

COMING SOON

GATES OPEN RESEARCH



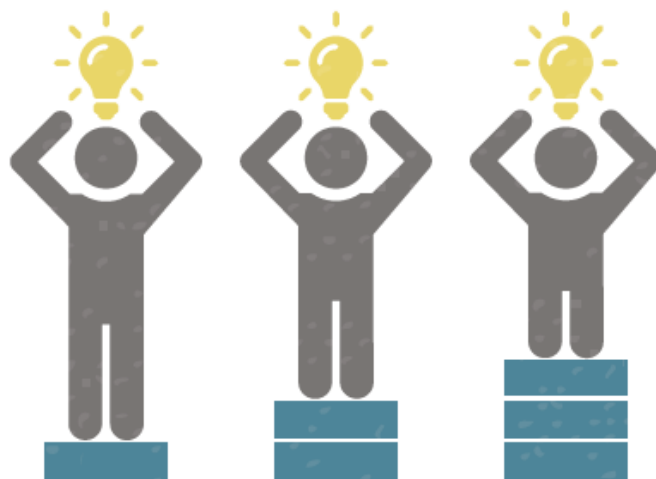
CEGA
May 26, 2017

Ashley Farley, Associate Officer, Knowledge & Research Services, Bill & Melinda Gates Foundation

Phil Dooner, Associate Publisher, F1000

Gates Commitment to Open Access is Mission Driven

Barrier-free access to foundation-funded research advances innovation and helps create a world where everyone has the opportunity to lead a healthy and productive life.



Open Access Policy: Four requirements and a commitment

The Gates Foundation's Open Access Policy enables the unrestricted access and reuse of all its peer-reviewed published research funded, in whole or in part, by the foundation, including any underlying data sets.

REQUIREMENT #1: Publications are discoverable and accessible online

REQUIREMENT #2: Publications will be on Open Access terms, i.e., published under a CC-BY license

REQUIREMENT #3: Publication will be accessible and open immediately, i.e., no embargo

REQUIREMENT #4: Underlying data supporting the published research must also be accessible and open immediately

COMMITMENT: Foundation will pay reasonable fees to publish on the above requirements*

*Special Issues/Supplements – only the APC's will be covered

What does this mean for Gates Foundation grantees?

- All grant agreements signed after January 1st, 2015 contain the following clause:

PUBLICATION IN PEER-REVIEWED JOURNALS

If You seek publication of Funded Developments in a peer-reviewed journal, such publication shall be under “open access” terms and conditions consistent with the Foundation’s Open Access Policy available at: <http://www.gatesfoundation.org/How-We-Work/General-Information/Open-Access-Policy>, which may be modified from time to time.

- This clause is non-negotiable – no exceptions will be made
- Grantee who have signed agreements prior to January 1, 2015, can opt-in to publish on open access terms and the foundation will pay the necessary fees to do so.
- Our goal is to reach 100% compliancy so that all Gates funded research is freely available without barrier or restriction.

