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Zoonotic *Acinetobacter baumannii*: the need for genomic epidemiology in a One Health context

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The ongoing COVID-19 pandemic has clearly highlighted two research aspects that are relevant to other human pathogens. First, the pandemic has shown that genomic epidemiology is extremely useful for tracking the dissemination patterns of pathogens at a high resolution and, thus, taking proper measures to deal with outbreaks. Second, it has also shown the need to consider animal hosts when analysing the pathogens' transmission patterns, given the zoonotic potential of many human pathogens. In this Comment I argue that genomic epidemiology of *Acinetobacter baumannii* sampled from animals is of paramount importance if we are to deal with this important human pathogen. *A baumannii* is a very important nosocomial pathogen and is a frequent cause of multidrug-resistant infections in hospitals. According to WHO, *A baumannii* is the top bacterial pathogen for which novel antibiotics are urgently needed.[1] Similar to other human pathogens, a lot of information has been gathered on clinical isolates yet very little is known about isolates from non-human sources. For some time, *A baumannii* was considered to be a hospital-associated pathogen that was just sporadically found outside of the clinic.[2] However, studies over the past decade have shown that this pathogen can be found in several animal (and even plant) species and in different environments. Remarkably, in 2020, it was proposed that *A baumannii* must be considered a One Health problem, as isolates from plants and animals have important antibiotic resistance genes.[3]

An important public health point regarding animal isolates is to what extent they represent distinct clones or populations with distinct characteristics. Under one scenario, human and animal *A baumannii* populations could be well differentiated from one another; thus, different clones are found in animals compared with humans. Supporting this scenario, a 2022 genomic epidemiology paper has shown that cattle and pig isolates belong to novel clones that are not found in humans.[4] Furthermore, some other animals (eg, donkey, goat, and goose) have clones of *A baumannii* that have not been described in clinical settings.[3,5] Another theory could be that animal and human *A baumannii* populations are not differentiated from one another and exhibit frequent gene flow between both populations. In this regard, when domesticated animals and poultry have been examined, the isolates found were identical or very similar to human clinical isolates.[6,7] Of note, there have also been cases of non-domesticated animals having isolates associated with human (clinical) clones of *A baumannii*.[7,8] Another relevant public health point is the antibiotic resistance genes residing within the animal clones of *A baumannii*. Even if the clones circulating in animals are different from those in humans, these clones can still harbour clinically relevant antibiotic resistance genes.[3] Importantly, a 2022 study has shown that the resistome of *A baumannii* is highly mobile, showing many cases of horizontal gene transfer with other important human pathogens such as *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*.[9] In connection with the previous point, even if the animal clones of *A baumannii* do not pose a public health risk per se, the antibiotic genes within them can be horizontally transferred to isolates from other human relevant bacterial species, which could be risky.

Genotyping *A baumannii* requires the high resolution provided by whole-genome sequencing (WGS), as more traditional strategies, such as multilocus sequence typing, are not reliable due to the dynamic genome of this pathogen.[10] An extra perk of WGS is that the transmission dynamics of the isolates' resistome can also be analysed.

There are three important considerations to the sampling of *A baumannii* animal isolates. First, attention should be paid to sampling from different types of animals and not only the most relevant to humans. In this regard, most studies about animal isolates have been on companion animals and animals used for food, yet sampling from wild animals has been neglected. Second, geographically homogenous sampling is desirable; most studies about animal isolates have been conducted in just a few countries, but for most countries there is no information about animal isolates. Finally, we should not only sample sick animals but also healthy animals.

Whether identical or different to human clones, it is clear that animal clones of *A baumannii* are a potential

reservoir of antibiotic resistance genes. In coming years, studies about animal and other non-human isolates will help us to better understand the transmission dynamics of this important pathogen. Ideally, in a One Health context, we should not only analyse human and animal isolates but also environmental isolates. Clearly, in this endeavour WGS is the best genotyping strategy.

I declare no competing interests.

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