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Las dimensiones de la ciencia abierta y el futuro de la comunicación científica

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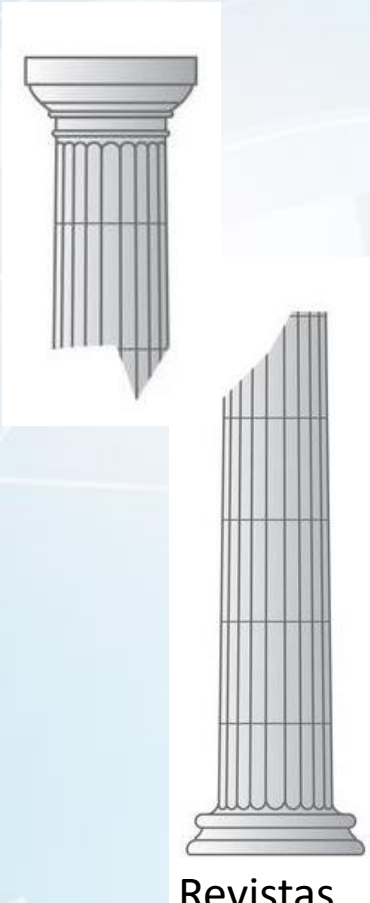
La ciencia al principio del Siglo XX

Revistas científicas
(como vehículo exclusivo para divulgar los resultados de investigación)

