

# Scientific Writing

魏桐

11/30/2022

- Manuscript editing
- Submission & revision
- How to prepare before the thesis season



# Part I

# Manuscript editing

- **TOP-DOWN** editing
- Read through the draft multiple times
- Do not try to fix everything once; fix on **one thing/error at a time** (tense, details, typo, etc.)

# The editing phase (continued)

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- Edit structure **section by section**
  - Move sentences/paragraphs to where they belong
  - Focus on the logic in each section
- Edit paragraph **line by line**
  - Look into each sentence, word, phrase, etc.
  - Language skills play an important role
  - Do it several rounds
- Seek for **professional feedbacks** after you have done a thorough editing
- Final check in spelling, grammar, numbers, figures & tables, etc.

# Outcomes from the editing phase

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- **Clear key questions**
- The main Figures and Results **in the same topic**
- An updated Discussion and Introduction **after a thorough review of literature**
- A rewritten Abstract with **answers to the 4 questions**
- A precise and interesting Title
- Methods, supplementary materials, data deposition, etc.

- That (referring to a specific thing) vs which (adding a clause)
- Correct/incorrect, not right/wrong
- Only use “significant” for statistics
- Give exact/approximate numbers instead of several, most, a few, etc.

# Tips for English writing (continued)

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- Articles: a, an or the
- Tense: past tense for results; present for facts; present tense in figure legends and formula; present perfect tense for continuous work
- Could, may, might
- Demonstrate, indicate, suggest
- Use short sentences
  
- Check grammar!



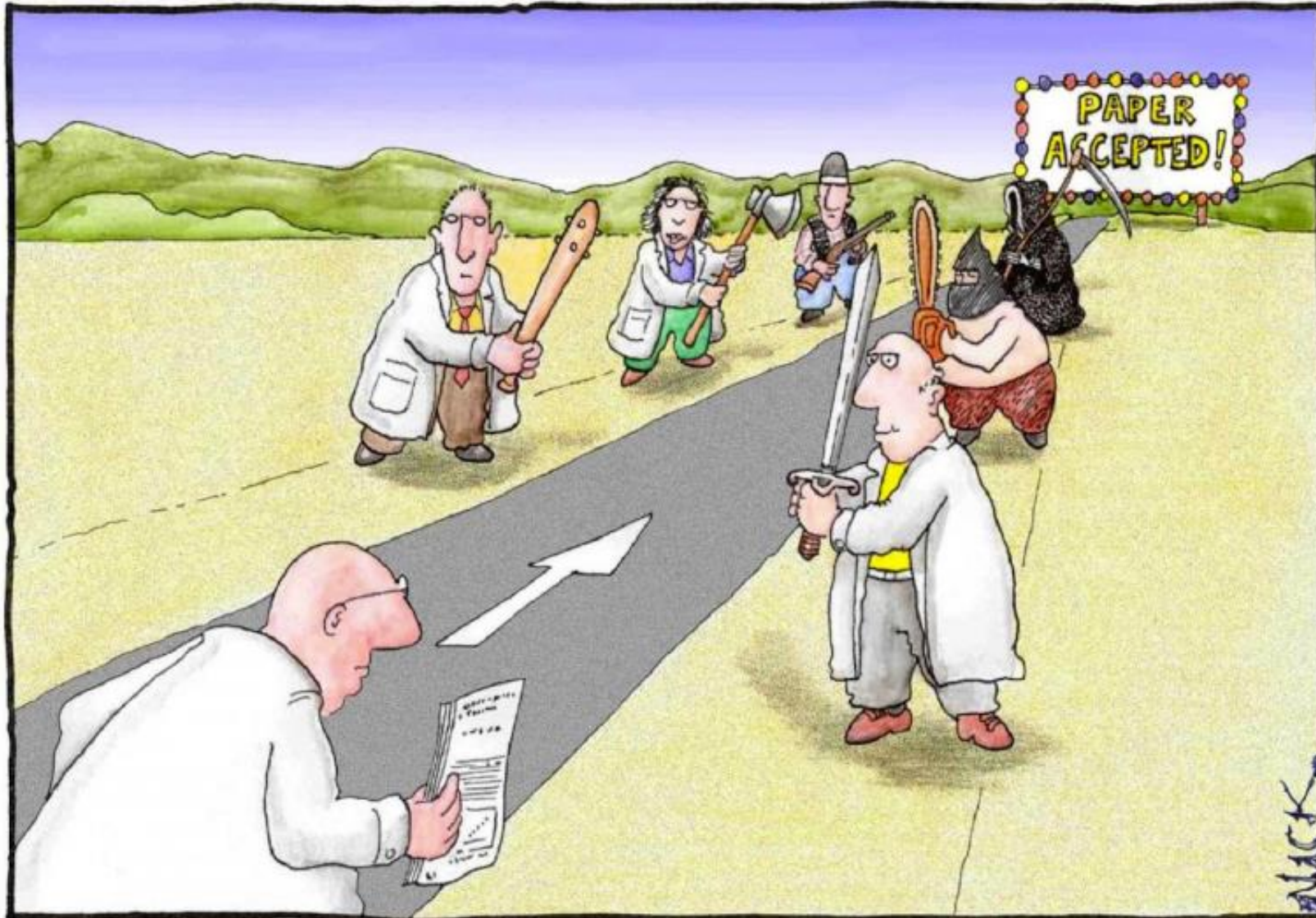
- Abstract is the essence of your manuscript
  - It is **the FIRST thing** readers see, and sometimes the ONLY thing
  - It **sets the stage** by telling what your work is about
  - It is **critical for the reviewing process**
- It should be one paragraph about,
  - Why you did the work
  - What you found
  - Why it matters

