



UNIVERSITÉ DE
TUNIS EL MANAR



NGS sequencing for monitoring Poliovirus strains in Patients with Primary Immunodeficiency

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Mediterranean Region

Institut Pasteur de Tunis



1st MENA Congress of Clinical Microbiology and Infectious Diseases

34th National Congress of the Tunisian Society of Infectious Diseases May, 22 - 24, 2025



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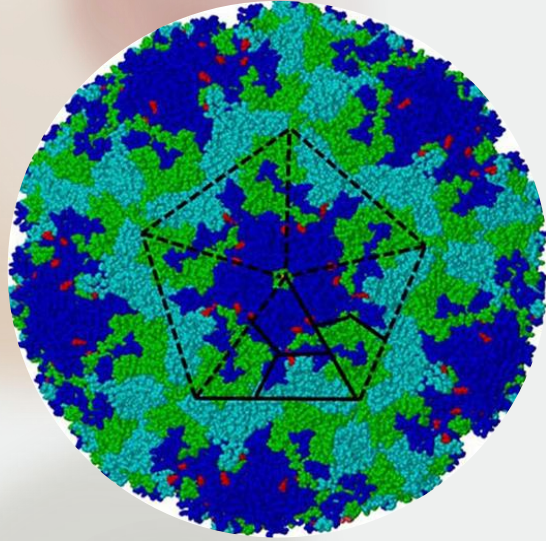


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01

PV & Eradication challenges

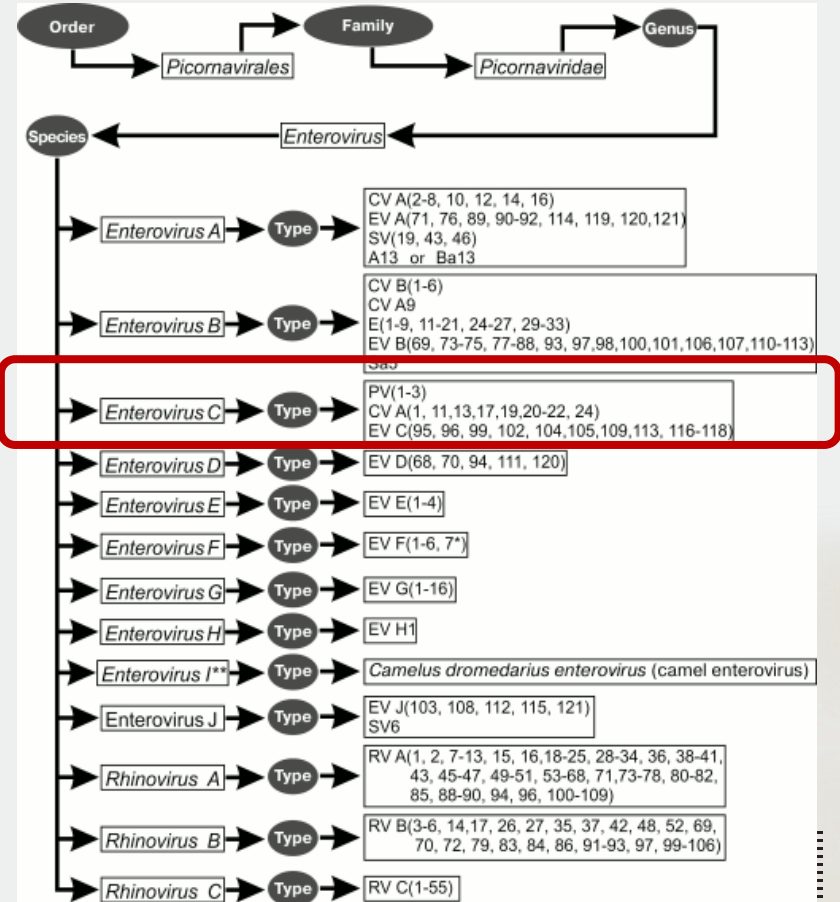
Poliovirus Classification

Family: Picornaviridae
(35 genus)

Genus: Enterovirus
(12 EV species & 3 RV)

Enterovirus C

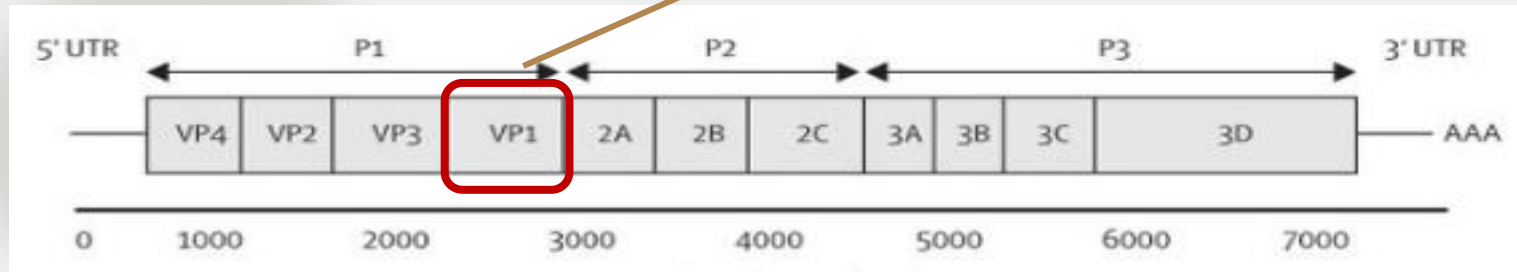
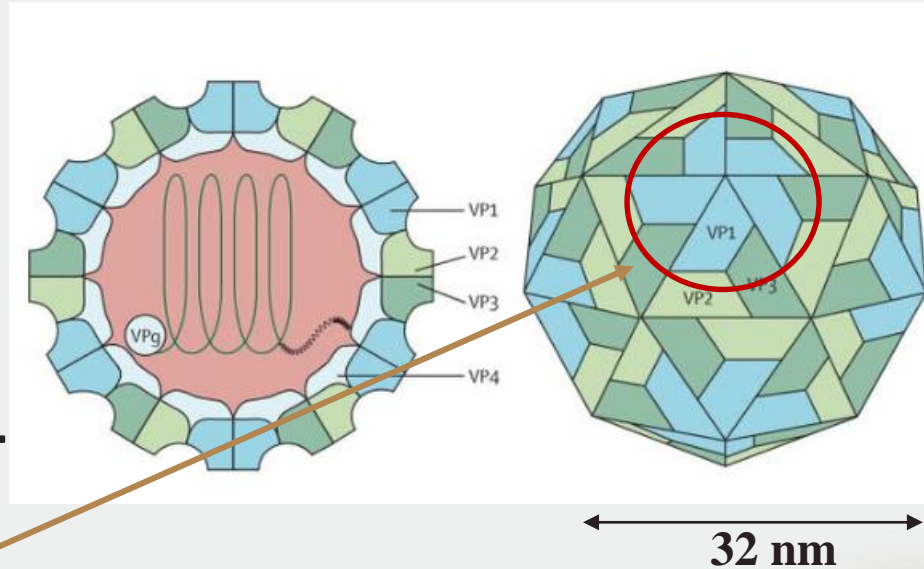
PV-1, PV-2, PV-3, CV-A21, CV-A24



Poliovirus : Structure

Single stranded naked RNA virus

Icosahedral capsid: 60 copies of VP1, VP2, VP3, VP4



Poliovirus Eradication challenges

Before Polio vaccines development



Épidémie à Newyork,1916; Unité de soins intensifs

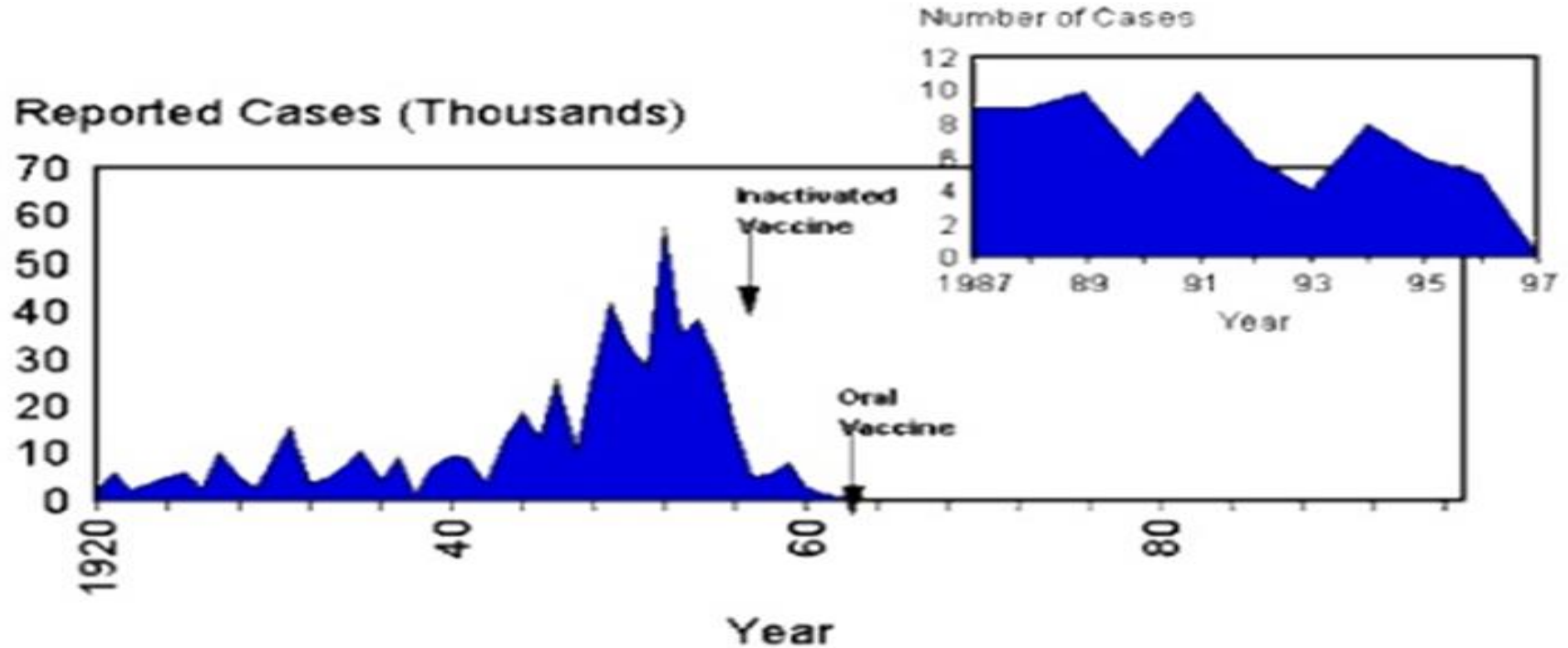


Franklin Rosvelt, 1932-45



Polio kiddies cheer news of successful vaccine., California 1955

Poliovirus Eradication challenges



Poliovirus Eradication challenges



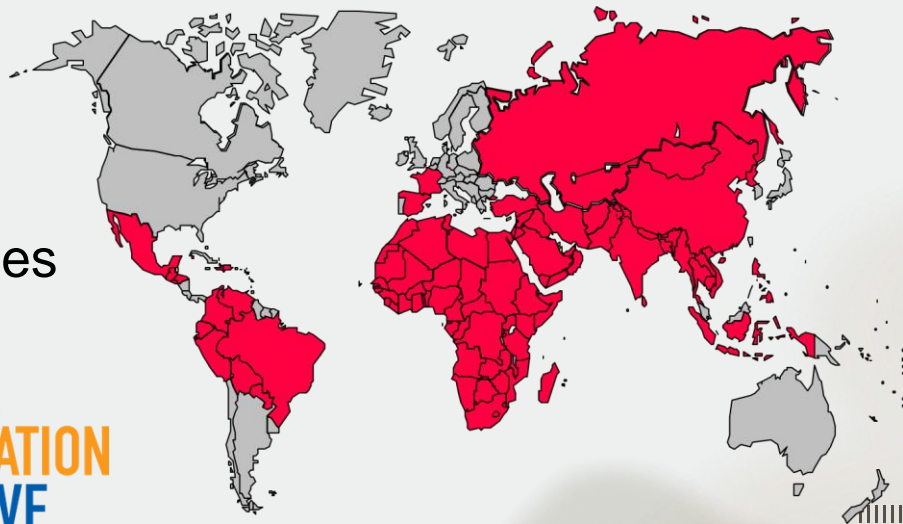
Since 50's

rare in developed countries

endemic in developing countries

1988

350 000 cases/ 125 countries



POLIO GLOBAL
ERADICATION
INITIATIVE

Poliovirus Eradication challenges

Since 2017



Source: Adapted from Global Polio Eradication Initiative (GPEI)

