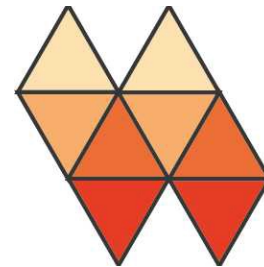


Sep 05, 2023 Version 2

Poliovirus direct detection and nanopore sequencing (DDNS) FAQs V.2



DOI

dx.doi.org/10.17504/protocols.io.bp2l619ezvqe/v2

Alex Shaw¹, Catherine Troman¹, Joyce Akello¹, Erika Bujaki², Manasi Majumdar², Javier Martin², Nick Grassly¹

¹Imperial College London; ²National Institute for Biological Standards and Control

Poliovirus Sequencing Co...



Nick Grassly

Imperial College London

OPEN  ACCESS



DOI: dx.doi.org/10.17504/protocols.io.bp2l619ezvqe/v2

Document Citation: Alex Shaw, Catherine Troman, Joyce Akello, Erika Bujaki, Manasi Majumdar, Javier Martin, Nick Grassly 2023. Poliovirus direct detection and nanopore sequencing (DDNS) FAQs. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.bp2l619ezvqe/v2> Version created by **Nick Grassly**.

License: This is an open access document distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Created: September 04, 2023

Last Modified: April 19, 2024

Document Integer ID: 87317

Funders Acknowledgement:

**Bill and Melinda Gates
Foundation**

Abstract

This short FAQ document summarises the poliovirus direct detection and nanopore sequencing (DDNS) protocol, the equipment and reagents required, the cost and staff-time involved (v1.7 updated 4 Sep 2023).

Poliovirus Direct Detection and Nanopore Sequencing (DDNS) FAQs

Overview

Direct Detection by Nanopore Sequencing (DDNS) allows rapid molecular detection and sequencing of poliovirus from stool samples in a simple integrated protocol [1]. It replaces cell culture, intratypic differentiation (ITD) and Sanger sequencing, allowing case confirmation by generating a VP1 sequence within 3 days of sample processing [2]. It can be performed in any laboratory with experience conducting PCR, bringing sequencing capacity to many more Global Polio Laboratory Network (GPLN) labs. This short FAQ document summarises the method, the equipment and reagents required, the cost and staff-time involved.

What is DDNS?

Poliovirus DDNS involves a nested PCR reaction [3] using custom barcoded primers, followed by nanopore sequencing of the VP1 product. Unlike traditional Sanger sequencing, nanopore allows samples containing multiple polioviruses or other enteroviruses to be correctly identified and sequenced. This is because individual, full length DNA strands are read as they pass through pores on a nanopore flow cell. Each flow cell contains 512 nanopores that rapidly read DNA strands, typically generating 1 million VP1 reads per hour. Flow cells can be re-used several times if washed with a nuclease solution after use. The protocol is summarised in the Appendix below and is available on protocols.io from the poliovirus sequencing consortium.

What do I need?

Laboratory Space: The DDNS protocol should be performed in a Biosafety level 2 (BSL-2, or equivalent) laboratory and ideally in three separate working areas:

- Area 1 RNA extraction is performed in a dedicated Class I or II biosafety cabinet
- Area 2 Nested PCR is performed in a dedicated PCR hood with a separate “clean” hood for the preparation of master mixes
- Area 3 Library preparation and sequencing area can be performed on the benchtop

Areas 2 and 3 could be combined if necessary.

Equipment: The equipment and ‘one-off’ purchases required to implement the DDNS protocol are:

A	B	C
Item	Number	Total cost (US\$)
Plate centrifuge	1	900
Vortex	1	270
Mini centrifuge	1	280
Micropipette p10	3	780
Micropipette p20	3	780
Micropipette p200	3	780
Micropipette p1000	3	780

A	B	C
Multichannel P10	1	1,690
Microtube magnetic stand	1	70
Qubit fluorometer	1	4000
Thermocycler	1	5,200
Gel electrophoresis tank or Tape station	1	370
High performance GPU laptop and MinION sequencer	1	5,000
<i>Kingfisher Duo* (optional)</i>	<i>1</i>	<i>22,100</i>
<i>Magnetic stand for 12 microtubes †</i>	<i>1</i>	<i>300</i>
Total (with Kingfisher Duo)		44,000
Total (without Kingfisher Duo)		22,200

*Helpful for high-throughput labs, allowing processing of 12 samples simultaneously for RNA extraction (or 96 samples for a Kingfisher Flex at USD\$ 57,000). Otherwise, manual RNA extractions can be performed, using the equipment marked with †.