# Part II

## Submission & revision



# Ready to submit your manuscript!



There is **no end of editing**, but there should be **a deadline for submission!**

- Everyone is satisfied (seldom).
- Major authors are satisfied (sometimes).
- Major authors are tired (most of the time).
- My advice
  - All the **major issues** raised by professionals are solved.
  - The logic is **easy to follow**.
  - The main text **reads well**.
  - There will not be any significant improvement in the next 2 months.

- Before pushing the SUBMIT button
  - Choose a **reasonable** journal
  - Write a **thoughtful Cover Letter**
  - Reformat according to the guideline
- Major or minor (unlikely) revisions
- Conditional acceptance -> copyediting -> formal acceptance

- Impact Factor
  - It shows how many times **on average** papers in one year have been cited **over the next two years**
  - The top journal is not always a good choice
- The potential readers
  - Make a list of journals with narrow to broad readership
- Open access
  - More read and cited
  - Required by funding agencies



# Choose a target journal (continued)

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- Time to publication
  - Competition
  - Graduation
  - Annual report
  - etc.

# Things to do for a particular journal

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- **A thoughtful cover letter**
  - to communicate with editor
- A well-written abstract
  - Answer the WHY, HOW, WHAT, and SO WHAT questions
- The checklist
  - Follow the author guideline

- Cover letter is for editors, who decide whether to send out your manuscript for reviewing.
- Do **NOT** copy Abstract. **ALWAYS** write a good letter!
  - One page
  - Start with a small paragraph about the paper you are submitting
  - Explain why it is **important and interesting**
  - Describe what you have concluded
  - Describe how it **fits into the scope**

Dear editor,

Hereby we submit our manuscript entitled "The Genome Sequence of the Domestic Cucumber (*Cucumis sativus* var. *sativus* L.)" to Science. The manuscript includes the text, one table, three figures, and supplementary material.

With our best regards,  
Corresponding authors

Dear editor,

I hereby we submit our manuscript entitled "The Genome Sequence of the Domestic Cucumber (*Cucumis sativus* var. *sativus* L.)" to Science. The manuscript includes the text, one table, three figures, and supplementary material.

Cucumbers are a great family in one of the most economically important botanical families. Collectively called as cucurbits, the family includes many important species as cucumbers, melons, watermelons, pumpkins and squashes. They provide vegetables, fruits, and edible seeds that are important for our daily diet.

Cucurbits are the model system for important biological processes. The female diploid is a dicentric system of 14 pairs, from numerous chromosomes in plants. The determination to complete are controlled by single genes, similar to the cucurbit. In nature, the cucurbit species of the plant, the cucurbit of the cucurbit species, cucurbit species and cucurbit species in developing cucurbit. Cucurbit is the cucurbit of the cucurbit species, cucurbit species and cucurbit species in developing cucurbit. Cucurbit is the cucurbit of the cucurbit species, cucurbit species and cucurbit species in developing cucurbit.

