Acinetobacter baumannii – a neglected pathogen in veterinary and environmental health in Germany

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Received: 25 October 2018 / Accepted: 6 December 2018 / Published online: 27 December 2018
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Abstract

The emergence and global spread of drug resistant *Acinetobacter* (*A.*) *baumannii* is a cause of great concern. The current knowledge on antibiotic resistance in *A. baumannii* from animal origin is mostly based on few internationally published case reports, investigations of strain collections and several whole genome analyses. This lack of data results in a somewhat sketchy picture on how to assess the possible impact of drug resistant *A. baumannii* strains on veterinary and public health in Germany. Consequently, there is an urgent need to intensify the surveillance of *A. baumannii* in pet animals, the farm animal population and wildlife.

Keywords *Acinetobacter baumannii* · Review · Antibiotic resistance · Germany

Introduction

Acinetobacter (*A.*) *baumannii* is a gram-negative opportunistic nosocomial pathogen belonging to the genus *Acinetobacter* and a member of the family *Moraxellaceae*. *Acinetobacter* spp. are non-motile, non-fastidious Gram-negative, non-fermenting, catalase positive, oxidase negative, strictly aerobic coccobacilli with a DNA G + C content between 39 and 47% (Peleg et al. 2008). Currently, there are 57 validly published species names (including 4 synonymous species) (Parte 2018). Of these, the species *A. baumannii*, *A. nosocomialis* and *A. pittii* are of clinical importance, as they have been isolated from human infections and hospital outbreaks (Visca et al. 2011). According to Bergogne-Bérézin and Towner (1996) the first reports on severe infections most likely caused by *A. baumannii* date back to the 1970ies. However, due to the numerous taxonomic changes the genus *Acinetobacter* has been subjected to, these earlier reports have to be regarded with caution as the species *A. baumannii* was formally just designated in 1986 by Bouvet and Grimont.

Strain typing by different techniques has revealed genotypic diversity within the species *A. baumannii*, however, only a

limited number of widespread clones appear to be responsible for hospital outbreaks in many countries (Diancourt et al. 2010). Eight international clonal lineages have been described so far and comparative typing of outbreak strains obtained all over Europe revealed the dominance of three clones, originally named European clones I–III (Dijkshoorn et al. 1996; Karah et al. 2012). These clones were re-named “international clones (IC) 1–3” after identifying them throughout the world. IC 1–3 correspond to the multi-locus sequence typing (MLST) clonal complexes (ST1–3) (Diancourt et al. 2010; Antunes et al. 2014).

In humans, *A. baumannii* can cause a multitude of severe nosocomial infections of the skin and soft tissue, wound infections, urinary tract infections and secondary meningitis. The highest mortality rates however, are seen in ventilator-associated pneumonia and bloodstream infections (Dijkshoorn et al. 2007). In comparison to human medicine, the data obtained from veterinary medicine are relatively limited (Müller et al. 2014; van der Kolk et al. 2018). In livestock (cattle, pig), *A. baumannii* has been observed as a cause of mastitis, pneumonia, and sepsis. Horses have been reported to develop wound infections, septicaemia, and bronchopneumonia as well as neonatal encephalopathy and eye infections. In dogs and cats *A. baumannii* has been isolated from wound, bloodstream and urinary tract infections (Müller et al. 2014; van der Kolk et al. 2018).

The genus *Acinetobacter* has the tendency to develop antibiotic resistance very rapidly, possibly due to its long-term