Poliovirus Eradication challenges

Possible importation of WPV1: Malawi, Mozambique

Morbidity and Mortality Weekly Report

Update on Wild Poliovirus Type 1 Outbreak — Southeastern Africa, 2021–2022

Elizabeth Davlantes, MD¹; Sharon A. Greene, PhD¹; Farrell A. Tobolowsky, DO¹; Oladayo Biya, MD¹; Eric Wiesen, DrPH¹; Fikru Abebe, MD²; Mesfin B. Weldersadik, MD²; Victor A. Eboh, MD²; Mike N. Chisema, MD³; Balbina da Conceição Mário, MPH⁴; Florian Tinuga⁵; Patricia Mupeta Bobo, MBChB⁶; Colline Koline Chigodo, MPH⁷; Ghanashyam Sethy, MBBS, MD⁸; Jan-Marcus Hellström, MSc⁹; Abdou Moumouni Goundara, MPH⁸; Marie-Eve Burny, MPH⁸; Jonas C. Mwale, MD⁸; Jaume Jorba, PhD⁹; Koketso S. Makua, MSc¹⁰; Wayne Howard, MSc¹⁰; Lerato Seakamela¹⁰; Samuel Okiror, MBChB¹¹; Andrea Thompson¹¹; Asma Ali, MD¹¹; Dhoud Samba, PhD¹¹; Chelumwanda Abo, MD¹²; Luambi Kabamba, MD¹³; Anshony Kasakala¹³; Dalene Lored Zamboon, MD¹³; Eudine Maseko, MPhil¹³.



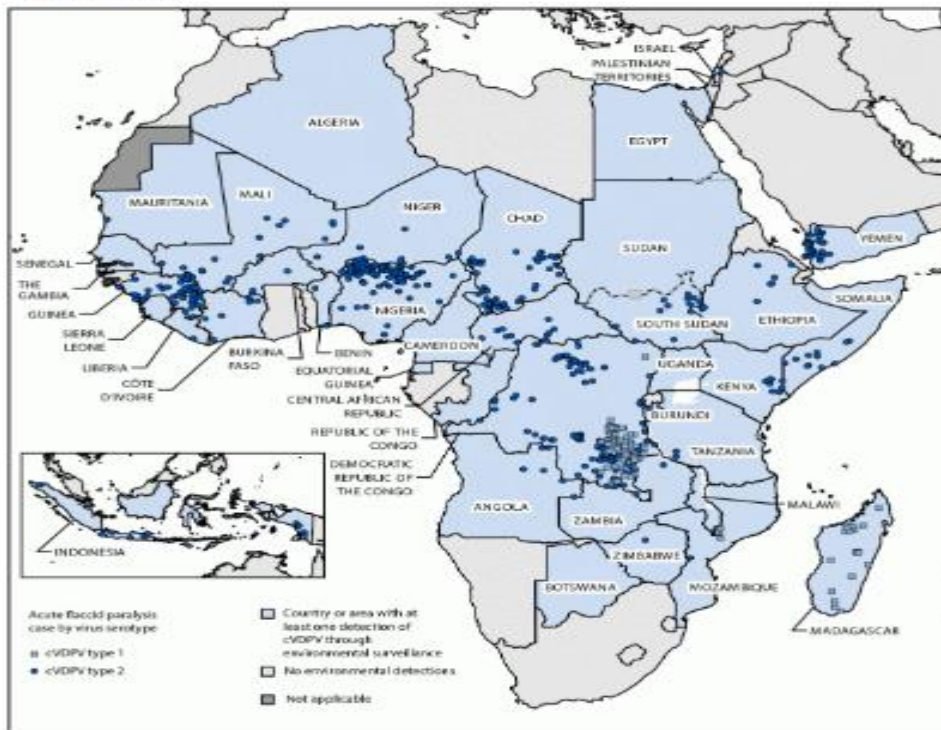
11 octobre 2022

<https://www.who.int/publications/i/item/global-vaccineaction-plan-2011-2020>

Poliovirus Eradication challenges

VDPV/cVDPV outbreaks

FIGURE 1. Pays et zones* signalant des flambées de polio en circulation dérivées d'une souche vaccinale (N = 39) — dans le monde, janvier 2023–juin 2024¹

