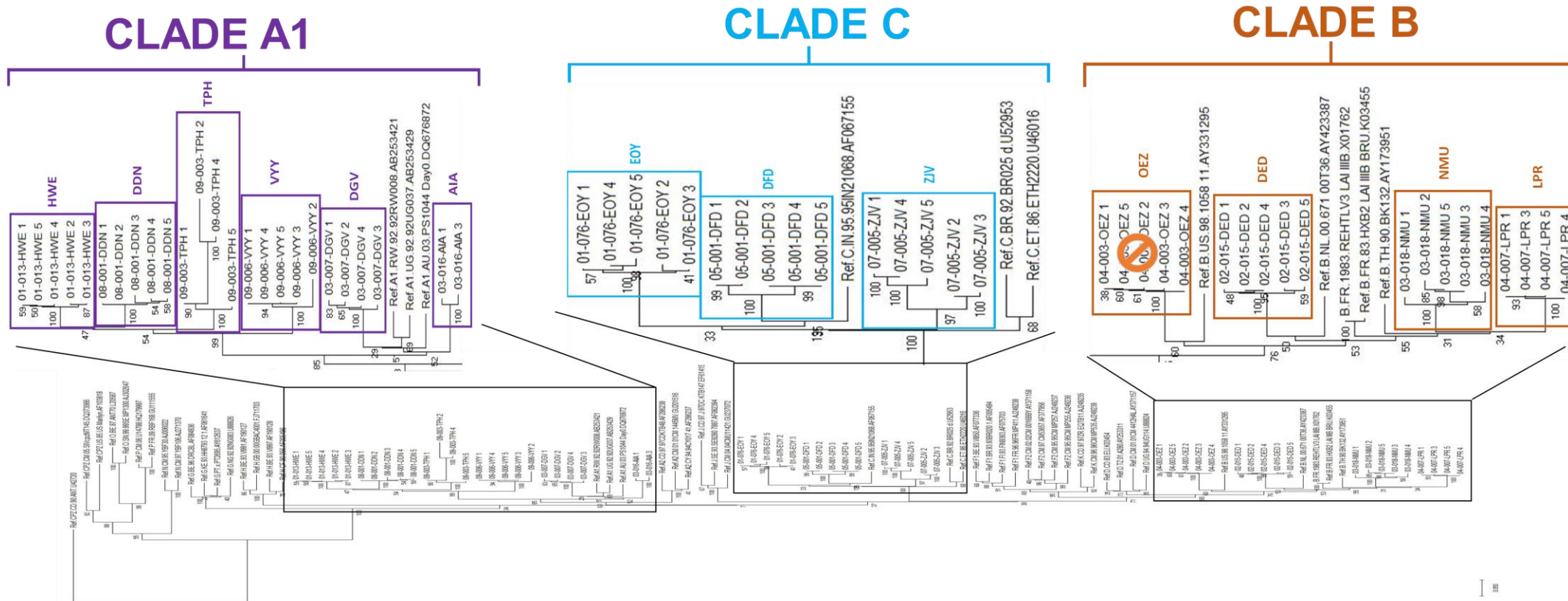


Vector
Extraction

SANGER SEQUENCING



PHYLOGENETIC ANALYSIS



Neighbor-joining method
Bootstrap = 1000

⊘ = Recombinant?

CONCLUSIONS

Genotyping was successful in 12 of 15 participants.

OEZ, who could be infected by a recombinant virus, presented the lowest proportion of CD4+ T cells (19%; Avg:36%), compatible with the fact that this was the only participant whose viremia remained detectable under cART.

The high prevalence of non-B subtypes our study group (75%) is consistent with the ethnic origin of study participants.

The increase of non-B infections in previously subtype B dominant regions such as Canada and Europe highlights the need to better understand the impacts of different HIV subtypes on the course of perinatal HIV infection.

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