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Proteus mirabilis carrying NTE$_{KPC-IId}$, *bla*$_{NDM-1}$, *bla*$_{OXA-10}$, *aph(3')-VI*, *qnrD1* and IncQ and Col3M plasmids from a hospital in Recife-PE, Brazil

Proteus mirabilis portador de NTE$_{KPC-IId}$, *bla*$_{NDM-1}$, *bla*$_{OXA-10}$, *aph(3')-VI*, *qnrD1* e plasmídeos *IncQ* e *Col3M* proveniente de paciente internado em hospital de Recife-PE, Brasil

Proteus mirabilis transportando NTE$_{KPC-IId}$, *bla*$_{NDM-1}$, *bla*$_{OXA-10}$, *aph(3')-VI*, *qnrD1* e plásmidos IncQ y Col3M de un hospital en Recife-PE, Brasil

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Abstract
The present study objective to characterize the clinical aspects of a patient infected with two strains of *P. mirabilis* and the presence of resistance determinants in the two isolates from a patient at a public hospital in Recife-PE, Brazil. The total DNA of the isolates was extracted and submitted to PCR and amplicon sequencing for the investigation of resistance genes, *bla*$_{KPC}$, *bla*$_{OXA-10}$, *bla*$_{OXA-23}$, *bla*$_{OXA-48}$, *bla*$_{OXA-58}$, *bla*$_{VIM}$, *bla*$_{IMP}$, *bla*$_{SPM}$, *bla*$_{GES}$, *bla*$_{NDM}$, *qnrD* and *aac(6')-Ib*). Isolate P21-A2 harbored the *aac(6')-Ib*, *bla*$_{OXA-10}$ and *qnrD* genes. One of the isolates, P20-A2, was selected for plasmid DNA sequencing. The results showed that the patient developed multiple infections with various pathogens including two strains of *P. mirabilis*. The patient was hospitalized for 103 days, had septic shock of skin, abdominal, pulmonary and ulcer focus, and died. Isolate P20-A2 harbored the genes *bla*$_{NDM}$, *qnrD, aph(3')-VI*, *bla*$_{KPC}$ and *bla*$_{OXA-10}$, and plasmids IncQ and Col3M, together with NTE$_{KPC-IId}$. To our knowledge, this is the first report of *P. mirabilis* harboring NTE$_{KPC-IId}$. Although *P. mirabilis* is standing out as a cause of nosocomial infections and a resistant multidrug pathogen, this species is still neglected, the emergence of these *P. mirabilis* isolates harboring aforementioned resistance determinants and the plasmids IncQ and Col3M demonstrate the potential for dissemination of important resistance genes, mainly in the case of *P. mirabilis*.
Keywords: *Proteus mirabilis*; NTE$_{KPC-IId}$; IncQ; Col3M.

Resumo
O presente estudo teve por objetivo caracterizar aspectos clínicos de um paciente com infecção por duas cepas de *P. mirabilis* e a presença de determinantes de resistência nos dois isolados provenientes de um paciente de um hospital público de Recife-PE, Brasil. O DNA total dos isolados foi extraído e submetido a PCR e sequenciamento dos amplicons para a investigação de genes de resistência, *bla*$_{KPC}$, *bla*$_{OXA-10}$, *bla*$_{OXA-23}$, *bla*$_{OXA-48}$, *bla*$_{OXA-58}$, *bla*$_{VIM}$, *bla*$_{IMP}$, *bla*$_{SPM}$, *bla*$_{GES}$, *bla*$_{NDM}$, *qnrD* e *aac(6')-Ib*). O isolado P21-A2 albergava os genes *aac(6')-Ib*, *bla*$_{OXA-10}$ e *qnrD*. Um dos isolados, P20-A2, foi selecionado para o sequenciamento do DNA plasmidial. Os resultados mostraram que o paciente desenvolveu diversas infecções por vários patógenos incluindo duas cepas de *P. mirabilis*. O paciente ficou internado por 103 dias, teve choque séptico de foco cutâneo, abdominal, pulmonar e úlcera, e veio a óbito. O isolado P20-A2 albergava os genes *bla*$_{NDM}$, *qnrD, aph(3')-VI*, *bla*$_{KPC}$ e *bla*$_{OXA-10}$, e os plasmídeos IncQ e Col3M, juntamente com

