

Bacteria: A New Chapter in a Rapidly Evolving Field

Vasco Ariston de Carvalho Azevedo 

Departamento de Genética, Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte 31270-901, MG, Brazil; vascoariston@gmail.com

1. A Maturing Forum for Bacterial Sciences

Scientific journals are, at their best, reflections of the disciplines they serve. When *Bacteria* was conceived in 2021 and launched in 2022, the field of bacteriology was already undergoing a profound transformation, one accelerated by the COVID-19 pandemic, which placed microbial sciences at the center of global public discourse. The founding vision, articulated by Prof. Dr. Bart C. Weimer in his inaugural editorial “Why a New Journal on Bacteria?” [1], was prescient: to create a platform where multi-omics, systems biology, and classical bacteriology could converge without disciplinary boundaries. Four years later, that vision has not only materialized but gained significant momentum.

The journal’s trajectory speaks for itself. After publishing its inaugural quarterly volume in 2022, *Bacteria* achieved Scopus indexing in 2024, earned its first CiteScore of 2.8 in early 2025 (ranked Q2 in Immunology and Microbiology), and in 2026 secured indexing in the Emerging Sources Citation Index (ESCI) of the Web of Science, accompanied by a CiteScore of 5.0 and a Q1 ranking in Agricultural and Biological Sciences. These milestones, rapid by any standard for a new journal, reflect the trust of a growing author community, the dedication of reviewers, and the editorial integrity established under Prof. Weimer’s leadership.

The founding Editor-in-Chief brought over three decades of transformative contributions to bacterial genomics to *Bacteria*. As Professor and Department Chair at the University of California, Davis, Director of the 100 K Pathogen Genome Project, and Co-founder of the Lactic Acid Bacteria Genome Consortium, Prof. Weimer shaped the genomic era of microbiology through nearly 200 peer-reviewed manuscripts, over 10,000 citations, and numerous books and patents. It is from this foundation, built with rigor, collegiality, and an unwavering commitment to scientific quality, that the journal now embarks on its next phase.

2. Bacteriology at a Crossroads

The field of bacteriology today stands at a remarkable intersection of technological capability and societal urgency. Several converging trends define the current landscape and, by extension, *Bacteria*’s editorial priorities.

The post-genomic revolution has moved beyond sequence acquisition into functional understanding. High-throughput transcriptomics, proteomics, and metabolomics now enable systems-level interrogation of bacterial physiology, revealing regulatory networks of extraordinary complexity. The challenge and opportunity lie in integrating these data streams into predictive models of bacterial behavior.

The antimicrobial resistance (AMR) crisis remains one of the defining public health challenges of the twenty-first century. The World Health Organization has identified AMR as a top-ten global health threat, and the need for novel therapeutic strategies, from phage therapy to CRISPR-based antimicrobials to microbiome modulation, has never been more



Received: 19 July 2026

Accepted: 21 July 2026

Published: 22 July 2026

Copyright: © 2026 by the author.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and conditions of the [Creative Commons Attribution \(CC BY\)](https://creativecommons.org/licenses/by/4.0/) license.

urgent. Bacteriology must deliver translational solutions while continuing to elucidate fundamental mechanisms of resistance.

The microbiome revolution has fundamentally altered our understanding of bacteria not as isolated pathogens or commensals, but as members of complex, dynamic ecosystems intimately linked to host physiology. The gut–brain axis, the role of the microbiome in immunotherapy response, and the metabolic contributions of bacterial communities to human health exemplify the frontier.

Artificial intelligence and machine learning are reshaping the analytical landscape. From predicting protein structures with atomic accuracy to mining metagenomic datasets for novel biosynthetic gene clusters, computational approaches are accelerating discovery at every scale of bacterial biology.

The One Health paradigm, recognizing the interconnectedness of human, animal, and environmental health, has moved from an aspirational framework to an operational necessity. Zoonotic pathogens, environmental resistomes, and climate-driven changes in microbial ecology demand integrated research approaches that transcend traditional disciplinary silos.

It is within this dynamic context that *Bacteria* must define its role not as a passive repository of knowledge, but as an active forum that shapes and accelerates the field's trajectory.

3. A New Chapter: Vision and Strategic Direction

As the second Editor-in-Chief of *Bacteria*, the author assumes leadership with both gratitude for the journal's achievements and a clear sense of the work ahead. With a CiteScore of 5.0 and Q1 ranking already established, the foundation is solid. The goal now is to build upward, increasing the journal's scientific impact, broadening its global reach, and strengthening its community.

Scientific rigor remains the non-negotiable cornerstone. As *Bacteria* approaches its first Journal Impact Factor, maintaining and enhancing peer-review standards is paramount. The journal currently achieves an average first-decision time of 26.6 days, a competitive turnaround time that must be maintained while further strengthening the depth and constructiveness of reviews. To this end, the Editorial Board will be expanded with colleagues who bring both scientific expertise and a commitment to rigorous, developmental peer review.

