

Acinetobacter baumannii's ecology– more than meets the eye

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Acinetobacter baumannii is mainly considered a human pathogen. Yet, its habitat range is uncertain. In a recent article, Wilharm et al. use a large multisource data set to show that decomposing plants and soil are natural habitats for this bacterium, thus advancing our understanding of *A. baumannii*'s ecology.

Over the last few decades, *Acinetobacter baumannii* has become one of the most important human nosocomial pathogens in many parts of the world. The World Health Organization considers it to be a high-priority bacterium for which we need to find novel therapies¹. Due to its impact on human health, research efforts on *A. baumannii* have mainly been directed to human clinical isolates. Recently, there have been some studies on *A. baumannii* from non-human sources^{2,3}. These studies have slowly started changing our perception of *A. baumannii*, but the notion that *A. baumannii* is mainly a human pathogen still prevails. A recent article published in this journal by Wilharm et al.⁴ is a significant step forward in debunking that notion.

Previous studies on non-human *A. baumannii* were comparatively limited in scope. First, most of the non-human isolates came from sources very close to humans, such as companion animals and livestock. Yet, very little is known about isolates from wildlife or pristine environments. Second, most of the previous studies were limited to a small number of isolates, usually less than 50 isolates, sampled over a relatively short period of time. Third, many of those studies focused on the antibiotic-resistance potential and the genetic identity of the non-human isolates, but not much else.

The paper by Wilharm and colleagues⁴ breaks the mold in attempting to address all the above-mentioned shortcomings. The authors gathered a large collection of 401 environmental isolates from multiple non-human sources, which allowed them to provide one of the most cohesive views of *A. baumannii* outside of the clinical settings. Starting from white stork nestlings, the authors sampled isolates from different sections of the food chain and surrounding environments, which, in my view, is the strongest point of their sampling strategy. In addition, they analysed their environmental genomes together with > 400 publicly available genomes from human isolates, thus providing a One Health view of *A. baumannii*. The main finding of the article is that decomposing plants and soil are habitats for this bacterium. Yet, on a more abstract level, the study makes a convincing case that the natural habitat for this species includes environments not directly related to human settings and with very small, if any, anthropogenic influence. Thus, in my opinion, the findings reported in this article are bound to change our perception of *A. baumannii*'s ecology.

Still, there are two aspects that future studies on non-human *A. baumannii* will need to address. First, a more global sampling is

desirable. Most studies, including the one by Wilharm and colleagues, carried out the sampling of isolates in a few European countries. The available data for non-human *A. baumannii* is very geographically biased, much more than the data for human *A. baumannii* (which is far from perfect). Thus, future studies should try to sample non-human sources from as many countries as possible and pay attention to neglected regions. For instance, hardly anything is known about non-human *A. baumannii* in Latin America. The second aspect has to do with the fact that genotyping based on whole-genome sequencing (WGS) relies on bacterial culture. Yet, in addition to WGS, future studies on non-human isolates should also consider metagenomics, particularly metagenome-assembled genomes (MAGs), to characterize understudied lineages of *A. baumannii*. This will be particularly relevant for lineages that dwell in sources where getting a proper bacterial culture is not feasible, as this will help to explore the whole range of habitats this bacterium can live in. In this regard, some recent studies^{5–7} have already shown the value of employing MAGs to study *A. baumannii* from rather unusual sources. Finally, it is important to highlight that improving our knowledge of the ecology of this bacterium beyond the clinical settings can, in turn, be very helpful for developing better strategies to deal with the *A. baumannii* residing in hospitals.

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Received: 19 March 2026; Accepted: 14 April 2026;

Published online: 21 April 2026

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Acknowledgements

S.C.-R. is supported by a PAPIIT grant (number IN209524) from UNAM.

Comment

Author contributions

S.C.-R. conceived and wrote this comment.

Competing interests

The author declares no competing interests.

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