



### Understanding the evolution of HIV using next generation sequencing technologies

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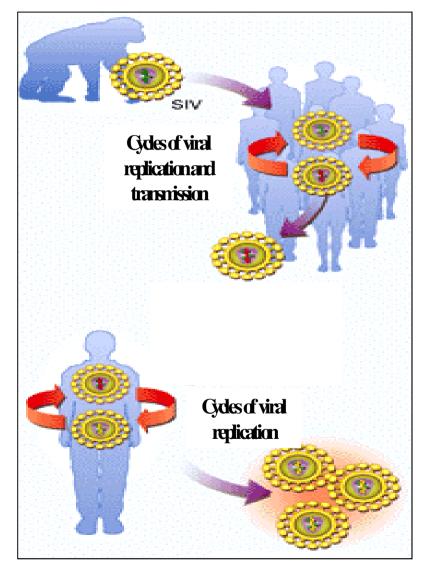
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# HIV diversity and continuing evolution is an impediment to vaccine design



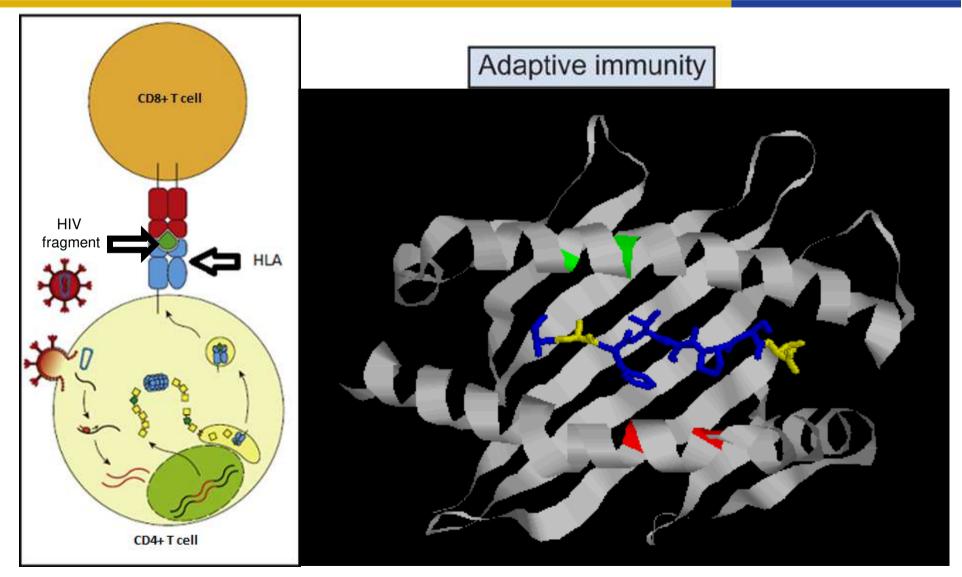
1996 global H3N2 viruses



What are the selection pressures driving evolution of HIV?

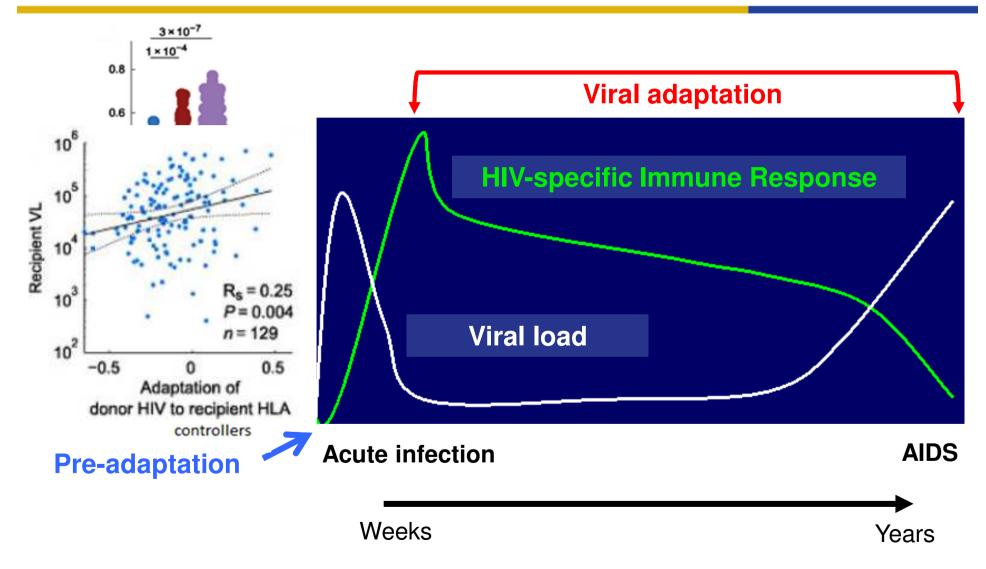
Host's immune response ("immune drug") known correlate of outcome

