


Preprints are a boon
for research integrity!

Deborah Sweet
VP of Editorial, Cell
Press/Elsevier

Record of form that precedes peer review

**bioRxiv**
THE PREPRINT SERVER FOR BIOLOGY

HOME | ABOUT

Search

21 Nov 2017

New Results

Comment on this paper

Cytoplasmic import and processing of mRNA amplify transcriptional bursts accounting for the majority of cellular noise

Maike M. K. Hansen, Ravi V. Desai, Michael L. Simpson, Leor S. Weinberger

doi: <https://doi.org/10.1101/222901>

Now published in *Cell Systems* doi: [10.1016/j.cels.2018.08.002](https://doi.org/10.1016/j.cels.2018.08.002)

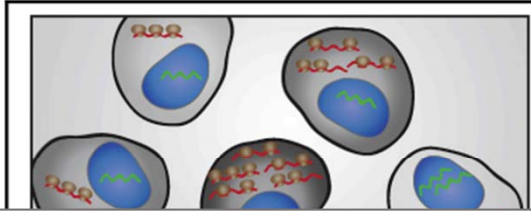
Abstract Full Text Info/History Metrics Preview

Received: April 18, 2018
Revised: June 14, 2018
Accepted: August 2, 2018
Published: September 19, 2018

Cell Systems 19 Sep 2018 Article

Cytoplasmic Amplification of Transcriptional Noise Generates Substantial Cell-to-Cell Variability

Graphical Abstract



Authors
Maike M.K. Hansen, Ravi V. Desai,
Michael L. Simpson,
Leor S. Weinberger

Correspondence
leor.weinberger@gladstone.ucsf.edu

In Brief

Cell Systems
Peer Review

Evaluation of Hansen et al.: Nuance Is Crucial in Comparisons of Noise

Noah Olsman,¹ Fangzhou Xiao,² and John Doyle^{1,*}

¹Department of Control and Dynamical Systems, California Institute of Technology, 1200 E. California Blvd, Pasadena, CA 91125, USA

²Division of Biology and Biological Engineering, California Institute of Technology, 1200 E. California Blvd, Pasadena, CA 91125, USA

*Correspondence: doyle@caltech.edu
<https://doi.org/10.1016/j.cels.2018.10.003>

One snapshot of the peer review process for "Cytoplasmic Amplification of Transcriptional Noise Generates Substantial Cell-to-Cell Variability" (Hansen et al., 2018).

Rapid communication of contradictory results

2 Aug 2017

ARTICLE

doi:10.1101/181255

Correction of a pathogenic gene mutation in human embryos

Hong Ma^{1,*}, Nuria Marti-Gutiérrez¹, Tomonari Hayama¹, Riffat Ahmed¹, Sang-Tae Kim², Jianhui Gong^{3,6}, Don P. Wolf¹, Stephen B. Heitner¹, Shoukhrat Mitalipov^{1,10}

Genome editing has potential to correct the heterozygous MYBPC3 mutation with accuracy and high homology-directed repair response. Induced double-strand breaks in the homologous wild-type maternal and paternal chromosomes of the DSB was induced, we were able to generate embryos carrying the wild-type MYBPC3 allele. The safety of the approach presented here for clinical applications, including the

bioRxiv preprint first posted online Aug. 28, 2017; doi: <http://dx.doi.org/10.1101/181255>. The copyright holder for this preprint (which was not peer-reviewed) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under a [CC-BY-NC-ND 4.0 International license](#).

Contradictory Results

Inter-homologue repair in fertilized human eggs?

Dieter Egli, Michael V. Zuccaro, Michal Kosicki, George M. Church, Allan Bradley, Maria Jasin

doi: <https://doi.org/10.1101/181255>

28 August 2017

August 2018

Inter-homologue repair in fertilized human eggs?