Compared to their economic and biological importance, cucurbits are very much under-investigated. Economic and genetic resources are scarce. Genetic improvement of cucurbits is further constrained since it is cross-incompatible with other species in the family.

One benefit shows the cucurbit genome is, although different, they have a similar genome size. This indicates that all genomes and one genome should tell story of cucurbit. I formed an international consortium to sequence the cucurbit genomes. Cucurbit Genome Consortium, there is 138 scientists in Australia.

Cucurbit genome by a novel computational method of the Cucurbit Genome Consortium (CGC) sequencing technology, the 35Mb genome size - 98% of the genetic regions. The abundance of satellite sequences and DNA. Cucurbit (1,000) in Arabidopsis, but not cucurbit whole genome. Cucurbit genome duplication was observed among the Cucurbit genome. Cucurbit genome duplication was observed among the Cucurbit genome. Cucurbit genome duplication was observed among the Cucurbit genome.

Cucurbit genome will greatly advance our understanding of cucurbit biology, life improvement, resources for their genetic improvement. Its progress was demonstrated in a meeting held in Nov. 2008 in Shenzhen, China. The Cucurbit Genome Consortium (CGC) assembled about 100 researchers from 7 countries. Eight of vegetable seed companies also sent their representatives. Several international projects are being developed based on the genome, such as the China-Watermelon Initiative, the Xian-Qin Cucumber Gene Expression Project, and others. 100 Cucurbit Genome Project.

Cucurbit genome was affordable in an only when Cucurbit Genome Consortium (CGC) was formed. The Cucurbit Genome Consortium (CGC) was formed in an only when Cucurbit Genome Consortium (CGC) was formed. The Cucurbit Genome Consortium (CGC) was formed in an only when Cucurbit Genome Consortium (CGC) was formed.

Best regards,  
Corresponding authors

- Format the manuscript according to the guideline
  - Word count (make each section close to the requirements)
  - Text formatting (title page, subtitles, spacing)
  - Figure formatting (citation, width, etc)
  - Supplementary materials

## PRINT PAPER

## LETTER

### Outgrowth of single oncogene-expressing cells from suppressive epithelial environments

©2000 E. J. Connel & David B. Clark

transcription is a shared cellular process that is believed to have evolved in the eukaryotic nuclear envelope. This process is regulated by a number of factors, including the basal transcription machinery, which is composed of RNA polymerase II and the basal transcription factors (TBP, TFIIB, TFIID, TFIIE, TFIIH, and TFIIF). The basal transcription machinery is responsible for the initiation of transcription, and its activity is regulated by a number of factors, including the basal transcription factors, which are themselves regulated by a number of factors, including the basal transcription factors. The basal transcription machinery is a complex of proteins that are involved in the initiation of transcription, and its activity is regulated by a number of factors, including the basal transcription factors, which are themselves regulated by a number of factors, including the basal transcription factors.

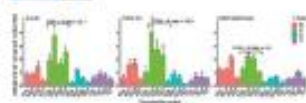
The outgrowth of synaptic axons onto cortical targets is a fundamental process in nervous development. However, synaptic development is not uniform across the cortex, and different subpopulations of neurons exhibit different patterns of outgrowth, particularly with respect to the timing of axon extension. Laminar and columnar organization of the cortex is a consequence of this process, and the development of synaptic connections is a critical step in the formation of the mature cortex. The development of synaptic connections is a critical step in the formation of the mature cortex. The development of synaptic connections is a critical step in the formation of the mature cortex.

In order to acquire a high  $\Delta G$  growth rate the *in vitro* system was first exposed to the appropriate temperature regime, and then cooled to 40°C. The initial 10 min of the 100°C heating cycle induced a 2.5-fold increase in the expression of *phosphoglycerate kinase* (Table 1). The 10 min of 40°C heating induced a 1.5-fold increase in the expression of *phosphoglycerate kinase* (Table 1). The 10 min of 40°C heating induced a 1.5-fold increase in the expression of *phosphoglycerate kinase* (Table 1). The 10 min of 40°C heating induced a 1.5-fold increase in the expression of *phosphoglycerate kinase* (Table 1).

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**On the Cover:** Authors, along with an additional Editorial Oversight team, submitted the *in situ* studies of the environment of the highly reduced pyrite in the Dabie orogen, as part of the special issue.

