Peer Community In
Infections

Advancing Pathogen Genomics: A Comprehensive Review of the Xanthomonas(*) Genome's Impact on Bacterial Research and Control Strategies

Damien François Meyer *based on peer reviews by* ***Boris Vinatzer*** *and 3 anonymous reviewers*

Ralf Koebnik, Sophie Cesbron, Nicolas W. G. Chen, Marion Fischer-Le Saux, Mathilde Hutin, Marie-Agnès Jacques, Laurent D. Noël, Alvaro Perez-Quintero, Perrine Portier, Olivier Pruvost, Adrien Rieux, And Boris Szurek (2023) Celebrating the 20th Anniversary of the First Xanthomonas Genome Sequences – How Genomics Revolutionized Taxonomy, Provided Insight into the Emergence of Pathogenic Bacteria, Enabled New Fundamental Discoveries and Helped Developing Novel Control Measures – A Perspective from the French Network on Xanthomonads. Zenodo, ver. 3, peer-reviewed and recommended by Peer Community in Infections. `https://doi.org/10.5281/zenodo.8223857`

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Meyer, D. (2024) Advancing Pathogen Genomics: A Comprehensive Review of the Xanthomonas(*) Genome's Impact on Bacterial Research and Control Strategies. *Peer Community in Infections*, 100193. 10.24072/pci.infections.100193

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The paper titled "Celebrating the 20th Anniversary of the First *Xanthomonas* Genome Sequences – How Genomics Revolutionized Taxonomy Provided Insight into the Emergence of Pathogenic Bacteria Enabled New Fundamental Discoveries and Helped Developing Novel Control Measures – A Perspective from the French Network on Xanthomonads" by Ralf Koebnik et al. (2023) is an insightful contribution to the field of genomics and its application in understanding pathogenic bacteria, particularly *Xanthomonas*. This comprehensive review offers a unique perspective from the French Network on Xanthomonads, underscoring the significant advancements in taxonomy, pathogen emergence, and development of control strategies due to genomic research.

One of the paper's main strengths is its thorough exploration of how genomics has revolutionized our understanding of *Xanthomonas* and other pathogenic bacteria. It sheds light on the evolution and emergence of these pathogens, contributing significantly to the development of novel and effective control measures. The authors' detailed account of the historical progress and current state of genomics in this field highlights its pivotal role in guiding future research and practical applications in managing bacterial diseases.

Moreover, the paper emphasizes the importance of collaborative efforts and the sharing of knowledge within scientific networks, as exemplified by the French Network on *Xanthomonas*. This approach not only enriches the study but also serves as a model for future collaborative research endeavors.

In conclusion, the work of Koebnik et al. is a valuable resource for researchers, policymakers, and practitioners in the field of plant pathology and genomics. It not only provides a comprehensive overview of the advances in genomics related to *Xanthomonas* but also illustrates the broader impact of genomic studies in understanding and managing pathogenic bacteria.

References:

Ralf Koebnik, Sophie Cesbron, Nicolas W. G. Chen, Marion Fischer-Le Saux, Mathilde Hutin, Marie-Agnès Jacques, Laurent D. Noël, Alvaro Perez-Quintero, Perrine Portier, Olivier Pruvost, Adrien Rieux, And Boris Szurek (2024) Celebrating the 20th anniversary of the first *Xanthomonas* genome gequences – How genomics revolutionized taxonomy, provided insight into the emergence of pathogenic bacteria, enabled new fundamental discoveries and helped developing novel control measures – A perspective from the French network on Xanthomonads. Zenodo ver. 3, peer-reviewed and recommended by Peer Community in Infections. https://doi.org/10.5281/zenodo.8223857

Reviews

Evaluation round #1

DOI or URL of the preprint: https://doi.org/10.5281/zenodo.8223857
Version of the preprint: 3

Authors' reply, 19 December 2023

Dear colleagues from the Managing Board of PCI Infections,
Dear Damien,

First of all, we would like to thank you for editing our manuscript. Special thanks go to the four reviewers for their positive and encouraging comments.

We have addressed and corrected all points raised by Reviewer 4 (Boris Vinatzer).

Anonymous reviewers 2 and 3 had no specific comments that needed to be considered in the revision of the manuscript.

Anonymous Reviewer 1 had the most comments, which we have addressed as explained below. Some comments called for further discussion on possible applications or implications. In order to maintain the balance of the individual contributions in this article, we have tried not to go into too much detail, but have nevertheless outlined important developments.

Our revisions are visible in the uploaded document with the modifications marked in TrackChange mode.

We hope that our revised manuscript is now suitable for publication in PCI Infections.

With kind regards,
Ralf Koebnik

Response to Reviewer 1:

Reviewer 1 – Page 7-9:
-The section could benefit from clearer organization and structure. It transitions between different topics, including the use of ancient DNA and taxonomic studies, without a clear delineation.
-The section could engage the reader more effectively by providing a clearer introduction or context for the importance of ancient genomics and taxonomic studies in the field of plant pathology. This would help readers understand why these topics are significant.

Our answer: We have reorganized this section and hope that it is now clearer. We prefer not to include taxonomic studies here, as this aspect will be developed later by Marion Fischer-Le Saux. However, we have changed the introduction on genomics and added a conclusion to the second paragraph to better structure the transition between the two paragraphs.