Dieter Egli^{1,*}, Michael V. Zuccaro², Michal Kosicki³, George M. Church⁴, Allan Bradley⁵, Maria Jasin⁶

¹Department of Obstetrics and Gynecology at Memorial Sloan-Kettering Cancer Center, 10032, USA; ²Graduate Program, Department of Biology, Memorial Sloan-Kettering Cancer Center, New York NY 10032, USA; ³Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridgeshire CB10 9RT, UK; ⁴Department of Genetics, Harvard Medical School, 77 Avenue Louis Pasteur, Boston, MA 02115, USA; ⁵Department of Genetics, Harvard Medical School, 77 Avenue Louis Pasteur, Boston, MA 02115, USA; ⁶Department of Genetics, Harvard Medical School, 77 Avenue Louis Pasteur, Boston, MA 02115, USA

* correspondence: de2220@cumc.columbia.edu

Change history

02 October 2017 Editorial Note: Readers should be aware that the conclusions of this paper are subject to ongoing investigation and are not considered by editors. Some of these issues have been resolved and deposited in preprint form. A further resolution of these issues.

nature
International journal of science

Brief Communications Arising | Published: 08 August 2018

Inter-homologue repair in fertilized human eggs?

Dieter Egli[✉], Michael V. Zuccaro, Michael Kosicki, George M. Church, Allan Bradley & Maria Jasin[✉]

Nature **560**, E5–E7 (2018) | [Download Citation](#)

ARISING FROM H. Ma et al. Nature **548**, 413–419 (2017); <https://doi.org/10.1038/nature23305>

Rapid highlighting of data problems

23 Nov 2015



Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade

Thomas C. Boothby^{a,1}, Jennifer R. Tenlen^{a,2}, Frank W. Smith^a, Jeremi Nishimura^a, Sophia C. Tintori^a, Qing Li^c, Corbin D. Jones^a, Mark Y. Patanella^a, and Bob Goldstein^a

^aDepartment of Biology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599; ^bEccles Institute of Human Genetics, University of Utah, Salt Lake City, UT 84143; ^cDepartment of Zoology, University of Oxford, Oxford OX1 3PS, United Kingdom

Edited by W. Ford Doolittle, Dalhousie University, Halifax, Canada, and approved September 1, 2015

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Horizontal gene transfer (HGT), or the transfer of genes between species, has been recognized recently as more pervasive than previously suspected. Here, we report evidence for an unprecedented degree of HGT in the draft genome of a tardigrade, *Hypsibius dujardini*.

The genome of *Hypsibius dujardini* contains a high fraction of genes that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.



bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

1 Dec 2015

New Results

No evidence for extensive horizontal gene transfer in the genome of the tardigrade *Hypsibius dujardini*

The genome of *Hypsibius dujardini*

No evidence for extensive horizontal gene transfer in the genome of the tardigrade *Hypsibius dujardini*

Georgios Koutsovoulos^a, Sujai Kumar^a, Dominik R. Laetsch^{a,b}, Lewis Steyer^a, Habib Maroon^a, Fran Thomas^a, Aziz A. Aboobaker^c, and Mark Blaxter^{a,1}

^aInstitute of Evolutionary Biology, University of Edinburgh, Edinburgh EH9 3FL, United Kingdom

^bThe James Hutton Institute, Invergowrie, Dundee DD9 8AT, United Kingdom

^cDepartment of Zoology, University of Oxford, Oxford OX1 3PS, United Kingdom

No evidence for extensive horizontal gene transfer in the genome of the tardigrade *Hypsibius dujardini*

Georgios Koutsovoulos^a, Sujai Kumar^a, Dominik R. Laetsch^{a,b}, Lewis Steyer^a, Habib Maroon^a, Fran Thomas^a, Aziz A. Aboobaker^c, and Mark Blaxter^{a,1}

^aInstitute of Evolutionary Biology, University of Edinburgh, Edinburgh EH9 3FL, United Kingdom; ^bDepartment of Zoology, University of Oxford, Oxford OX1 3PS, United Kingdom; and ^cDepartment of Zoology, University of Oxford, Oxford OX1 3PS, United Kingdom

Edited by W. Ford Doolittle, Dalhousie University, Halifax, Canada, and approved March 1, 2016