Received 18 May 2004; revised 10 July 2004; accepted 10 July 2004  
Published online 12 August 2004 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/anie.200400450

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12. Kasper, L., and S. C. Schreiber. *Antigen presentation by MHC class II molecules*. *Annu. Rev. Biochem.* 69: 439–476 (2000).
13. Kasper, L., and S. C. Schreiber. *Antigen presentation by MHC class II molecules*. *Annu. Rev. Biochem.* 69: 439–476 (2000).
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16. Kasper, L., and S. C. Schreiber. *Antigen presentation by MHC class II molecules*. *Annu. Rev. Biochem.* 69: 439–476 (2000).
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21. Kasper, L., and S. C. Schreiber. *Antigen presentation by MHC class II molecules*. *Annu. Rev. Biochem.* 69: 439–476 (2000).
22. Kasper, L., and S. C. Schreiber. *Antigen presentation by MHC class II molecules*. *Annu. Rev. Biochem.* 69: 439–476 (2000).

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### Key features:

- Includes main text and figures/tables/boxes plus references.
- Appears in print and online as a PDF and as full-text HTML.
- Text and figures are copy-edited to *Nature* style.
- Figure formats: colour artwork supplied in **RGB (recommended) or CMYK formats**; preferred formats are layered Photoshop (PSD) or TIFF for photographic images (minimum 300 p.p.i.), AI, Postscript, Vector EPS or PDF for line drawings and graphs.



## Formatting details in text

## Order of elements

Articles should be **ordered in the sequence:** title, authors, affiliations (plus present addresses), bold first paragraph, main text, references, tables, figure legends, (online-only) Methods (plus any associated references; data and code availability statements included at end of online Methods), acknowledgements, author contributions, competing interest declaration, additional information (containing supplementary information line (if any) and corresponding author line), Extended Data figure legends and Extended Data table titles and footnotes (any references unique to the Extended Data should be added to the end of the online-only reference list).

## Fonts

We prefer the use throughout of a 'standard' font, **preferably 12-point Times New Roman**. For superscripts or subscripts, please apply actual super/subscript format; do not use 'raised' or 'lowered' formats. For mathematical symbols, Greek letters, and other special characters, use 'insert', 'symbol' and then select '(normal text)' or 'symbol' as the font. Use of other fonts can cause translation problems. List non-standard keyboard symbols in the letter accompanying the final accepted version of your paper.

## Final print-only artwork

When preparing figures, authors are advised to refer to printed copies of Nature to get a sense of general size and style points. For an illustrated guide to preparing production-quality artwork after acceptance, see [this information document](#).