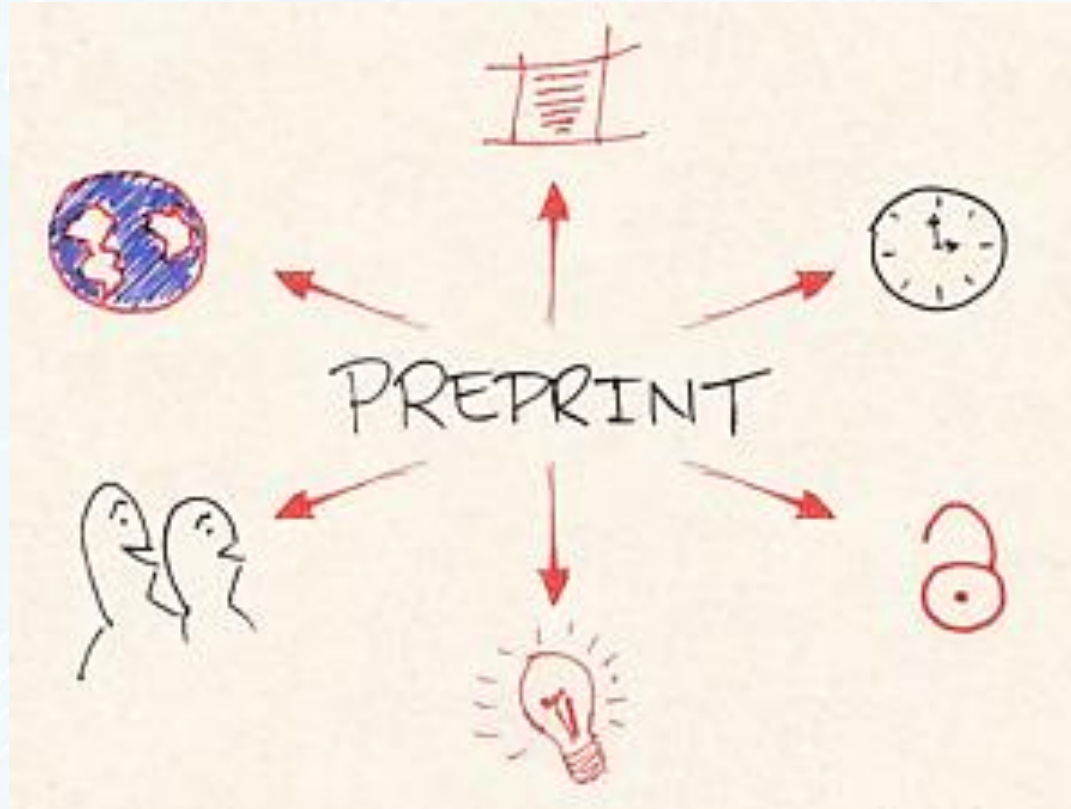
Revisión por pares
pré-publicación

Índices de impacto basados en citas





Revistas científicas



arXiv

bioRxiv

THE PREPRINT SERVER FOR BIOLOGY



SOC
ARXIV

medRxiv

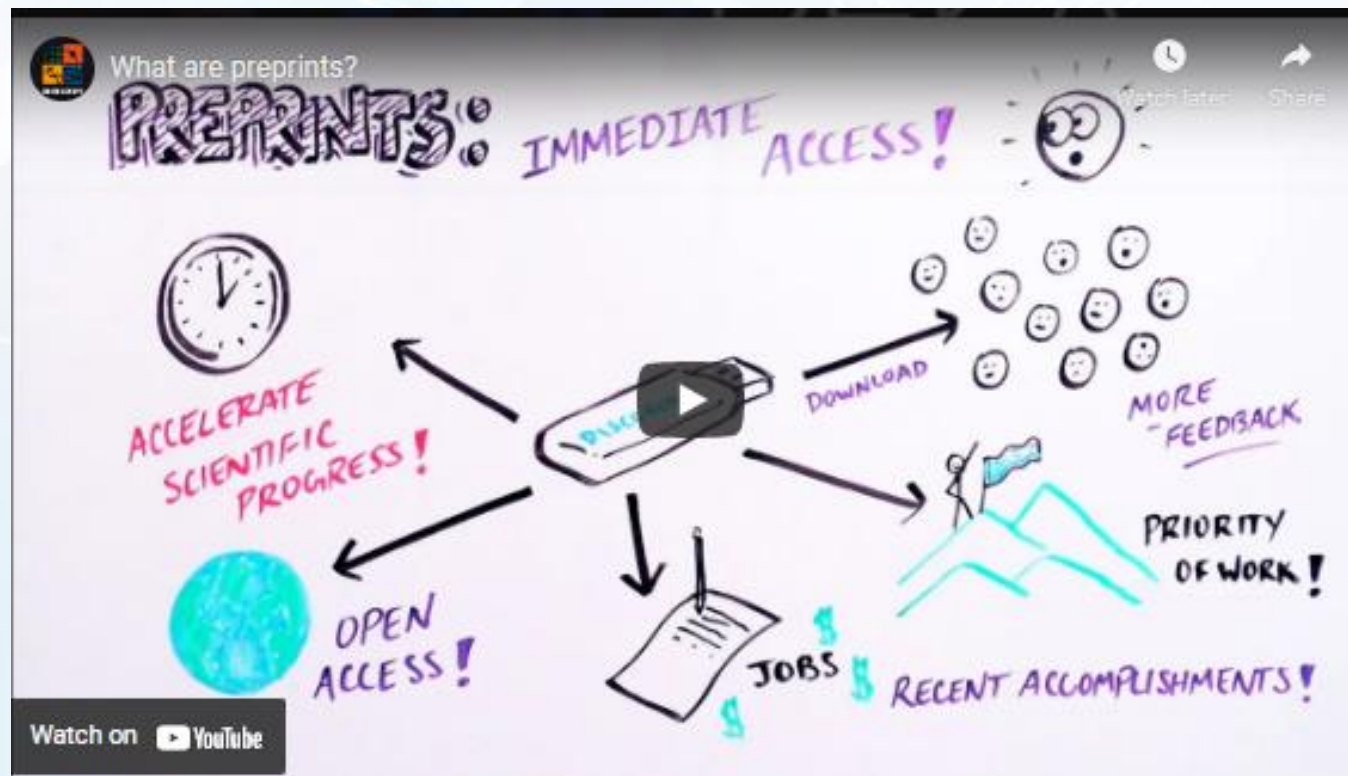


ChemRxiv™

Preprint es un **artículo científico completo** que es depositado por los autores en una plataforma (servidor) de acceso abierto. El preprint suele ser la misma versión o una versión anterior de un manuscrito enviado a una revista para revisión por pares y posible publicación.

En la mayoría de los casos, el mismo artículo publicado como preprint también se envía a una revista y, en este proceso, es evaluados por los pares. Los preprints (**rápidos, pero no revisados por pares**) y la publicación en revistas (**más lentos, pero revisados por los pares**) pueden funcionar en paralelo como **canales de comunicación complementares** para la investigación científica.

Qué son los preprints?