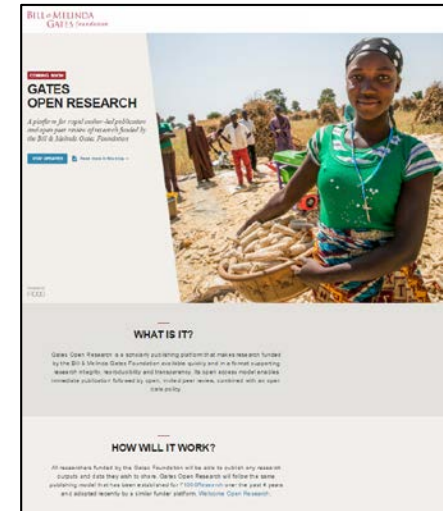
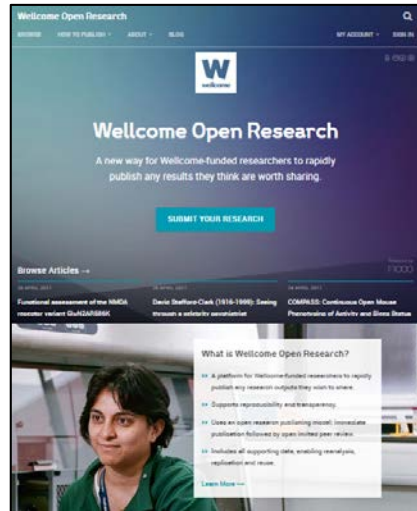
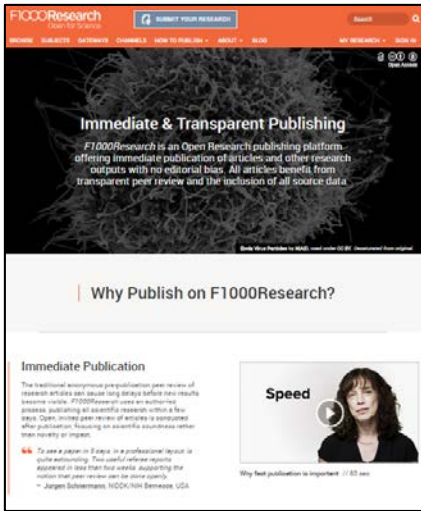
Introducing Gates Open Research

An open access publishing platform where Gates-funded researchers can publish any results they think are worth sharing.

- Allow research to be disseminated without delay - especially crucial during public health emergencies
- Increase transparency and make it easier for researchers to support reproducibility

<https://gatesopenresearch.org/>

Open Research publishing platforms



- F1000's own platform
- Launched 2013
- More than 1,600 open access articles published

- Controlled by Wellcome, operated by F1000
- Launched Nov 2016
- More than 60 articles published since launch

- Controlled by the Gates Foundation, operated by F1000
- To be launched in Q3 2017

What is different about Gates Open Research?

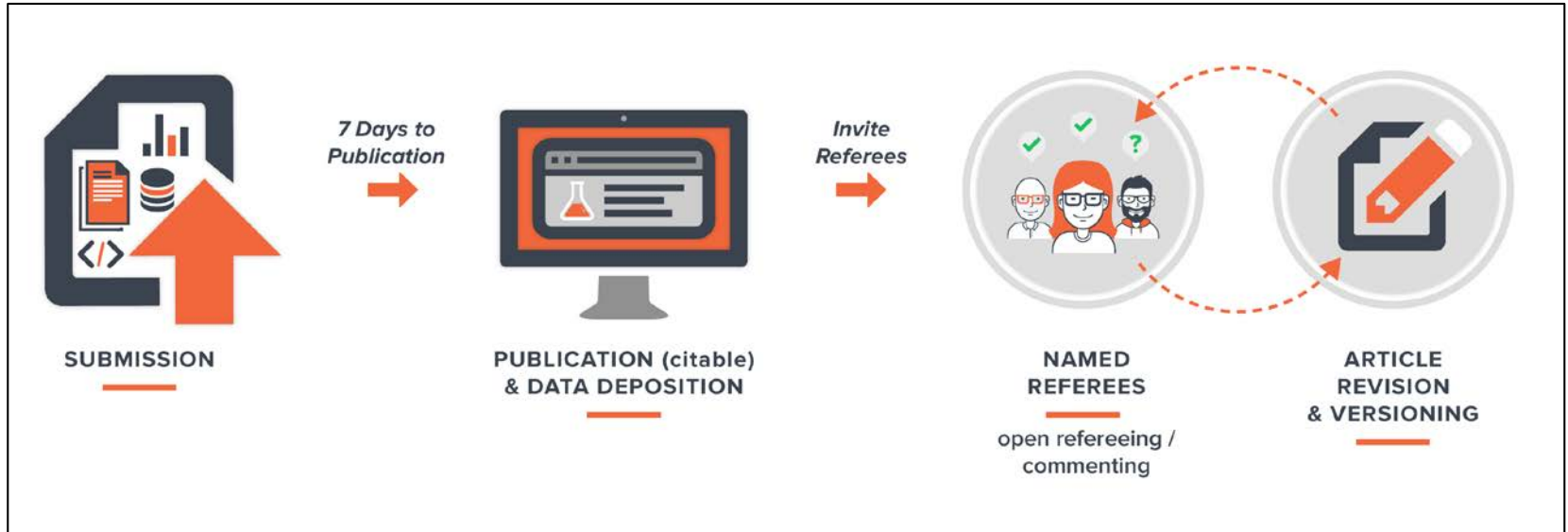
- **Fast** – articles published within a week
- **Inclusive** – *all* Gates-funded research outputs are suitable: traditional research articles, methods, software, data sets, protocols, negative and confirmatory results etc.
- **Open** – fulfils the foundation's OA and data sharing requirements
- **Reproducible** - source data and code published alongside article
- **Transparent** – open, author-led publishing
- **Easy** – all costs are directly covered by the Gates Foundation