$NTE_{KPC-IId}$. Para o nosso conhecimento, este é o primeiro relato de *P. mirabilis* albergando $NTE_{KPC-IId}$. Apesar de *P. mirabilis* estar se destacando como causador de infecções nosocomiais e patógeno multidroga resistente, esta espécie ainda é negligência, a emergência desses isolados de *P. mirabilis* albergando determinantes de resistência antes mencionados e os plasmídeos IncQ e Col3M demonstra o potencial de disseminação de importantes genes de resistência, principalmente se tratando de *P. mirabilis*.
Palavras-chave: *Proteus mirabilis*; $NTE_{KPC-IId}$; IncQ; Col3M.

Resumen
El presente estudio tuvo como objetivo caracterizar los aspectos clínicos de un paciente infectado con dos cepas de P. mirabilis y la presencia de determinantes de resistencia en los dos aislamientos de un paciente de un hospital público de Recife-PE, Brasil. El DNA total de los aislamientos fue extraído y sometido a PCR y secuenciación de amplicones para la investigación de genes de resistencia, bla_{KPC}, bla_{OXA-10}, bla_{OXA-23}, bla_{OXA-48}, bla_{OXA-58}, bla_{VIM}, bla_{IMP}, bla_{SPM}, bla_{GES}, bla_{NDM}, *qnrD* y *aac(6')-Ib*). El aislamiento P21-A2 albergaba los genes *aac(6')-Ib*, bla_{OXA-10} y *qnrD*. Uno de los aislados, P20-A2, se seleccionó para la secuenciación del DNA plasmídico. Los resultados mostraron que el paciente desarrolló múltiples infecciones con varios patógenos, incluidas dos cepas de *P. mirabilis*. El paciente estuvo hospitalizado durante 103 días, presentó shock séptico de piel, foco abdominal, pulmonar y ulceroso, y falleció. El aislamiento P20-A2 albergaba los genes bla_{NDM}, *qnrD*, *aph(3')-VI*, bla_{KPC} y bla_{OXA-10}, y los plásmidos IncQ y Col3M, junto con $NTE_{KPC-IId}$. Hasta donde sabemos, este es el primer informe de P. mirabilis que alberga $NTE_{KPC-IId}$. Aunque *P. mirabilis* se destaca como una causa de infecciones nosocomiales y un patógeno resistente a múltiples fármacos, esta especie aún se descuida, la aparición de estos aislados de *P. mirabilis* que albergan los determinantes de resistencia antes mencionados y los plásmidos IncQ y Col3M demuestran el potencial de diseminación de importantes genes de resistencia, principalmente en el caso de *P. mirabilis*.
Palabras clave: *Proteus mirabilis*; $NTE_{KPC-IId}$; IncQ; Col3M.

1. Introduction

Health care-related infections (HAI) continue to be of great concern to public epidemiological surveillance agencies, due to the increase in antimicrobial resistance, mainly due to the plasmid spread of resistance genes, along with the spread of opportunistic pathogens, such as *Proteus mirabilis.* Its consequences are associated with increased morbidity and mortality, increased length of hospital stay, as well as increased selective pressure (Cantón et al., 2002; Del Franco et al., 2015).

The genus *Proteus* contains six known species: *Proteus vulgaris*, *Proteus mirabilis*, *Proteus myxofaciens*, *Proteus cibarius*, *Proteus penneri* and *Proteus hauseri*. Being *P. mirabilis*, *P. vulgaris* and *P. penneri* are commonly described as opportunistic pathogens (Beltrão et al., 2021; Girlich et al., 2020). *Proteus mirabilis* is a gram-negative bacillus belonging to the order *Enterobacterales* (Oliveira et al., 2021).