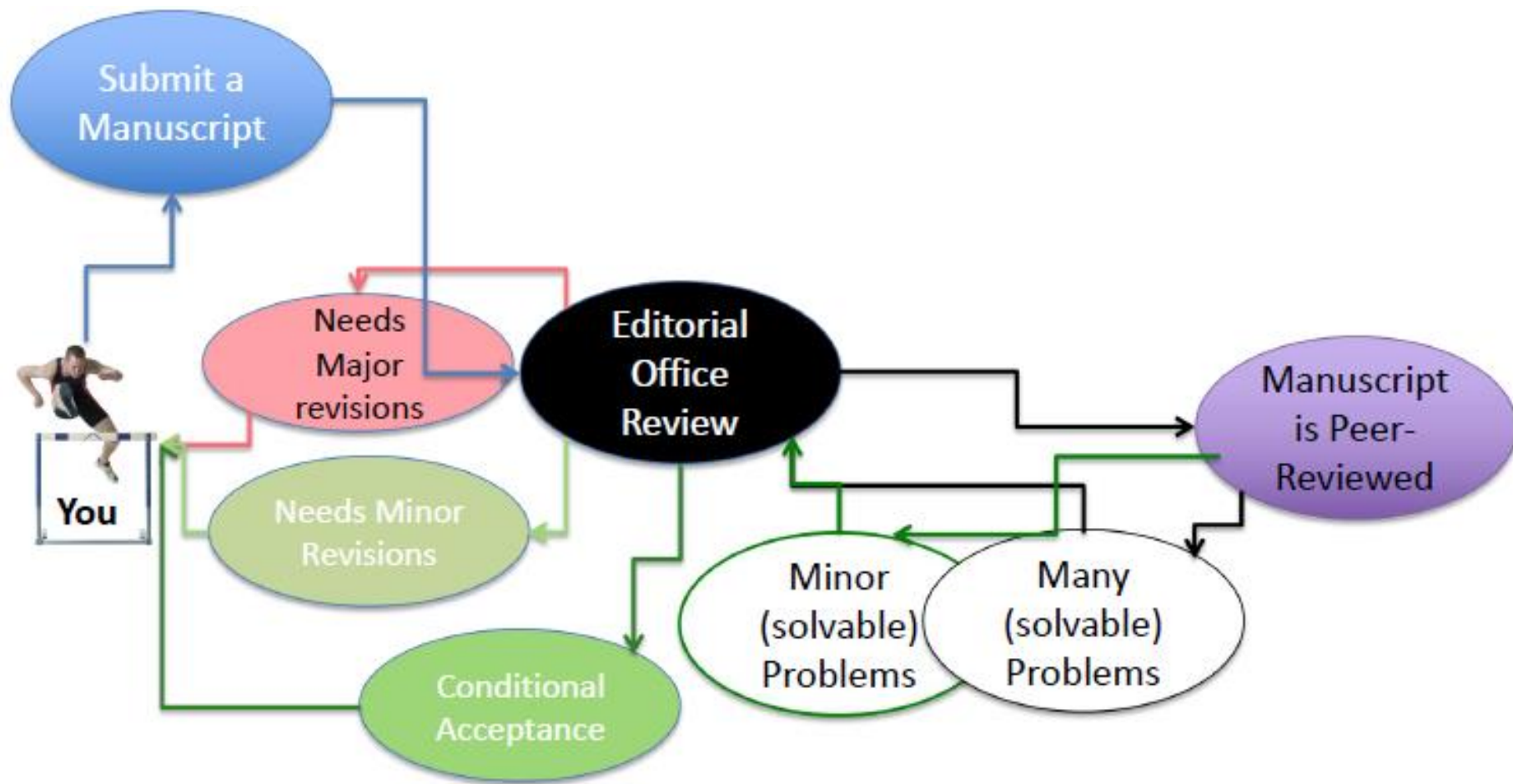
## Lettering

Lettering should be in a sans-serif typeface, preferably Helvetica or Arial, the same font throughout all figures in the paper. Units, capitalization, etc. should follow Nature style. Where practical, avoid placing lettering directly over images or shaded areas.