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evolutionary exposure to antibiotic-producing organisms in the soil environment (Bergogne-Bérzin and Towner 1996). Moreover, a major feature of *A. baumannii*, enabling its prolonged survival and spread within the healthcare system, is its ability to not only upregulate intrinsic but also to acquire foreign mechanisms of antimicrobial resistance (Pogue et al. 2013). The European Committee on Antimicrobial Susceptibility Testing (EUCAST) expert rules V 3.1 state that *A. baumannii* is naturally (or intrinsically) resistant to the following antimicrobials: ampicillin, amoxicillin-clavulanic acid, cefazolin, cefalothin, cephalexin, cefadroxil, cefotaxime, ceftriaxone, aztreonam, ertapenem, trimethoprim and fosfomycin. It is still a matter of debate as to whether the augmented antimicrobial resistance found in clinical *Acinetobacter baumannii* isolates may also lead to reduced susceptibility to disinfectants. While Ivancovic et al. (2017), Babaei et al. (2015) and Kawamura-Sato et al. (2010) were able to demonstrate reduced susceptibility to disinfectants, no correlation was found by Martro et al. (2003).

A wide array of resistance mechanisms have been described for *A. baumannii* such as β -lactamases, outer membrane proteins (OMPs), efflux influencing proteins, aminoglycoside modifying enzymes, chromosomal mutations in the quinolone resistance determining region (QRDR), enzymes targeting tetracycline-specific efflux, glycosylases as well as ribosomal methylation (Peleg et al. 2008; Evans et al. 2013). A particular challenge is the resistance to carbapenems, which is predominantly mediated by Ambler Class D β -lactamases, such as the intrinsic carbapenem-hydrolysing oxacillinase OXA-51, which confers resistance to carbapenems when overexpressed or the acquisition and production of the oxacillinases OXA-23-like, OXA-24/40-like, OXA-58-like, OXA-143-like and OXA-235-like (da Silva et al. 2016). Their corresponding genes can be upregulated by insertion sequences (IS) located upstream of these genes, e.g. IS*Aba*-1. Metallo- β -lactamases such as imipenemase (IMP), Verona integrin-encoded-metallo- β -lactamase (VIM) and New Delhi metallo- β -lactamase (NDM) have been reported in Europe but currently appear to play a minor role (Evans et al. 2013). The production of *K. pneumoniae* carbapenemase (KPC) and OXA-48 oxacillinase has been reported from the Middle East and South America, respectively (Elsherif et al. 2016; Martinez et al. 2016).

The emergence of drug resistant *Acinetobacter* spp., especially *A. baumannii* in hospitals, but also in veterinary clinics and the environment has been observed throughout the world and has become a cause of concern (Dijkshoorn et al. 2007; Diancourt et al. 2010; Mller et al. 2014; van der Kolk et al. 2018). Severe nosocomial infections are recurrently associated with epidemic spread, outbreak strains are frequently multi-drug resistant (MDR) and the increasing occurrence of strains resistant to carbapenems or to last resource antimicrobial agents such as colistin is alarming (Diancourt et al. 2010; Zordan et al. 2011; Zarrilli et al. 2013; Guerra et al. 2014).

The aim of this short review is to summarise the current knowledge and data on antimicrobial resistance determined in *A. baumannii* strains isolated from animal and environmental sources in Germany.

Antimicrobial resistance in *A. baumannii* originating from animal hosts

To date, only few reports exist on the prevalence of antibiotic resistance in *A. baumannii* isolated from animal origin in Germany (Table 1). The earliest study on multidrug resistant *Acinetobacter* spp. in Germany analysed 52 *A. baumannii*, 3 *A. pittii* strains and one non defined *Acinetobacter* isolate from hospitalised animals (dog, cat, horse, cow) collected between 2000 and 2008. The isolates could be allocated to the international clones 1, 2 and 3, respectively, and were resistant to oxacillin, penicillin, cephalothin, erythromycin, clindamycin, chloramphenicol, and, with the exception of two isolates, to colistin. Bar of one isolate, all strains were sensitive to imipenem and amikacin, respectively. This study also revealed the possible endemic occurrence of *Acinetobacter* spp. within an animal clinic (Zordan et al. 2011).

