

“Polio Immunization: Moving Forward”
NIH- Bethesda 19-20 September 2007

**Co-circulation and evolution of polioviruses and species C
enteroviruses in Madagascar**

Polio Epidemics due to cVDPVs in Madagascar in 2001-2002 and 2005

Type 2 cVDPVs

- Oct. 2001: Toliara - 1 case
- March 2002: Tolagnaro - 3 cases
- April 2002: Tolagnaro - 1 case

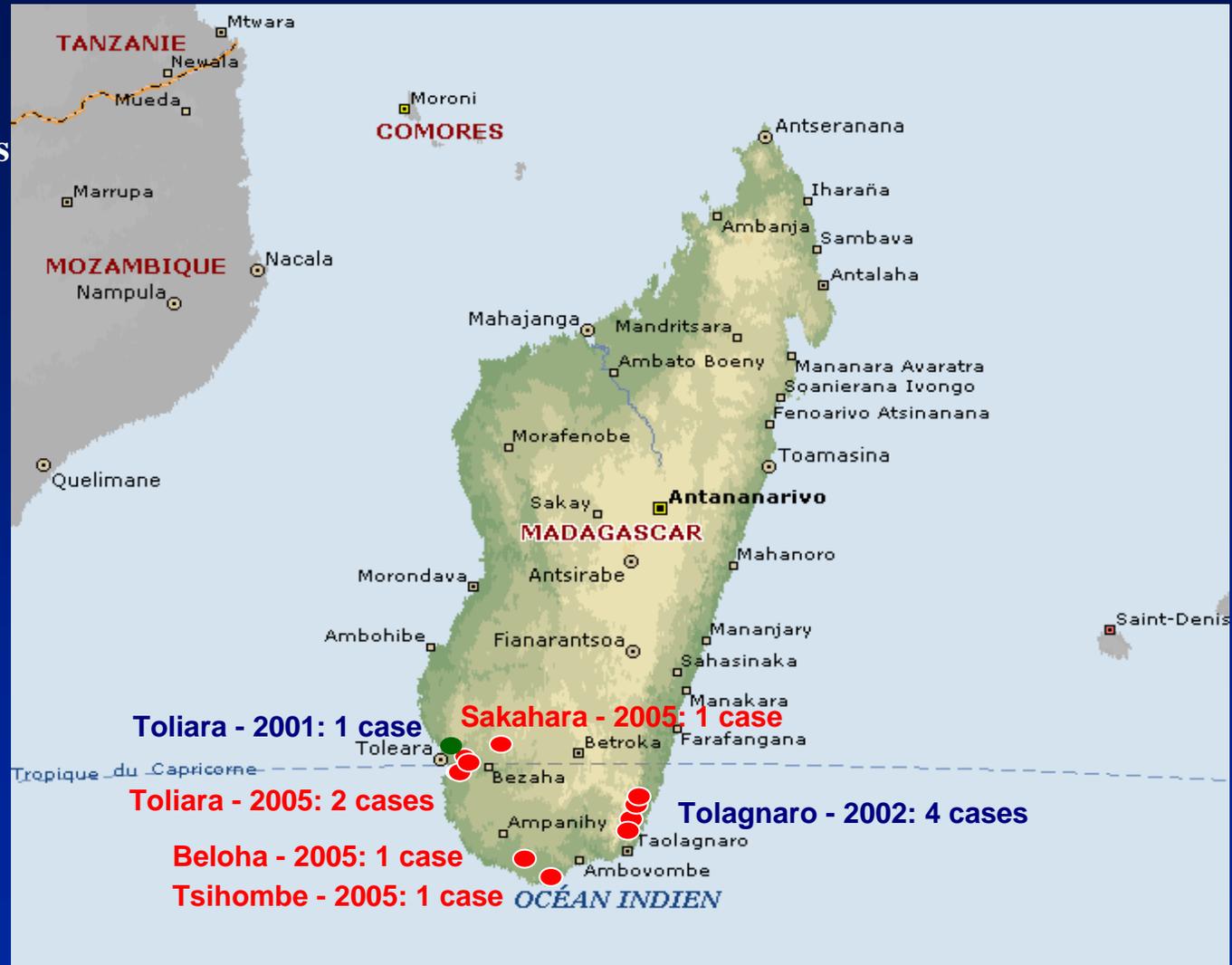
Type 3 cVDPVs

- April 2005: Toliara - 1 case

Type 2 cVDPVs

- June 2005: Tsihombe - 1 case
- June 2005: Beloha - 1 case
- July 2005: Toliara - 1 case
- August 2005: Sakahara - 1 case

- Type 2 cVDPV
- Type 3 cVDPV



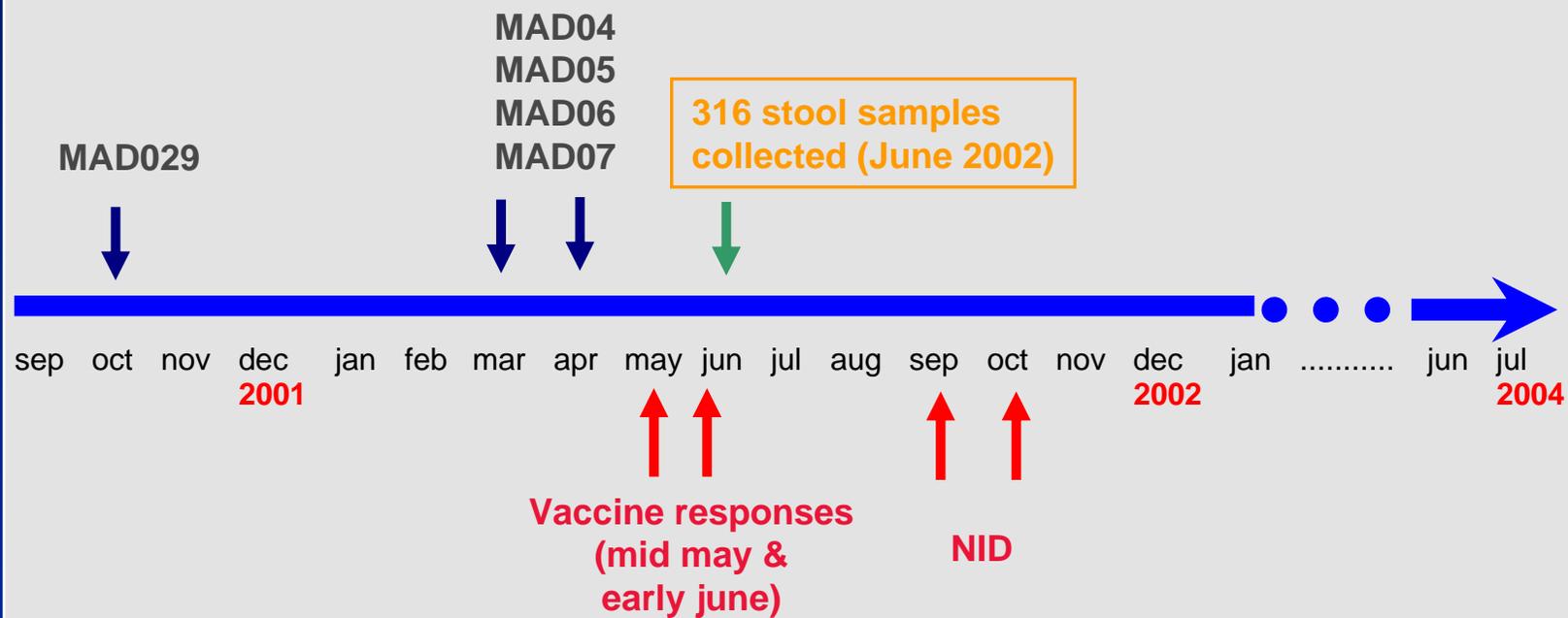
Characteristics of cVDPVs isolated in Madagascar .