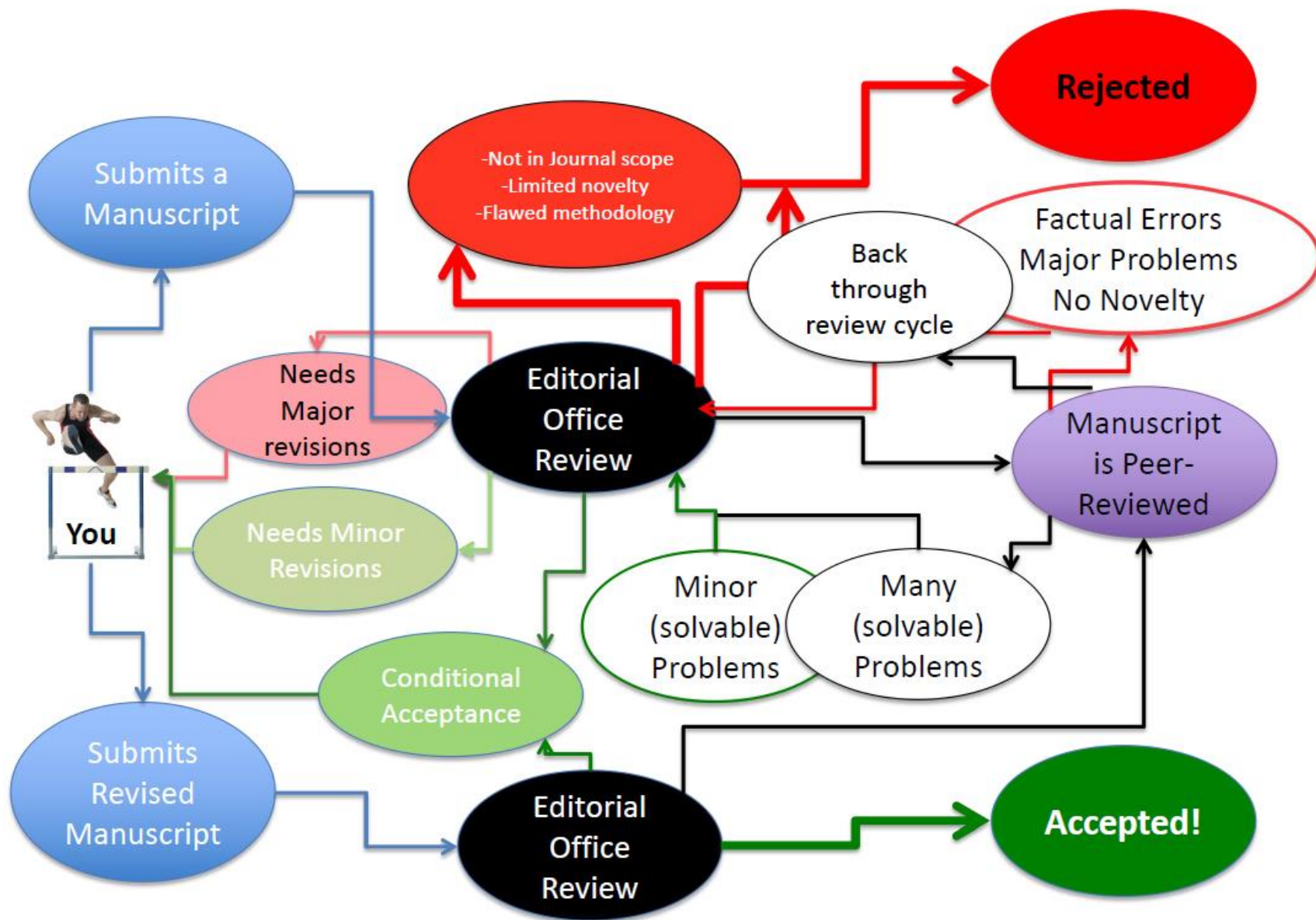
Separate panels in multi-part figures should each be labelled with **8 pt bold, upright** (not italic) a, b, c. **Maximum text size for all other text should be 7 pt; minimum text size should be 5 pt.** Amino-acid sequences should be presented in one-letter code in Courier.

Do not rasterize or covert text to outlines.

# Theoretical reviewing process



# Actual reviewing process



# Common reasons for rejections

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- No novelty
- Data do not support conclusions
- Not significant enough for your target journal
- Inappropriate experimental setup
- Inappropriate methods for the analysis
- Plagiarism
- Lack of ethical approval or missing data

- Novelty
  - “There is very little biological novelty”
  - “The work is unlikely to have broad interest”
- Scientific questions
  - “Paper is mostly descriptive”
- English writing
  - “The English is difficult to follow”
  - “The methods are uninterpretable”



- Make a plan on,
  - What experiments/analyses to be done
  - What mistakes/typos need to be corrected
  - Which parts need to be re-written
  - Which comments need to be argued
- Focus on **the major issues**
- Fix the minor ones
- Highlight the changes in MS and indicate the line numbers in Response

- Thumb of rules
  - **Respond politely**
  - Do NOT argue; take it easy
  - Response to EVERY issue
  - Provide new evidence if you did what the reviewers asked
  - Explain clearly the reason if you decide not to do
- It is difficult to argue with No Novelty
  - Highlight the novelty in the first submission
  - Point out the novelty if reviewers miss it

- Fill out required forms, author consent letter, checklist, statements, etc.
- Meet the requirements for final submission, word count, figure size, acknowledgements, etc.
- **Data and code availability**
- There is another round of copyediting.

nature  
genetics

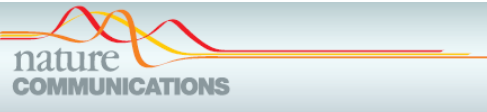
ARTICLES

<https://doi.org/10.1038/s41588-021-00831-0>



## Whole-genome resequencing of 445 *Lactuca* accessions reveals the domestication history of cultivated lettuce

Year	2017	2021
Sample	One reference genome	445 germplasm lines
Key finding	Whole-genome triplication	Domestication history
Journal	Nature Communications	Nature Genetics