Consumables: In addition to the setup costs, consumables and reagents are:

A	B	C
Items	Storage/Shipping	Supplier
SuperScript III One-Step RT-PCR System (Platinum Taq)	Frozen	Thermo Fisher, Carramore
DreamTaq	Frozen	Thermo Fisher, Carramore
NEB Quick Ligase	Frozen	New England Biolabs, Carramore
NEB End preparation module	Frozen	New England Biolabs, Carramore
Agencourt AMPure XP beads	Refrigerated	Beckman Coulter, Carramore
Ligation Sequencing Kit	Refrigerated	Oxford Nanopore, Carramore
MinION Flow cells	Refrigerated	Oxford Nanopore, Carramore
Flow cell wash kits	Refrigerated	Oxford Nanopore, Carramore
PanEV primers and barcoded VP1 primers	Room temp	Eurofins, IDT, etc.
Plasticware (tips, 1.5 mL microtubes, 0.2 mL PCR tubes, Qubit assay tubes, racking for tubes, chiller racks)	Room temp	Local

Staff: The DDNS protocol can be performed by staff familiar with PCR and molecular biology techniques. The PIRANHA software is self-explanatory. We recommend laboratories implementing DDNS carefully plan their data management

process. Piranha produces a detailed run report based on a barcode file provided by the user that can be used to store and report data. Staff time requirements are given in the appendix.

How much does it cost?

Estimated costs without any bulk discounts are given below, based on automated RNA extraction via the Kingfisher. Sequencing batches containing greater numbers of samples (up to 96, including controls) give better value per sample, as the cost of performing a sequencing run is fixed, regardless of the number of samples included.

A	B
Samples processed per week	Cost per sample (\$US)
25	25
50	19
90+	16

*Low through-put laboratories can perform manual RNA extractions (e.g. via Magmax viral RNA kit for a similar price.

How sensitive and specific is it?

Preliminary data from pilot GPLN laboratories indicate that DDNS has equivalent sensitivity and specificity to cell culture when testing fresh or recently frozen samples (<2 months old). [1,4]

What QA/QC procedures are in place?

The protocol has been streamlined to mitigate human error and the techniques involved will be familiar to staff who have performed ITD by qPCR. Once RNA extraction is completed, samples and barcoded primers can be handled with multichannel pipettes, facilitating accurate and high-throughput sample processing, minimising risks of cross contamination. A positive control for RNA extraction, nested PCR and nanopore sequencing is available from NIBSC and is undergoing review by WHO ECBS as an international standard. A detailed quality assurance program is in development.

Can it be used for environmental surveillance samples?

The method can be used with RNA extracted from environmental surveillance (ES) samples, although sensitivity depends on sample processing and sample volume undergoing RNA extraction. Pilot DDNS with ES samples is underway in selected GPLN labs.

References

1. Shaw AG, Majumdar M, Troman C, Toole Á, Benny B, Abraham D, Prahara J, Kang G, Sharif S, Alam MM, Shaikat S, Angez M, Khurshid A, Mahmood N, Arshad Y, Rehman L, Mujtaba G, Akthar R, Salman M, Klapsa D, Hajarha Y, Asghar H, Bandyopadhyay A, Rambaut A, Martin J, Grassly N. Rapid and Sensitive Direct Detection and Identification of Poliovirus from Stool and Environmental Surveillance Samples by Use of Nanopore Sequencing. *J Clin Microbiol* **2020**; 58.

<https://pubmed.ncbi.nlm.nih.gov/32611795/>

2. Shaw AG, Cooper LV, Gumede N, Bandyopadhyay AS, Grassly NC, Blake IM. Time Taken to Detect and Respond to Polio Outbreaks in Africa and the Potential Impact of Direct Molecular Detection and Nanopore Sequencing. *The Journal of Infectious Diseases* **2021**:jjab518. <https://pubmed.ncbi.nlm.nih.gov/34623444/>

3. Arita M, Kilpatrick DR, Nakamura T, et al. Development of an efficient entire-capsid-coding-region amplification method for direct detection of poliovirus from stool extracts. *J Clin Microbiol* **2015**; 53:73-8.