This pathogen is frequently reported to cause Urinary Tract Infections (UTI), especially in patients with prolonged use of indwelling catheters and urinary catheters. In addition, *P. mirabilis* has intrinsic resistance to tigecycline, nitrofurantoin, polymyxins and tetracycline (Cunha et al., 2017; Beltrão et al., 2020). And has reduced susceptibility to imipenem (Bontron et al., 2019). This characteristic of intrinsic resistance added to horizontal gene transfer through plasmid dissemination makes this pathogen, an agent of HAI, a matter of great concern. Highlighting that *P. mirabilis* belongs to the normal intestinal microbiota of humans, and can eventually migrate to other tissues and cause serious infections. In this context, infections caused by *P. mirabilis* that are resistant to beta-lactams, mainly due to the bla_{GES}, bla_{NDM} and bla_{KPC} genes are considered challenging issues for antimicrobial therapy (Beltrão et al., 2021).

Taking into account the importance of investigating the clinical and microbiological aspects of *P. mirabilis* resistance, the present study aimed to characterize the clinical aspects of a patient infected with two strains of *P. mirabilis* in a public hospital in Recife in 2018, and the presence of determinants of resistance to carbapenems and quinolones.

2. Methodology

Two clinical isolates of *P. mirabilis* recovered from a patient admitted to a tertiary hospital in Recife-PE, Brazil, were selected. Biochemical identification and antimicrobial susceptibility profile were performed by automated Phoenix-BD system

and data were interpreted according to CLSI, 2018 specifications. The study was approved by the Research Ethics Committee involving human beings (CEP/Plataforma Brasil) and opinion number 3.007.636.

For susceptibility tests, the following antimicrobials were tested: Amikacin, Amoxicillin-clavulanic acid, Ampicillin; Aztreonam, Cephalotin, Cefepime, Cefoxitin, Ceftazidime, Ceftriaxone, Cefuroxime, Ciprofloxacin; Gentamicin, Ertapenem, Imipenem, Meropenem, Levofloxacin, Piperacillin-tazobactam and Sulfametaxazol-trimethoprim.

Genomic DNA from the isolates was extracted using the Wizard Genomic DNA Purification Kit (Promega) and the resistance genes *bla*$_{KPC}$, *bla*$_{OXA-10}$, *bla*$_{OXA-23}$, *bla*$_{OXA-48}$, *bla*$_{OXA-58}$, *bla*$_{VIM}$, *bla*$_{IMP}$, *bla*$_{SPM}$, *bla*$_{GES}$, *bla*$_{NDM}$ and *qnrD*, aac(6')-Ib were investigated by PCR. The amplification conditions and the used primers were shown in table 1. Positive and negative controls were included in each PCR.

The Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction (ERIC-PCR) technique was performed to determine the relationship between the two isolates, P20-A2 and P21-A2. Primers described in Table 1 were used. For the analysis of the ERIC results, the GelAnalyzer and DARwin 6.0 programs were used.