Reviewer 1 – Pages 10-22:
Constantin and Co-workers' Taxonomic Reclassification: The work by Constantin and co-workers on the taxonomic reclassification of *Xanthomonas* strains is commendable. However, it's essential to acknowledge that there are still unresolved taxonomic issues, particularly in Rademaker group 9.1 and some unclassified pathovars. The absence of a clear classification for these strains might hinder precise research and diagnostics in the field. Addressing these ambiguities should be a priority for future taxonomic studies.

Our answer: We have commented on the problem with Rademaker group 9.1, which was unfortunately not addressed by Constantin et al. in their study on the taxonomic revision of the so-called *X. axonopodis* species complex, which correspond to Rademaker group 9.

Reviewer 1 – Emergence of Xylella fastidiosa in Europe:
The emergence of *Xylella fastidiosa* and its comparison with *Xanthomonas* is indeed a fascinating area of research. However, it's important to note that while these bacteria share phylogenetic relations, their biological characteristics and niches significantly differ. The section provides valuable insights into the epidemiology and ecological impact of *X. fastidiosa*, but further discussions on potential preventive measures and strategies to mitigate its spread would be beneficial.

Our answer: We have added our perspective on potential preventive measures and strategies to mitigate its spread.

Reviewer 1 – Type 4 Protein Secretion and Bacterial Competition: The discovery of type 4 protein secretion as a mechanism for bacterial competition in *Xanthomonas* is groundbreaking. However, this subsection primarily focuses on the historical context and initial discoveries. To enhance the reader's understanding, it would be helpful to include more recent developments and ongoing research in this area. Additionally, discussing potential applications or implications of this discovery in biotechnology or agriculture could add value.

Our answer: We have added some implications of this discovery in the context of biological control, where two genera related to *Xanthomonas*, *Lysobacter* and *Stenotrophomonas*, contain potential biological control organisms and where knowledge of contact-dependent killing will facilitate the engineering of beneficial synthetic communities.

Reviewer 1 – Cracking the DNA-binding Code of TAL Effectors: The TAL effector research has indeed been a captivating field, especially with the discovery of the TAL code. However, the subsection briefly mentions this significant discovery without delving into its broader implications or recent advancements. Providing more context on how this code has revolutionized our understanding of TAL effectors and its applications

Our answer: We have added some stunning applications of TALENs and discuss their advantages over CRISPR-Cas technologies in the context of organelle genome engineering. Such striking applications are of course a matter of taste, and as this essay reflects the personal opinions of the authors, others may think of other applications in this rapidly developing field.

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Decision by Damien François Meyer, posted 30 November 2023, validated 30 November 2023

Acceptation with minor modifications

Dear corresponding author,

First of all, I would like to apologize for the delay of my answer. It took us time to find some reviewers that have no conflict of interests and accept to revise your manuscript. It took time also to get all the reviews.

Anyway, your opinion article is of high interest for the Xanthomonas community and beyond.

As you will see, it is a point of view shared by all the reviewers. Nevertheless, some suggested some minor revisions that should enhance the paper before a final official recommendation in PCI infections.

I am looking forward to read the final version of the paper.

Regards

Damien

Reviewed by anonymous reviewer 3, 01 October 2023

Download the review

Reviewed by anonymous reviewer 1, 21 November 2023

I found the essay celebrating the importance of the first *Xanthomonas* Genome Sequences scratches the surface of research done but gives us a great picture of how quickly we have moved the research forward in 20 years. We have made such progress in such a short time in so many different pathosystems as a result of this seminal work.

Reviewed by anonymous reviewer 2, 30 October 2023

This manuscript is a series of personal perspectives on recent progress on the biology of Xanthomonas. Because it does not claim to be a comprehensive review and does not present any new results, I do not have any comments on the content. It is a perspective or commentary piece, which do not typically go through traditional peer review.

Reviewed by Boris Vinatzer, 05 November 2023

The perspective paper by Koebnik and colleagues is a wonderful read to get an overview of 20 years of genome-based research on the Xanthomonads/Lysobacteraceae. As a perspective paper, I think it is really up to the authors what they want to include and write about. I learned a lot by reading it and I did not find any major issues with any of the sections. I just found a couple of sentences hard to understand. Below I list small suggested language edits and these sentence that, I think, should be revised:

L143 delete the ”a” at tehe of the line

L157 Not sure to which ”their holistic study” refers to. I suggest to rephrase and make that clear.

L173 change ”without the” to ”without performing the”

L175 change ”long-life” to ”long-lived”

L177 change ”brings no” to ”does not include”

L196 consider `https://www.pnas.org/doi/abs/10.1073/pnas.0409727102` instead

L199 change ”has” to ”had”

L274 consider chngeing ”works” to ”investigations”

L301/302 Not sure what ”biological specificities” means in this context. Consider revising.

L327 I am not sure what ”very contrasted management” means

L336/337 I suggest ”having expanding geographic and host ranges”

L354 I suggest ”X. fastidiosa are naturally conpement bacteria” or ”... that bacteria in the X. fastidiosa species are naturally competent ...”

L363-365 I suggest: ”Evidende of extensive ... recombination that occurred in the course of X. fastidipsa evolution was found.”

L374 change ”a same ecological niche” to ”the same echological niche”

L381 change ”and developing” to ”and was developing”

L393 change ”authors speculate to ”authors to speculate”

L397 change ”provides these” to ”provides to these”

L402 add a reference to the sentence that ends with ”interactions”.

L421 change ”producing bacteria” to ”bacteria that produce them”