



First report of NDM-1 in an *Acinetobacter baumannii* strain from a pet animal in Europe

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Sir,

Multidrug-resistant *Acinetobacter baumannii*, including carbapenem-resistant strains carrying New Delhi metallo- β -lactamase 1 (NDM-1), have emerged as a major cause of healthcare-associated infections worldwide [1]. Although carbapenem-resistant *Acinetobacter* spp. strains have been reported from animals, NDM-1-producing strains are still rare. They mainly occurred in livestock animals in China and were often identified in non-*baumannii* strains [2–4].

Here we report an NDM-1-positive, carbapenem-resistant *A. baumannii* strain belonging to a globally distributed clonal lineage isolated from a dog suffering from a urinary tract infection in Europe. Strain IHIT38008, identified as *A. baumannii* by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF/MS) (Bruker Daltonik, Bremen, Germany), was isolated from the urine of a dog from Italy during routine diagnostics in a veterinary microbiology laboratory in Germany in 2018. Antimicrobial susceptibility was determined using VITEK®2 (bioMérieux, Nürtingen, Germany; cards AST-GN38 and AST-N248), antibiotic gradient strips in the case of carbapenems (Liofilchem, Roseto degli Abruzzi, Italy) and a MICRONAUT system (Merlin Diagnostika GmbH, Bornheim-Hersel, Germany) for colistin. According to Clinical and Laboratory Standards Institute (CLSI) breakpoints, the isolate was resistant to all β -lactams, including the carbapenems imipenem [minimum inhibitory concentration (MIC) = 8 mg/L], doripenem (MIC > 32 mg/L) and meropenem (MIC = 8 mg/L). It was also resistant to enrofloxacin (MIC \geq 4 mg/L), marbofloxacin (MIC \geq 4 mg/L) and nitrofurantoin (MIC \geq 512 mg/L) but showed susceptibility to amikacin, gentamicin, tobramycin, trimethoprim/sulfamethoxazole and colistin. The genome was sequenced using MiSeq (Illumina Inc., San Diego, CA, USA) (Sequence Read Archive no. [SDSK000000001](https://www.ncbi.nlm.nih.gov/sra/SDSK000000001)), and de novo assembly and annotation of sequences were performed with SPAdes v.3.15.1 (<http://cab.spbu.ru/software/spades/>) and RAST v.2.0 (<http://rast.nmpdr.org/>), respectively. Using ResFinder 4.1 (<https://cge.cbs.dtu.dk/services/ResFinder/>), we identified the carbapenemase gene *bla*_{NDM-1} and the intrinsic β -lactamase genes *bla*_{OXA-64} and *bla*_{ADC-25-like}. In accordance with the resistance observed for fluoroquinolones, we identified mutations in the quinolone resistance-determining region of DNA gyrase (GyrA; S83L) and topoisomerase IV (ParC; E84K). Other known resistance genes or mechanisms were not present.

NDM-producing *Acinetobacter* spp. strains have been frequently reported from humans [1,5], but there are much fewer findings in animals [2–4,6]. In China, the *bla*_{NDM-1} gene was identified in *A. baumannii* and *Acinetobacter calcoaceticus* isolated from pigs, in

Acinetobacter lwoffii from chicken and cat, and recently in *Acinetobacter indicus*, *Acinetobacter schindleri* and *A. lwoffii* from waterfowl [2,4]. So far, there is only one report regarding an NDM-1-positive *Acinetobacter* sp. strain in Europe, namely an *Acinetobacter radioresistens* strain isolated from a rectal swab of a hospitalised dog in Italy in 2014 [6].