## Mutations in HIV genome allow immune escape (adaptations)



(Image from Carlson et al., 2015)

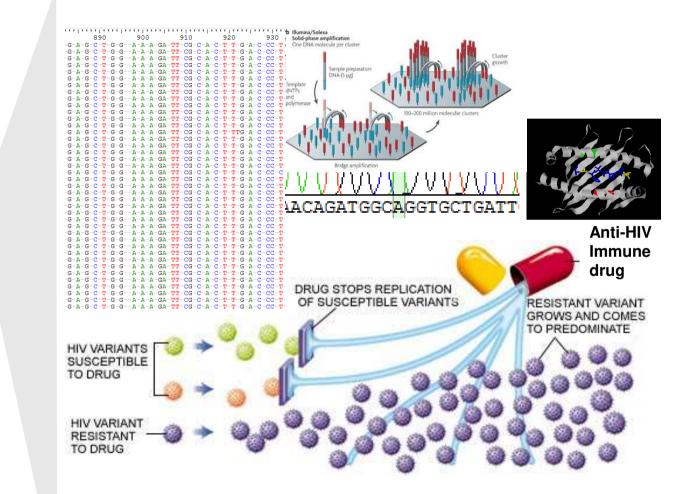
# Adaptation an important factor influencing HIV evolution and outcome



1 Moore et al Science 2002; 2 Carlson et al., Nat Medicine 2016

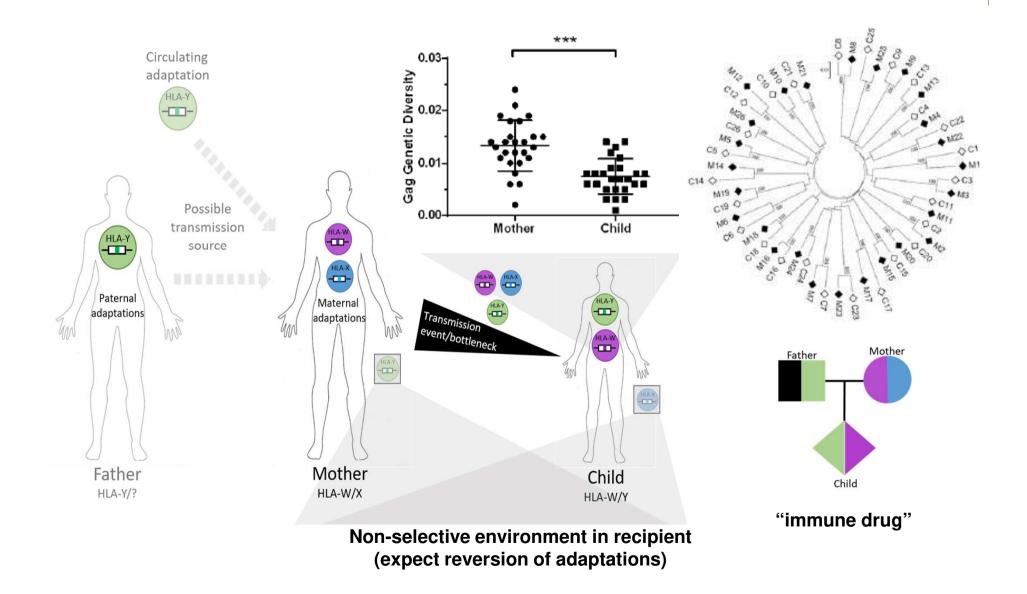
### How can we understand dynamics of these HIV mutations (adaptations) and how they contribute to HIV evolution?

Next generation sequencing provides high-resolution snapshot of HIV quasispecies

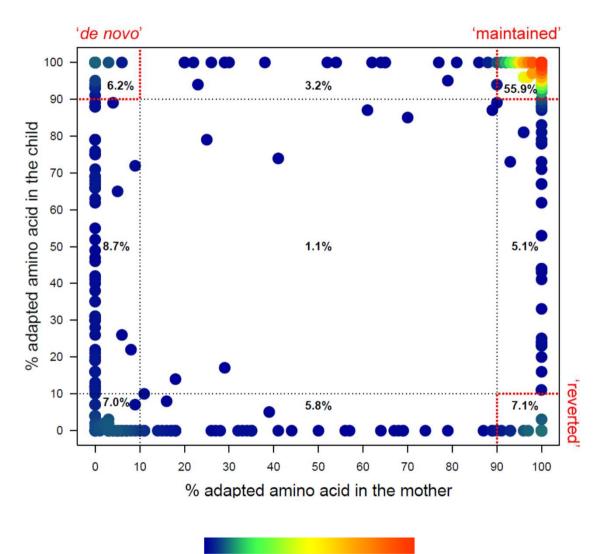


Adaptation can become dominant strain but if drug is removed could go back to wildtype (reversion)