- All cVDPVs were recombinant with species C enteroviruses (simple recombinant or mosaic genomes)
- cVDPVs showed phenotypes similar to those of wild polioviruses (loss of attenuated and ts phenotypes) .
- cVDPVs were widespread in the population (present in faeces of healthy children)

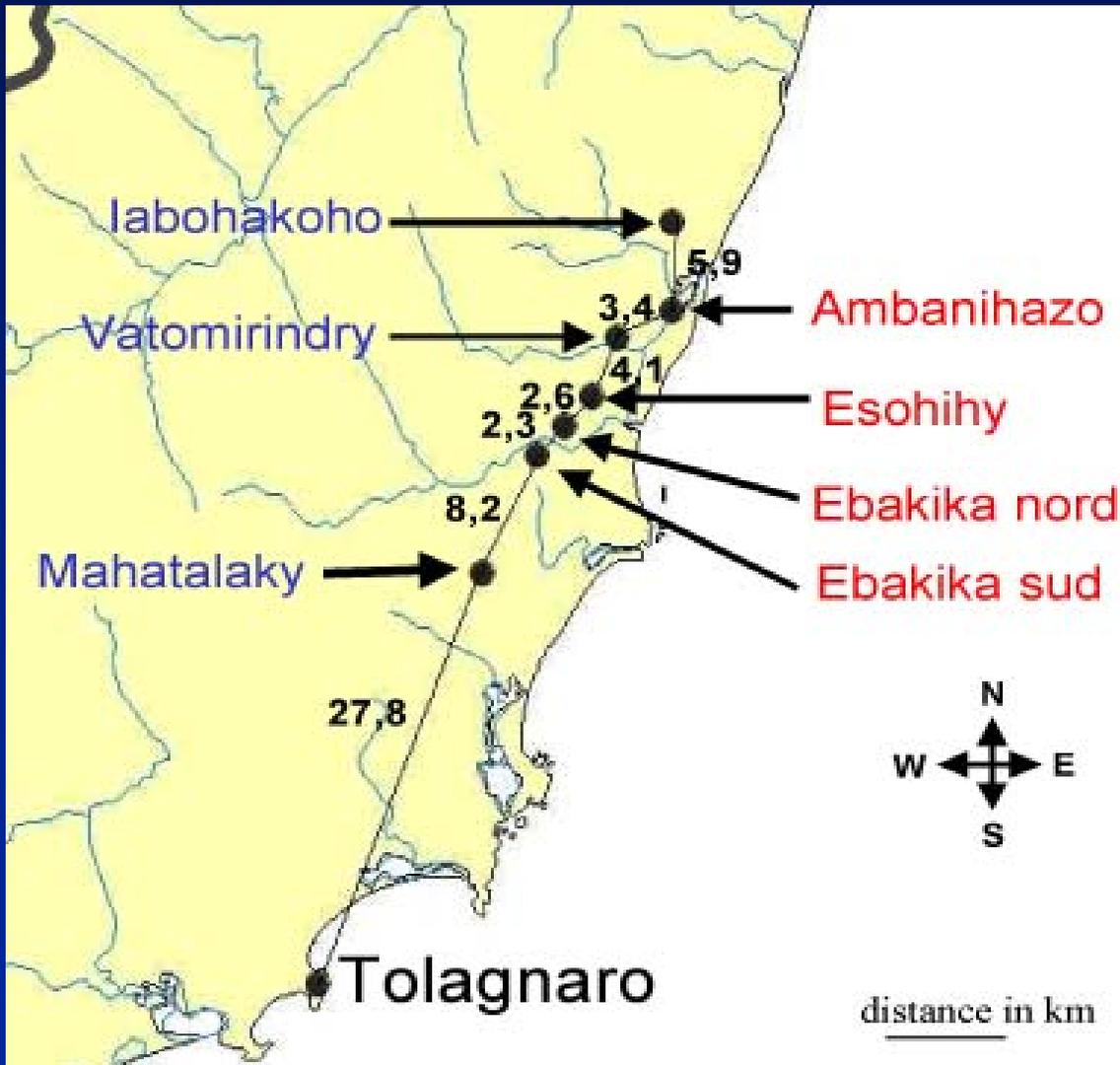
cVDPV outbreaks in the Toliara province - Madagascar 2001/2002-2005.

