

# 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

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](#)

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 Genetics



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

Review

### Stay Connected: A Germ Cell Strategy

Kevin Lu <sup>1,2,3</sup>, Lindy Jensen <sup>3,4</sup>, Lei Lei <sup>5</sup>, Yukiko M. Yamashita <sup>1,3,5,6,8</sup> 

## Trends in Genetics



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

Science & Society

### Raw Genomic Data: Storage, Access, and Sharing

Mahsa Shabani <sup>1</sup> , Danya Vears <sup>1</sup>, Pascal Borry <sup>1</sup>

## Trends in Genetics



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

Forum

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

Ellie J. Maas <sup>1</sup> , Brigid Betz-Stablein <sup>1</sup>, Lauren G. Aoude <sup>2</sup>, H. Peter Soyer <sup>1,3</sup>, Aideen M. McInerney-Leo <sup>1</sup> 

## 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

Great attention has in the past been paid to the mechanisms of evolution by gene duplication (that is, neofunctionalization and subfunctionalization)<sup>1,2</sup>. 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](#)

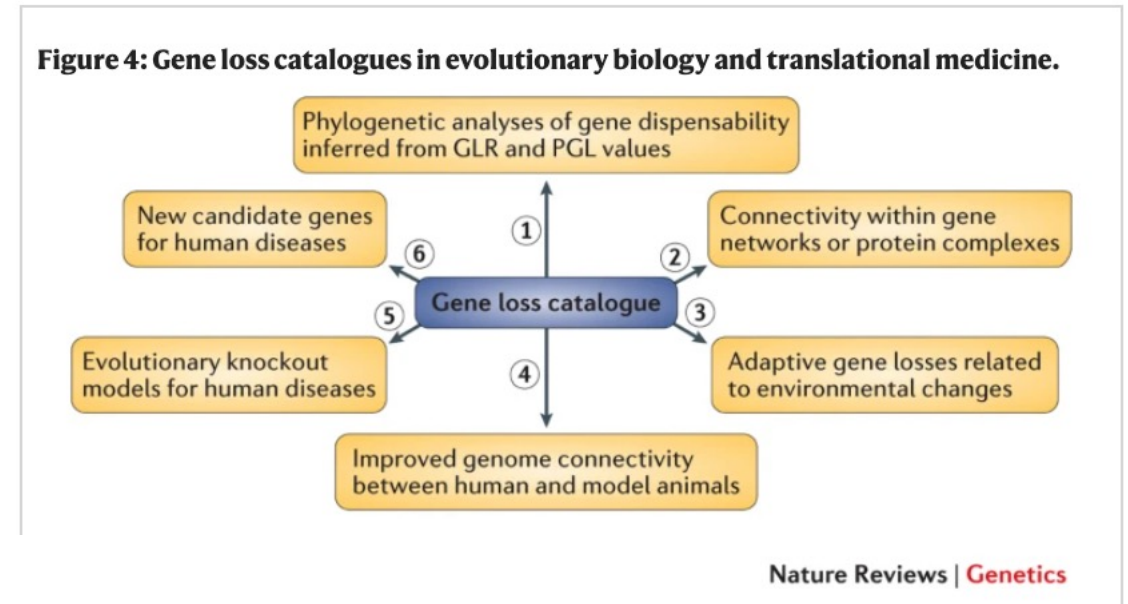
19k Accesses | 340 Citations | 209 Altmetric | [Metrics](#)

# 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).



## Evolution by gene loss

Ricard Albalat & Cristian Cañestro

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

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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**

**W**E 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<sup>1</sup>. 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  $\beta$ -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.



# Responding to Reviewers



# Things to keep in mind when responding to reviewers

- Structure
- Thoroughness
- Attitude
- Strategy

# Responding to Reviewers: Structure (of the response)

- Provide an overview, then quote the full set of reviews
- Use typography to help the reviewer navigate your response

P24 fig 5 right: we see here that the MSAs are very good, with ~90% of well aligned residue pairs. What about harder cases with (say) 50% of errors? Is this representative of real cases, e.g. with large number of taxa? A bit of discussion is needed there ...

**Response:** We agree. As we now explain in the manuscript, 90% pairwise accuracy is roughly in line with the performance of typical aligners on empirical benchmarks such as Balibase. Note that the score is computed on a pairwise-residue level and so is not very sensitive to the number of taxa, in contrast to column-wise scores, which rapidly degrade with increasing number of taxa.

P25 “to fare better”

**Response:** the formulation seems correct to us. We use “to fare better” in the sense “to perform better”.

P26 “to leave our some”

**Response:** fixed.

# Make the response self-contained

- Quote the changes directly in the response
  - Refer to specific line number
- Makes it easier for the reviewer to understand exactly what you did without having to flip back and forth between your manuscript and the response
  - Reduces the chance that reviewer will read the whole paper and find new things to complain about
- Except when a large chunk of modified text (e.g., a new section) is too long to quote.
  - Refer to it explicitly in the response (e.g., give title of the new section)

# Responding to Reviewers: Thoroughness

- Respond to every point raised by the reviewer
- Be clear about what changed relative to the previous version
- Typical ways to respond to each point:
  - *You are right, here's how we addressed the criticism...*
  - *This is a misunderstanding because things were unclearly formulated. We have clarified...*
  - *This is a legitimate/pertinent concern in general, but in this specific case...*



# Responding to Reviewers: Attitude

- Don't be scared by major revisions
- Accept the blame
- Be polite and respectful of all reviewers
- Remember that reviewers are typical readers



# Responding to Reviewers: Strategy

- When possible, do what the reviewer asks
- Be prepared for discrepancies
- Compromise
  - *You can't do everything*
  - *When in doubt, ask the editor*



# TO DO

- Make the revisions according to the peer reviews
- Submit two versions– one with tracked changes, and another that is the “clean copy”
- ~~Submit the cover letter~~
- Submit the Response to Reviewers



# How to easily track changes

- Starting from google doc:
- Make your revisions either on a separate copy of the document and rename it with a new title
- OR, make your revisions in the same document
  - “suggest mode” during the collaborative editing process, but accept all changes in end
  - Name the original version and the new version (Version history)
- Download word documents of both version

# How to easily track changes

- From Word:
- Open Word -> Tools -> Combine documents
- Load original vs. revised document
- Review -> Markup Options -> Balloons -> Show only formatting in balloons

# How to get your scientific paper published: Responding to Reviewers

- <https://www.youtube.com/watch?v=j2cfcH1P8E8>



# Check out the other videos in the “How to get published” series:

- The writing process:

<https://www.youtube.com/watch?v=JQrJyDsddZc&t=4s>

- Journal selection:

<https://www.youtube.com/watch?v=xFnIsWrljLQ&t=1s>

- Responding to reviewers:

<https://www.youtube.com/watch?v=j2cfcH1P8E8>