<https://youtu.be/2zMgY8Dx9co> - video muy claro en inglés sobre preprints, 4:00 min



arXiv

1990



AgriXiv

2017



AUTHOREA

2019



AfricArXiv

2019



bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

2013



medRxiv

THE PREPRINT SERVER FOR HEALTH SCIENCES

2019



ChinaXiv
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2016



EarthArXiv

2017



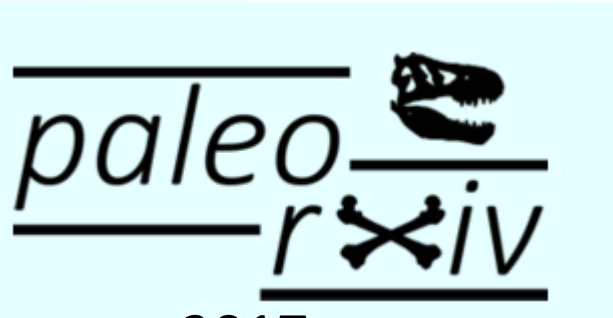
LawArXiv
Legal Scholarship in the Open

2017



NutriXiv

2017



paleoRxiv

2017



SciELO Preprints

2020



Open Access 20th Anniversary
1997-2022 55

New Results

Genetics of single-cell protein abundance variation in large yeast populations

Frank Albert, Sebastian Treusch, Arthur H Shockley, Joshua S Bloom, Leonid Kruglyak

doi: <https://doi.org/10.1101/000067>Now published in *Nature* doi: [10.1038/nature12904](https://doi.org/10.1038/nature12904)

Abstract

Info/History

Metrics

 Preview PDF**Abstract**

Many DNA sequence variants influence phenotypes by altering gene expression. Our understanding of these variants is limited by sample sizes of current studies and by measurements of mRNA rather than protein abundance. We developed a powerful method for identifying genetic loci that influence protein expression in very large populations of the yeast *Saccharomyces cerevisiae*. The method measures single-cell protein abundance through the use of green-fluorescent-protein tags. We applied this method to 160 genes and detected many more loci per gene than previous studies. We also observed closer correspondence between loci that influence protein abundance and loci that influence mRNA abundance of a given gene. Most loci cluster at hotspot locations that influence multiple proteins—in some cases, more than half of those examined. The variants that underlie these hotspots have profound effects on the gene regulatory network and provide insights into genetic variation in cell physiology between yeast strains.

Tweets referencing this article:



Paul Macklin

@MathCancer

RT @leonidkruglyak: @CancerConnector our experience: <https://t.co/8qCVwsVeL2> Nature policy: <https://t.co/EnFQFKkgMh> @NimaSharifiMD

12 Sep 2016



Nima Sharifi

@NimaSharifiMD

RT @leonidkruglyak: @CancerConnector our experience: <https://t.co/8qCVwsVeL2> Nature policy: <https://t.co/EnFQFKkgMh> @NimaSharifiMD

12 Sep 2016



Jacob G Scott

View comments on earlier versions of this paper

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Name



Animesh Ray · 4 years ago

Very nice idea, which can be immediately applicable to other organisms where at least some GFP tagged proteins are available and cells of a specific type can be isolated and sorted. This is probably the first instance where genome wide protein abundance has been related to segregating alleles. Two questions arise. (1) Single cell expression studies have revealed noise (variance of expression levels) uncorrelated to the precise allele expression levels (extrinsic noise) and this noise is under genetic control. One normally understands this noise as the result of stochastic perturbation of a network of genes of which the observed (tagged) gene is a member. I realize that because only one (GFP-tagged) allele is considered (in a haploid), extrinsic noise is not registered by this method. Could some of the effects of the segregating alleles be on the noise in expression rather than on expression level itself? Since only extremes of the GFP fluorescence distribution are selected in the measurement, if the noise effect is non-Gaussian, one could potentially confound the mean expression with the noise in expression. Would it not be better to look at the full distribution of expression levels? Or am I off to a wrong track? (2) I wonder whether including an internal control for general protein synthesis rate in each cell--say, by a homozygous CFP tagged ribosomal protein (very long half-life) or some such protein that shows minimal variation under most genetic backgrounds, in the starting diploid--could be used as a normalizing standard, to compensate for pool size effects that are known to affect protein synthesis rates within the time scale of 1 cell division. On a second thought, after sleeping on it, perhaps you could normalize against nuclear DNA amount by DAPI fluorescence or against cell aspect ratio (unless you already do that and I haven't yet read the details). In any event, the results are beautiful and set the stage for further progress into figuring the effects of modifier alleles on protein expression levels. Terrific work.

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Los comentarios funcionan como
revisión por pares pospublicación

Además, los repositorios de preprints hacen parcerías con ciertas revistas. Los autores pueden presentar los preprints depositados a las revistas, que irá evaluarlos de acuerdo con sus practicas editoriales, con objetivo de publicación.



bioRxiv posts many COVID-19-related papers. A reminder: they have not been formally peer-reviewed and should not guide health-related behavior or be reported in the press as conclusive.

