Editing

Reviews in Quantitative Biology

18 Nov 2022

Macrostructure: paragraphs, sentences, flow

The Title

- Signals the field and scope
- Includes your main point
- Arouses interest of the readers

Trends in Genetics

Volume 33, Issue 12, December 2017, Pages 971-978

Review

Stay Connected: A Germ Cell Strategy

Kevin Lu [1, 2, 3], Lindy Jensen [3, 4], Lei Lei [5], Yukiko M. Yamashita [1, 3, 5, 6]

Trends in Genetics

Volume 34, Issue 1, January 2018, Pages 8-10

Science & Society

Raw Genomic Data: Storage, Access, and Sharing

Mahsa Shabani [1], Danya Vears [1], Pascal Borry [1]

Review Article | Published: 11 August 2021

Exploring tissue architecture using spatial transcriptomics

Anjali Rao, Dalia Barkley, Gustavo S. França & Itai Yanai

Nature **596**, 211–220 (2021) | Cite this article

Trends in Genetics

Volume 38, Issue 12, December 2022, Pages 1204-1207

Forum

Unusual suspects in hereditary melanoma: *POT1*, *POLE*, *BAP1*

Ellie J. Maas [1], Brigid Betz-Stablein [1], Lauren G. Aoude [2], H. Peter Soyer [1, 3], Aideen M. McInerney-Leo [1]

Review | Published: 10 February 2021

Origins of modern human ancestry

Anders Bergström, Chris Stringer, Mateja Hajdinjak, Eleanor M. L. Scerri & Pontus Skoglund

Nature **590**, 229–237 (2021) | Cite this article

Trends in Ecology & Evolution

Volume 18, Issue 6, June 2003, Pages 292-298

Evolution by gene duplication: an update

Jianzhi Zhang

The Introduction

- Set the context from general to specific
  - Show that the research area is important/interesting/relevant
- Establish a niche
  - Show need for your work
- Occupy the niche
  - Announce your main points
  - Announce structure of article

Loss is nothing else but change, and change is Nature's delight – Marcus Aurelius, AD 121–180

Great attention has in the past been paid to the mechanisms of evolution by gene duplication (that is, neofunctionalization and subfunctionalization)[1,2]. By contrast, gene loss has often been associated with the loss of redundant gene duplicates without apparent functional consequences, and therefore this process has mostly been neglected as an evolutionary force. However, genomic data, which is accumulating as a result of recent technological and methodological advances, such as next-generation sequencing, is revealing a new perspective of gene loss as a pervasive source of genetic change that has great potential to cause adaptive phenotypic diversity.

Two main molecular mechanisms can lead to the loss of a gene from a given genome. First, the loss of a gene can be the consequence of an abrupt mutational event, such as an unequal crossing over during meiosis or the mobilization of a transposable or viral element that leads to the sudden physical removal of the gene from an organism's genome. Second, the loss of a gene can be the consequence of a slow process of accumulation of mutations during the pseudogenization that follows an initial loss-of-function mutation. This initial mutation can be caused by nonsense mutations that generate truncated proteins, insertions or deletions that cause a frameshift, missense mutations that affect crucial amino acid positions, changes involving splice sites that lead to aberrant transcripts or mutations in regulatory regions that abolish gene expression. In this Review, the term 'gene loss' is used in a broad sense, not only referring to the absence of a gene that is identified when different species are compared, but also to any allelic variant carrying a loss-of-function (that is, non-functionalization) mutation that is found within a population.

Here, we address some of the fundamental questions in evolutionary biology that have emerged from this novel perspective of evolution by gene loss. Examples from all life kingdoms are covered, from bacteria to fungi and from plants to animals, including key examples of gene loss in humans. We review how gene loss has affected the evolution of different phyla and address key questions, including how genes can become dispensable, how many of our current genes are actually dispensable, how patterns of gene loss are biased, and whether the effects of gene loss are mostly neutral or whether gene loss can actually be an effective way of adaptation. Finally, promising future perspectives on the study of gene loss are discussed. These include the development of computational pipelines to identify the complete catalogue of gene losses that have occurred during the evolution of a given species, the effect that anticipated findings have on the fields of evolutionary biology and biomedicine, and the means by which comparative population genomics approaches and the measure of 'population gene dispensability' can help to discover new genes that are relevant for human health.