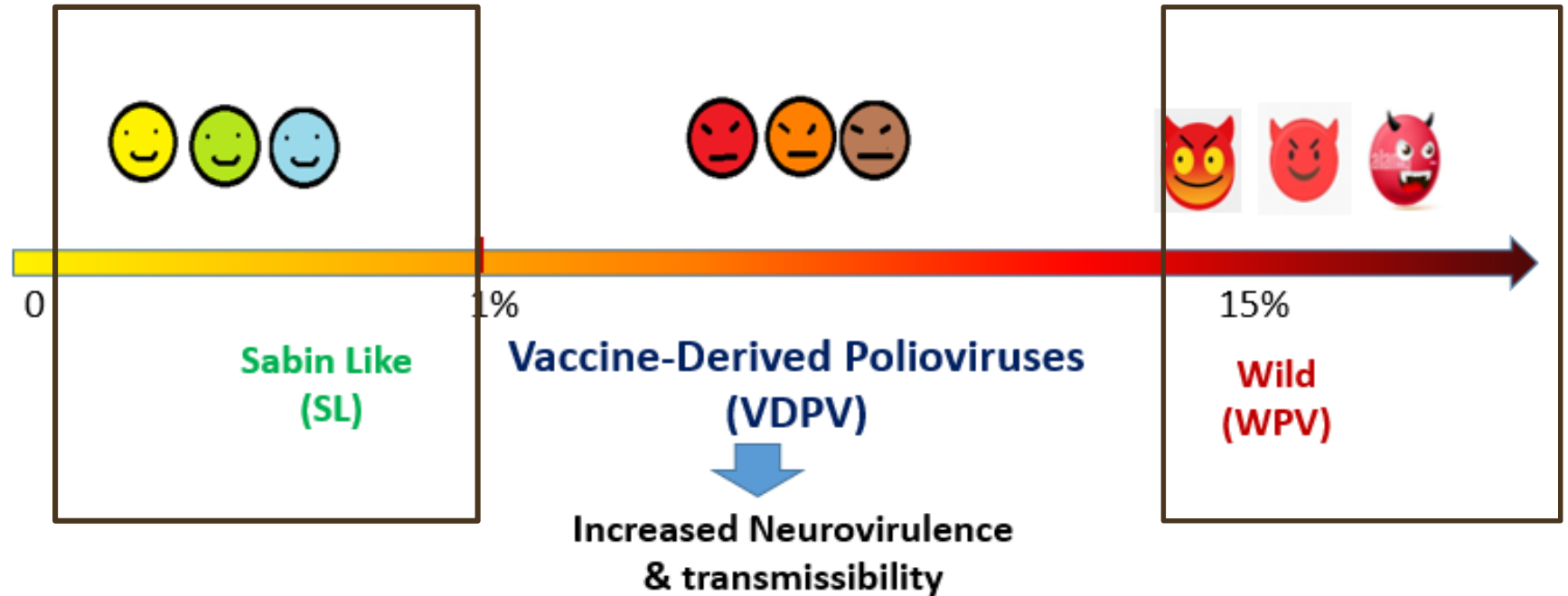


Jan 2023- June 2024:
74 outbreaks in 39
countries

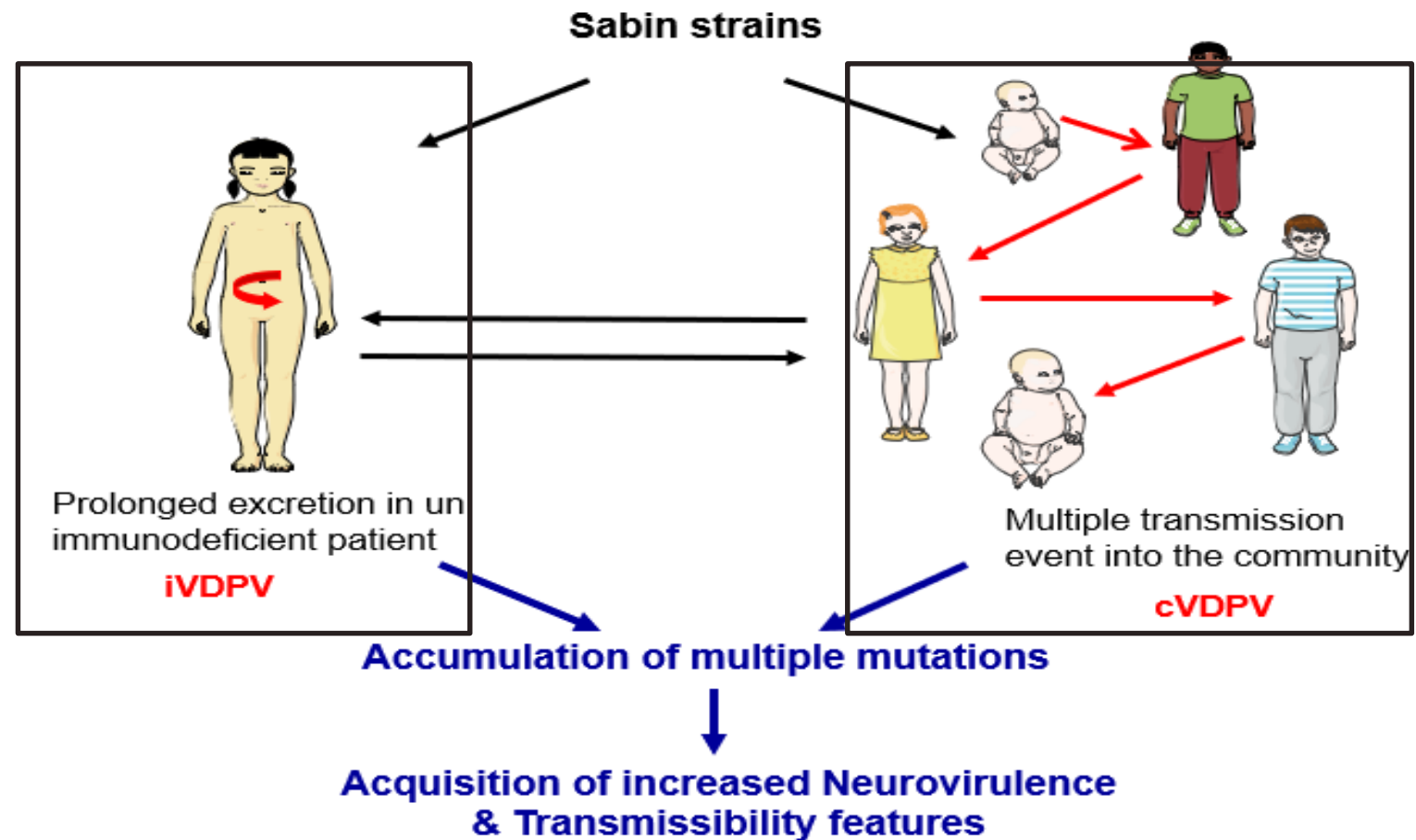
672 AFP cases

Poliovirus Eradication challenges

Nucleotidic divergence in VP1 gene



Poliovirus Eradication challenges



Poliovirus Eradication challenges

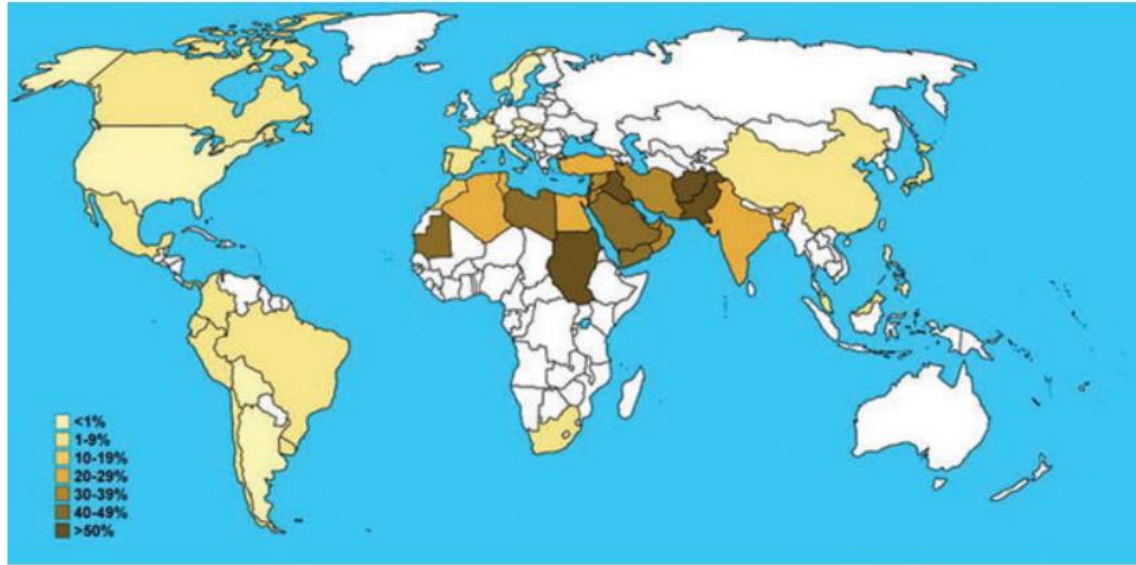


Figure 1. Available data on the worldwide consanguinity rate, with obvious high consanguinity in the Middle Eastern countries.

MENA region:
High rate of consanguineous marriages
High prevalence of autosomal
recessive forms of PIDs.

doi: 10.1111/j.1749-6632.2011.06379.x

<https://doi.org/10.1080/1744666X.2020.1801422>

Poliovirus Eradication challenges

Up to date, rare community spread of iVDPV : only three iVDPV circulation

Paralysis Case and Contact Spread of Recombinant Vaccine-derived Poliovirus, Spain

To the Editor: The World Health Organization Polio Eradication Initiative

encephalitis developed. The case was

Transmissior Poliovirus in Minnesota



Vaccine

journal homepage: www.elsevier.com/locate/vaccine



Concurrent outbreaks of circulating vaccine-derived poliovirus types 1 and 2 affecting the Republic of the Philippines and Malaysia, 2019–2021 [☆]



After wild poliovirus eradication,

- Global reduction of poliovirus immunity
- Improvement of PID health conditions

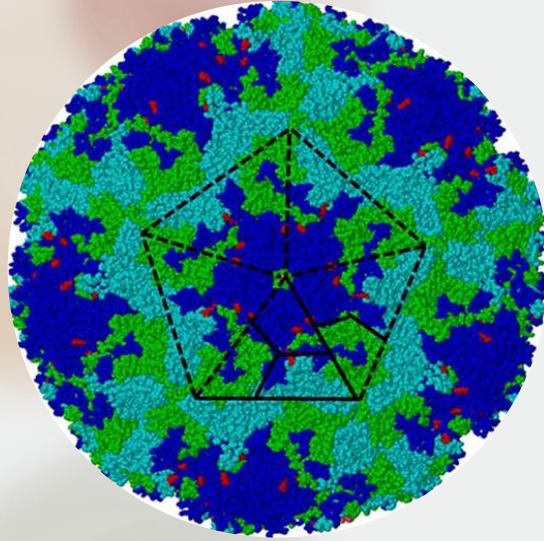
OPEN ACCESS

Edited by:
Antonio Condino-Neto,
University of São Paulo, Brazil

Patients with Primary Immunodeficiencies Are a Reservoir of Poliovirus and a Risk to Polio Eradication

iVDPV excretors will constitute a significant risk for poliovirus re-emergence

02



**Increased susceptibility &
persistence PV/EV in PID**

PV/EV Increased susceptibility in PID

Prolonged poliovirus excretion is associated with
Primary immunodeficiency disorders (PIDs)

Published in final edited form as:

Vaccine. 2015 March 03; 33(10): 1235–1242. doi:10.1016/j.vaccine.2015.01.018.

Immunodeficiency-related vaccine-derived poliovirus (iVDPV)
cases: A systematic review and implications for polio
eradication

SUPPLEMENT ARTICLE

Immunodeficiency-related vaccine-derived poliovirus (iVDPV)
cases: A systematic review and implications for polio
eradication

Jean Guo^{a,*}, Sara Bolivar-Wagers^b, Nivedita Srinivas^a, Marisa Holubar^a, and Yvonne
Maldonado^a

Poliovirus Excretion Among Persons With
Primary Immune Deficiency Disorders:
Summary of a Seven-Country Study Series

Primary Antibody Deficiency:

Hypogammaglobulinemia, Agammaglobulinemia, Hypergammaglobulinemia
M (hyper IgM)

Combined antibody and cellular immunodeficiency disorders: Severe
Combined Immunodeficiency Disorder (SCID) , Common Variable
Immunodeficiency Disorder (CVID), Major Histocompatibility complex
deficiencies and other disorders .



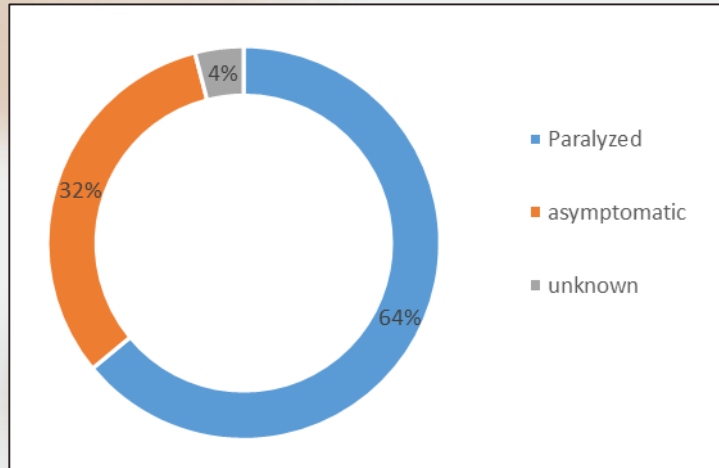
PV/EV Increased susceptibility in PID

The iVDPV excretors are classified into 3 categories:

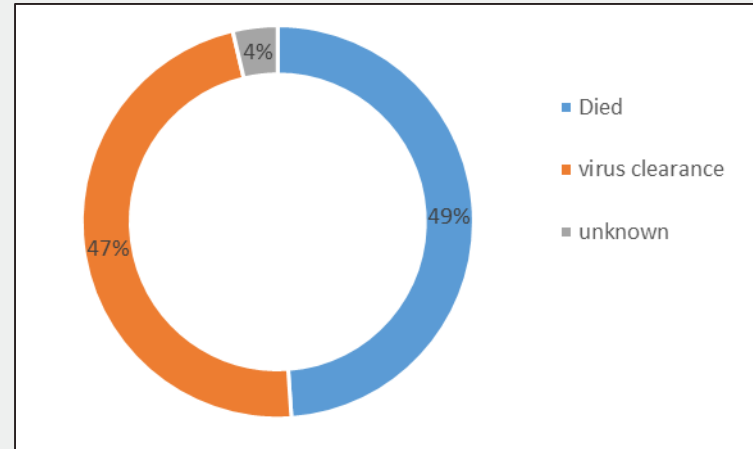
- Excretors of less than 6 months period
- Prolonged excretors when it's comprised between 6 months and 5 years
- Chronic excretors when excretion period exceeds 5 years

PV/EV Increased susceptibility in PID

According to Macklin et al. (2020), 149 cases of iVDPV (with or without AFP) were reported to the WHO from 1961 to 2019.

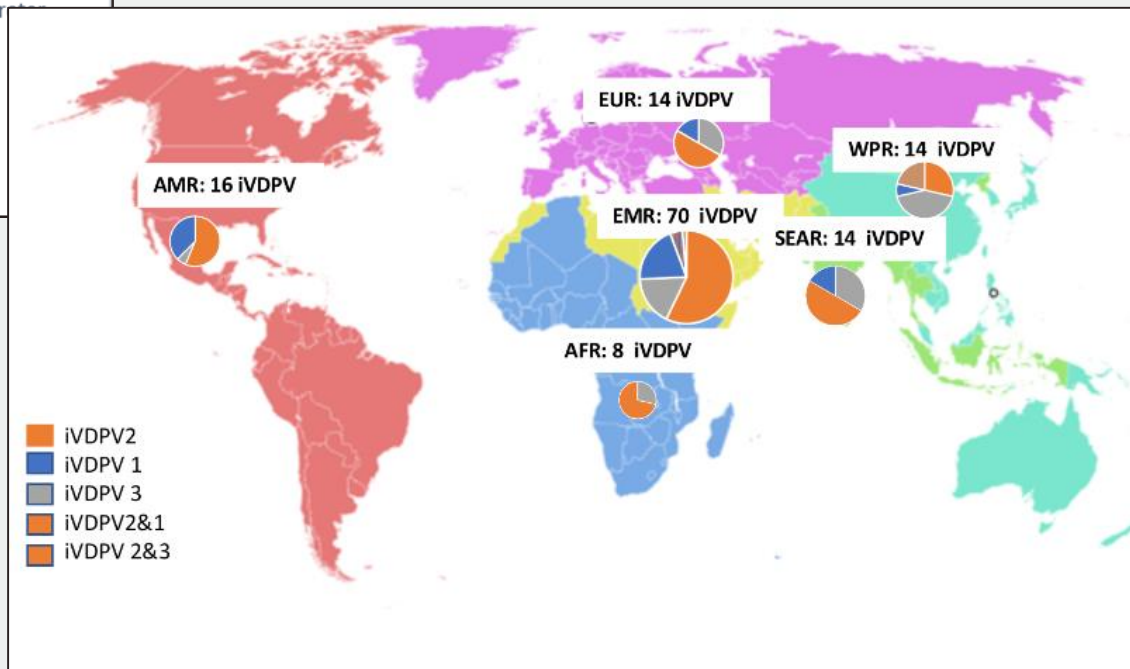
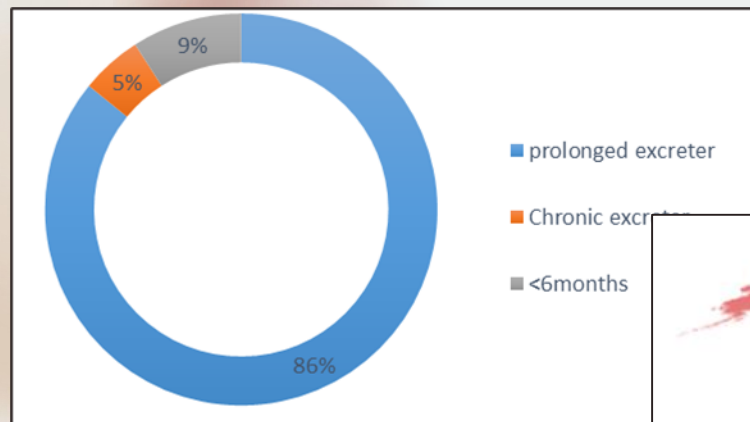