Tardigrades are meiofaunal ecdysozoans that are key to understanding the origins of Arthropoda. Many species of Tardigrada can survive extreme conditions through cryptobiosis. In a recent paper [Boothby et al. (2015) *Proc Natl Acad Sci USA* 112(52):15976–15981], the authors concluded that the tardigrade *Hypsibius dujardini* had an unprecedented proportion (17%) of genes originating through functional horizontal gene transfer (fHGT) and speculated that fHGT was likely formative in the evolution of cryptobiosis. We independently sequenced the genome of *H. dujardini*. As expected from whole-organism DNA sampling, our raw data contained reads from nontarget genomes. Filtering using metagenomics approaches generated a draft *H. dujardini* genome assembly of 135 Mb with superior assembly metrics to the previously published assembly. Additional microbial contamination likely remains. We found no support for extensive fHGT. Among 23,021 gene predictions we identified 0.2% strong candidates for fHGT from bacteria and 0.2% strong candidates for fHGT from nonmetazoan eukaryotes. Cross-comparison of assemblies showed that the overwhelming majority of HGT candidates in the Boothby et al. genome derived from contaminants. We conclude that fHGT into *H. dujardini* accounts for at most 1–2% of genes and that the proposal that one-sixth of tardigrade genes originate from functional HGT events is an artifact of undetected contamination.

tardigrade | blobtools | contamination | metagenomics | horizontal gene transfer

LETTER

12 May 2016

No evidence for extensive horizontal gene transfer from the draft genome of a tardigrade

Kazuharu Arakawa^{a,1}

LETTER

LETTER

12 May 2016

REPLY TO BEMM ET AL. AND ARAKAWA:

Identifying foreign genes in independent *Hypsibius dujardini* genome assemblies

Thomas C. Boothby^{a,1} and Bob Goldstein^a

Our report (1) describing the discovery of extensive horizontal gene transfer in a tardigrade genome raised questions from other groups who were sequencing the *Hypsibius dujardini* genome in parallel or who have done new experiments and analyses since our report (2–5). Bemm et al. (2) now reporting our data for likely contaminants, resulting in a new, prefiltered genome assembly. Arakawa (3) sequenced genomes of starved, washed, and incubated animals that had been treated with antibiotics for 48 h, and used this genomic sequence and RNA-seq data to identify likely bona fide tardigrade genes. Two other reports have contributed data and analyses (4, 5). In our new assembly, we set out to reduce the impact of bacterial contamination on the assembly process dramatically.

A central finding of our original report (1) is a high fraction of genes in the *H. dujardini* genome that are not found in any other species, as well as a high fraction of genes that are found in multiple species. We speculate that the high fraction of genes found in multiple species is due to horizontal gene transfer.

Correction

22 Aug 2016

GENETICS

Correction for “Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade,” by Thomas C. Boothby, Jennifer R. Tenlen, Frank W. Smith, Jeremy R. Wang, Kiera A. Patanella, Erin Osborne Nishimura, Sophia C. Tintori, Qing Li, Corbin D. Jones, Mark Yandell, David N. Messina, Jarret Glasscock, and Bob Goldstein, which appeared in issue 52, December 29, 2015, of *Proc Natl Acad Sci USA* (112:15976–15981; first published November 23, 2015; 10.1073/pnas.1510461112).

The authors wish to note the following: “The data deposition footnote included in our published manuscript provides a link to an outdated version of our genome assembly. The version of the assembly that was used in our paper has been uploaded to GitHub and is available at the following link: https://github.com/Hd-tg-genome/PNAS_response/tree/master/Postfiltered_assembly.”

www.pnas.org/cgi/doi/10.1073/pnas.1613046113

Think of all the things preprints can do....

1. Record what a paper was like before peer review
2. Allow authors to counter criticism/respond to discussion
3. Speedy communication of contradictory results
4. Highlighting problems with data/analysis
- 5. Helping authors refine their paper before they formally submit**
- 6. Giving a home to negative results**
- 7. Validation and confirmation of results**

Think about a paper you know that turned out to be problematic.

Would that situation have been different if the paper had been put out as a preprint first?