Evolution by gene loss

Ricard Albalat ✉ & Cristian Cañestro ✉

Nature Reviews Genetics **17**, 379–391 (2016) | Cite this article

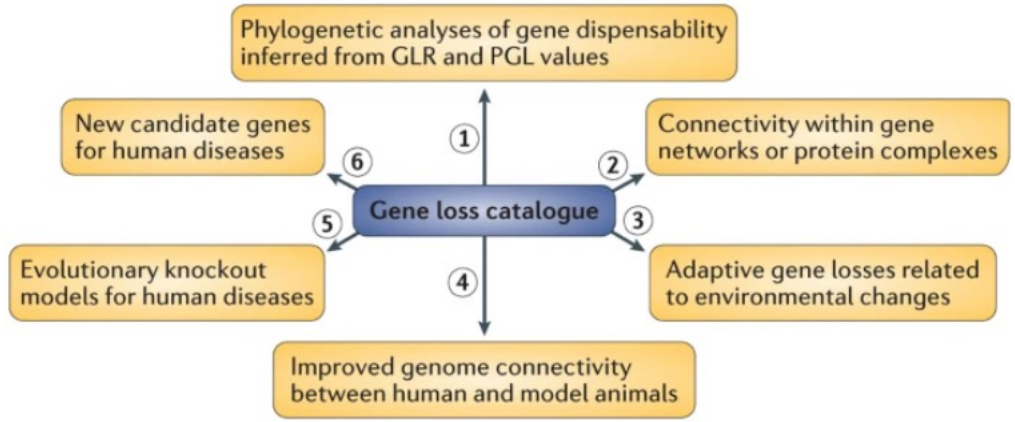
The Conclusion

- Specific → general
  - Repeat key points
  - Broader implications, future directions

Future directions

A future challenge in the area of gene loss research will be to use comparative genomics to map all instances of gene loss in the tree of life and to identify genes that have been lost during the evolution of any given species or taxon in relation to its last common ancestor with another given species or taxon. Comprehensive gene loss catalogues that cover a wide range of diverse groups of organisms would provide valuable information for many fields of biology, including evolutionary biology and translational medicine (Fig. 4).

Figure 4: Gene loss catalogues in evolutionary biology and translational medicine.



Nature Reviews | Genetics

Evolution by gene loss

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Microstructure: paragraphs, sentences, flow

Paragraph

- Paragraph usually starts with a topic sentence which summarises its “point”.

Published: 25 April 1953

Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid

J. D. WATSON & F. H. C. CRICK

Nature **171**, 737–738 (1953) | Cite this article

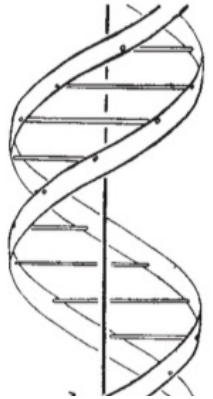
MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.



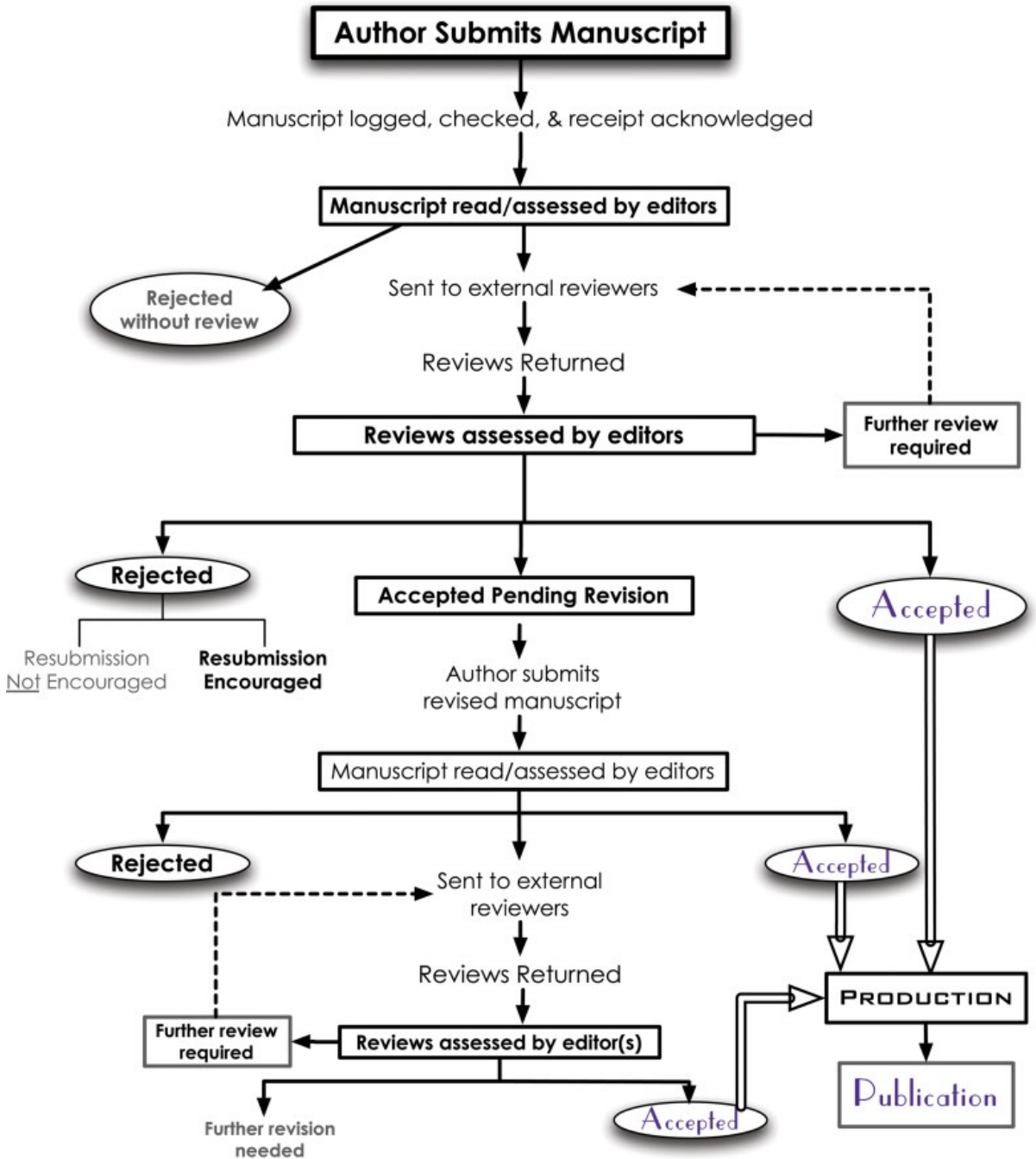
We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a