- Beside low vaccine coverage (< 50% in 2002 and 2004), what are the factors that favor the circulation of OPV and that allow the emergence of cVDPVs ?

Field investigations to determine the extent of cVDPVs and circulation of NPEV in Tolagnaro district 2002



Field investigations to determine the extent of cVDPVs
and circulation of NPEV in Tolagnaro district 2002



Isolated enteroviruses : 91

Polioviruses : 23 -
Sab 1, 2, 3 and VDPVs

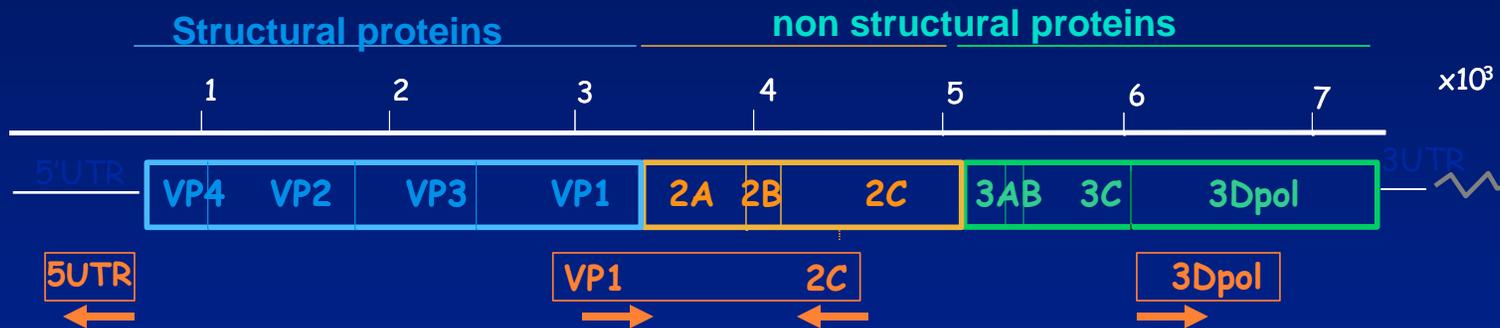
Non-polio enteroviruses: 68

HEV-B: 13
EV14, EV25, EV19

HEV-C: 51
CAV13, CAV11,
CAV17, CAV20, CAV24

Genetic characterization of the NPEV co-circulating with cVDPVs in the Tolaganaro district

☒ Séquencing 4 different genomic regions:



☒ Alignment & sequences comparison

☒ phylogenetic analysis

Co-circulating and evolution of polioviruses and NPEV
in Tolagnaro district - 2002.
Conclusion

- Co-circulation of VDPVs, some HEV-B and several HEV-C.
- Genetic exchanges between polioviruses, Cox. A17 and Cox. A13 (or common ancestors). Molecular vestiges of past co-evolution of HEV-C and wild PVs.
- Evolution of poliovirus and HEV-C by recombination results in unexpectedly extensive viral genetic diversity (5 HEV-C serotypes and at least 19 different recombinant HEV-C lineages) in a small human population and area (316 children - 6 villages - 10 x 20 km).

Co-circulating and evolution of polioviruses and HEV-C. Conclusion

- Poliovirus appears to be the «black sheep» of a diversified viral tribe in which it has been co-circulating and evolving, (at least in some parts of the world).
- This diversified PV/HEV-C population gives a further insight into viral ecosystems and the evolutionary processes that shape viral biodiversity.
- This kind of viral ecosystem may favor OPV strains circulation and indirect immunity as well as OPV strains evolution and emergence of VDPVs.

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