



## OPEN ACCESS

EDITED AND REVIEWED BY  
Ludmila Chistoserdova,  
University of Washington, United States

## \*CORRESPONDENCE

Ernesto Perez-Rueda  
✉ ernesto.perez@iimas.unam.mx  
Feng Gao  
✉ fgao@tju.edu.cn

RECEIVED 31 July 2023  
ACCEPTED 10 August 2023  
PUBLISHED 21 August 2023

## CITATION

Perez-Rueda E and Gao F (2023) Editorial:  
Insights in evolutionary & genomic  
microbiology: 2022.  
*Front. Microbiol.* 14:1269933.  
doi: 10.3389/fmicb.2023.1269933

## COPYRIGHT

© 2023 Perez-Rueda and Gao. This is an  
open-access article distributed under the terms  
of the [Creative Commons Attribution License  
\(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution or reproduction  
in other forums is permitted, provided the  
original author(s) and the copyright owner(s)  
are credited and that the original publication in  
this journal is cited, in accordance with  
accepted academic practice. No use,  
distribution or reproduction is permitted which  
does not comply with these terms.

# Editorial: Insights in evolutionary & genomic microbiology: 2022

Ernesto Perez-Rueda<sup>1\*</sup> and Feng Gao<sup>2,3,4\*</sup>

<sup>1</sup>Instituto de Investigaciones en Matemáticas Aplicadas y en Sistemas, Universidad Nacional Autónoma de México, Unidad Académica del Estado de Yucatán, Mérida, Mexico, <sup>2</sup>Department of Physics, School of Science, Tianjin University, Tianjin, China, <sup>3</sup>Frontier Science Center of Synthetic Biology (MOE), Key Laboratory of Systems Bioengineering (MOE), Tianjin University, Tianjin, China, <sup>4</sup>SynBio Research Platform, Collaborative Innovation Center of Chemical Science and Engineering (Tianjin), Tianjin, China

## KEYWORDS

bacteria, fungi, evolution, phylogenetics, genomic epidemiology, gene regulation and expression

## Editorial on the Research Topic

### Insights in evolutionary & genomic microbiology: 2022

During the past decade, the field of evolutionary and genomic microbiology has witnessed significant advancements, with development of high-throughput “omics” technologies, bioinformatics, and artificial intelligence (Gao et al., 2022), shedding new light on the intricate mechanisms that shape microbial evolution and genomic diversity (Shu and Huang, 2022). As Topic Editors, Drs. Daniel Yero, Feng Gao, and Baolei Jia organized the Research Topic “*Insights in evolutionary and genomic microbiology: 2021*” for Frontiers in Microbiology (Yero et al., 2022), which has been recommended by the Chief Editors and journal team as 2022 outstanding Research Topic in terms of views and downloads. Given its previous success, this Research Topic was revisited by Dr. Ernesto Perez-Rueda and Dr. Feng Gao in 2022. After rigorous peer review, a total of 10 articles have been published in this topic, including 8 original research articles, one review, and one mini-review.

Majority of the articles focus on various studies on evolution in bacteria via the omics methods. Among the review articles, Vanacker et al. systematically reviewed the potential fitness cost of antimicrobial resistance (AMR) in *Escherichia coli* with the meta-analysis of related high-quality studies. Fujihara et al. summarized the evolutionary mechanisms regarding degradation gene systems by analyzing the genome sequences of isolated bacteria degrading xenobiotics.

Among the original research articles, Wang et al. discovered that the evolution of morphological development of *Streptomyces* is in accord with the species phylogeny by using a comparative phylogenetic approach. Through the genomic epidemiology analysis, Zhao et al. provided an overview of the prevalence of clinical multidrug-resistant *Pseudomonas aeruginosa* infections and the emergence of high-risk clones in Guangdong, China. Based on the growth rate-associated transcriptome, Matsui et al. found the occurrence of the environmental stressors remarkably decreased the growth rate of the wild-type instead of reduced-genome *Escherichia coli* when investigating whether and how bacterial growth was affected by the genomic, environmental, and evolutionary interruptions. By a pan-genome wide association study, Zhou et al. highlighted the genes associated with virulence and biofilm formation for further investigation in *Glaesserella parasuis*. Based on the comparative genomics and phylogenetic analysis, Santana-Molina et al. investigated early origin and evolution of the FtsZ/tubulin protein family, which would provide valuable insights into the diversification of the three domains of life.

Facilitated by the mutant obtained by Tn5 mutagenesis, [Wei et al.](#) found *rpoZ* was an important regulator of antibiotic 2,4-diacetylphloroglucinol (2,4-DAPG) production and quorum sensing system in *Pseudomonas fluorescens* 2P24.

In addition to the studies on bacteria, there are two original research articles about fungi in this topic. Through *de novo* sequencing, assembly, and comparative analyses, [Jiang et al.](#) found more carbohydrate-active enzymes (CAZymes) and distinct genes related to vesicular fusion and autophagy in an *Aspergillus sydowii* strain 29R-4-F02 compared to the terrestrial strain CBS593.65, which revealed the survival and environmental adaptation mechanism of this seafloor fungus. Based on the genomic data newly generated or retrieved from GenBank, [Meng et al.](#) explored the origin, evolution, and historical biogeography of the *Morchella* fungi in the Qinghai-Tibet Plateau subkingdoms (QTPs), particularly focusing on the Elata and Esculenta clades, which provided strong evidence for the origin theory of the QTPs.

## Author contributions

FG: Writing—original draft, Writing—review and editing.  
EP-R: Writing—original draft, Writing—review and editing.

## Funding

FG was supported by the National Key Research and Development Program of China (grant number 2018YFA0903700)

## References

Gao, F., Huang, K., and Xing, Y. (2022). Artificial intelligence in omics. *Genom. Proteom. Bioinform.* 20, 811–813. doi: 10.1016/j.gpb.2023.01.002

Shu, W. S., and Huang, L. N. (2022). Microbial diversity in extreme environments. *Nat. Rev. Microbiol.* 20, 219–235. doi: 10.1038/s41579-021-00648-y

and the National Natural Science Foundation of China (grant numbers 32270692 and 31571358). EP-R was supported by the Dirección General de Asuntos del Personal Académico-Universidad Nacional Autónoma de México (IN-220523) and CONAHCYT (320012).

## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author(s) declared that they were an editorial board member of *Frontiers*, at the time of submission. This had no impact on the peer review process and the final decision.

## Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

Yero, D., Jia, B., and Gao, F. (2022). Editorial: insights in evolutionary and genomic microbiology: 2021. *Front. Microbiol.* 13, 915593. doi: 10.3389/fmicb.2022.915593