The *bla*_{NDM-1} gene in strain IHIT38008 was identified on a whole-genome sequencing contig of 345 993 bp in size. This, together with the results from mlplasmids (<https://sarredondo.shinyapps.io/mlplasmids/>) analysis, indicated the chromosomal location of the gene, which was confirmed by *S1* nuclease digestion and subsequent pulsed-field gel electrophoresis (PFGE) and Southern blot hybridisation. By analysing the genetic environment of *bla*_{NDM-1} using Geneious v.R8.1 (Biomatters Ltd., Auckland, New Zealand), we could locate the gene inside the composite transposon Tn125 (Fig. 1). This transposon structure was first described in a clinical *A. baumannii* strain (161/07) from a hospitalised patient in Germany with travel history to Serbia in 2007 [5]. Of note, the ~10.1-kb transposon structure of IHIT38008 (GenBank accession no. [MK467522.1](https://www.ncbi.nlm.nih.gov/nuccore/MK467522.1)) revealed > 99.9% sequence identity with that of the human strain 161/07. In addition, it was also almost similar to transposon sequences previously identified in *A. baumannii* strain JH from Switzerland and on plasmid pNDM-lz4b of feline *A. lwoffii* strain lz4b [1,3,5]. In addition, the NDM-1-positive *A. radioresistens* strain from a hospitalised dog in Italy shows this genetic environment [6]. In contrast, plasmids pNDM-AB and pAL-1, both identified in *Acinetobacter* spp. from livestock animals in China, differed from the previous ones by carrying a partial Tn125 (Fig. 1). In strain IHIT38008, Tn125 was inserted into a gene encoding a protein of unknown function (GenBank no. [MK467522.1](https://www.ncbi.nlm.nih.gov/nuccore/MK467522.1), locus_id QBQ02716.1). This insertion site differs from those previously published (Fig. 1). These data further confirm that independent transposition events targeted the chromosomes and plasmids of different *Acinetobacter* spp. strains and that the Tn125 transposon likely contributes to the global spread of NDM-1 [1,2].

Our strain was assigned to ST25^{Pasteur} (<https://cge.cbs.dtu.dk/services/MLST/>) and international clone VII, an emerging genotype that has been associated with epidemics in humans worldwide.

A core genome comparison of 39 *A. baumannii* ST25 strains (Supplementary Table S1) revealed that IHIT38008 clustered closely [maximum of 568 single nucleotide polymorphisms (SNPs) among 2,222 orthologous genes] to strains previously isolated from human patients (Supplementary Fig. S1). Only 179 SNPs distinguished IHIT38008 from strain 1429530 obtained from a perirectal swab of a human in the USA. Strains from Europe were less related, as exemplified by 161/07 (Germany; 1,861 SNPs), RUH1486 (The Netherlands; 2,882 SNPs) and 4190 (Italy; 5,708 SNPs).

In summary, we describe the first case of an NDM-1-producing *A. baumannii* belonging to the successful clonal ST25 lineage from a pet in Europe. Together with the finding that *bla*_{NDM-1} was integrated into transposon Tn125, which is a major vehicle for NDM-