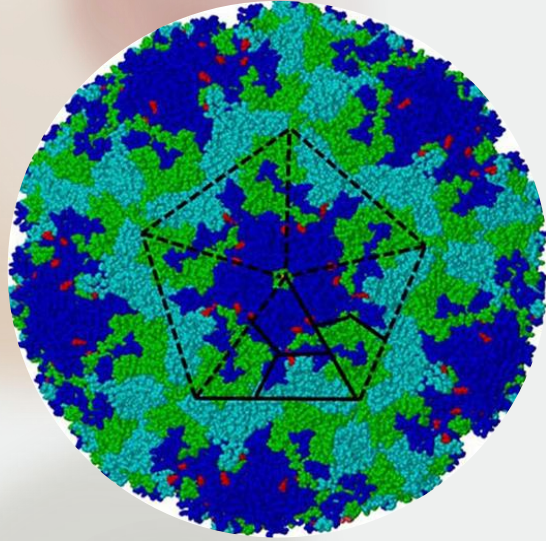
Clinical status



Outcome status

PV/EV Increased susceptibility in PID





03

Genetic Variability of PV/EV

Genetic variability of PV/EV

PV/EV, as with all RNA viruses, are in a constant process of evolution driven by different mechanisms: .

1- Generation of **point mutations** followed by genetic drift and selection: absence of proof-reading/repair mechanism.

Based on VP1 region, the **mutation rate of WPV/ EV/ cVDPV: $1-3 \times 10^{-2}$ mutations/ site/year**

Genetic variability of PV/EV

the mutation rate of iVDPV: 2– 6 10^{-2} mutations/ site/year

circulating VDPV using genetic information. Genetic characteristics distinguishing between cVDPV and iVDPV include [1,2]:

- A higher proportion of mixed-base nucleotide sites in iVDPV sequences.
- Extensive antigenic divergence from the OPV strains in iVDPV sequences.
- Multiple viral lineages observed in iVDPV sequences.

Global Polio Laboratory Network

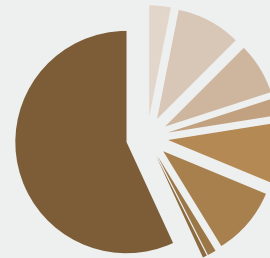
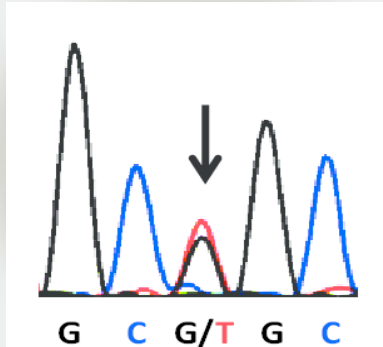
Guidance
Paper 5

Reporting Vaccine
Derived Polioviruses
(VDPVs)

Mixed Bases +++



Intra-host diversity +++



Mixed bases
43%

Genetic variability of PV/EV

Recombination:

Homologous recombination:

Both parental RNAs are homologous

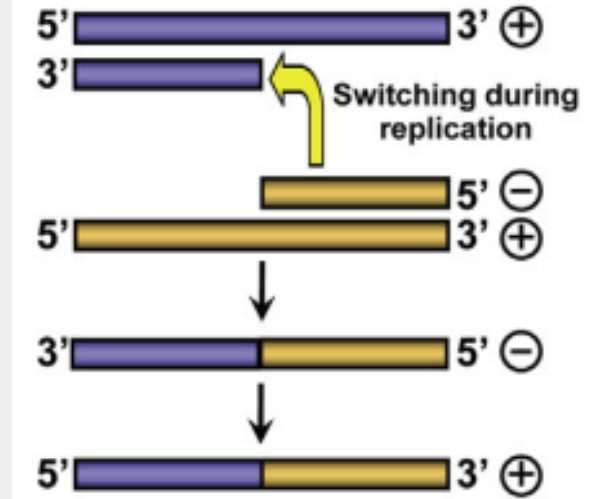
The crossovers occur at homologous sites.

After OPV vaccination, Intratypic recombinaison is frequent (20%) (Haddad-Boubaker et al, 2007)

Tableau 2
Fréquences et types de recombinants retrouvés.

Souches excrétées en cours de vaccination (n = 137)

Total	Profil RFLP VP1/3D	Souches non recombinantes	Souches recombinantes	
			No	%
S1 (n = 31)	S1/S1	30		2
	S1/S2		1	
	S1/S3		—	
S2 (n = 33)	S2/S2	31		6
	S2/S1		2	
	S2/S3		—	
S3 (n = 73)	S3/S3	36		34
	S3/S1		14	
	S3/S2		11	



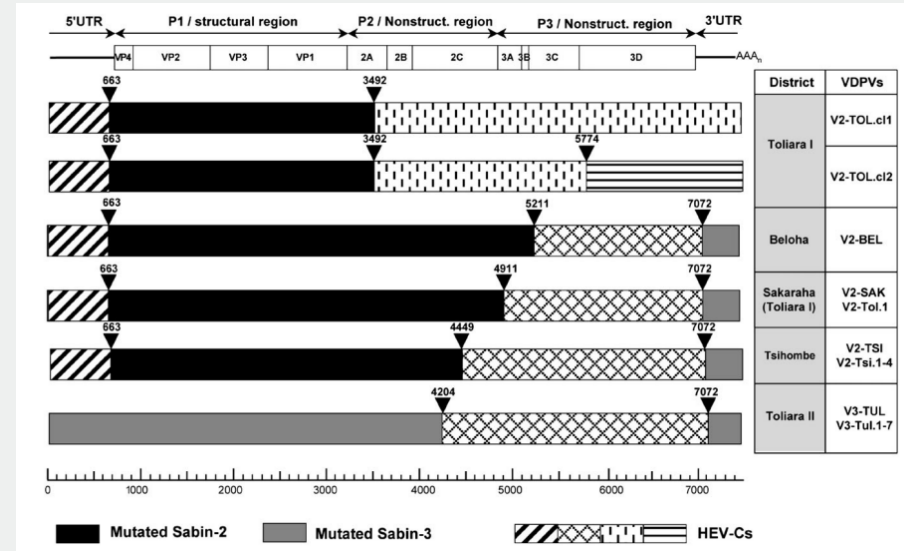
<https://doi.org/10.1016/B978-0-12-816331-3.00002-7>

Genetic variability of PV/EV

cVDPV outbreaks

Recombinant Sabin /EV-C

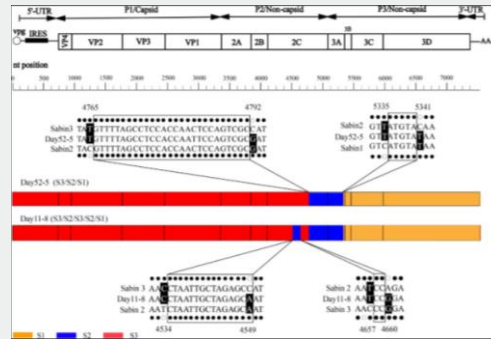
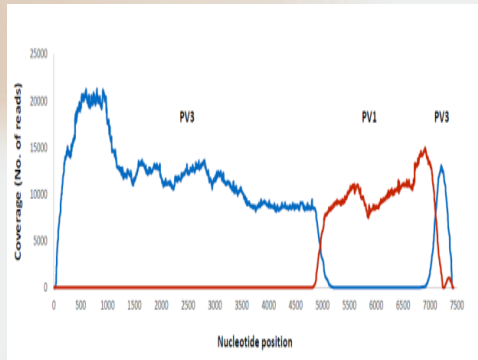
coxsackievirus A (CV-A) type 13 (CV-A13) and CV-A17



Genetic variability of PV/EV

iVDPV excretors

Intertypic recombination has been found occasionally in iVDPVs

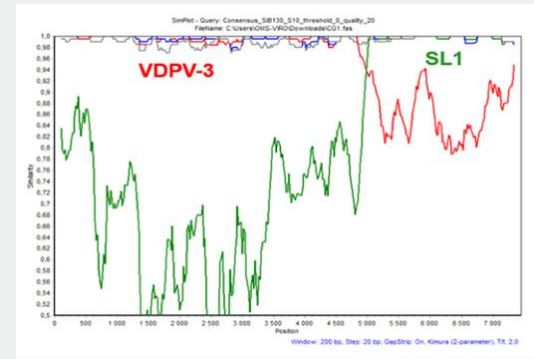


Paralysis Case and Contact Spread of Recombinant Vaccine-derived Poliovirus, Spain

To the Editor: The World Health Organization Polio Eradication Initiative

encephalitis developed. The case was immediately considered suspicious and was therefore monitored at least monthly until the boy died. Sampling was conducted, coinciding with his visits to the hospital to receive therapy with immunoglobulin (γ globulin 0.5 g/kg). His contacts were studied, environmental surveillance was conducted, and molecular analysis of

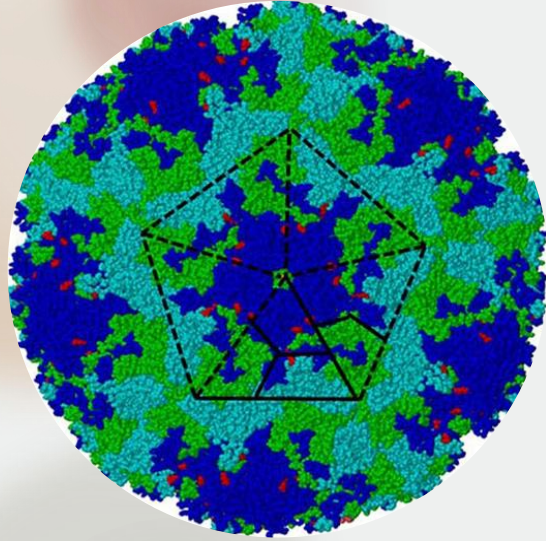
iVDPV spread



Prolonged iVDPV
asymptomatic excretor
(Singanayagam et al., 2023)