<https://pubmed.ncbi.nlm.nih.gov/25339406/>

4. Shaw AG, Mampuela TK, Lofiko EL, Pratt C, Troman C, Bujaki E, O'Toole Á, Akello JO, Aziza AA, Lusamaki EK, Makangara JC, Akonga M, Lay Y, Nsunda B, White B, Jorgensen D, Pukuta E, Riziki Y, Rankin KE, Rambaut A, Ahuka-Mundeké S, Muyembe J-J, Martin J, Grassly NC, Mbala-Kingebeni P. Sensitive poliovirus detection using nested PCR and nanopore sequencing: a prospective validation study. *Nature Microbiology* **2023**; 8: 1634-40

<https://www.nature.com/articles/s41564-023-01453-4>

Appendix: protocol summary

The DDNS method can be performed directly on stool suspension and involves the following steps (summarised in Figure 1):

1) RNA extraction – Extraction can be manual or automated (e.g. using a Kingfisher machine). We recommend the Thermofisher MagMAX Viral RNA kit.

2) Nested RT-PCR - Amplification of the VP1 region is performed using a nested PCR; the sensitivity of this approach has been validated for a wide range of polioviruses. First, the enterovirus capsid region is amplified by RT-PCR, then the product is added directly to a VP1 PCR using barcoded primers. A set of 96 barcoded primers in plate format allow multiplexing of up to 96 samples.

3) Sample pooling - 2 µL of all samples tested are pooled together. This reduces both the cost and time required for sample cleaning and quantification, and the associated potential for error or cross-contamination during these steps. Including samples negative for poliovirus does not use significant sequencing chemistry (other than to identify any non-polio enteroviruses amplified by the nested PCR).

4) Sequencing library preparation - The sample pool is cleaned with AMPure beads to remove enzymes and primers, and the sequencing adaptor ligated onto the amplified DNA.

5) Nanopore sequencing - Sequencing of the VP1 amplicons can be performed on any Oxford Nanopore Technologies device. For data to be processed in real-time, a MinION Mk1B controlled by a high-specification GPU laptop is recommended.

6) Data analysis - Sequencing reads are split between samples, mapped to a poliovirus reference database and consensus sequences generated using PIRANHA (<https://github.com/polio-nanopore/piranha>). The software is available as a command line version or with a graphical user interface for Linux, Mac or Windows machines.

The complete protocol is maintained and freely available at <https://www.protocols.io/workspaces/poliovirus-sequencing-consortium/>

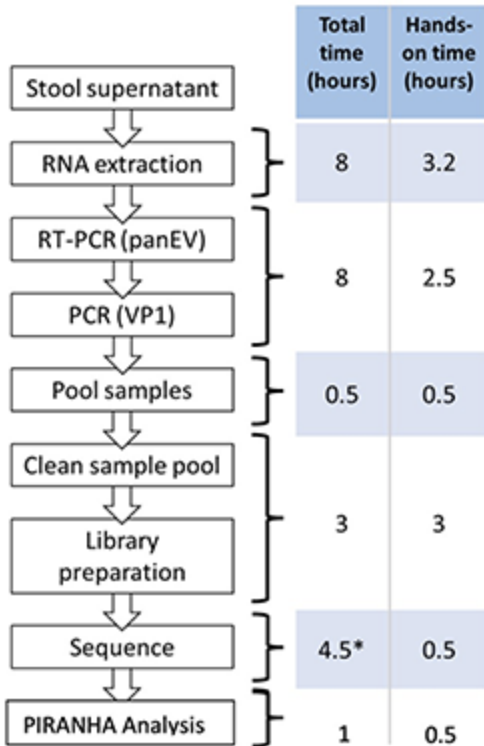


Figure 1 – Steps of the DDNS protocol. Timings shown are for 96 samples with automated extraction (batches of 12, Kingfisher Duo). Manual extractions will require 1.25 hours per batch of 12 (kit dependent). High throughput extraction (Kingfisher FLEX) can process 96 samples in one hour.

* Run duration can be varied.