Sentences

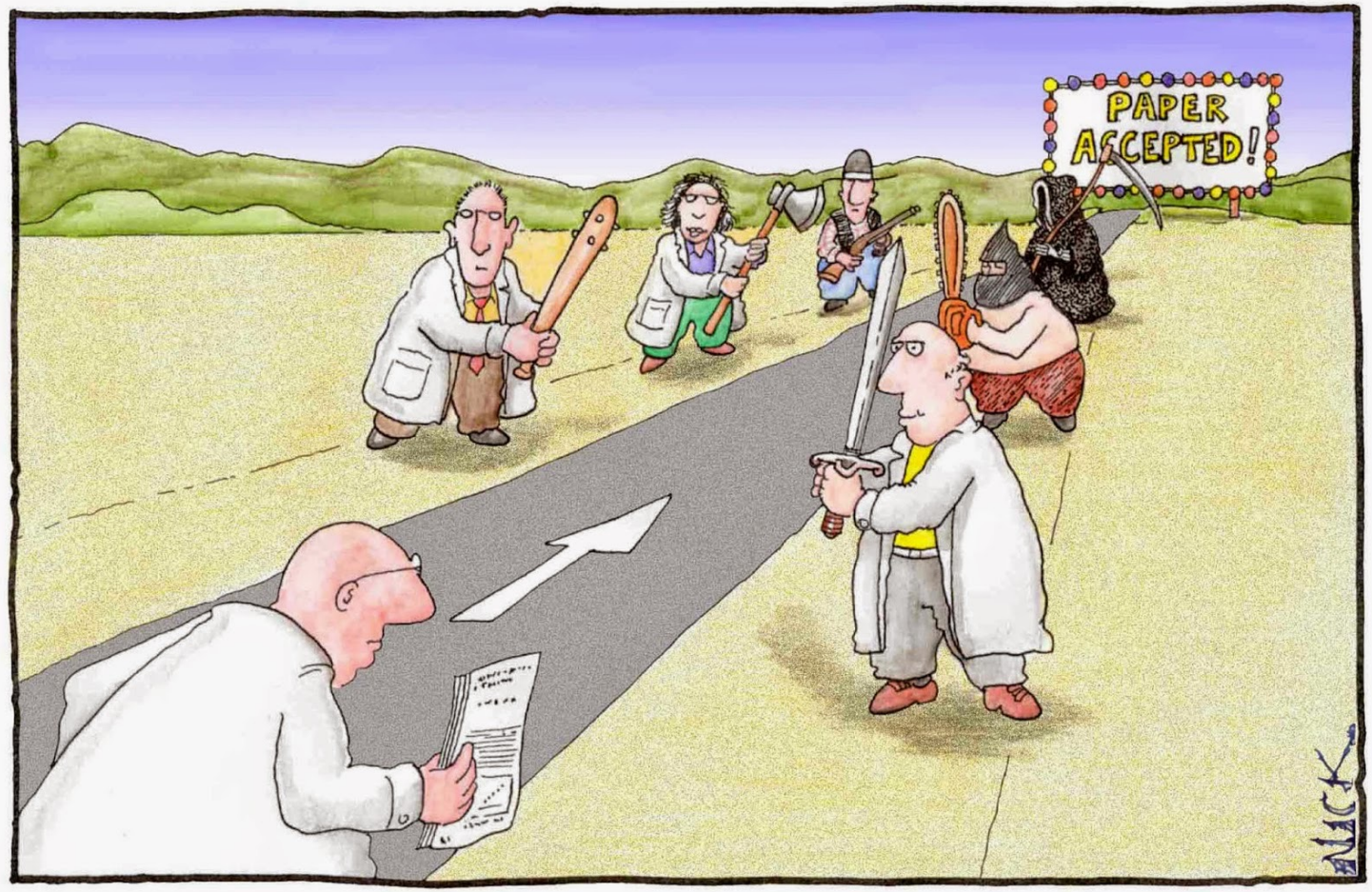
- Don’t pack more than one idea into one sentence.
- Goal, solution
  - e.g. To infer the origin of the Ebola outbreak, we …
- Old/new information pattern
  - e.g. There are a number of methods for multilocus phylogenetic analysis (Bininda-Emonds et al. 2002; de Queiroz and Gatesy 2007; Liu et al. 2009). Many of these methods proceed by inferring the single evolutionary tree that best fits the entire data set. Such “averaging” over multiple loci presumes that these loci share a common evolutionary history.