Excretors with paralysis & fatal outcome
(Guo et al., 2023; Ben Salem et al., 2024)

04

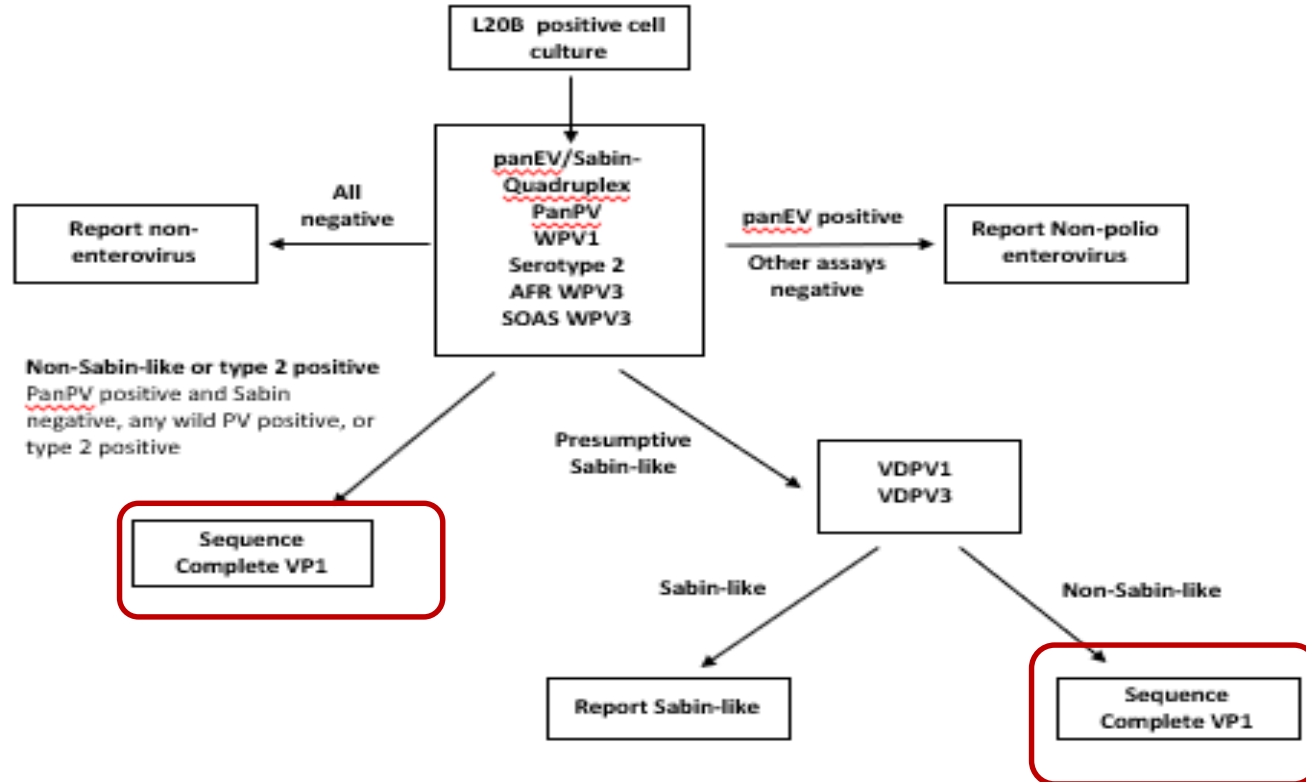


Apport of NGS sequencing

Apport of NGS sequencing



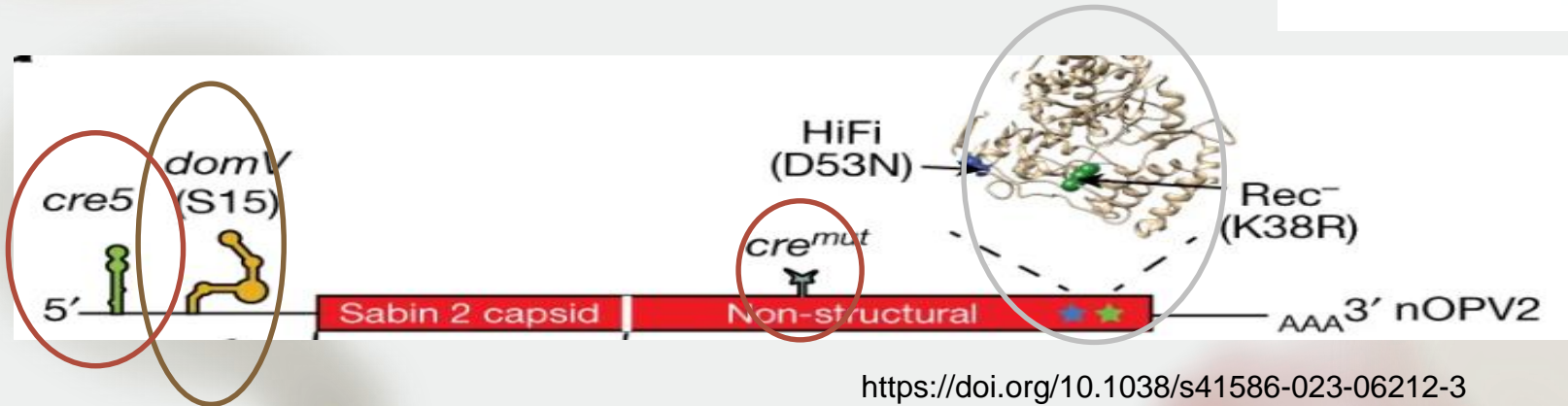
Global Polio Laboratory Network



Apport of NGS sequencing

- COVID-19 pandemic: Democratisation of NGS sequencing
- PV2 identification (cVDPV2, SL2, nOPV2)

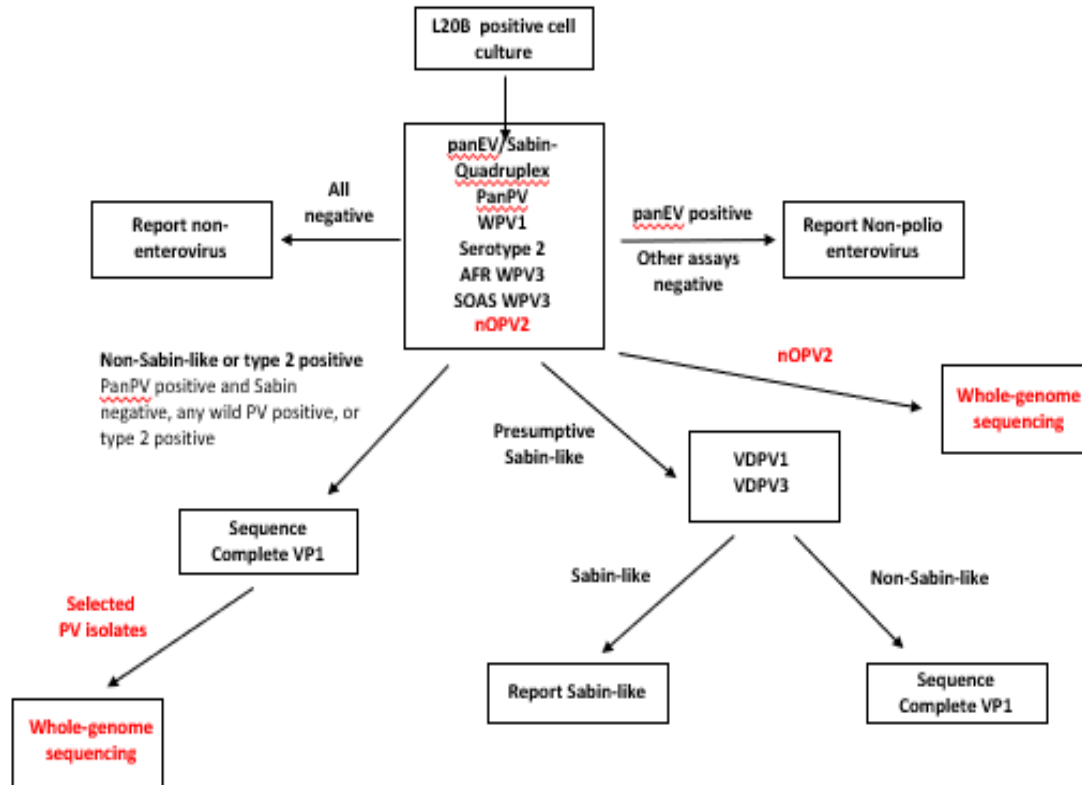
nOPV2: modified Sabin 2 strain



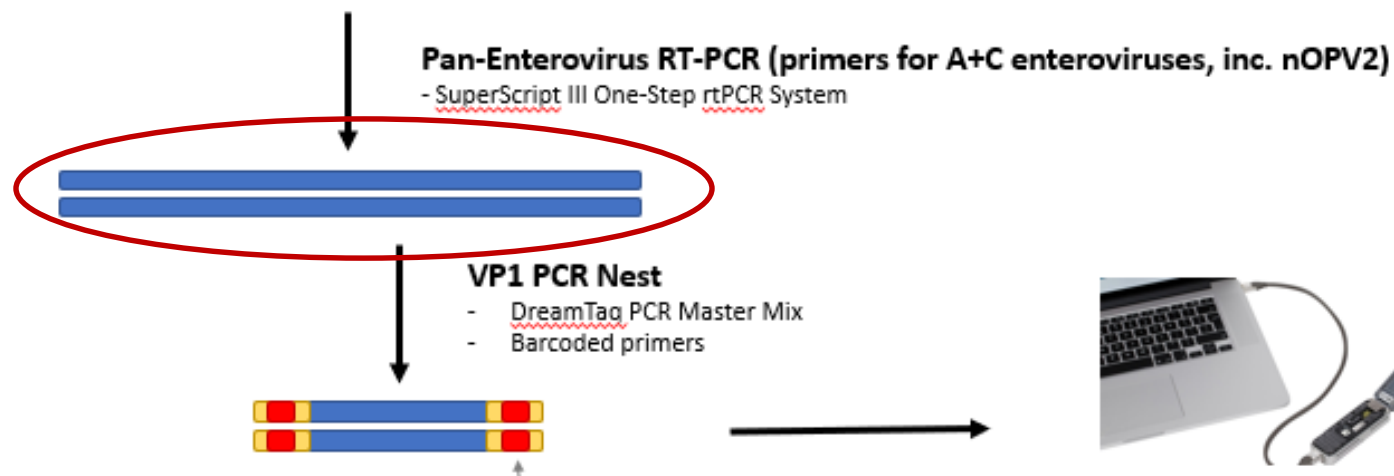
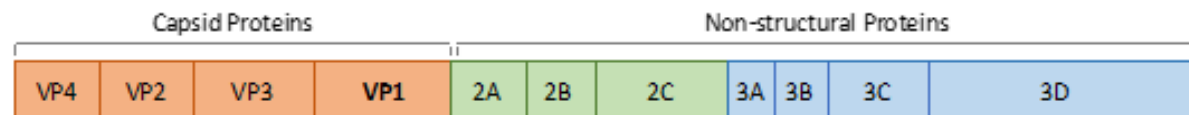
Apport of NGS sequencing