The first description and genome sequence of a carbapenem-resistant *A. baumannii* strain isolated in 2000 and originating from a cat was in 2016 by Ewers and co-workers. Phylogenetic analyses revealed that the isolate belonged to the globally distributed international clone IC1 and displayed a close resemblance to clonal lineages causing severe infections in humans. The strain harboured a plasmid encoding for *bla*_{OXA-23}; other resistance coding genes detected in the genome were aminoglycoside resistance genes, *bla*_{OXA-51-like} gene encoding OXA-69, a phenicol resistance gene (*catA1*), a sulfonamide (*sul1*) and a tetracycline (*tetA*) resistance coding gene, respectively. High MIC breakpoints were determined for imipenem, piperacillin, ceftazidime, gentamycin, tetracycline and trimethoprim/sulfamethoxazole (Ewers et al. 2016). A later study by the same group screened 223 *A. baumannii* isolates collected between 2000 and 2013 from companion animals (dog, cat, rabbit, ferret, snake, rat, duck) for carbapenem-non-susceptibility testing (Ewers et al. 2017). Fifty-eight isolates carried *bla*_{OXA-66} with the upstream insertion sequence element IS*Aba*1; further three isolates (cat; dogs) harboured *bla*_{OXA-23}, belonged to the IC 1 and 8, respectively, and were resistant to piperacillin, piperacillin/tazobactam, ampicillin/sulbactam, ceftazidime, cefuroxime, cefpodoxime, imipenem, meropenem and trimethoprim/sulphamethazole. All three isolates carried the aminoglycoside-modifying enzyme gene *aadA1*, and one isolate *aacC1*. The 58 IS*Aba*1- *bla*_{OXA-66}-positive isolates belonged to the IC 2, 53 were resistant to piperacillin, 11 to piperacillin/tazobactam, 20 to ampicillin/sulbactam, 9 to

Table 1 Summary of studies on *A. baumannii* from animal and environmental origin in Germany

Source	No. of isolates	AST/MIC	Resistance genes	EC/IC	Sampling period	Reference
Animal						
Companion animals/cow	52	oxacillin, penicillin, cephalotin, erythromycin, clindamycin, chloramphenicol, colistin	not determined	1, 2, 3	2000–2008	Zordan et al. 2011
cat	1	imipenem (≥ 16 mg/L), piperacillin (≥ 16 mg/L), cefpirome (≥ 64 mg/L), gentamicin (≥ 16 mg/L), tetracycline (≥ 16 mg/L), trimethoprim/sulfamethoxazole (≥ 32 mg/L); enrofloxacin (2 mg/L) marbofloxacin (≥ 4 mg/L) piperacillin, piperacillin/tazobactam, ampicillin/sulbactam, ceftazidime, cefuroxime, cefpodoxime, gentamycin, levofloxacin trimethoprim/sulphametazole	<i>bla</i> _{OXA-23} ; <i>strA</i> ; <i>strB</i> ; OXA-69; <i>aadA1</i> ; <i>aph(3)</i> ; <i>aac(3)-Ia</i> <i>catA1</i> ; <i>su1</i> ; <i>tetA</i>	1	2000	Ewers et al. 2016
Companion animals	223	piperacillin, piperacillin/tazobactam, ampicillin/sulbactam, ceftazidime, cefuroxime, cefpodoxime, gentamycin, levofloxacin trimethoprim/sulphametazole	<i>bla</i> _{OXA-66} with <i>ISAba1</i> <i>bla</i> _{OXA-23} ; <i>aadA1</i> ; <i>aacC1</i>	1, 2, 8	2000–2013	Ewers et al. 2017
Chicken geese	6	gentamycin, kanamycin	OXA-68; OXA-385	unknown	2012	Wilharm et al. 2018
	3	kanamycin, sulfamerazine, sulfamerazine/trimethoprim	OXA-314; OXA-71; OXA-95		2013	
Horses	9	ceftiofur, gentamycin, tetracycline, tobramycin, trimethoprim/sulphametazole	no carbapenemase activity	not stated	2014–2015	Walther et al. 2018
Environment						
Tap water/tea		sensitive to cotrimaxole	n. d.	not stated	1998	Hauer et al. 1999
Moth fly	15	cephalosporinase and β -lactamase-resistance; third-generation cephalosporins, penicillins; aminoglycosides chloramphenicol, oxacillin	n. d.	not stated	2011–2012	Faulde and Spiesberger 2013
Milk powder	42		<i>bla</i> _{OXA-51} ; <i>bla</i> _{OXA-530} ; <i>bla</i> _{OXA-91} ; <i>bla</i> _{OXA-430} ; <i>bla</i> _{ADC-25-like}	II, III	not stated	Cho et al. 2018

