Global Grand Challenges: Application of Metagenomic Next Gen Sequencing to Detect & Identify Pathogens

Sponsor

Bill & Melinda Gates Foundation

Program

Global Grand Challenges Explorations (GCE) (Round 22)

For More Information

Grand Challenges Explorations - New Call [1]

Tips from Reviewers [2]

Frequently Asked Questions [3]

Grand Challenges Explorations - General Rules & Guidelines [4]

Description

In order to identify and treat existing and emergent infectious disease efficiently, clinicians and the global health community must have access to accurate and timely estimates of disease burden and distribution. Traditionally, summaries of these data have been manually reported by national health ministries from regional clinical data, aggregated from local health centers. Local institutions, however, face multiple challenges to accurately assess the emerging needs of their community with current toolsets.

Recent breakthroughs in pathogen sequencing technology - both at the hardware and software level - enable the combination of rapid deep sequencing of patient samples with subsequent sequence mapping to a custom, continuously updated reference database to provide near-real-time pathogen detection. Yet, these advancements alone have not been sufficient to provide metagenomic sequencing to patients in low- and middle-resource settings that could benefit the most, largely due to limitations in access or availability of the following essential components: a) expensive equipment/reagents, b) specialized biochemical training, c) accurate reference pathogen sequence databases, d) and advanced computational analytics.

The Bill & Melinda Gates Foundation has partnered with the Chan Zuckerberg Biohub and the

Chan Zuckerberg Initiative to enable patients in low- and middle-resource settings to benefit from cutting-edge pathogen detection and discovery. This partnership will provide highly specialized training in biosample preparation and sequencing to technical staff from awardee global health centers. Trainees will learn to use the open-source, open-access IDseq [5] software developed by CZ-Biohub for the global health community to upload and analyze patient sequencing data. The BMGF-CZ-Biohub partnership will therefore aim to provide selected applicants the benefits of onsite next generation sequencing and rapid pathogen detection to better understand their local pathogen landscape. The Foundation is specifically seeking projects that endeavor to build upon their initial locally-focused effort to contribute to future data-informed decision-making at the population level via data sharing and pathogen data comparison across sites.

Examples of insights could include:

1.
    Deciphering unknown medical cases

2.
    Identification of new pathogens

3.
    Detection of local outbreaks

4.
    Characterization of the local pathogen landscape, including vector-borne diseases

5.
    Detection and classification of AMR Markers, with potential for insight into antibiotic treatment discordance

6.
    Data-informed healthcare and resource allocation

Grantees will be expected to partner closely with scientists and engineers and provide feedback to help guide the cloud computing software's development. Sites will also be expected to share data and collaborate with other labs in the network.

Eligibility

Applicants can be at any experience level; in any discipline; and from any type of organization, including colleges and universities, government laboratories, research institutions, non-profit organizations and for-profit companies.

Eligible Projects & Sites:

- Provide a clearly scoped initial project that demonstrates why this technology will provide insights that are not currently possible.
- Have space and capacity to run samples on a basic, globally rugged sequencer once provided with training, reagents, sequencer, and a dedicated computer.
- Have consistent access to electricity and the ability to upload data via internet to a designated cloud server at least once a day.
- Are willing to give product feedback and collaborate with an engineering team through scheduled video calls, email, or other messaging service.
- Are committed to open science, preprints, and data sharing.
- Already have, or can rapidly acquire, necessary IRB approval for pathogen DNA and RNA sequence sharing from patients.
- Include neonatal and infant patients as a substantial fraction of overall sampling
- Are representative of larger geographic regions

Ineligible Projects & Sites:

- Do not articulate how they will leverage the value of next generation sequencing to impact health outcomes.
- Are interested exclusively in Whole Genome Sequencing
- Do not plan to share their pathogen data and discoveries.
- Have extremely limited internet access.
- Are limited to previously stored samples, without substantial potential for prospective sample collection.

Maximum Project Value

Initial grants are for $100,000 USD (Phase I) and successful projects are eligible to receive follow-on funding of up to $1M USD (Phase II).

Indirect Costs

0%

Project Duration

Through this GCE award, BMGF will support travel and accommodation of grantees for pilot analysis of samples from their home region during hands-on, intensive mentoring provided by the CZ-Biohub in San Francisco. This two week instructional period will include both biochemical sample preparation for sequencing and bioinformatic analysis using the IDseq software platform. Specifically, the hands-on training for bench scientists will include best practices and standards for sample processing, DNA & RNA extraction, library preparation and data analysis on the Global IDseq software platform. Upon completion of training at CZ-Biohub, laboratory teams are expected to use the remaining GCE award primarily on the following items: 1) a sequencer suitable for the global health environment, 2) a dedicated sequencing technician, and 3) sequencing reagents for the duration of the award.

The combination of intensive training with molecular, capital equipment, reagent, and personnel support is intended to maximize the potential for sustainable, prospective, onsite analysis of patient samples upon return to the home site.

Please see the list of compatible sequencers appropriate for global health use . [6]

Deadlines

If College-level review is required, your College will communicate its earlier internal deadlines.

Type	Date	Notes
Internal Deadline	Wednesday, November 21, 2018 - 4:30pm	Please submit your application/proposal, along with a complete OR-5 to research.services@uoguelph.ca [7]
External Deadline	Wednesday, December 5, 2018 - 2:30pm	PI to submit full application directly to the sponsor by 2:30pm EST (11:30am PST) using the GCE online portal. [8]

How to Apply

Full application instructions can be accessed here: https://gcgh.grandchallenges.org/application-instructions [9]

If you are an existing user, you can log in to your existing account [10]. New users must create an account [11] and submit proposals through the online portal.

Applicants are encouraged to use the provided application form (see Attachments). Applicants are required to submit either a Microsoft Word or PDF document; no more than two pages in length. Please do not include a cover sheet with your proposal. A cover sheet will be automatically generated from your registration data.

Attachment(s)

Attachment	Size
GCE Application Form [12]	60 KB

Attachment	Size
📊 GCE Rules & Guidelines [13]	264.19 KB

For Questions, please contact

Please direct all questions about this initiative, selection criteria, or application instructions by e-mail to the following address: GCEhelp@gatesfoundation.org [14].

Office of Research

Carolyn Osborn, Senior Manager, Grants & Contracts
Research Services Office
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Alert Classifications**Category:**
Funding Opportunities and Sponsor News

Disciplines:

Health and Life Sciences
Information and Communications Technology
Physical Sciences and Engineering

**Source
URL:**https://www-research.uoguelph.ca/research/alerts/content/global-grand-challenges-application-metagenomic-next-gen-sequencing-detect-identify

Links

[1] https://gcgh.grandchallenges.org/challenge/application-metagenomic-next-generation-sequencing-detect-and-identify-pathogens-round-22
[2] https://gcgh.grandchallenges.org/sites/default/files/GCE_ApplicantTips.pdf
[3] https://gcgh.grandchallenges.org/grant-opportunities/faq/gce#t16n37081
[4] https://gcgh.grandchallenges.org/sites/default/files/additional-materials/GCE_Rules_and_Guidelines_Round22.pdf
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