Global Polio Laboratory Network



Our PCR strategy



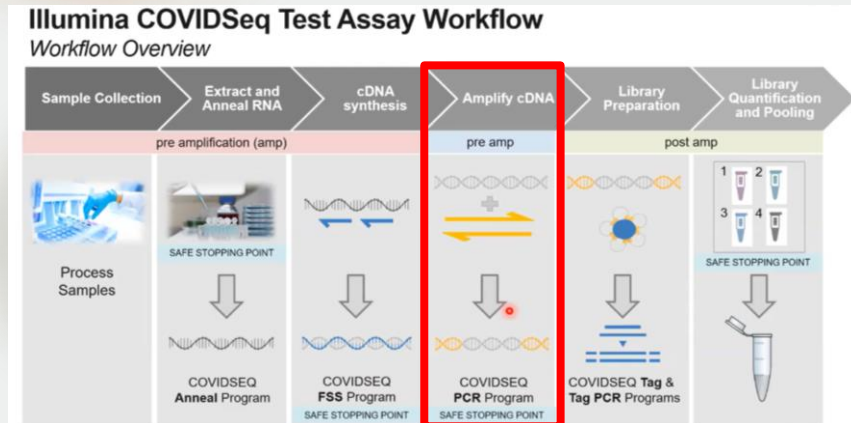
Apport of NGS sequencing

Amplification and next generation sequencing of near full-length human enteroviruses for identification and characterisation from clinical samples

[Sonia R Isaacs](#)^{1,2}, [Ki Wook Kim](#)^{1,2}, [Junipearl X Cheng](#)³, [Rowena A Bull](#)^{3,4}, [Sacha Stelzer-Braid](#)^{2,3}, [Fabio Luciani](#)^{3,4}, [William D Rawlinson](#)^{1,2,3,5,6}, [Maria E Craig](#)^{1,2,7,8,✉}



Conception specific primers pools nOPV2/ PV/EV:





ELSEVIER

Virus Research

journal homepage: www.elsevier.com/locate/virusres

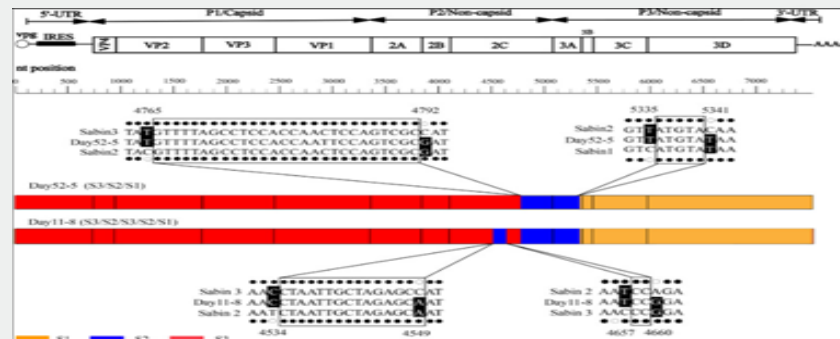
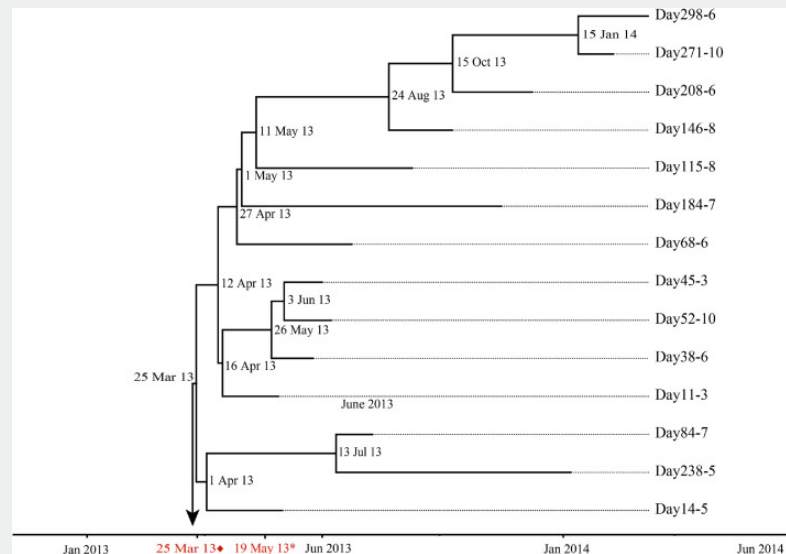
Genetic characterization and molecular evolution of type 3 vaccine-derived polioviruses from an immunodeficient patient in China

The patient was a 7-month-old boy born on 7 October 2012, in Yichun, Jiangxi Province, China. A total of three OPV vaccinations were given. The last vaccination was given on 20 February 2013, and the remaining vaccination dates were unknown. The child developed symptoms of paralysis on 19 May 2013 and then immediately went to the hospital for treatment. Tests revealed that the child's immune function was lower than normal, and the Jiangxi Provincial and National Polio diagnosis experts group diagnosed the child as a case of iVDPV. A total of 15 stool specimens for virological examination were obtained from 30 May 2013 to 12 April 2014 at approximately monthly intervals. Finally, the child died on 18 April 2014.

Multiple variants
and lineages have been diverged

All iVDPVs were vaccine
recombinants,

Modification in Ag sites all along
the genome



Apport of NGS sequencing

nature communications



Article

<https://doi.org/10.1038/s41467-023-39094-0>

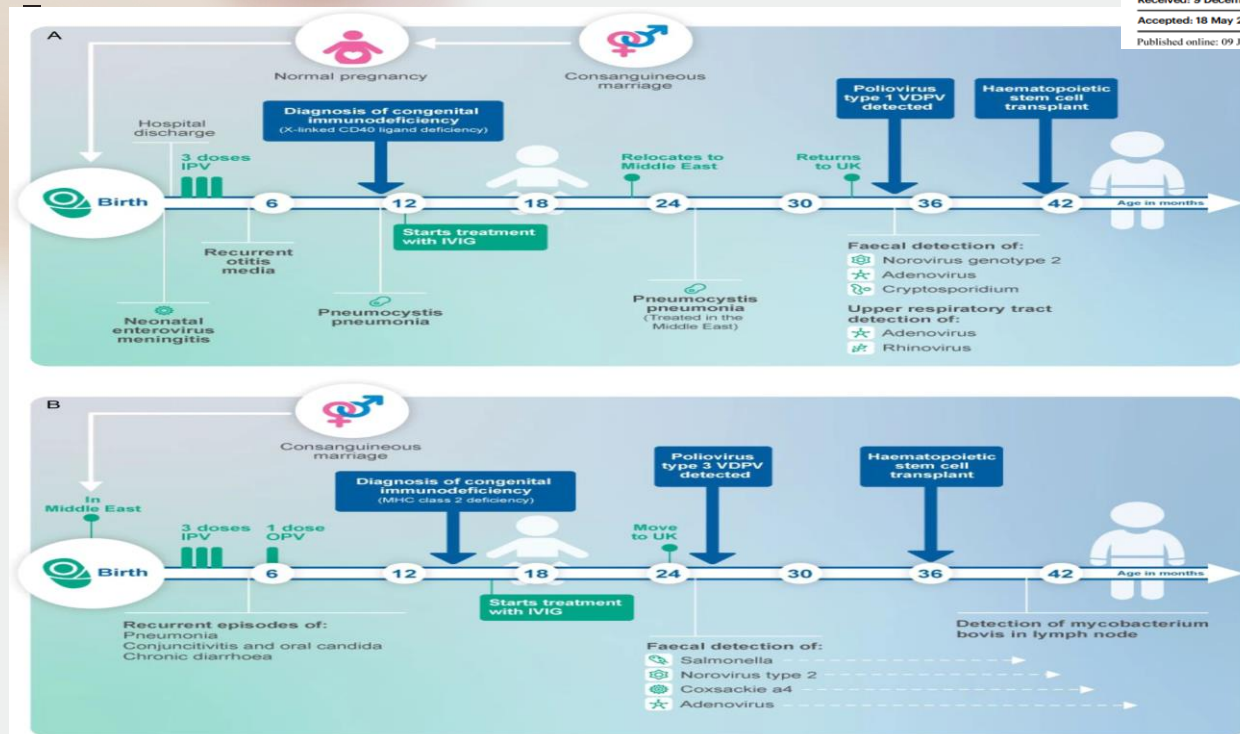
Asymptomatic immunodeficiency-associated vaccine-derived poliovirus infections in two UK children

Received: 9 December 2022

Accepted: 18 May 2023

Published online: 09 June 2023

Anika Singanayagam^{1,2}, Dimitra Klapa³, Shirelle Burton-Fanning⁴,
Julian Hand⁵, Thomas Wilson⁶, Laura Stephens⁷, Ryan Mate⁸,
Benjamin Shillito^{9,10}, Cristina Celma¹¹, Mary Slatter¹², Terry Flood⁶,
Robin Gopal¹, Javier Martin¹³ & Maria Zamboni¹ ✉



6 weeks & 3 months
excretion periods

Article

<https://doi.org/10.1038/s41467-023-39094-0>

Asymptomatic immunodeficiency-associated vaccine-derived poliovirus infections in two UK children

Received: 9 December 2022

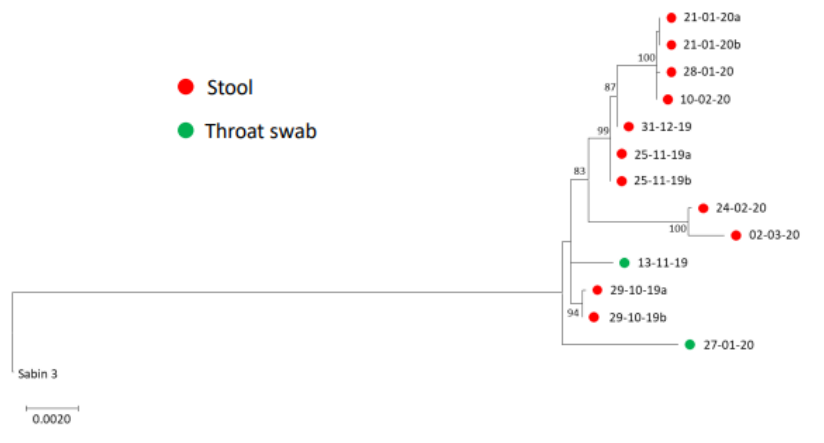
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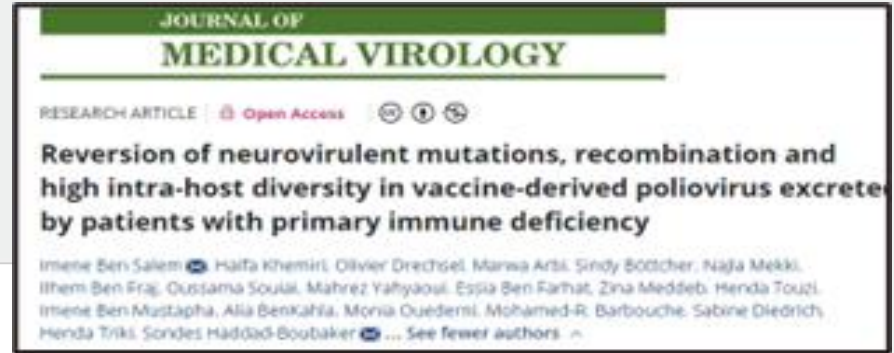
Anika Singanayagam^{1,2} , Dimitra Klapsa³, Shirelle Burton-Fanning⁴, Julian Hand¹, Thomas Wilton⁵, Laura Stephens⁶, Ryan Mate⁶, Benjamin Shillitoe^{6,6}, Cristina Celma⁶, Mary Slatter^{6,7}, Terry Flood⁵, Robin Gopal¹, Javier Martin⁶ & Maria Zamboni¹ 