Strategic thematic expansion will be pursued through commissioned Special Issues and Topical Collections in areas of high current impact and future promise:

- The microbiome–host interface and its therapeutic implications;
- Bacterial persistence, persister cells, and chronic infections;
- Antimicrobial resistance within the One Health framework;
- Phage biology, engineering, and therapeutic applications;
- Synthetic biology and metabolic engineering in prokaryotes;
- Artificial intelligence and machine learning in bacterial systems biology;
- Climate change and microbial ecology;
- Bacterial extracellular vesicles and interkingdom communication.

The journal will particularly welcome submissions that bridge fundamental bacteriology with translational applications in human and veterinary medicine, agriculture, and environmental science, reflecting the integrative spirit of the One Health paradigm.

Global representation and inclusivity constitute a strategic priority. As a scientist from the Global South, the author recognizes both the outstanding research conducted outside traditional centers and the structural barriers that limit its visibility. The bacterial diseases that impose the greatest burden on human health—tuberculosis, diarrheal diseases,

and neglected tropical infections—disproportionately affect low- and middle-income countries, yet research from these regions remains underrepresented in the scientific literature. *Bacteria* will actively work to address this imbalance through deliberate diversification of the Editorial Board, targeted calls for papers from Latin America, Africa, the Middle East, and Southeast Asia, and mentorship programs designed to support early-career researchers and authors from underrepresented regions throughout the publication process.

Community building and dialogue will be cultivated through initiatives that extend beyond the printed page. The “Bacteria Dialogues” webinar series, to be launched in 2026, will feature emerging topics in microbiology presented by leading and early-career researchers alike. Interactive workshops on scientific writing and peer review will support the next generation of authors. A structured mentorship program will pair experienced Editorial Board members with prospective authors from underrepresented regions. Upcoming editorials will address pressing topics such as bacteriology’s role in global health equity, the integration of artificial intelligence into microbial research, and the ethical dimensions of microbiome engineering.

These initiatives share a common purpose: to make *Bacteria* not merely a journal of record, but a dynamic intellectual community—one that serves the full breadth of bacteriology and the global diversity of its practitioners.

4. Looking Forward

Scientific publishing, like the science it communicates, is a collective endeavor. The achievements that *Bacteria* has attained since its launch belong to its authors, who entrusted the journal with their work; its reviewers, whose critical insights uphold quality; its Editorial Board members, whose expertise guides its direction; and its founding Editor-in-Chief, Prof. Dr. Bart C. Weimer, whose vision established the foundation upon which all future growth will be built.

The author extends sincere gratitude to MDPI and the Editorial Board for the opportunity to serve, and to the broader bacteriology community for its continued engagement. The torch has been passed. The work continues, with purpose and with the shared conviction that understanding the bacterial world in all its complexity, diversity, and profound impact on life remains one of the most consequential scientific endeavors of our time.

Acknowledgments: The author used Grammarly Pro (Premium), an AI-powered writing assistant, to review and refine the English language of this manuscript.

Conflicts of Interest: The author declares no conflicts of interest.

References

1. Weimer, B.C. Why a New Journal on Bacteria? *Bacteria* **2022**, *1*, 1–2. [[CrossRef](#)]
2. Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; et al. The Complete Genome Sequence of the Gram-Positive Bacterium *Bacillus subtilis*. *Nature* **1997**, *390*, 249–256. [[CrossRef](#)] [[PubMed](#)]
3. Faria, N.R.; Kraemer, M.U.G.; Hill, S.C.; Goes de Jesus, J.; Aguiar, R.S.; Iani, F.C.M.; Xavier, J.; Quick, J.; Du Plessis, L.; Dellicour, S.; et al. Genomic and Epidemiological Monitoring of Yellow Fever Virus Transmission Potential. *Science* **2018**, *361*, 894–899. [[CrossRef](#)] [[PubMed](#)]

Short Biography of Author



Prof. Dr. Vasco Ariston de Carvalho Azevedo is a Full Professor of Genetics at the Institute of Biological Sciences, Federal University of Minas Gerais (UFMG), Brazil, where he leads the Cellular and Molecular Genetics Laboratory. He earned his DVM from the Federal University of Bahia (1986), followed by an MSc (1989) and PhD (1993) in Microbial Genetics from the Institut National Agronomique Paris-Grignon (France). He completed postdoctoral training at the University of Pennsylvania (USA), obtained a *Livre-docência* from the University of São Paulo (2004), and earned a second PhD in Bioinformatics from UFMG (2017). Prof. Azevedo is a Titular Member of the Brazilian Academy of Sciences and a Corresponding Member of the Göttingen Academy of Sciences and Humanities (Germany). His research program spans genomics, transcriptomics, proteomics, metabolomics, and functional gene analysis, with a focus on bacterial pathogens of veterinary and zoonotic importance including *Corynebacterium pseudotuberculosis*, *Brucella abortus*, and lactic acid bacteria engineered as live delivery vehicles for vaccines and therapeutics. He has mentored 92 master's students, 65 doctoral candidates, and 20 postdoctoral fellows, and has authored over 800 peer-reviewed publications, including contributions to *Nature* and *Science* [2,3]. He previously served on the Editorial Board of *Bacteria*, gaining direct insight into the journal's editorial processes and community.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.