Peer Reviewing

The Peer Review Process



Voight ML, Hoogenboom BJ. Publishing your work in a journal: understanding the peer review process. *Int J Sports Phys Ther*. 2012;7(5):452–460.



Most scientists regarded the new streamlined peer-review process as ‘quite an improvement.’

What is peer review?

- Independent evaluation of an academic article, usually by an anonymous expert
- Helps the editor decide what to publish
- Helps the authors improve their work

Why peer review?

- Be a good citizen
- Stay at forefront of research
- Sharpen your critical thinking skills
- Impress the editor
- For review papers specifically:
  - They are designed to be short and easy to read
  - You might learn something
  - You can have a say in developing a consensus for your field

How does peer reviewing a review article compare with reviewing a research article?

Similarities

- Be professional and objective
- Understand the journal's guidelines and expectations
- Your task is to help improve the manuscript

Differences

- Good communication and accessible writing are important for research but **essential** for review articles
- No methods, statistics, analyses to evaluate in reviews
- Novelty should be assessed on the discussion rather than on results
- Distinguish consensus from author opinion in reviews
- Timeliness of a review article is critical

https://researcheracademy.elsevier.com/navigating-peer-review/certified-peer-reviewer-course/33-peer-review-review-article

Duties as Referee

Specifically for reviewing review papers:

- Assess significance
- Verify accuracy
- Improve clarity

Significance

- Is the topic addressed important/interesting? (Does the review say why?)
- How original is the review? (Compared with existing reviews of field?)
  - Considers the topic from a different angle
  - Different interpretation of the same results
  - Writing for a different audience
- Are the results reported significant?

Accuracy

- Are all claims backed by evidence?
- Are the evidences relevant/reliable/sufficient?
- Are methods/results appropriate and well-described?
- Is important relevant work omitted?
- Does the review suffer from any bias?
- Is the review balanced?

Accuracy

- Are the concepts explained correctly according to the current understanding in the field?
- Is terminology defined and used in a consistent and accepted way?
- Does the manuscript cite important recent research? Are the data and conclusions from the cited publications faithfully represented? Does the manuscript cite any disputed or discredited studies?
- Are author hypothesis vs. prevailing opinion vs. undisputed fact accurately delineated?
- **Would a non-expert reader come away with a correct understanding of the topic?**

https://researcheracademy.elsevier.com/navigating-peer-review/certified-peer-reviewer-course/33-peer-review-review-article

Clarity

- Is the review well-organised?
- Do title/abstract accurately reflect content?
- Is there the right level of detail?
- Are there language issues or typos?
  - It’s crucial that language and phrasing is clear and unambiguous to avoid confusion or misinterpretation.

https://thenode.biologists.com/another-look-at-peer-review-reviewing-review-articles/resources/

Clarity

Figures

- Are the figures well designed, well presented and intuitive?
  - Would additional figures, boxes or tables help to clarify text and illustrate important key points?
- Schematic/abstraction vs. reproduction of research results
- Legibility of small text

Courtesy

- Criticise the work, not the authors
- Mention also positive aspects
- Offer constructive criticism
- Don’t write things that you would not say in person

Be specific

- Try to be specific – refer to line or page numbers if you have concerns with a particular statement.

Iteration Process

- Reviewers' comments sent to the Editor
- Authors make changes and respond to comments
- Revision with comments sent back to the reviewers
- Editor asks reviewers if they are happy?...
- If not repeat...

Normal Timescale to do a peer review

- Normally from 1 week to 1 month
- Repeated duration if iterated
- If delayed, the Editor might decide instead