New Results [Follow this preprint](#)

Recombinant single-cycle influenza virus as a new tool to augment antitumour immunity with immune checkpoint inhibitors

Matheswaran Kandasamy, Uzi Gileadi, Pramila Rijal, Tiong Kit Tan, Lian Ni Lee, Jili Chen, Gennaro Prota, Jing Zhang, Terence Rabbitts, Alain Townsend, Vincenzo Cerundolo
 doi: <https://doi.org/10.1101/2021.07.31.454512>

This article is a preprint and has not been certified by peer review [what does this mean?]



Abstract Full Text Info/History Metrics [Preview PDF](#)

Abstract

Virus-based tumour vaccines offer many advantages compared to other antigen delivering systems. They generate concerted innate and adaptive immune response, and robust CD8⁺T cell responses. We engineered a non-replicating pseudotyped influenza virus (S-FLU) to deliver the well-known cancer testis antigen, NY-ESO-1 (S-NY-ESO-1 FLU). Intranasal or intramuscular immunization of NY-ESO-1 S-FLU virus in mice elicited a strong NY-ESO-1 specific CD8⁺T cell response in lungs and spleen that resulted in the regression of NY-ESO-1 expressing lung tumour and subcutaneous tumour respectively. Combined administration with anti PD-1 antibody, NY-ESO-1 S-FLU virus augmented the tumour protection by reducing the tumour metastasis. We propose that the antigen delivery through S-FLU is highly efficient in inducing antigen specific CD8⁺T cell response and protection against tumour development in combination with PD-1 blockade.

Competing Interest Statement

The authors have declared no competing interest.

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Evaluation/discussion of this paper



TRIP

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Evaluation Summary:

This paper describes an approach in which a non-replicating influenza virus expressing a cancer testis antigen is used to induce a systemic and mucosal antigen specific T cell responses. The authors find that this immune response is sufficient to reduce tumor burden following intravenous or subcutaneous tumor challenge. This paper is potentially interesting to tumor-immunity researchers.

(This preprint has been reviewed by eLife. We include the public reviews from the reviewers here; the authors also receive private feedback with suggested changes to the manuscript. The reviewers remained anonymous to the authors.)

[Less](#)

Reviewer #1 (Public Review):

This paper is potentially interesting to many researchers who are looking for ways to enhance the CTL response to tumor immunity in combination with checkpoint antibodies.

Strengths:

- The authors engineered a non-replicating pseudotyped influenza virus to deliver the well-known cancer testis antigen, NY-ESO-1 (NY-ESO-1 S-FLU). One problem in using virus vectors for vaccination is the immune reaction to viral protein. They clearly showed that Switching HA coat of virus in S-FLU construct would easily overcome the pre-existing anti FLU immunity. This finding is new and interesting.
- The authors also showed that intranasal or intramuscular immunization of NY-ESO-1 S-FLU virus in mice elicited a strong NY-ESO-1 specific CD8⁺T cell response in lungs and spleen that resulted in the regression of NY-ESO-1 expressing lung tumor and subcutaneous tumor respectively. In addition, they demonstrated that NY-ESO-1 S-FLU synergistically works with anti-PD1, which is also interesting.

Weaknesses:

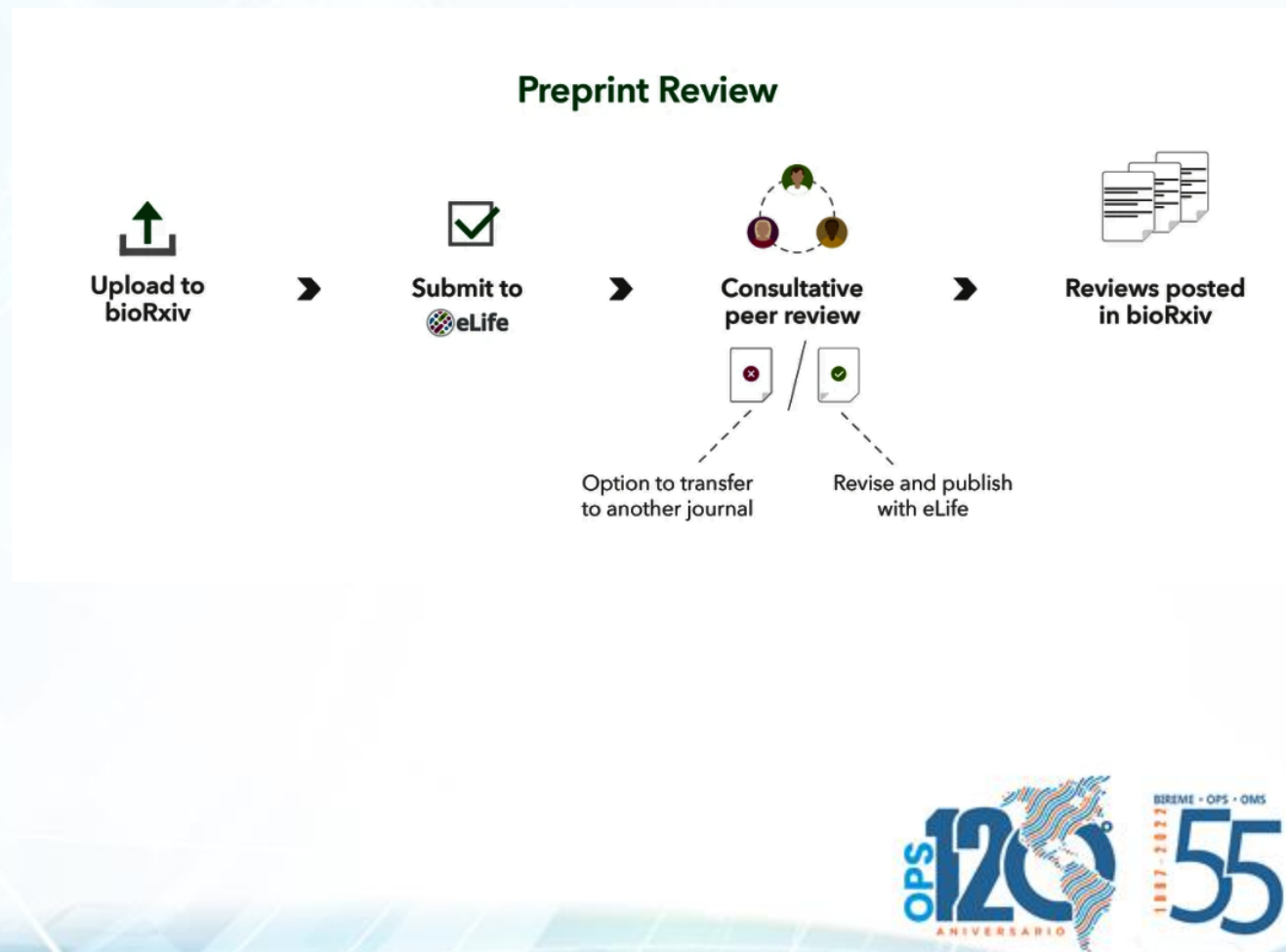
- Mechanisms by which NY-ESO-1 S-FLU works better than other types of viral vectors are unclear.
- To most readers who do not have much information on cancer vaccine, it is unclear whether the anti-tumor effect of NY-ESO-1 S-FLU was high or modest compared with those reported in the similar studies using other types of vaccines (e.g., peptide vaccine, mRNA vaccine, ...).

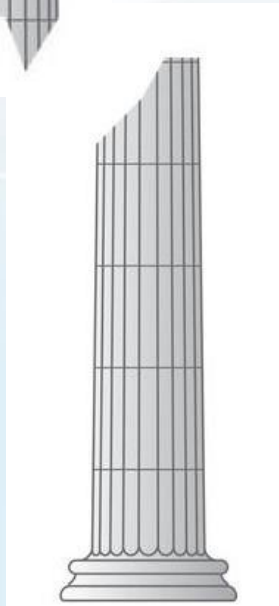
[Less](#)

Reviewer #2 (Public Review):

Virus-based tumor vaccines can induce a robust T cell response capable of limiting tumor progression. The authors sought to investigate whether the influenza virus can be used to induce a protective tumor antigen-specific T cell response. They generated a replication deficient influenza

[More](#)





Índices de impacto
basados en citas

Impacto



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Peer review

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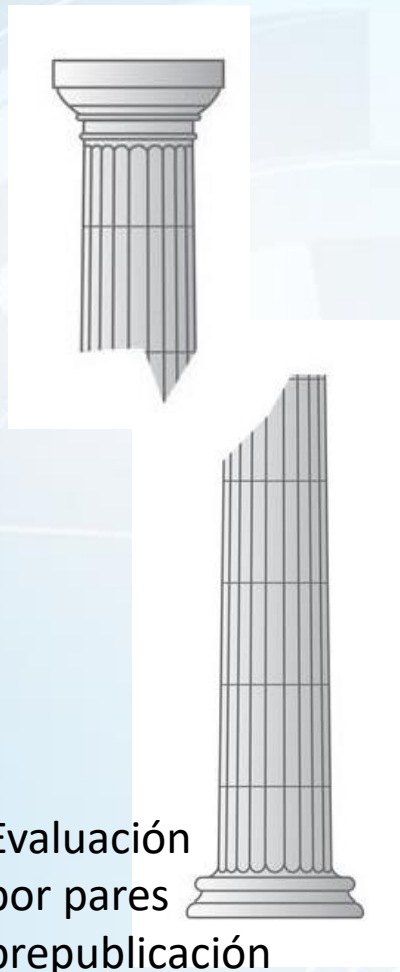
Citas