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How does it work?



- **Peer review *after* publication** (no 'Editor', but in-house pre-pub checks)
- Fully transparent peer review (referee names, report and rating)
- Access to source data
- "living articles": **Versioning** (also in PubMed) for revisions, corrections, updates

Publication without delay

The screenshot shows a research article page on Wellcome Open Research. The article title is "Geographic-genetic analysis of *Plasmodium falciparum* parasite populations from surveys of primary school children in Western Kenya [version 1; referees: awaiting peer review]". The authors listed are Irene Omedo, Polycarp Mogeni, Kirk Rockett, Alice Kamau, Christina Hubbard, Anna Jeffreys, Lynette Isabella Ochola-Oyier, Etienne P. de Villiers, Caroline W. Gitonga, Abdisalan M. Noor, Robert W. Snow, Dominic Kwiatkowski, and Phillip Bejon. The article is in a "RESEARCH ARTICLE" state with an "EDIT VERSION" button. A "Check for updates" button is also present. The article is annotated with three callouts: "Usage data" pointing to the metrics sidebar, "Version and peer review status" pointing to the article title, and "Article is immediately citable, with DOI" pointing to the "Cite" button in the sidebar. The sidebar includes metrics (92 views, 27 downloads) and options to get PDF, XML, or cite. The "Open Peer Review" section shows a status of "AWAITING PEER REVIEW". The "Comments on this article" section shows 0 comments. A "Sign up for Table of Contents Alerts" form is also visible.

Wellcome Open Research

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Version and peer review status

RESEARCH ARTICLE EDIT VERSION

Check for updates

Geographic-genetic analysis of *Plasmodium falciparum* parasite populations from surveys of primary school children in Western Kenya [version 1; referees: awaiting peer review]

Irene Omedo¹, Polycarp Mogeni¹, Kirk Rockett², Alice Kamau¹, Christina Hubbard², Anna Jeffreys², Lynette Isabella Ochola-Oyier¹, Etienne P. de Villiers^{1,3,4}, Caroline W. Gitonga⁵, Abdisalan M. Noor^{3,5}, Robert W. Snow^{3,5}, Dominic Kwiatkowski^{2,6}, Phillip Bejon^{1,7}

Author affiliations

Grant information

Abstract

Background. Malaria control, and finally malaria elimination, requires the identification and targeting of residual foci or hotspots of transmission. However, the level of parasite mixing within and between geographical locations is likely to impact the effectiveness and durability of control interventions and thus should be taken into consideration when developing control programs.

Methods. In order to determine the geographic-genetic patterns of *Plasmodium falciparum* parasite populations at a sub-national level in Kenya, we used the Sequenom platform to genotype 111 genome-wide distributed single nucleotide polymorphic (SNP) positions in 2486 isolates collected from children in 95 primary schools in western Kenya. We analysed these parasite genotypes for genetic structure using principal component analysis and assessed local and global clustering using statistical measures of spatial autocorrelation. We further examined the region for spatial barriers to parasite movement as well as directionality in the patterns of parasite movement.

Results. We found no evidence of population structure and little evidence of spatial autocorrelation of parasite genotypes (correlation coefficients <0.03 among parasite pairs in distance classes of 1km, 2km and 5km; p value<0.01). An analysis of the geographical distribution of allele frequencies showed weak evidence of variation in distribution of alleles, with clusters representing a higher than expected number of samples with the major allele being identified for 5 SNPs.

