

1                   **Detection of NDM-1, CTX-M-15 and qnrB4-producing *Enterobacter***

2   ***hormaechei* isolates in Brazil**

3  
4 Ana Paula D'A. Carvalho-Assef,<sup>a</sup> Polyana S. Pereira,<sup>a</sup> Rodolpho M. Albano,<sup>b</sup>, Gabriela Casemiro  
5 Berião,<sup>a</sup> Carolina Padilha Tavares,<sup>a</sup> Thiago Pavoni Gomes Chagas,<sup>a</sup> Elizabeth A. Marques,<sup>c</sup> Loeci  
6 N. Timm,<sup>d</sup> Renato C.F. Da Silva,<sup>e</sup> Diego R. Falci,<sup>c</sup> Marise D. Asensi<sup>a#</sup>

7  
8 Laboratório de Pesquisa em Infecção Hospitalar (LAPIH), Instituto Oswaldo Cruz-FIOCRUZ, Rio  
9 de Janeiro, RJ, Brazil<sup>a</sup>; Departamento de Bioquímica, Instituto de Biologia Roberto Alcântara  
10 Gomes, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil<sup>b</sup>; Departamento de  
11 Microbiologia, Imunologia e Parasitologia, Faculdade de Ciências Médicas, Universidade do Estado  
12 do Rio de Janeiro, Rio de Janeiro, RJ, Brazil<sup>c</sup>; Fundação Estadual de Produção e Pesquisa em Saúde  
13 (FEPPS IPB-LACEN-RS), Porto Alegre, RS, Brazil<sup>d</sup>; Hospital Nossa Senhora da Conceição, Porto  
14 Alegre, RS, Brazil<sup>e</sup>.

15  
16 Running Title: NDM-1-producing *E. hormaechei* in Brazil

17  
18 #Address correspondence to Marise Dutra Asensi, marise@ioc.fiocruz.br and  
19 anapdca@ioc.fiocruz.br.

20  
21 **Keywords:** NDM-1; CTX-M-15; qnrB4; *Enterobacter hormaechei* subps. *Oharae*; Brazil

22  
23 **Abstract:** Not applicable

24

25 **Text:**

26 After the first description of NDM-1-carbapenemase in a *Providencia rettgeri* isolate in  
27 Brazil in February 2013 (1), the public hospital where this isolate was recovered began an active  
28 surveillance in search of asymptomatic carriers and at the hospital environment. Furthermore, a  
29 retrospective study of carbapenem-resistant isolates stored at that hospital since 2012 was performed.  
30 Six NDM-1-producing *Enterobacter hormaechei* subsp. *oharae* isolates, identified by the Vitek2  
31 system and *hsp60*-genotyping, were recovered and characterized by phenotypic assays and molecular  
32 techniques, such as PCR and DNA sequencing (2,3). One isolate (CCBH10892) was recovered from  
33 a rectal swab of a patient at the Intensive Care Unit (ICU) in September 2012 (a time period prior to  
34 the isolation of NDM-positive *P. rettgeri*). The others were isolated from March to May 2013 from  
35 rectal swabs of patients (n=4) and a sink (n=1) located in the same ICU.

36 PFGE of *Xba*-I-digested DNA (4) showed that all isolates belonged to the same clone,  
37 considered to be multidrug-resistant as they were susceptible only to amikacin (MIC range to 8-  
38 16mg/L) and polymyxin B (MIC  $\leq$ 1mg/L) by E-test method (Figure 1). Besides *bla*<sub>NDM-1</sub>, all these  
39 isolates carried *bla*<sub>CTX-M-15</sub>, *qnrB4* and *aac(6)-Ib* genes, detected by PCR and sequencing. Plasmid  
40 analysis by restriction digests with S1 nuclease and southern blotting (5) showed that the *bla*<sub>NDM-1</sub>  
41 and *qnrB4* genes were located on the same plasmids, ranging in size from 420 to 490kb (Figure 1).

42 To obtain a comprehensive in-depth view of the genetic structure surrounding the *bla*<sub>NDM-1</sub>,  
43 *bla*<sub>CTX-M-15</sub> and *qnrB4* genes, the genomic sequence of the CCBH10892 isolate was determined on an  
44 Illumina MiSeq system. A total of 1,149,470 reads (5,373,710bp) were assembled with Geneious  
45 assembler (Biomatters) to generate 56 contigs. We found *bla*<sub>NDM-1</sub> in a 94,795bp contig flanked by a  
46 truncated IS*Aba*125 at the right boundary and by a bleomycin-resistance gene (*ble*<sub>MBL</sub>) at the left  
47 (GeneBank accession number KF727591). This region shared 99% identity with the NDM region  
48 present in a plasmid carried by a *K. pneumoniae* isolate from Taiwan (6). In this contig, some

49 conjugation and plasmid transfer genes and a replication protein gene belonging to the IncF group  
50 were also observed. However, this replicon could not be detected by the PBRT scheme (7).