FI, índice h

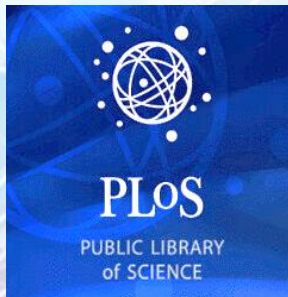


Altmetric





- Críticas al modelo de revisión por pares prepublicación
- Sobrecarga de los revisores
- *San Francisco Declaration on Research Assessment (DORA)*
- Evaluación por pares abierta (Open peer review - OPR)
 - Identidades abiertas
 - Revisiones abiertas
 - Evaluación pospublicación
 - Revisores no formalmente invitados pueden opinar
- OPR Permite generar informes y estadísticas sobre la revisión por pares



Críticas al modelo actual de revisión por pares

1. **Poco fidedigno e inconsistente.** No siempre detecta errores, o puede haber inconsistencias entre los informes de los revisores.
2. **Los plazos son muy largo y costosos.** Ocasiona largos tiempos entre el envío y la publicación.
3. **Falta de responsabilidades y riesgo de sesgos.** Permite sesgos sociales y de publicación. Los revisores no son capacitados para la función
4. **Sin incentivo para los revisores.** Ellos no reciben créditos por su trabajo. Plataformas como Publons y ReviewerCredits buscan llenar este vacío
5. **Desperdicio de esfuerzo.** El mismo manuscrito puede ser revisado muchas veces, en la medida que pasa por ciclos de envíos y rechazos.

Formas alternativas de revisión por pares

PLoS – Realiza evaluación **prepublicación objetiva**, *no evalúa impacto*. Publica la identidad del editor asociado que sigue el artículo.

The BMJ – Realiza evaluación **prepublicación abierta**. Publica el contenido de las revisiones y la respuesta de los autores. Además, revela la identidad de los revisores.

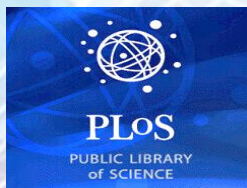
F1000 Research – Realiza **evaluación abierta pospublicación**, en la cual sucesivos ciclos que resulta en modificaciones del manuscrito por los autores, según las recomendaciones de los revisores, hasta que el artículo sea finalmente publicado. Los comentarios de los revisores y respuestas de los autores se publican como suplemento del artículo. Se aceptan comentarios de lectores (también publicados).

PeerJ – Realiza evaluación por pares objetiva. **Revisiones y la identidad de los revisores se divulgan de forma opcional**, con la anuencia de autores y revisores.

eLife – Realiza revisión prepublicación simple ciego objetiva. Toda la historia de la revisión consolidadas se **publican opcionalmente de forma abierta** y se divulga la identidad de los revisores.

BioMed Central – Se trata de un publisher de más de 250 revistas. En las revistas que realizan la revisión abierta, autores y revisores conocen la identidad uno del otro, y en caso del artículo aceptado, **se publican las revisiones y las respuestas de los autores**, junto con la identidad de los revisores.

Nature Communications - Revisión por pares transparente, lo que significa que publican los **comentarios de los revisores y las respuestas de los autores**, pero no la identidad de los revisores.



Research

Effect of fish oil supplementation in pregnancy on bone, lean, and fat mass at six years: randomised clinical trial

BMJ 2018 ; 362 doi: <https://doi.org/10.1136/bmj.k3312> (Published 04 September 2018)
Cite this as: BMJ 2018;362:k3312

Opinion

How we built vikings

- Article
- Related content
- Metrics
- Responses
- Peer review

Rebecca Kofod Vinding, medical doctor^{1,2}, Jakob Stokholm, senior researcher¹, Astrid Sevelsted, statistician¹, Tobias Sejersen, medical doctor^{1,2}, Bo L Chawes, associate professor¹, Klaus Bennelykke, associate professor¹, Jonathan Thorsen, medical doctor¹, Laura D Howe, epidemiologist³, Martin Krakauer, nuclear medicine consultant⁴, Hans Bisgaard, professor¹

Author affiliations ▾

Correspondence to: H Bisgaard bisgaard@copscac.com

Accepted 17 July 2018

Abstract

Objective To examine the effect of supplementation with n-3 long chain polyunsaturated fatty acids (n-3 LCPUFA) in pregnancy on anthropometry and body composition in offspring.