Usage data

METRICS

92 VIEWS

27 DOWNLOADS

Open Peer Review

Referee Status: AWAITING PEER REVIEW

Comments on this article

All comments (0)

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Article is immediately citable, with DOI

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Cite

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Post-publication peer review and revisions

The screenshot shows the Wellcome Open Research interface for a research article. The article title is "Free serum haemoglobin is associated with brain atrophy in secondary progressive multiple sclerosis [version 2; referees: 3 approved]". The article is marked as "REVISED". The authors listed are Alex Lewin, Shea Hamilton, Aviva Witkovter, Paul Langford, Richard Nicholas, Jeremy Chataway, and Charles R.M. Bangham. The article has 1142 views and 168 downloads. The peer review section shows three referees: Hans Lassmann, Simon Hametner, and Franz Fazekas. The review history table shows that Version 2 (published 23 Dec 2016) is the current version, and it has received three approved reports. Version 1 (published 15 Nov 2016) also has three reports, but one is a question mark and one is a question mark with a question mark. The article is citable and has a DOI. The abstract and methods sections are also visible.




Wellcome Open Research

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Check for updates

RESEARCH ARTICLE

REVISED Free serum haemoglobin is associated with brain atrophy in secondary progressive multiple sclerosis [version 2; referees: 3 approved]

✉ Alex Lewin^{1,5*}, ✉ Shea Hamilton ^{2*}, Aviva Witkovter², Paul Langford ², Richard Nicholas³, Jeremy Chataway⁴, ✉ Charles R.M. Bangham ²

* Equal contributors

✚ Author affiliations

✚ Grant information

Abstract

Background: A major cause of disability in secondary progressive multiple sclerosis (SPMS) is progressive brain atrophy, whose pathogenesis is not fully understood. The objective of this study was to identify protein biomarkers of brain atrophy in SPMS.

Methods: We used surface-enhanced laser desorption-ionization time-of-flight mass spectrometry to carry out an unbiased search for serum proteins whose concentration correlated with the rate of brain atrophy, measured by serial MRI scans over a 2-year period in a well-characterized cohort of 140 patients with SPMS. Protein species were identified by liquid chromatography-electrospray ionization tandem mass spectrometry.

Results: There was a significant ($p < 0.004$) correlation between the rate of brain atrophy and a rise in the concentration of proteins at 15.1 kDa and 15.9 kDa in the serum. Tandem mass spectrometry identified these proteins as alpha-haemoglobin and beta-haemoglobin, respectively. The abnormal concentration of free serum haemoglobin was confirmed by ELISA ($p < 0.001$). The serum lactate dehydrogenase activity was also elevated in patients with secondary progressive multiple sclerosis.

METRICS

1142 VIEWS

168 DOWNLOADS

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Get XML

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Open Peer Review

Referee Status: ✓✓✓

Version(s)	1	2	3
REVISED Version 2 published 23 Dec 2016		✓ read report	✓ read report
Version 1 published 15 Nov 2016	✓ read report	? read report	? read report

1 Hans Lassmann, Medical University of Vienna, Austria
Simon Hametner, Medical University of Vienna, Austria

2 George Harauz, University of Guelph, Canada
Vladimir V. Bamm, University of Guelph, Canada

3 Franz Fazekas, Medical University of Graz, Austria
Michael Khalil, Department of Neurology, Medical University of Graz, Graz, Austria, Austria

All reports (5)

Comments on this article

All comments (1)

Add a Comment

Full review history

All versions are citable and have separate DOIs

Open peer review

Referee Report 21 Nov 2016

George Harauz, Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada
 Vladimir V. Bamm, Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada

Views

71

Cite

? Approved with Reservations

Summary – This article describes a proteomics analysis of serum proteins derived from 140 patients with secondary progressive multiple sclerosis (MS), 20 healthy adult volunteers, 20 patients with human T-lymphotropic virus (HTLV-1) causing symptoms resembling spinal MS, and 20 asymptomatic HTLV-1 carriers. Half of the MS patients were undergoing treatment with simvastatin, a drug used to lower blood cholesterol and shown to have immunomodulatory and anti-inflammatory properties. Protein profiling of sera was achieved by mass spectrometry of 475 serum samples collected at 0, 12, and 24 months. (A 6-month time point is mentioned in some places and is queried below). The MS patients had concurrent MRI scans at 0, 12, and 25 months to measure whole brain volume (BBSI – brain boundary shift integral), presumably amongst other measures. Serum samples were “enriched” and analysed by 1D SDS-PAGE followed by LC-MS/MS of in gel digested protein. Free haemoglobin (Hb) levels were assessed by ELISA, and activity of lactate dehydrogenase (LDH), an indicator of general tissue damage, and particularly of haemolysis was measured. The proteomics analysis suggested that a 15.1-kDa protein peak correlated with the rate of brain atrophy in seemingly all MS patients, regardless of treatment regime. Following protein enrichment, 15.1-kDa and 15.9-kDa peaks were observed and confirmed to represent the α - and β -chains of haemoglobin, respectively. In all MS patients, levels of both free Hb chains and of LDH activity were elevated compared to all controls. The results are consistent with the idea that Hb is released into serum by chronic and low-grade intravascular haemolysis, with subsequent translocation into the CNS where it has great potential to cause oxidative damage.

Comments on title and abstract –

1. We suggest that the word “associated” needs to be substituted by “correlated”
2. Conclusions in the abstract must be linked to the objectives of the study rather than be a speculative claim.

Comments on study design and data interpretation – Several points require clarification, in our view.

1. There were 140 patents, and 60 controls (3 groups of 20). So the total number is supposed to be 200 serum samples per time point. What are the other 275 samples? The question of sample numbers, both of patients and controls, arises again later when 138 patients are mentioned. Additionally, a valuable control could be a group of

Author Response 23 Dec 2016

Charles Bangham, Department of Immunology, Imperial College London, UK

Lewin *et al.* – response to reviewers

We thank the three pairs of reviewers of our article, each of whom made helpful suggestions and raised salient points for clarification or further discussion. We have revised the article in the light of these comments, and cite further relevant literature (8 references have been added). The response to individual points is given below.

4. The Top 12 Protein Depletion Spin Columns are a good way to partially fractionate the serum or to enrich the protein of interest. However, several very important proteins (haptoglobin, transferrin, and Apo A1) related to iron homeostasis will be removed by this procedure. In the context of this study, it is important to see the specific expression patterns of haptoglobin, hemopexin, and HO-1 since they represent different levels of defence mechanisms against extracellular Hb. Also, it could be beneficial to try and correlate different haptoglobin phenotypes with BBSI.
5. In the same vein, the ELISA kit will detect extracellular Hb from two sources: free Hb and haptoglobin-bound Hb. The latter form could have been removed by the spin column that was used for protein enrichment.
6. Why and how were only 20 patients selected for ELISA?

Comments on discussion – We believe that the Discussion can be augmented to give a broader picture as follows.

Referee ratings:



Approved



Approved with reservations



Not approved

Minimal requirements for indexing:



Referees can update the status:

Open Peer Review

Referee Status: ✓✓✓

	Invited Referees		
Version(s)	1	2	3
<div style="background-color: #007bff; color: white; padding: 2px; border-radius: 4px; display: inline-block;">REVISED</div> Version 2 published 23 Dec 2016	✓ read report	✓ read report	
Version 1 published 15 Nov 2016	✓ read report	? read report	? read report

Reproducibility

Data and software policy:

- Access to source data underlying results
- Data must be hosted in a stable open repository (e.g. Open Science Framework, Dataverse, Zenodo)
- Data must be clearly described and formatted
- Data must be openly available (with some exceptions)
- Source code for new software must be provided (Software tool articles)

Data and software availability section

Wellcome Open Research

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METHOD ARTICLE EDIT VERSION Check for updates

UPDATE A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast [version 3; referees: 2 approved]