Table 1. Sequence of the PCR primers that were used in the study**.**

Genes	Sequence of primers	Fragment Size	Annealing Temperature	Ref.
***bla*$_{KPC}$**	TGTCACTGTATCGCCGTC CTCAGTGCTCTACAGAAAACC	882bp	63°C	(YIGIT et al., 2001a)
***bla*$_{GES}$**	ATCAGCCACCTCTCAATGG TAGCATCGGGACACATGAC	860bp	55°C	(BOYD et al., 2015)
***bla*$_{NDM}$**	TGCCCAATATTATGCACCCGG CGAAACCCGGCATGTCGAGA	621bp	60°C	(HUANG et al., 2017)
***bla*$_{VIM}$**	CAGATTGCCGATGGTGTTTGG AGGTGGGCCATTCAGCCAGA	ND	62°C	(CABRAL et al., 2012)
***bla*$_{IMP}$**	GGAATAGAGTGGCTTAATTCTC GTGATGCGTCYCCAAYTT CACT	232bp	60°C	(CABRAL et al., 2012)
***bla*$_{SPM}$**	CCTACAATCTAACGGCGACC TCGCCGTGTCCAGGTATAAC	271bp	63°C	(GALES et al., 2003b)
***bla*$_{OXA-10}$**	TCAACAAATCGCCAGAGAAG TCCCACACCAGAAAAACCAG	276bp	62°C	(BERT et al., 2002)
***bla*$_{OXA-23}$**	GATCGGATTGGAGAACCAGA ATTTCTGACCGCATTTCCA	501bp	57°C	(RANJBAR; ZAYERI; MIRZAIE, 2020)
***bla*$_{OXA-48}$**	TTGGTGGCATCGATTATCGG GAGCACTTCTTTTGTGATGGC	743bp	55ºC	(POIREL et al., 2004)
***bla*$_{OXA-58}$**	CGATCAGAATGTTCAAGCGC ACGATTCTCCCCTCTGCGC	800bp	ND	(POIREL; NORDMANN, 2006b)
qnrD	CGAGATCAATTTACGGGGAATA AACAAGCTGAAGCGCCTG	500bp	61°C	(CAVACO et al., 2009)
aac(6')-Ib	CCCGCTTTCTCGTAGCA TATGAGTGGCTAAATCGAT	500bp	52°C	(FIRMO et al., 2020)
ERIC	ATGTAAGCTCCTGGGGATTAAC AAGTAAGTGACTGGGGTGAGCG	ND	36°C	(DUAN et al., 2009)

ND – Not determined. Source: Authors.

To carry out the plasmid DNA sequencing, the isolate P20-A2 was selected because it harbors the *bla*$_{KPC}$ and *bla*$_{NDM}$ genes.

Plasmid DNA from isolate P20-A2 was extracted using the PureYieldTM Plasmid Miniprep System kit (Promega) according to the manufacturer's specifications. Isolates were characterized by Illumina MiSeq sequencing (Nextera XT libraries).

Data were processed to remove low quality readings using the Trimmomatic tool. Subsequently, the filtered readings were used for reassembly by applying the Velvet tool, whose parameters were optimized using the Velvet Optimiser program. Velvet results were also used as input to another assembly program, CAP3, in order to improve the assemblies. Gene prediction and annotation were performed using the Prokka program. Plasmid DNA sequences were analyzed using Artemis Sanger software. In addition, the Resfinder and PlasmidFinder platforms were used.

3. Results

Clinical patient information

In December 2017, a 43-year-old man was admitted for preoperative bariatric surgery. The patient had grade III obesity (216kg at admission) with a BMI of 71.4, hypertensive crisis, edema (with a restrictive disorder), Systemic Arterial Hypertension (SAH) and depression. After 16 days of hospitalization, the patient underwent open Roux-en-Y gastroplasty under balanced general anesthesia. The patient used a Blake drain in the abdominal cavity and elastic stockings in the lower limbs. The length of stay was 103 days. After surgery, the patient had several bacterial infections and died. The reason for death was pulmonary insufficiency, septic shock of skin, abdominal, pulmonary and ulcer focus. During the 103-day hospital stay, the patient used meropenem, vancomycin, polymyxin B, ampicillin, amikacin, daptomycin and amphotericin.

Proteus mirabilis isolates profile

A tissue sample and a sample of tracheal secretions from the patient were sent to the hospital's microbiology laboratory within 3 days of collection of both samples. Two clinical isolates of *P. mirabilis* (P20-A2 and P21-A2) multidrug resistant and possibly ESBL producers were recovered (Table 2). Isolate P20-A2 showed resistance to most antimicrobials, including first, second and third generation cephalosporins, sulfonamides, monobactams, carbapenems and quinolones. Isolate P21-A2 differed by not having resistance to carbapenems (Table 2). Isolates P20-A2 and P21-A2 did not show clonal relationship by Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction (ERIC-PCR), by previous study (Beltrão et al., 2021).