Design Double blinded, randomised controlled trial.

Setting Copenhagen Prospective Studies on Asthma in Childhood₂₀₁₀ cohort.

Participants 736 pregnant women and their offspring.

Intervention n-3 LCPUFA (fish oil) or control (olive oil) daily from pregnancy week 24 until one week after birth.

Main outcome measures Height/length, weight, head, and waist measurements and body composition from dual energy x ray absorptiometry (all pre-specified secondary endpoints of the n-3 LCPUFA trial; the primary outcome for the trial was persistent wheeze/asthma).

Results The mean body mass index (BMI) z score was increased between age 0 and 6 years in the fish oil supplementation group compared with the control group (0.14 (95% confidence interval 0.04 to 0.23); P=0.006). At 6 years, supplementation was associated with a higher BMI z score (0.19 (0.06 to 0.32); P=0.004), a higher weight/height (3.48 (0.38 to 6.57) g/cm; P=0.03), and a larger waist circumference (0.6 (0.0 to 1.2) cm; P=0.04) but not a higher proportion of obese children, using International Obesity Task Force grades. The dual energy x ray absorptiometry scan at age 6 years showed a higher total mass (395.4 (86.6 to 704.3) g; P=0.01) in the supplementation versus the control group, explained by a higher lean mass (280.7 (98.9 to 462.4) g; P=0.002), a higher bone mineral content (10.3 (2.3 to 18.1) g; P=0.01), and a non-significantly higher fat mass (116.3 (-92.9 to 325.5) g; P=0.28), but no differences were seen in total body fat or lean mass percentage.

Conclusion Fish oil supplementation from the 24th week of pregnancy led to a higher BMI in the offspring from 0 to 6 years of age but not an increased risk of obesity at age 6. The body composition at age 6 years in children given fish oil supplementation was characterised by a proportional increase in lean, bone, and fat

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We thank the Editors and Reviewers for their constructive comments, which we address individually below. We believe that the manuscript has been significantly improved through the additional analyses and manuscript corrections and hope that you now find it acceptable for publication in the British Medical Journal.

Reviewer: 1

Comments:

This is an interesting manuscript.

It is based on a well-conducted and comprehensive randomised controlled trial with fish oil vs olive oil supplementation during pregnancy. The study follows up children to the age of 6y with anthropometric measurements. The study is not the first of its kind, but it is relatively large, it has repeated measurements during follow up and has an extensive battery of measurements. Generally, the manuscript is well written and overall it complies with the Consort Statement. There are however a few general and some more specific comments.

Response: We thank the reviewer for the appreciation of our study. We have addressed the individual comments below.

General comments:

Attrition is generally low but there is some attrition in the study up to the age of 6y (particularly for the DEXA scans). Have the authors considered whether exchangeability between the two interventions groups is still present after 6 years? Did you consider adjusting for potential risk factors for the outcome?

Response 1: Since we had a successful randomization (refer to table 1), we follow the typical guidelines for reporting of randomized controlled trials, which is without confounder adjustment. We only adjust for sex and age, which is crucial for comparison of growth endpoints. Furthermore, the attrition in relation to DEXA scans at 3.5 and 6 years was similar for the two supplementation groups; please also see Response 9 and 10.

A number of sub-analyses are described in the result section, which have not been described in the method section (consort checklist 12b). This includes both stratified analyses, interaction analyses and also the sub-analysis concerning FADS. I suggest that these analyses also should be included in the method section.

Response 2: This has been done as suggested, please refer to response 4 and 8 for details.

Specific comments:

pp6 line 9: Is "growth" the right word to use?

Response 3: We have now changed this to "anthropometry."

pp8 line 33-38: It is unclear at this point what this information should be used for. I suggest that

either it is introduced as a secondary aim or that it is shortly explained here in the method section.

Response 4: We have added this sentence to the methods section.

Page 8, line 179: *"The FADS genotype was used to perform a genetic validation of our findings."*

pp9 line 28-29: Self-reported birth weight and length were validated against information from the Danish National Birth Register. How valid was the self-reported information? What did you do in case of discrepancy? What was the correlation? Generally it is unclear what this validation showed and what you used the information for.