AST/MIC Susceptibility testing; minimum inhibitory concentration, EC/IC European clone/International clone, n. d. not determined

ceftazidime, 22 to cefuroxime, 21 to cefpodoxime, 0 to imipenem, 0 to meropenem, 53 to gentamycin, 5 to levofloxacin and 28 to trimethoprim/sulphamethazole. Of the 58 isolates 35 carried the aminoglycoside-modifying enzyme gene *aadA1*, and 55 isolates *aacC1*. This study demonstrated that two of the most common mechanisms of carbapenem-non-susceptibility found in human *A. baumannii* isolates, i.e. the acquisition of the carbapenemase-hydrolysing enzyme *bla_{oxa-23}* and possession of the insertion sequence *ISAbal* upstream of the *bla_{oxa-51}*-like gene, are also found in isolates originating from companion animals.

A further study tested the hypothesis whether birds might be a reservoir for *A. baumannii* (Wilharm et al. 2018). Two hundred and twenty chickens from 37 flocks were sampled between 2012 and 2013, yielding six *A. baumannii* isolates from three independent farms. Three isolates originated from the same farm from chicks at fledgling state, two from a flock at a different farm with 1 day old chicks and one from a hen at a further farm. The isolates of the fledglings and the hen were closely related as determined by *ApaI* macrorestriction analyses, but distinct from the closely related isolates obtained from the 1 day old chicks. These results were further corroborated by sequencing of the *bla_{oxa-51}*-like gene, revealing an OXA-68 variant in the fledglings and the hen. The isolates of the one day old chicks harboured a novel *bla_{oxa-51}*-like gene variant, OXA-385 and were resistant to gentamycin and kanamycin. None of the chicken isolates could be matched to the international clonal lineages. Further screening of 40 goslings at a single farm yielded three *A. baumannii* isolates carrying different variants of the *bla_{oxa-51}*-like gene encoding OXA-314, OXA-71 and OXA-95, respectively. Also here a match to the international clonal lineages was not possible. Only one of the isolates was submitted to antimicrobial resistance testing to reveal intermediate susceptibility to kanamycin and resistance to sulfamerazine and sulfamerazine/trimethoprim.

The most recent published work studying extended spectrum β -lactamase producing *E. coli* (ESBL) in 341 horses entering a veterinary teaching hospital between 2014 and 2015, found nine *A. baumannii* isolates (Walther et al. 2018). No carbapenemase activity was observed in these isolates, one isolate displayed a MDR phenotype (ceftiofur, gentamycin, tetracycline, tobramycin, trimethoprim/sulphamethazole), whereas the remaining eight were resistant to ceftiofur. The authors stated that veterinary infection control measures must be implemented into the clinical setting.

Antimicrobial resistance in *A. baumannii* originating from non-clinical samples

Several publications on *A. baumannii* from non-clinical origin exist (Table 1). A short note by Hauer et al. (1999), reports on the isolation of *A. baumannii* from tap water and anti-splash

nozzles in a hospital in 1998, which ultimately contaminated the tea used for mouth washes. The isolates were sensitive to cotrimaxole, no further information on antimicrobial resistance testing was provided.