51 The *qnrB4* gene was found in a 16,569bp contig in which were also observed *ISCR1*, genes  
52 encoding permeases (*sapA-B-C*), phage shock proteins (*pspA-B-C-D*) and AmpC *bla<sub>DHA-1</sub>*  
53 (GeneBank accession number KF646592). This same region has been reported in different plasmids  
54 of other bacterial species (8).

55 *bla<sub>CTX-M-15</sub>* was integrated in the chromosome associated with an upstream *ISEcp1* element in  
56 a 277,989bp contig (part of it is in GeneBank accession number KF727590). This transposition unit  
57 was inserted into the *flhC* gene that encodes a flagellar transcriptional activator protein (9). In fact,  
58 these isolates showed no motility.

59 This study showed the detection of a multiresistant *E. hormaechei* clone carrying relevant  
60 resistance genes (*bla<sub>NDM-1</sub>*, *bla<sub>CTX-M-15</sub>* and *qnrB4*) in asymptomatic carriers and at the hospital  
61 environment, alerting that our current views on the extent of the spread of NDM in Brazil may well  
62 be underestimated.

63

#### 64 **Acknowledgments**

65 This work was funded by research grants from Conselho Nacional de Desenvolvimento  
66 Científico e Tecnológico – CNPq, Fundação Carlos Chagas de Amparo a Pesquisa – FAPERJ and  
67 Instituto Oswaldo Cruz – IOC – FIOCRUZ. We thank the Genomic Platform for DNA Sequencing  
68 PDTIS (Instituto Oswaldo Cruz).

69

70

71

72

73

74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97

## References

1. **Carvalho-Assef AP, Pereira PS, Albano RM, Berião GC, Chagas TPG, Timm LN, Da Silva RCF, Falci DR, Asensi MD.** 2013. Isolation of NDM-producing *Providencia rettgeri* in Brazil. *J. Antimicrob. Chemother.* **68**: 2956-2957.
2. **Nordmann P, Poirel L, Carrër A, Toleman MA, Walsh TR.** 2011. How to detect NDM-1 producers. *J. Clin. Microbiol.* **49**: 718-721.
3. **Hoffmann H, Roggenkamp A.** 2003. Population genetics of the nomenclatures *Enterobacter cloacae*. *Appl. Environ. Microbiol.* **69**: 5306–5318.
4. **Seki LM, Pereira PS, de Souza Conceição M, Souza MJ, Marques EA, Carballido JM, de Carvalho ME, Assef AP, Asensi MD.** 2013. Molecular epidemiology of CTX-M producing *Enterobacteriaceae* isolated from bloodstream infections in Rio de Janeiro, Brazil: emergence of CTX-M-15. *Braz J Infect Dis* **17**: 640-646.
5. **Barton BM, Harding GP, Zuccarelli AJ.** 1995. A general method for detecting and sizing large plasmids. *Anal. Biochem.* **226**: 235-240.
6. **Huang TW, Chen TL, Chen YT, Lauderdale TL, Liao TL, Lee YT, Chen CP, Liu YM, Lin AC, Chang YH, Wu KM, Kirby R, Lai JF, Tan MC, Siu LK, Chang CM, Fung CP, Tsai SF.** 2013. Copy Number Change of the NDM-1 sequence in a multidrug-resistant *Klebsiella pneumoniae* clinical isolate. *PLoS One.* **8**: e62774.
7. **Carattoli A, Bertini A, Villa L, Falbo V, Hopkins KL, Threlfall EJ.** 2005. Identification of plasmids by PCR-based replicon typing. *J. Microbiol. Methods.* **63**: 219–228.
8. **Pérez-Moreno MO, Estepa V, Sáenz Y, Cortell-Ortolá M, Fort-Gallifa I, Ruiz J, Torres C.** 2012. Intrahospitalary dissemination of *Klebsiella pneumoniae* carrying *bla*<sub>DHA-1</sub> and *qnrB4* genes within a novel complex class 1 integron. *Diagn. Microbiol. Infect. Dis.* **73**: 210-211.

- 98 9. **Lehti TA, Bauchart P, Dobrindt U, Korhonen TK, Westerlund-Wikstro B.** 2012. The  
99 fimbriae activator MatA switches off motility in *Escherichia coli* by repression of the  
100 flagellar master operon *flhDC*. *Microbiology*. **158**: 1444–1455.

101

102 Figure 1: Characteristics of 6 NDM-producing *E. hormaechei* subsp. *oharae* isolates obtained in a  
103 hospital in Rio Grande do Sul, Brazil.

104 \*CCBH14397 – *E. hormaechei* isolate epidemiologically unrelated to NDM-producing isolates

105 Results of antimicrobial susceptibility were interpreted according to CLSI breakpoints, except for  
106 tygeciline and polymixin in which the EUCAST breakpoints were used.