ARTICLE

Received 15 Aug 2016 | Accepted 15 Feb 2017 | Published 12 Apr 2017


DOI: 10.1038/ncomms14953

OPEN

Genome assembly with *in vitro* proximity ligation data and whole-genome triplication in lettuce

Sebastian Reyes-Chin-Wo<sup>1,\*</sup>, Zhiwen Wang<sup>2,\*,†</sup>, Xinhua Yang<sup>2,\*</sup>, Alexander Kozik<sup>1</sup>, Siwaret Arikrit<sup>3,†</sup>, Chi Song<sup>2</sup>, Liangfeng Xia<sup>2</sup>, Lutz Froenicke<sup>1</sup>, Dean O. Lavelle<sup>1</sup>, Maria-José Truco<sup>1</sup>, Rui Xia<sup>4</sup>, Shilin Zhu<sup>2</sup>, Chunyan Xu<sup>2</sup>, Huaqin Xu<sup>1</sup>, Xun Xu<sup>2</sup>, Kyle Cox<sup>1</sup>, Ian Korf<sup>1,5</sup>, Blake C. Meyers<sup>3,4</sup> & Richard W. Michelmore<sup>1,5,6,7</sup>

Lettuce (*Lactuca sativa*) is a major crop and a member of the large, highly successful Compositae family of flowering plants. Here we present a reference assembly for the species and family. This was generated using whole-genome shotgun Illumina reads plus *in vitro* proximity ligation data to create large superscaffolds; it was validated genetically and superscaffolds were oriented in genetic bins ordered along nine chromosomal pseudomolecules. We identify several genomic features that may have contributed to the success of the family, including genes encoding Cycloidea-like transcription factors, kinases, enzymes involved in rubber biosynthesis and disease resistance proteins that are expanded in the genome. We characterize 21 novel microRNAs, one of which may trigger phasiRNAs from numerous kinase transcripts. We provide evidence for a whole-genome triplication event specific but basal to the Compositae. We detect 26% of the genome in triplicated regions containing 30% of all genes that are enriched for regulatory sequences and depleted for genes involved in defence.



ARTICLES

<https://doi.org/10.1038/s41588-021-00831-0>

Check for updates

Whole-genome resequencing of 445 *Lactuca* accessions reveals the domestication history of cultivated lettuce

Tong Wei<sup>1,11</sup>, Rob van Treuren<sup>2,11</sup>, Xinjiang Liu<sup>1,11</sup>, Zhaowu Zhang<sup>1,3</sup>, Jiongjiong Chen<sup>4</sup>, Yang Liu<sup>1</sup>, Shanshan Dong<sup>5</sup>, Peinan Sun<sup>4</sup>, Ting Yang<sup>1</sup>, Tianming Lan<sup>1,6</sup>, Xiaogang Wang<sup>7</sup>, Zhouquan Xiong<sup>7</sup>, Yaqiong Liu<sup>8</sup>, Jinpu Wei<sup>8</sup>, Haorong Lu<sup>8</sup>, Shengping Han<sup>8</sup>, Jason C. Chen<sup>8</sup>, Xuemei Ni<sup>1</sup>, Jian Wang<sup>1,9</sup>, Huanming Yang<sup>1,9</sup>, Xun Xu<sup>1,10</sup>, Hanhui Kuang<sup>4</sup>, Theo van Hintum<sup>2</sup>, Xin Liu<sup>1</sup> and Huan Liu<sup>1</sup>

Lettuce (*Lactuca sativa*) is an important vegetable crop worldwide. Cultivated lettuce is believed to be domesticated from *L. serriola*; however, its origins and domestication history remain to be elucidated. Here, we sequenced a total of 445 *Lactuca* accessions, including major lettuce crop types and wild relative species, and generated a comprehensive map of lettuce genome variations. In-depth analyses of population structure and demography revealed that lettuce was first domesticated near the Caucasus, which was marked by loss of seed shattering. We also identified the genetic architecture of other domestication traits and wild introgressions in major resistance clusters in the lettuce genome. This study provides valuable genomic resources for crop breeding and sheds light on the domestication history of cultivated lettuce.

# Part III

## Writing practice



Issue	Solution
Manuscript structure	<b>Structured</b> report
Results description & interpretation	<b>Write immediately</b> after analyses is done
Context writing	<b>Take notes</b> for literature
Procrastination	<b>Picture</b> your goal and start writing

# Write your way out