1998	C → T	VP3	79	UCG → UTG	S → L	15%
2020	A → G	VP3	86	UCA → UCG		100%
2032	A → T	VP3	90	GCA → GCT		100%
2034	T → C	VP3	91	UUU → UCU	F → S	100%
2041	G → A	VP3	93	CCG → CCA		100%
2047	G → A	VP3	95	UUG → UUA		100%
2128	T → C	VP3	122	GGU → GGC		8%
2239	C → T	VP3	159	GGC → GGT		31%
2285	A → G	VP3	175	ACA → GCA	T → A	100%
2323	C → T	VP3	187	GGC → GGT		31%
2383	T → C	VP3	207	AGU → AGC		100%
2440	A → T	VP3	226	CGA → CGT		100%
2455	T → C	VP3	231	AUU → AUC		100%
2464	T → C	VP3	234	UCU → UCC		8%
2493	C → T	VP1	6	ACU → ATU	T → I	100%
2547	G → C	VP1	24	AGC → ACC	S → T	4%
2572	C → T	VP1	32	GGC → GGT		100%
2577	C → T	VP1	34	GCG → GTG	A → V	8%
2602	C → T	VP1	42	CUC → CUT		15%
2636	G → A	VP1	54	GCA → ACA	A → T	100%
2668	A → G	VP1	64	GUA → GUG		8%
2677	A → G	VP1	67	CGA → CGG		100%
2695	C → T	VP1	73	UCC → UCT		100%
2719	C → A	VP1	81	CGC → CGA		8%
2722	G → A	VP1	82	GGG → GGA		100%
2749	C → T	VP1	91	GAC → GAT		92%
2878	C → T	VP1	134	UUC → UUT		8%
2887	C → T	VP1	137	ACC → ACT		54%
2903	G → A	VP1	143	GCU → ACU	A → T	100%
2908	T → C	VP1	144	AAU → AAC		8%
2911	T → C	VP1	145	AAU → AAC		100%

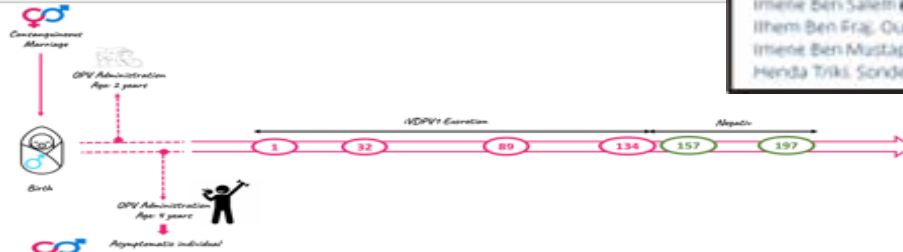


Apport of NGS sequencing



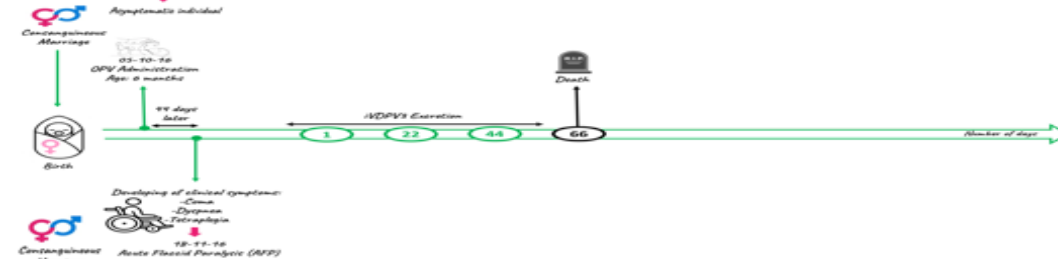
Patient A

VDVP1
2009



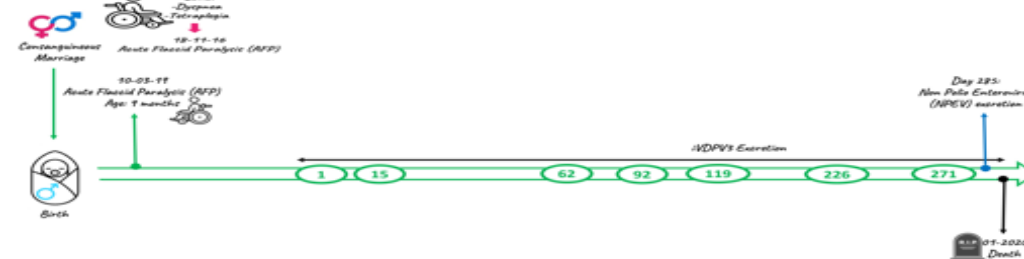
Patient B

VDVP3
2016



Patient C

VDVP3
2019

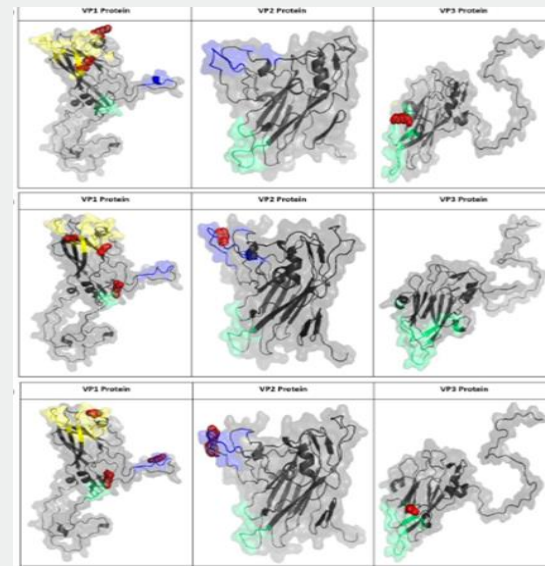
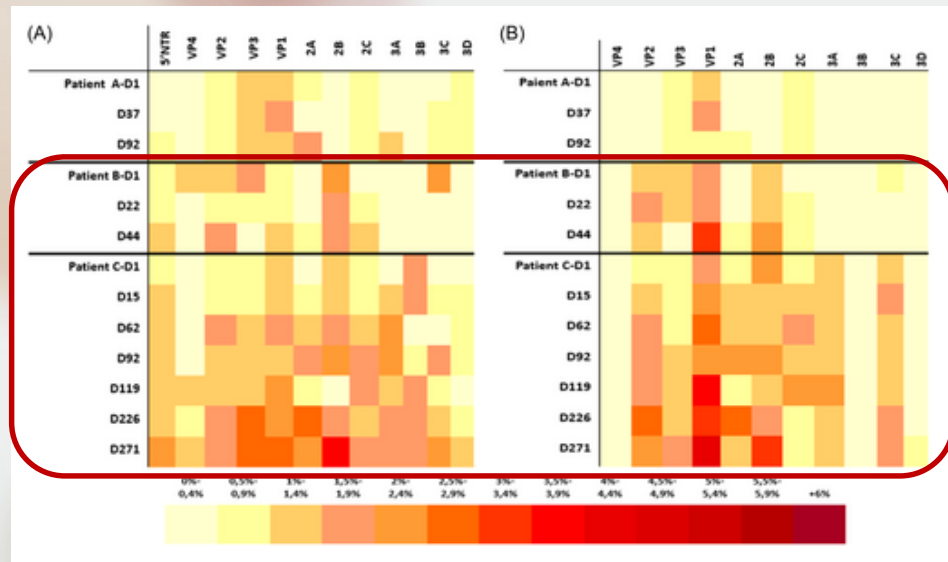


SCAN ME

Apport of NGS sequencing

Table 2. Neurovirulence reverse mutations.

Patient	Region	Serotype	Function	Position	Amino acid change and positions
Patient A	5'UTR	Type 1 VDPV	Affect the RNA secondary structure ³⁵	G480A*	No change
	VP1		Temperature resistance ³⁶	A2775C*	Lys99Thr*
				A2749G*	Ile90Met*
				A2795G*	Thr106Ala*
Patient B and Patient C	5'UTR	Type 3 VDPV	Affect the RNA secondary structure ^{31, 34}	T472C*	No change
	VP3		ts* phenotype ^{31, 34}	T2034C*	Ser91Phe*

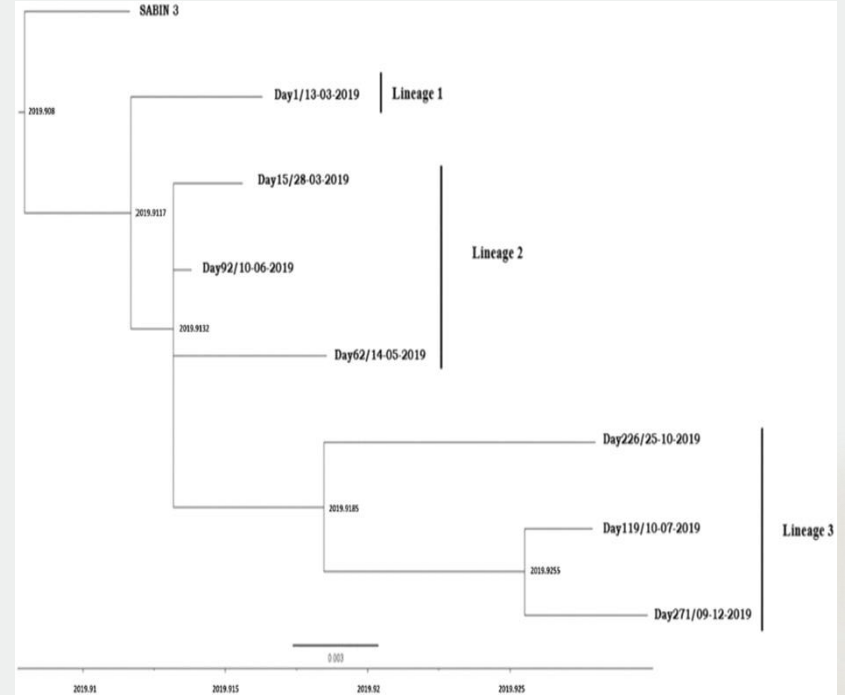


Apport of NGS sequencing

Patient 2

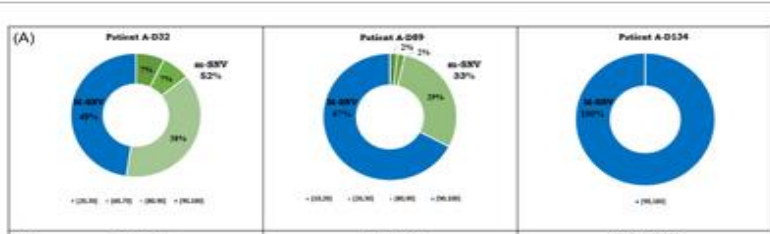


Patient 3

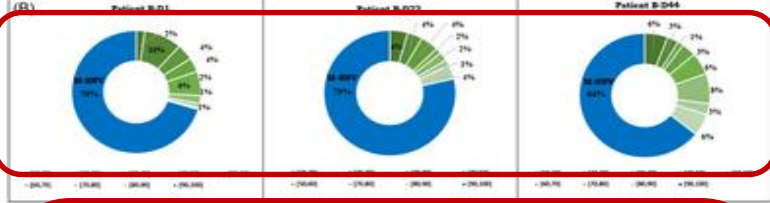


PV/EV surveillance of PID in Tunisia

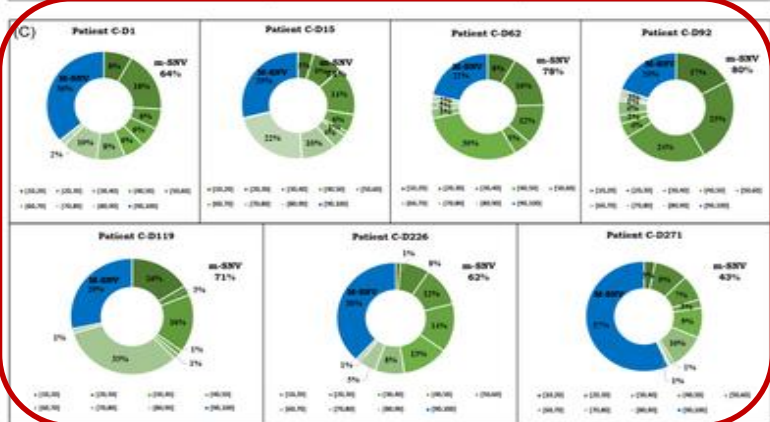
Patient 1



Patient 2



Patient 3



Possible role of genetic and intra-host diversity in the prolonged virus shedding as well as the genesis of virulent strains.