In 2013, Faulde and Spiesberger reported on the role of the moth fly *Clogima (C.) albipunctata* as a mechanical vector of bacterial pathogens in four infested hospitals. A total of 15 *A. baumannii* strains was isolated from 271 adult *C. albipunctata* collected between 2011 and 2012 from shower cubicles, patient wards, rest rooms and hospital kitchens. Antimicrobial resistance testing revealed comparable cephalosporinase and β -lactamase-positive resistance patterns, one strain showed partial drug resistance to three groups of antibiotics, i.e. third-generation cephalosporins, penicillins and two aminoglycosides and thus qualified as a MDR strain. The authors stated that *C. albipunctata* is an indicator of poor hygiene, water and pest control in hospitals, but that bacterial investigation of the moth flies might be an option for monitoring contaminated hospital environments and for nosocomial pathogens.

The most recent study on *A. baumannii* in Germany addressed the question whether isolates from food harboured antibiotic resistances and if the food route had an impact on the dissemination of resistance genes (Cho et al. 2018). Forty-two *A. baumannii* isolates obtained from dry milk samples were tested for antimicrobial resistance by means of the Kirby-Bauer disc diffusion method. All strains could be allocated to the European clonal lineages II and III, were PCR positive for *bla_{oxa-51}* and resistant to chloramphenicol and oxacillin. Genome sequencing of nine *A. baumannii* isolates revealed four isolates to be positive for *bla_{oxa-530}* and further four to be positive for *bla_{oxa-91}* and *bla_{oxa-430}* genes, all belonging to the *bla_{oxa-51}*-like family. The strains moreover contained a *bla_{ADC-25}*-like gene encoding for an intrinsic AmpC β -lactamase. As the tested strains were generally not resistant to clinically relevant antibiotics such as tobramycin, ciprofloxacin, cefepime and meropenem, the authors concluded that the food route currently poses only a low risk for MDR *Acinetobacter* strains and transmission of resistance genes.

Discussion

Antibiotic resistance in human *A. baumannii* infections is closely monitored among the medical profession in Germany and numerous case studies, epidemiological surveys and reviews are regularly published (Huenges et al. 2016; Katchanov et al. 2018; Schleicher et al. 2012). This however, does not apply to veterinary medicine. The current knowledge on antibiotic resistance in *A. baumannii* from animal origin is mostly based on internationally published case reports, investigations of strain collections and several whole genome

analyses as summarised by Müller et al. (2014) and van der Kolk et al. (2018). This lack of data results in a somewhat sketchy picture on how to assess the impact of drug resistant *A. baumannii* strains on veterinary and public health. It is not yet clear if animals indeed pose a risk as reservoir for *A. baumannii*; genetically distinct animal isolates have been reported by Wilharm et al. (2018) and by van der Kolk et al. (2018), whereas companion animals have been found to carry isolates more closely related to human strains (Ewers et al. 2017; Walther et al. 2018), which could be an indication for humans possibly infecting their pets.

Hardly any data exist regarding the presence of drug resistant *A. baumannii* in food and food-producing animals in Germany. *A. baumannii* are regularly found in milk samples, however the majority of antimicrobial susceptibility patterns detected were not against clinically relevant antibiotics (Cho et al. 2018), which is in agreement with a similar study from Korea (Gurung et al. 2013). In a recent study, Klotz et al. (2018) isolated carbapenem-resistant *Acinetobacter indicus* harbouring *bla*_{oxa-23} on transposable elements from cattle. Despite the presumptive low pathogenicity of *A. indicus*, these isolates could contribute to the spreading of the *bla*_{oxa-23} gene to other receptive bacterial species and to their dissemination into the environment via manure, thus further contributing to the contamination of e.g. vegetables for human consumption.

Notwithstanding the global distribution of drug resistant *A. baumannii* in the animal population, it is still not clear if the higher reporting rates are due to increased awareness of the agent, close human animal contact, changes in animal husbandry, a spill over from humans to animals or the detection of the agent in a statistically skewed population.

Conclusions

Data on the general distribution of *A. baumannii* in the farm animal population in Germany are next to none and scarce for pet animals. Information on *A. baumannii* in wildlife, i.e. game and birds is missing and the possible influence of these animals on the dissemination of the agent to livestock and pets is unknown. Due to the ability of *A. baumannii* to survive in the environment for prolonged time and its ability to acquire resistance genes with relative ease, screening and implementation of hygiene strategies to minimise transmission and spread is recommended.

