

Short report on type 2 polioviruses detected in the USA, ISRAEL and the UK

As of 28 July 2022

In the past week the Global Polio Laboratory Network had convened several meetings to collate and analyze genetic data on PV2 detections in several countries. The following narrative is a summary of critical findings.

In July 2022, sequencing by the Global Specialized Laboratory at US CDC of three sewage samples obtained on June 6th, 13th and 21st 2022 in Rockland County (New York, USA) yielded identical VP1 sequences characterized as SL2 with four nucleotide differences from Sabin 2. Stool samples collected from a paralytic case in the same county on June 28th and 29th yielded a VP1 sequence presenting 10 mutations from Sabin 2 that is genetically linked to the sewage sequences (99.34% identity; four shared nucleotide differences from Sabin 2).

Comparison between VP1 sequences obtained from the sewage samples and the AFP case in Rockland County (NY) with SL2 isolates, obtained from sewage samples collected in Israel between January and June 2022 and shared by the National Polio Laboratory in Tel-Aviv, show the following results:

- 1) The SL2 sequence collected on June 5th, 2022, in the Sorek Waste Water Treatment Plant (which shows five nucleotide differences from Sabin 2 reference strain, i.e 99.45% identity) had only one nucleotide difference to the Rockland County (NY) sewage sequence (99.89% identity between the two).
- 2) The closest match for the Rockland County sewage sequence is the Sorek (ISR) sequence (99.89% identity between the two).
- 3) The four VP1 nucleotide substitutions from Sabin 2 detected in the Rockland sewage are also found in the Sorek sequence. Sorek and Rockland sewage sequences share 80% of all variable sites (nucleotide differences from Sabin 2). This is evidence of genetic linkage.



Furthermore, guided by epidemiological findings a wider comparative analysis of available complete genomes from Israel, USA and United Kingdom samples (shared by the Global Specialized Laboratory at NIBSC, MHRA) showed significant shared genetic ancestry for PV2s isolated in the three countries. Indeed during February-June 2022, UK reported PV2 detections collected from environmental sites in London. Complete capsid sequences of Israel, USA, and UK isolates clearly showed evidence of shared genetic ancestry (>99.0% identity). In addition, they showed a common recombinant block with possibly an unknown species C enterovirus at the P3/Non Capsid region, providing further evidence of the genetic relationships among the isolates from the three countries (ISR, USA and UK).

In summary, VP1 sequences from sewage samples collected in Israel (Sorek Waste Water Treatment Plant), USA (Rockland County), UK (Beckton Waste Water Treatment Plant) and the VP1 sequence from the AFP case in Rockland, showed genetic linkage between the isolates. Further analysis of the whole genome sequences of these viruses will continue at the USA Global Specialized Laboratory (US CDC), the National Polio Laboratory in Tel-Aviv, and the UK Global Specialized Laboratory (NIBSC, MHRA) for in-depth characterization of all relevant viruses and results will continue to be reported to the GPEI as soon as they are available.