María Rodríguez-López¹, Cristina Cotoab¹, Oscar Fernández-Sánchez¹, Natalia Borbarán Bravo¹, Risky Oktriari¹, Heike Abendroth¹, Dardan Uka¹, Mimoza Hoti¹, Jin Wang¹, Mikel Zaratigui², Jürg Bähler¹

Author affiliations Grant information

Abstract

In the fission yeast *Schizosaccharomyces pombe* the prevailing approach for gene manipulations is based on homologous recombination of a PCR product that contains genomic target sequences and a selectable marker. The CRISPR/Cas9 system has recently been implemented in fission yeast, which allows for seamless genome editing without integration of a selection marker or leaving any other genomic 'scars'. The published method involves manual design of the single guide RNA (sgRNA), and digestion of a large plasmid with a problematic restriction enzyme to clone the sgRNA. To increase the efficiency of this approach, we have established and optimized a PCR-based system to clone the sgRNA without restriction enzymes into a plasmid with a dominant *natMX6* (nourseothricin) selection marker. We also provide a web-tool, CRISPR4R to support the design of the sgRNAs and the primers required for the entire process of seamless DNA deletion. Moreover, we report the preparation of G1-synchronized and cryopreserved *S. pombe* cells, which greatly increases the efficiency and speed for transformations, and may also facilitate standard gene manipulations. Applying this optimized CRISPR/Cas9-based approach, we have successfully deleted over 80 different non-coding RNA genes, which are generally lowly expressed, and have inserted 7 point mutations in 4 different genomic regions.

Open Peer Review

Referee Status: ✓✓

Version(s)	1	2
UPDATE Version 3 published 05 May 2017		
REVISED Version 2 published 03 Jan 2017	read report ✓	read report ✓
Version 1 published 23 Nov 2016	read report ✓	read report ?

1 Silke Hauf, Virginia Tech, USA
2 Damien Hermand, The University of Namur, Belgium
Carlo Yague-Sanz, The University of Namur, Belgium
Olivier Finet, The University of Namur, Belgium

All reports (4), Responses and comments (2)

Comments on this article

[...]

At-a-glance summary:
Dataset and source code DOIs and direct citations

Data and software availability

CRISPR4P software available from: bahlerlab.info/crispr4p

Latest source code: <https://github.com/Bahler-Lab/crispr4p>

Archived source code: DOI: [10.5281/zenodo.164683](https://doi.org/10.5281/zenodo.164683)¹⁴

License: MIT

Raw data are deposited in OSF (<https://osf.io/5de22/>) DOI: [10.17605/OSF.IO/5DE22](https://doi.org/10.17605/OSF.IO/5DE22)²⁸

References

14. Sinan Shi, osfesa: Bahler-Lab/crispr4p v1.0. Zenodo. 2016. [Data Source](https://doi.org/10.5281/zenodo.164683)

28. Rodriguez-Lopez M: A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. 2016. [Data Source](https://doi.org/10.17605/OSF.IO/5DE22)

Data visualization


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METHOD ARTICLE [EDIT VERSION](#) [Check for updates](#) METRICS

Examples of movements of a mouse required to activate PIR sensors at different heights from the cage floor

77 views 0 shares 22 downloads



Invited Referees

	2	3	4
Invited Referees	2	3	4
Referee 1	✓	✓	?
Referee 2	✓	✓	✓
Referee 3	✓	✓	✓

royal Veterinary College, UK
to Italiano di Tecnologia (IIT),

Data widget:
Figshare-hosted data

Responses and comments (4)