Several mechanisms conferring resistance to carbapenems in *A. baumannii* have been detected both in isolates originating from humans and companion animals in Germany. However, the impact of these findings on German veterinary and public health is difficult to assess, as conclusive data on antibiotic resistance in *A. baumannii* from animal and environmental origin in Germany are limited.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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References

- Antunes LC, Visca P, Towner KJ (2014) *Acinetobacter baumannii*: evolution of a global pathogen. *Pathog Dis* 71:292–301. <https://doi.org/10.1111/2049-632X.12125>
- Babaei M, Sulong A, Hamat R, Nordin S, Neela V (2015) Extremely high prevalence of antiseptic resistant Quaternary Ammonium Compound E gene among clinical isolates of multiple drug resistant *Acinetobacter baumannii* in Malaysia. *Ann Clin Microbiol Antimicrob* 14:11. <https://doi.org/10.1186/s12941-015-0071-7>
- Bergogne-Bérézin E, Towner KJ (1996) *Acinetobacter* spp. as nosocomial pathogens: microbiological, clinical, and epidemiological features. *CMR* 9:148–165. <https://doi.org/10.1128/CMR.9.2.148>
- Cho GS, Li B, Rostalsky A, Fiedler G, Rösch N, Igbinosa E, Kabisch J, Bockelmann W, Hammer P, Huys G, Franz CMAP (2018) Diversity and antibiotic susceptibility of *Acinetobacter* strains from Milk powder produced in Germany. *Front Microbiol* 9:536. <https://doi.org/10.3389/fmicb.2018.00536>
- Da Silva GJ, Domingues S (2016) Insights on the Horizontal Gene Transfer of Carbapenemase Determinants in the Opportunistic Pathogen *Acinetobacter baumannii*. *Microorganisms* 4(3). <https://doi.org/10.3390/microorganisms4030029>
- Diancourt L, Passet V, Nemec A, Dijkshoorn L, Brisse S (2010) The population structure of *Acinetobacter baumannii*: expanding multiresistant clones from an ancestral susceptible genetic pool. *PLoS One* 5(4):e10034. <https://doi.org/10.1371/journal.pone.0010034>
- Dijkshoorn L, Aucken H, Gerner-Smidt P, Janssen P, Kaufmann ME, Garaizar J, Ursing J, Pitt TL (1996) Comparison of outbreak and nonoutbreak *Acinetobacter baumannii* strains by genotypic and phenotypic methods. *JCM* 34:1519–1525
- Dijkshoorn L, Nemec A, Seifert H (2007) An increasing threat in hospitals: multidrug-resistant *Acinetobacter baumannii*. *Nat Rev Microbiol* 5:939–951. <https://doi.org/10.1038/nrmicro1789>
- Elsherif R, Ismail D, Elawady S, Jastaniah S, Al-Masaudi S, Harakeh S, Karrouf G (2016) Boronic acid disk diffusion for the phenotypic detection of polymerase chain reaction-confirmed, carbapenem-resistant, gram-negative bacilli isolates. *BMC Microbiol* 16:135
- Evans BA, Hamouda A, Amyes SG (2013) The rise of carbapenem-resistant *Acinetobacter baumannii*. *Curr Pharm Des* 19:223–238. <https://doi.org/10.2174/1381612811306020223>
- Ewers C, Klotz P, Scheufen S, Leidner U, Göttig S, Semmler T (2016) Genome sequence of OXA-23 producing *Acinetobacter baumannii* IHIT7853, a carbapenem-resistant strain from a cat belonging to international clone IC1. *Gut Pathog* 8:37. <https://doi.org/10.1186/s13099-016-0119-z>