Table 2. Phenotypic resistance profile and presence of resistance genes investigated by PCR for the two *Proteus mirabilis* isolates (P20-A2 e P21-A2). Id.- Identification; ICU – Intensive care unit, UCO –Coronary Unit; Int – intermediary.

Id.	Harvest date (dd/mm/yyyy)	Insulation sample	Sector	Resistance profile		Resistance genes
				Antimicrobial groups	Antimicrobials (MIC)	
P20-A2	23/03/2018	Tissue	ICU	Aminoglycosides	Gentamicine (=8)(Int)	*aph(3')-VI* *bla*$_{OXA-10}$ *bla*$_{KPC-2}$ *bla*$_{NDM-1}$ *qnrD1*
				Cephalosporins	Cefepime (>16); Cefoxitine (>16); Ceftriaxone (>32); Ceftazidime (>16); Cefuroxime (>16)	
				Carbapenemics	Imipenem (>8); Meropenem (=4); Ertapenem	
				Penicillins	Ampicillin (>16); Amoxicillin-acid clavulanic (>16/8); Piperacillin-tazobactam (=64/4)(Int)	
				Quinolones and fluoroquinolones	Levofloxacin (>4); Ciprofloxacin (>2)	
				Sulfonamide	Sulfamethoxazole-trimethoprim (>4/76)	
				Monobactam	Aztreonam	
P21-A2	25/03/2018	Tracheal secretion	UCO	Aminoglycosides	Gentamicine (=8)(Int)	*aac(6')-Ib* *bla*$_{OXA-10}$ *qnrD1*
				Cephalosporins	Cefepim (>16); Ceftriaxone (>32); Ceftazidime; Cefuroxime (>16);	
				Penicillins	Ampicillin (>16) Amoxicillin+clavulanic acid	
				Quinolones and fluoroquinolones	Levofloxacin (>4); Ciprofloxacin (>2)	
				Sulfonamide	Sulfamethoxazole-trimethoprim (>4/76)	
				Monobactam	Aztreonam	

Source: Beltrão et al., (2021).

In addition to *P. mirabilis*, the patient also acquired infections at different sites. *Morganella morganii* and *Klebsiella pneumoniae* were isolated from abdominal cavity fluid, *P. mirabilis* (P21-A2) and *Acinetobacter baummanii* were isolated from tracheal secretions, from blood culture *Enterococcus faecalis*, from *Morganella morgannii* wound secretion and from a tissue sample from *P. mirabilis* (P20-A2).

Analysis of the genetic environment of the *bla*$_{KPC}$ gene and Plasmidial Incompatibility group (Inc)

The plasmid sequencing results showed that the P20-A2 isolate had a GC content of 47.8%, with a total of 31,899 bases. In summary, all sequenced content was assembled into 27 contigs, produced with 333.0x coverage. And 33 CDS were obtained (Table 3).

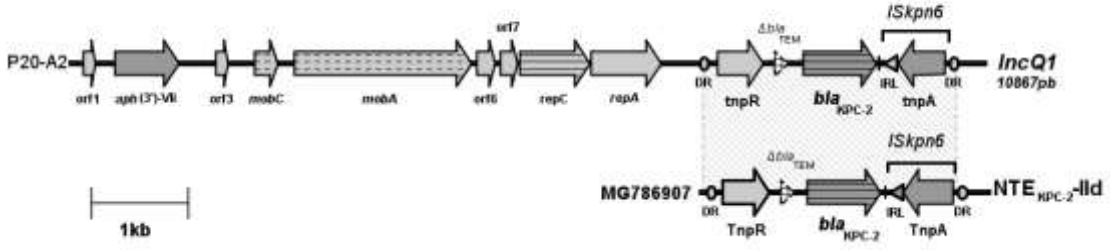
Table 3. Plasmid DNA characterization of *Proteus mirabilis* isolate P20-A2.