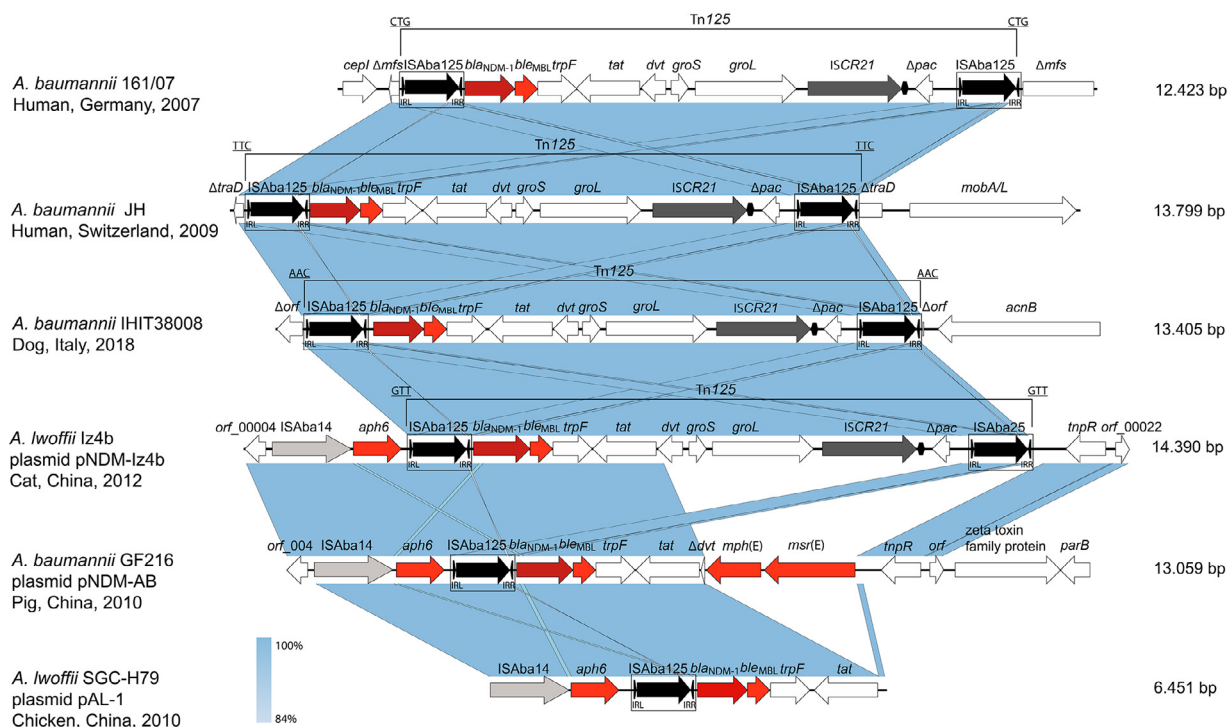


Fig. 1. Genetic environment of the *bla*_{NDM-1} gene in canine *Acinetobacter baumannii* strain IHIT38008 (GenBank accession no. [MK467522.1](https://www.ncbi.nlm.nih.gov/nuccore/MK467522.1)) and comparison with the corresponding genetic regions in strains of human origin [*A. baumannii* 161/07 ([HQ857107](https://www.ncbi.nlm.nih.gov/nuccore/HQ857107) and [JZCA00000000.1](https://www.ncbi.nlm.nih.gov/nuccore/JZCA00000000.1)); *A. baumannii* JH, Switzerland ([JN872329.1](https://www.ncbi.nlm.nih.gov/nuccore/JN872329.1))] and animal origin [*Acinetobacter Iwoffii* SGC-H79 plasmid pAL-1 ([JN616388.1](https://www.ncbi.nlm.nih.gov/nuccore/JN616388.1)); *A. Iwoffii* Iz4b plasmid pNDM-Iz4b ([KJ547696.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ547696.1)); *A. baumannii* GF216 plasmid pNDM-AB ([KC503911.1](https://www.ncbi.nlm.nih.gov/nuccore/KC503911.1))]. Genes and their transcription orientations are presented by arrows. Resistance genes are indicated by red arrowed boxes and insertion sequences by grey and black arrowed boxes. In the four Tn125-carrying strains, the transposon is bracketed by a 3-bp target site duplication (transposon signature; underlined and uppercase). IRR and IRL indicate inverted repeats left and right, respectively. Tn125 was inserted into different genes in these strains, encoding a protein of unknown function (IHIT38008), a transfer protein (*traD*; JH) and a putative major facilitator superfamily metabolite/H⁺ symporter (*mfs*; 161/07), or an intergenic region (pNDM-Iz4b) located between *aphA6* and *ISAbal25* on the left site and between two copies of *ISAbal25*. Map generation was performed with Easyfig v.2.2.2 (<http://mjsoull.github.io/Easyfig/>).

1 in human *Acinetobacter* spp. and *Enterobacteriales*, our data suggest that companion animals may incidentally acquire NDM-1-producing strains from humans. These findings warrant further investigation of the epidemiology of carbapenem resistance in *Acinetobacter* spp. strains from animals and the processes that may favour the emergence and spread of such bacteria in veterinary settings.

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Competing interests

None declared.

Ethical approval

Not required.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.jgar.2021.05.003](https://doi.org/10.1016/j.jgar.2021.05.003).

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