- Ewers C, Klotz P, Leidner U, Stamm I, Prenger-Berninghoff E, Göttig S, Semmler T, Scheufen S (2017) OXA-23 and ISAbal-OXA-66 class D β -lactamases in *Acinetobacter baumannii* isolates from companion animals. *Int J Antimicrob Agents* 49:37–44. <https://doi.org/10.1016/j.ijantimicag.2016.09.033>
- Faulde M, Spiesberger M (2013) Role of the moth fly *Clogmia albipunctata* (Diptera: Psychodinae) as a mechanical vector of bacterial pathogens in German hospitals. *J Hosp Infect* 83:51–60. <https://doi.org/10.1016/j.jhin.2012.09.019>
- Guerra B, Fischer J, Helmuth R (2014) An emerging public health problem: acquired carbapenemase-producing microorganisms are present in food-producing animals, their environment, companion animals and wild birds. *Vet Microbiol* 171:290–297. <https://doi.org/10.1016/j.vetmic.2014.02.001>
- Gurung M, Nam HM, Tamang MD, Chae MH, Jang GC, Jung SC, Lim SK (2013) Prevalence and antimicrobial susceptibility of *Acinetobacter* from raw bulk tank milk in Korea. *J Dairy Sci* 96:1997–2002. <https://doi.org/10.3168/jds.2012-5965>
- Hauer T, Jonas D, Dettenkofer M, Daschner FD (1999) Tea as a source of *Acinetobacter baumannii* ventilator-associated pneumonia? *Infect Control Hosp Epidemiol* 20:594. <https://doi.org/10.1086/503149>
- Huenges K, Reinecke A, Bewig B, Haneya A, Cremer J (2016) Lung Transplantation in a Multidrug-Resistant Gram-Negative *Acinetobacter Baumannii*-Colonized Patient: A Case Report. *Thorac Cardiovasc Surg Rep* 5:16–17. <https://doi.org/10.1055/s-0035-1569993>
- Ivanković T, Goić-Barišić I, Hrenović J (2017) Reduced susceptibility to disinfectants of *Acinetobacter baumannii* biofilms on glass and ceramic. *Arh Hig Rada Toksikol* 68:99–108. <https://doi.org/10.1515/aht-2017-68-2946>
- Karah N, Sundsfjord A, Towner K, Samuelsen Ø (2012) Insights into the global molecular epidemiology of carbapenem non-susceptible clones of *Acinetobacter baumannii*. *Drug Resist Updat* 15:237–247. <https://doi.org/10.1016/j.drup.2012.06.001>
- Kawamura-Sato K, Wachino J, Kondo T, Ito H, Arakawa Y (2010) Correlation between reduced susceptibility to disinfectants and multidrug resistance among clinical isolates of *Acinetobacter* species. *J Antimicrob Chemother* 65(9):1975–1983. <https://doi.org/10.1093/jac/dkq227>
- Katchanov J, Asar L, Klupp EM, Both A, Rothe C, König C, Rohde H, Kluge S, Maurer FP (2018) Carbapenem-resistant Gram-negative pathogens in a German university medical center: Prevalence, clinical implications and the role of novel β -lactam/ β -lactamase inhibitor combinations. *PLoS One* 13(4):e0195757. <https://doi.org/10.1371/journal.pone.0195757>
- Klotz P, Jacobmeyer L, Stamm I, Leidner U, Pfeifer Y, Semmler T, Prenger-Berninghoff E, Ewers C (2018) Carbapenem-resistant *Acinetobacter baumannii* ST294 harbouring the OXA-72 carbapenemase from a captive grey parrot. *J Antimicrob Chemother* 73:1098–1100. <https://doi.org/10.1093/jac/dkx490>
- Martínez T, Ropelewski AJ, González-Mendez R, Vázquez GJ, Robledo IE (2016) Draft Genome Sequence of a Multidrug-Resistant *Klebsiella pneumoniae* Carbapenemase-Producing *Acinetobacter baumannii* Sequence Type 2 Isolate from Puerto Rico. *Genome Announc* 4(4). <https://mra.asm.org/content/4/4/e00758-16>. Accessed 9 Oct 2018