#### Understanding dynamics of adaptations using samples from 26 Mother-child pairs – known source and child at least 50% haplo-identical with mother



## Maintenance or reversion of adaptations reflects immune environment of new host



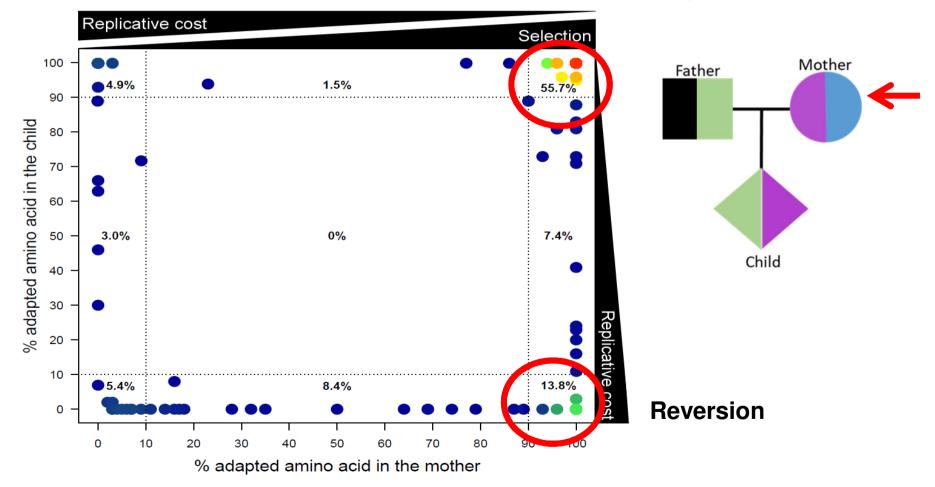
max

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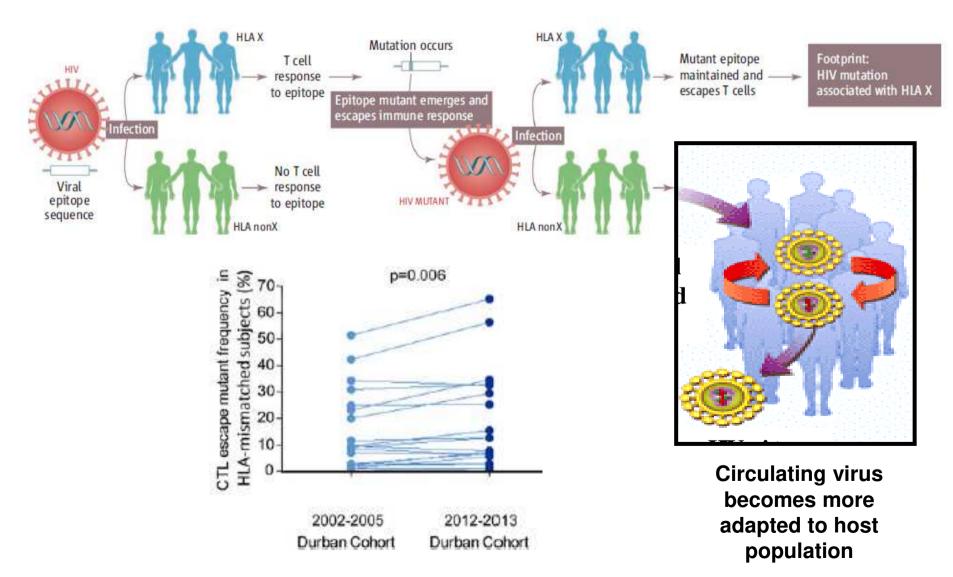
- More <u>maintenance</u> of adaptations in the child for adaptations in a selective environment
- More <u>reversion</u> of adaptations in the child when not in a selective environment
- More <u>de novo</u> adaptations in the child at sites under selection pressure in the child only

# Lack of reversion suggests low fitness cost and/or compensatory mutations

Mother only HLA allele (blue allele; no immune pressure in child – expect reversion in child)



#### Accumulation of adaptations in circulating viruses: implications for future vaccine designs



### Acknowledgements





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