In this article

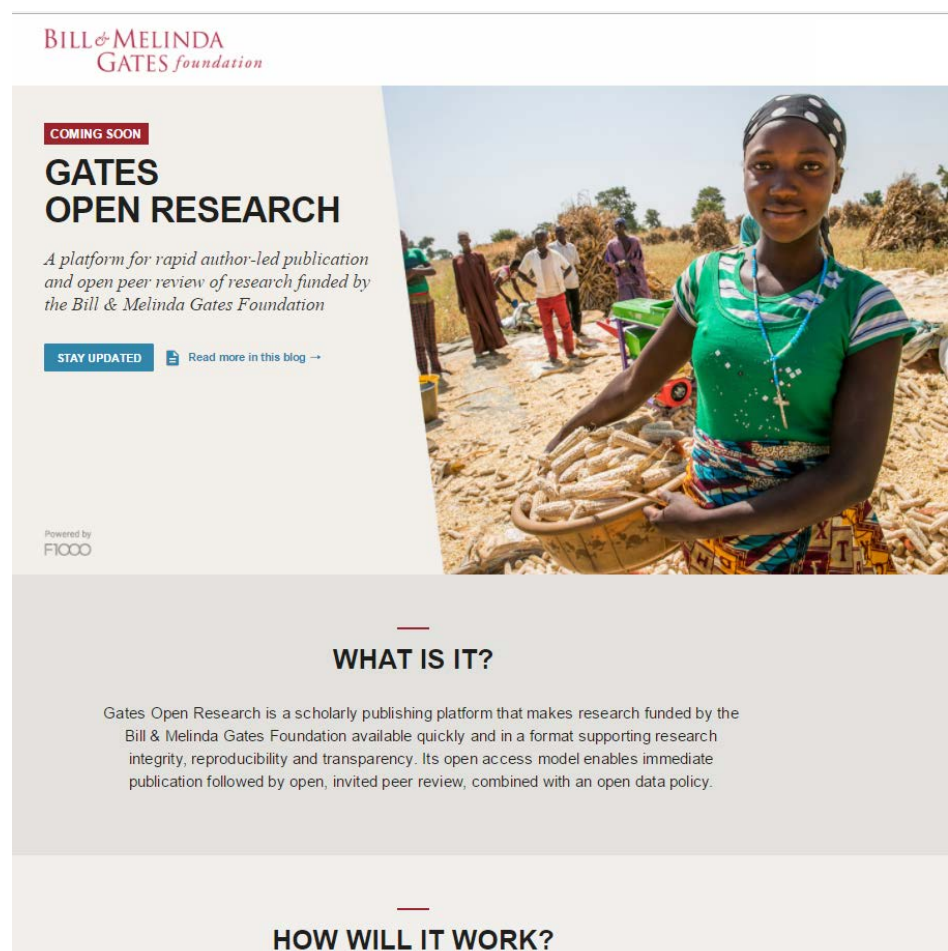
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When will Gates Open Research launch?

- Instructions for authors published in July
- Submission system launch planned for August
- First articles published in late September

<https://gatesopenresearch.org/>



The screenshot shows the top portion of the Gates Open Research website. At the top left, the logo for the Bill & Melinda Gates Foundation is displayed in red. Below it, a white box contains the text 'COMING SOON' in a red box, followed by 'GATES OPEN RESEARCH' in large black letters. A subtitle reads: 'A platform for rapid author-led publication and open peer review of research funded by the Bill & Melinda Gates Foundation'. Below this is a blue button labeled 'STAY UPDATED' and a link 'Read more in this blog ->'. To the right of the text is a photograph of a young woman in a green and white striped shirt, smiling and holding a large basket of harvested corn. The background of the photo shows other people in a rural, agricultural setting. At the bottom left of the white box, it says 'Powered by F1000'. Below the white box, the text 'WHAT IS IT?' is centered, followed by a paragraph of text describing the platform. At the very bottom, the text 'HOW WILL IT WORK?' is centered.

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WHAT IS IT?

Gates Open Research is a scholarly publishing platform that makes research funded by the Bill & Melinda Gates Foundation available quickly and in a format supporting research integrity, reproducibility and transparency. Its open access model enables immediate publication followed by open, invited peer review, combined with an open data policy.

HOW WILL IT WORK?

Questions?



Get in touch:

Gates Foundation:

Jennifer Hansen, Senior Officer, Knowledge & Research Services

Jennifer.Hansen@gatesfoundation.org

Ashley Farley, Associate Officer, Knowledge & Research Services

Ashley.Farley@gatesfoundation.org

F1000:

Michaela Torkar, Publishing Director, Michaela.Torkar@f1000.com

Philip Dooner, Associate Publisher, Philip.Dooner@f1000.com