- Martó E, Hernández A, Ariza J, Domínguez MA, Matas L, Argerich MJ, Martín R, Ausina V (2003) Assessment of *Acinetobacter baumannii* susceptibility to antiseptics and disinfectants. *J Hosp Infect* 55(1):39–46. [https://doi.org/10.1016/S0195-6701\(03\)00220-2](https://doi.org/10.1016/S0195-6701(03)00220-2)
- Müller S, Janssen T, Wieler LH (2014) Multidrug resistant *Acinetobacter baumannii* in veterinary medicine - emergence of an underestimated pathogen? *BMTW* 127:435–446
- Parte AC (2018) LPSN – list of prokaryotic names with standing in nomenclature (bacterio.net), 20 years on. *IJSEM* 68:1825–1829. <https://doi.org/10.1099/ijsem.0.002786>
- Peleg AY, Seifert H, Paterson DL (2008) *Acinetobacter baumannii*: emergence of a successful pathogen. *CMR* 21:538–582. <https://doi.org/10.1128/CMR.00058-07>
- Pogue JM, Mann T, Barber KE, Kaye KS (2013) Carbapenem-resistant *Acinetobacter baumannii*: epidemiology, surveillance and management. *Expert Rev Anti-Infect Ther* 11:383–393. <https://doi.org/10.1586/eri.13.14>
- Schleicher X, Higgins PG, Wisplinghoff H, Körber-Irrgang B, Kresken M, Seifert H (2013) Molecular epidemiology of *Acinetobacter baumannii* and *Acinetobacter nosocomialis* in Germany over a 5-year period (2005–2009). *Clin Microbiol Infect* 19:737–742. <https://doi.org/10.1111/1469-0691.12026>
- van der Kolk JH, Endimiani A, Graubner C, Gerber V, Perreten V (2018) *Acinetobacter* in Veterinary Medicine with emphasis on *A. baumannii*. *J Glob Antimicrob Resist*. <https://doi.org/10.1016/j.jgar.2018.08.011>
- Visca P, Seifert H, Towner KJ (2011) *Acinetobacter infection*—an emerging threat to human health. *IUBMB Life* 63:1048–1054. <https://doi.org/10.1002/iub.534>
- Walther B, Klein KS, Barton AK, Semmler T, Huber C, Wolf SA, Tedin K, Merle R, Mitrach F, Guenther S, Lübke-Becker A, Gehlen H (2018) Extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* and *Acinetobacter baumannii* among horses entering a veterinary teaching hospital: the contemporary "Trojan horse". *PLoS One* 13:e0191873. <https://doi.org/10.1371/journal.pone.0191873>
- Wilharm G, Skiebe E, Higgins PG, Poppel MT, Blaschke U, Leser S, Heider C, Heindorf M, Brauner P, Jäckel U, Böhland K, Cuny C, Łopińska A, Kaminski P, Kasprzak M, Bochenski M, Ciebiera O, Tobółka M, Żołnierowicz KM, Siekiera J, Seifert H, Gagné S, Salcedo SP, Kaatz M, Leyer F, Bender JK, Fuchs S, Semmler T, Pfeifer Y, Jerzak L (2018) Relatedness of wildlife and livestock avian isolates of the nosocomial pathogen *Acinetobacter baumannii* to lineages spread in hospitals worldwide. *Environ Microbiol* 19:4349–4364. <https://doi.org/10.1111/1462-2920.13931>
- Zarrilli R, Poumaras S, Giannouli M, Tsakris A (2013) Global evolution of multidrug-resistant *Acinetobacter baumannii* clonal lineages. *Int J Antimicrob Agents* 41:11–19. <https://doi.org/10.1016/j.ijantimicag.2012.09.008>
- Zordan S, Prenger-Berninghoff E, Weiss R, van der Reijden T, van den Broek P, Baljer G, Dijkshoorn L (2011) Multidrug-resistant *Acinetobacter baumannii* in veterinary clinics, Germany. *EID* 17:1751–1754. <https://doi.org/10.3201/eid1709.101931>