Isolated	P20-A2
GC content	47,8%,
Plasmid DNA sequence size	31.899bp
Contigs	27
CDS	33
Found plasmids	IncQ1 Col3M
Resistance Genes	*bla*$_{KPC-2}$ *aph(3')-VI* *qnrD1*
Other genes found in plasmids	*tnpA; tnpR; mobA; mobC; oriV; repA; repC; maze; mazF; traU; higA; dinG*

Source: Authors.

Analysis using the Resfinder and GenBank databases showed 100% identity for the *bla*$_{KPC-2}$, *aph(3')-VI* and *qnrD1* resistance genes in the plasmid DNA of the P20-A2 isolate. Incompatibility replicons were found for plasmid IncQ and a small plasmid from the Col3M family (Figure 1).

Figure 1. Complete sequence of plasmid IncQ1 and non-Tn4401 mobile genetic element (NTE$_{KPC-IId}$) that harbors the *bla*$_{KPC-2}$ gene in the study isolate P20-A2 and comparison with reference sequences from GenBank (NTEKPC-IId:MG786907 (Beltrão et al., 2020)). Protein coding sequences were represented as arrows and marked with the gene name. Gray dashed represents shared homologous regions (>95%) The NTE$_{KPC-IId}$ IR sequence is represented by a circle.



Source: Authors.

The *bla*$_{KPC-2}$ gene was found inserted between the partial IS*Kpn6* insertion sequence (ΔIS*Kpn6*) with an associated left IR (IRL) and *tnpR* resolvase (Figure 1). A 21 bp fragment corresponding to the Δ*bla*$_{TEM}$ gene was found upstream of the *bla*$_{KPC-2}$ gene. When comparing the genetic environment of the bla$_{KPC-2}$ gene with the sequences deposited in GenBank, we observed the NTE$_{KPC-IId}$ variant (GenBank accession number: MG786907) with approximately 100% identity for the isolates.

The other genes *mobA, mobC, oriV, repA, repC, mazE, mazF, traU, higA* and *dinG* were identified using Blast/NCBI.

4. Discussion

In addition to other HAIs, *P. mirabilis* can cause infections in the colonized skin and oral mucosa of hospitalized patients (Wasfi et al., 2020). It can cause serious infections, in addition to contributing to the increase in hospitalization time and the use of various antimicrobials. The patient in the present study acquired infections by *Morganella morganii*, *K. pneumoniae*, *P. mirabilis* (P21-A2), *Acinetobacter baummanii* and *Enterococcus faecalis* in different infection sites, for a period of 103 days. Patients who acquire infections in the hospital have a history of recurrent infections, especially if the hospital stay is prolonged (Wasfi et al., 2020). The most common clinical manifestations caused by *P. mirabilis* are urinary tract infections (UTIs), but little is known about other infections caused by this pathogen, as in the case of the patient in the present study with respiratory tract and tissue infections.

In addition to the establishment of serious infections in the host by pathogenic strains, bacterial resistance to antimicrobials has been a matter of great concern to world health agencies, especially in strains that harbor resistance determinants to carbapenems. The isolates analyzed in the present study harbored resistance determinants, including the *aph(3')-VI*, *aac(6')-Ib* and *bla*$_{OXA-10}$ genes, widely reported in other species such as *K. pneumoniae* or *Pseudomonas aeruginosa* (Firmo et al., 2020).

However, in *P. mirabilis*, these resistance genes are little investigated when compared to other bacterial species. In the present study, clinical characteristics of the patient and genetic and resistance aspects of the two isolated strains were analyzed. Isolate P20-A2 harbored the *bla*$_{KPC-2}$ and *bla*$_{NDM-1}$ genes. The presence of these genes represents a real challenge, since the identification of this resistance phenotype by routine laboratory tests in the hospital does not have the sensitivity of molecular

methods (Beirão et al., 2011). In addition, the available options for treating such infections caused by this species are reduced, as this species has intrinsic resistance to several antimicrobials that could be used alternatively for the treatment of serious infections.