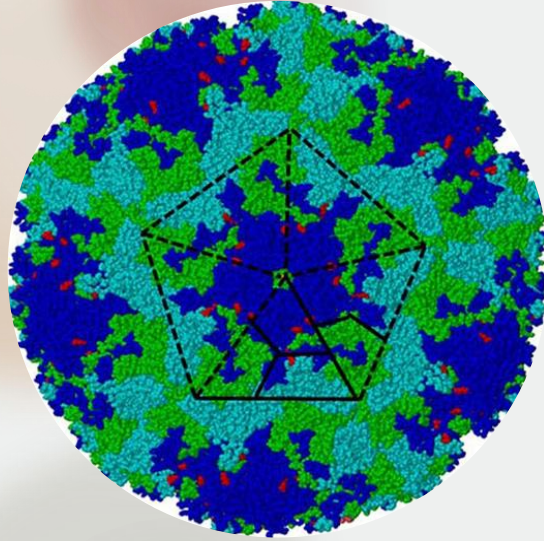
Apport of NGS sequencing

Complete genome characterization provides valuable information

for the patient management and treatment

as well as rapid detect of potential epidemic strains

establishment of an efficient public health responses for any VDPV
emergence and spread.



05

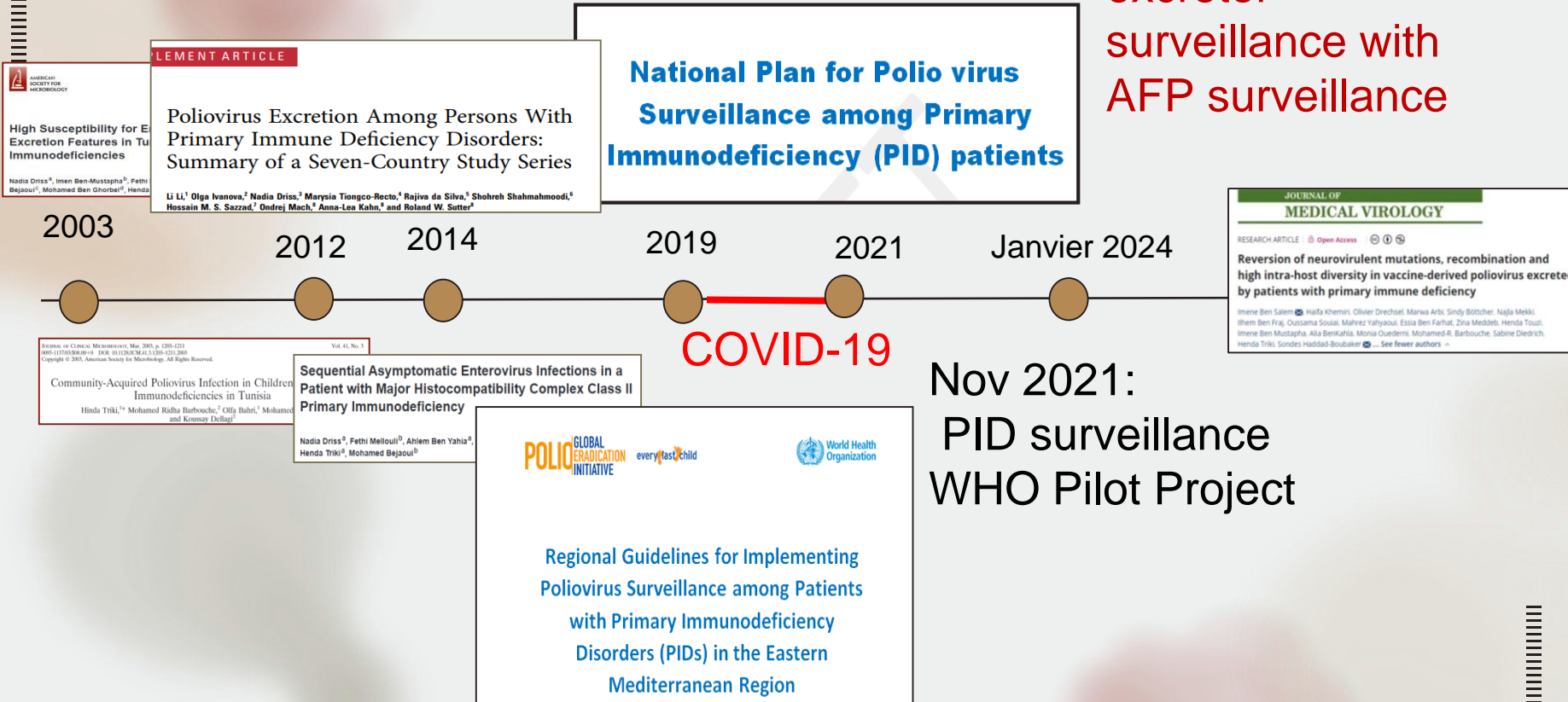
PV/EV surveillance of PID in Tunisia

PV/EV surveillance of PID in Tunisia

- Last Paralytic case due to WPV: 1992
- Last detection in asymptomatic case: 1994
- No epidemic due to cVDPV
- No WPV importation but it is still possible
- Good vaccination coverage & performant AFP surveillance system
- No regular surveillance of poliovirus/enterovirus excretion in ID patients in Tunisia, until November 2021

PV/EV surveillance of PID in Tunisia

Integration of PID
excretor
surveillance with
AFP surveillance



PID line list

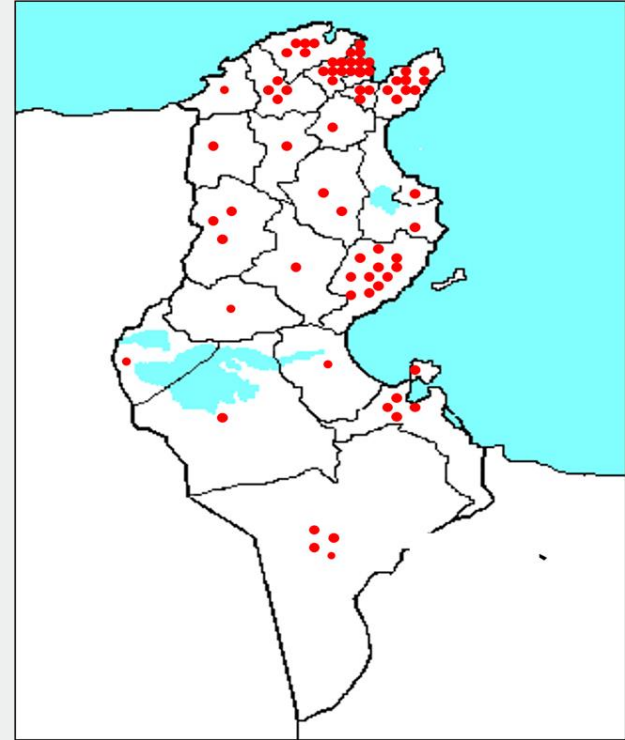
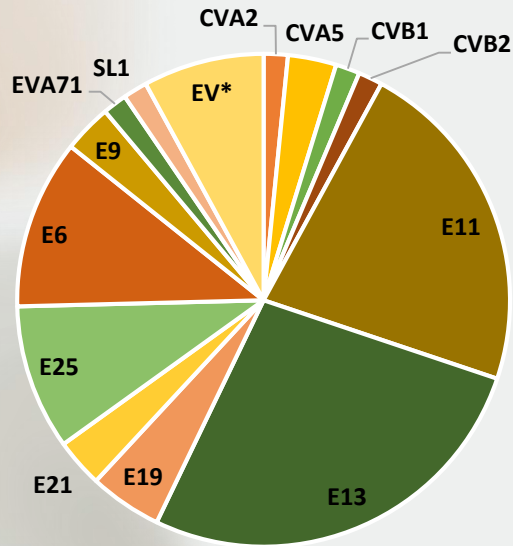
As of 19 May 2025

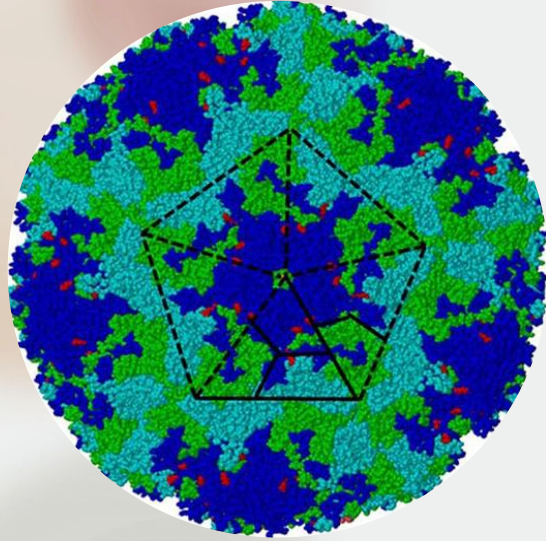
Included patients: 144

Patients refusing sampling: 4

Died patients: 11

Transplanted patients: 9





06

Conclusion

- The prolonged excretion and evolution of PVs in patients with Primary Immunodeficiency (PID) pose **major concerns for the Global Polio Eradication Initiative (GPEI)**.
- in-depth genetic characterization of complete genomes of the excreted PV/EV strains adds **new genomic data and knowledges, on the limited global PV/EV excretion**.
- Studies showed **Huge genomic diversity, Multiple variants and lineages** that have been diverged for rapid adaptation to new environments and resistance to host immune stress.
- Complete genome characterization provides valuable information for the **patient management and treatment** as well as establishment of **an efficient public health responses** for any VDPV emergence and spread.

Acknowledgments



WHO: HQ- EMRO – WR-TUN
Collaborators



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[illegible]

Pleconaril antiviral is a 3C protease inhibitor, developed by Pfizer [58] against picornaviruses including most Enteroviruses and Rhinoviruses.

The safety of Pleconaril was proved in adults [60] and pediatric population such as children [61] and neonates [62-63] for enteroviral and Rhinoviral treatment. Nevertheless, pleconaril resistant strain against Echovirus 11 was identified in immunocompromised patient and it was also resistant to intravenous immunoglobulin, used in combined treatment [64]. Thus, further investigation was suggested since multiple factors such as immunity status may play a role in the development of resistant strains [64].