Response 5: We have added this to the methods section:

Page 9, line 204-206: *"Furthermore, if there was a difference larger than 10g and 5cm, data were validated against the length and weight measures at 1 week from the research clinic."*

pp10 line 14: Twins were excluded. They usually come in pairs. How come three twins are excluded from the LCPUFA group?

Response 6: It was twin pregnancies which were excluded, the word "pregnancies" has been added to the text.

pp10 line 17 and 22. The use of "cross sectional" in this context is a bit confusing.

Response 7: We have rewritten the methods section:

Page 10, line 232-235: *"The effect of n-3 LCPUFA supplementation on cross-sectional anthropometric outcomes at 6 years of age (defined as the specific anthropometric measurement closest to 6 years ± 6 months) was analysed using Student's t-test for normally distributed continuous variables and chi-square tests for categorical variables."*

pp10 statistical analysis: A number of sub-analyses have been performed. They should be described in this section.

Response 8: We have added a methods section regarding sub-analyses:

Page 10, line 250-255: *"We analyzed for interaction in regards to sex, age, size for gestational age, FADS-genotype and maternal pre-intervention blood levels of EPA and DHA. A subgroup from this pregnancy cohort also participated in a nested; factorial designed, double-blind, RCT of 2,400IU/day of vitamin D3 supplementation (N=576). We performed a sub-analysis excluding children with asthma at age 6 years and/or with lower respiratory tract infections before age 3 years. In a sub analysis we adjusted our primary outcomes for size for gestational age and birth weight."*

pp11 line 19-21: The sentence is a bit unclear. Consider revising.

Response 9: We have changed the sentence to this:

Aspectos positivos y negativos de la revisión por pares abierta



Fuente: NASSI-CALÒ, L. Ventajas y desventajas potenciales en la publicación de opiniones de evaluación SciELO en Perspectiva, 2019.

<https://blog.scielo.org/es/2019/04/30/ventajas-y-desventajas-potenciales-en-la-publicacion-de-opiniones-de-evaluacion/>

Datos abiertos

Motivación:

- Compartir recursos entre disciplinas
- Aumentar la transparencia en todas las etapas de la investigación

Desafíos:

- Demostrar a los varios actores las ventajas de operar con un sistema transparente de generación, evaluación, compartición y uso del conocimiento
- Nuevos paradigmas >> aceptar cambios

Datos brutos son un ejemplo de bien publico global. Si no son compartidos, se pierden, son corrompidos y no se pueden acceder a ellos después de cierto tiempo.

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Datos abiertos, así como los artículos, en formato *machine readable* (legible por máquina) son colocados a disposición en repositorios específicos para esta finalidad, asociados a una licencia de distribución.

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Buenas practicas en la presentación de datos abiertos

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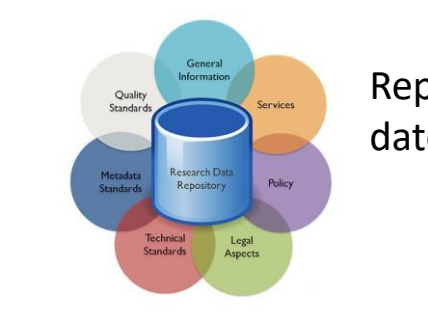
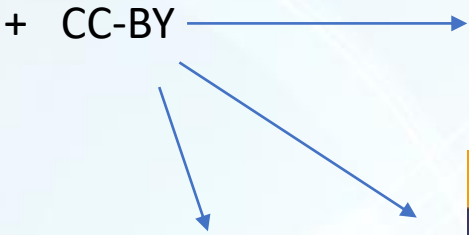
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- En un repositorio de datos de acceso abierto
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- Para estimular el compartimiento de datos, hay repositorios que disponen de herramientas para la generación automática de *data papers* a partir del articulo principal

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Data sets - Machine readable



Repositorio de datos abiertos



Data papers



Data journals



Data papers

<http://dx.doi.org/10.1037/a0028240>

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Recomendación de la UNESCO sobre la Ciencia Abierta



*"promover la ciencia abierta desde el inicio del proceso de investigación y ampliar los principios de apertura a todas las etapas del proceso científico, entre otros mediante el **fomento de los preprints**, a fin de acelerar la difusión e impulsar el rápido crecimiento del conocimiento científico"*

Recomendación aprobada en la 41° Asamblea General de la UNESCO en París, noviembre de 2021

Texto Completo: https://unesdoc.unesco.org/ark:/48223/pf0000379949_spa

Ciencia Abierta

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