The genetic environment of the bla_{KPC-2} gene has been widely investigated around the world. The Tn4401 transposon is commonly reported to harbor this gene and has been widely studied. To date, this transposon has nine variants named Tn4401a to Tn4401i, differentiated by deletions in its structure. The structure of Tn4401 comprises two *tnpA*, one *tnpR*, the insertion sequences ISKpn6 and ISKpn7, the bla_{KPC} gene and the *istA* and *istB* genes, all these structures help in the transferability of this transposon. In addition to the Tn4401 transposon, other transposons may harbor the bla_{KPC-2} gene, such as the Tn3000 transposon and the non-Tn4401 mobile element (NTE). $NTE_{KPC-IId}$ has been reported in Brazil in K. pneumoniae and *Klebsiella aerogenes*, including in hospitals in Recife-PE, Brazil (Cerdeira et al., 2017; Beltrão et al., 2020; Fuga et al., 2020; Lima et al., 2020). There is evidence that $NTE_{KPC-IId}$ is the variant circulating in Recife harboring the bla_{KPC} gene in *K. pneumoniae* and *K. aerogenes*, together with the plasmid IncQ (Beltrão et al., 2020b; Lima et al., 2020; Oliveira et al., 2020). Since bla_{KPC} is widely disseminated in our country (Almeida et al., 2012; Pereira et al., 2013, 2015; Dalmolin et al., 2018; Oliveira et al., 2020). In addition, $NTE_{KPC-IId}$ may decrease or enhance the spread of bla_{KPC} (Beltrão et al., 2020). In addition, to our knowledge $NTE_{KPC-IId}$ has not yet been reported in *P. mirabilis*.

Plasmid IncQ1 found in isolate P20-A2 is a small, promiscuous, non-conjugative plasmid. However, this plasmid has the ability to bind to conjugative plasmids at the time of conjugation, which can facilitate its dissemination in pathogenic bacteria of the same species and different species (Beltrão et al., 2020; Lima et al., 2020; Oliveira et al., 2020). In addition to plasmid IncQ1, a small plasmid belonging to the Col3M family was found harboring the qnrD1 gene, which confers resistance to quinolones, in isolate P20-A2. The presence of *qnrD* transported by plasmid Col3M has been little reported, what is known is that the *qnrD* gene is widely disseminated in *P. mirabilis* isolates causing infections in humans and animals (Sanches et al., 2019). Plasmid-mediated resistance mechanisms are of concern as they have a greater capacity to spread by horizontal gene transfer (Rozwandowicz *et al.*, 2018; Lerminiaux e Cameron, 2019).

5. Conclusion

In conclusion, although *P. mirabilis* is gaining prominence as a cause of nosocomial infections and resistant multidrug pathogen, this species is still neglected. The emergence of these *P. mirabilis* isolates harboring resistance determinants such as *qnrD1*, bla_{KPC-2}, bla_{NDM-1}, *aph(3')-VI*, *aac(6')-Ib* and bla_{OXA-10} and the plasmids IncQ and Col3M demonstrates the potential for dissemination of important resistance genes, especially in the case of *P. mirabilis*. Additionally, the mobile genetic element $NTE_{KPC-IId}$, together with IncQ may be related to the high spread of the bla_{KPC} gene in Recife. Co-infections can contribute to a poor prognosis, especially in immunocompromised patients with prolonged hospitalization, as in the present study. Additionally, further studies are needed on the transferability of the non-Tn4401 mobile element ($NTE_{KPC-IId}$) and investigations of the genetic environment of the bla_{KPC} gene in other circulating isolates from Pernambuco.

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Conflict of interest

The authors declare that there are conflicts of interest.

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