BMC Genomics

RESEARCH Open Access

Characterization of a novel multi-resistant *Pseudomonas juntendi* strain from China with chromosomal bla_{VIM-2} and a megaplasmid coharboring $bla_{IMP-1-like}$ and bla_{OXA-1}

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Abstract

Background *Pseudomonas juntendi* is a newly identified opportunistic pathogen, of which we have limited understanding. *P. juntendi* strains are often multidrug resistant, which complicates clinical management of infection.

Methods A strain of *Pseudomonas juntendi* (strain L4326) isolated from feces was characterized by MALDI-TOF-MS and Average Nucleotide Identity BLAST. This strain was further subject to whole-genome sequencing and Maximum Likelihood phylogenetic analysis. The strain was phenotypically characterized by antimicrobial susceptibility testing and conjugation assays.

Results We have isolated the novel *P. juntendi* strain L4236, which was multidrug resistant, but retained sensitivity to amikacin. L4236 harbored a megaplasmid that encoded bla_{OXA-1} and a novel bla_{IMP-1} resistance gene variant. *P. juntendi* strain L4236 was phylogenetically related to *P. juntendi* strain SAMN30525517.

Conclusion A rare *P. juntendi* strain was isolated from human feces in southern China with a megaplasmid coharboring $bla_{IMP-1-like}$ and bla_{OXA-1}. Antimicrobial selection pressures may have driven acquisition of drug-resistance gene mutations and carriage of the megaplasmid.

Keywords *Pseudomonas juntendi*, $bla_{IMP-1-like}$, bla_{OXA-1}, bla_{VIM-2}, Average nucleotide identity, Phylogenetics

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Background

In recent years, novel members of the genus *Pseudomonas* have been described due to the development of identification techniques [1]. The *Pseudomonas putida* group (*P. putida* G) consists of over 21 environmental species, which are largely sensitive to antibiotics [2]. However, in recent years, *P. putida* G strains harboring resistance genes have been detected. *Pseudomonas juntendi* is an understudied member of the *putida* group. In Brazil, a carbapenem-resistant *P. juntendi* clinical isolate harboring bla_{BKC-1} was recently reported [3]. Similarly, a carbapenem-resistant *P. juntendi* urine isolate encoding bla_{IMP-1} was identified in China [4]. A *P. juntendi* strain isolated from a farm in China was found to encode tmexCD3-toprJ3 [5], and a metallo-β-lactamase (MBLs) producing strain isolated from Poland was found to belong to the MBL-producing *P. putida* (MPPP) group [6].

MBLs are well known determinants of carbapenem resistance, and consist of NDM, VIM, IMP, AIM, SPM, DIM, KPC, and OXA variants [7]. VIM and IMP belong to Class B, while OXA belongs to Class D, in accordance with the classification proposed by Ambler [8]. Acquisition of carbapenemase genes are not random with respect to strain phylogeny [9]. Most IMP variants can be expressed in conjunction with other drug-resistance genes, and more than 29 IMP variants have been identified in clinically important Gram-negative bacilli [10]. First detected in Japan in 1994 [11], IMP-1 shares a comparable capacity as NDM-1 for hydrolyzing meropenem [12]. VIM-2 is a soluble MBL [13], which was identified in a strain isolated from a Portuguese patient in 1995 [14]. Members of *P. putida* G have been suggested to be a reservoir of bla_{VIM-2} genes [15]. Furthermore, OXA, first identified in the 1960s [16], promotes resistance to aminopenicillins and ureidopenicillin, and displays high-level capacity to hydrolyze oxacillin, methicillin, and cloxacillin [17]. Antibiotic resistance genes can integrate into plasmids which are then acquired by clinical pathogens, leading to difficulties in clinical management, and a substantial burden on world health [18].

Our study has identified a novel *Pseudomonas juntendi* strain, L4326, which co-harbors $bla_{IMP-1-like}$, bla_{OXA-1} genes on a large plasmid, and bla_{VIM-2} gene on a chromosome. We also identified a novel variant of IMP-1 (IMP-1-like), and provide mechanistic insights into the development of drug resistance in this emerging pathogen.

Materials and methods

Strain identification and antimicrobial susceptibility testing (AST)

A strain was isolated from the feces of a patient at a teaching hospital in the Zhejiang province, China. The isolate was characterized as *Pseudomonas juntendi* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS) (Bruker Daltonik, Bremen, Germany) [19], and Basic Local Alignment Search Tool (BLAST) analysis, and was designated strain L4326.

Subsequently, AST [20] was performed by broth microdilution for polymyxin B, or agar dilution for other drugs, according to the criteria of the Clinical and Laboratory Standards Institute (CLSI) and the European Committee on Antimicrobial Susceptibility Testing (EUCAST). *Escherichia coli* ATCC25922 and *Pseudomonas aeruginosa* ATCC27853 were used as control strains. *P. juntendi* L4326 plated on Mueller-Hinton (MH) agar medium was incubated at 37℃ for 20 h, and the minimum inhibitory concentrations were taken as the first concentration to inhibit growth.

Bacterial whole-genome sequencing and downstream analysis

Total DNA from *P. juntendi* L4326 was extracted using the QIAamp DNA Microbiome kit (QIAamp, Germany) according to the manufacturer's instructions. Genome sequencing was performed using the Illumina NovaSeq 6000 (Illumina, San Diego, CA, United States), and Oxford Nanopore sequencing (Oxford Nanopore Technologies, Oxford, UK) platforms. The whole genome was assembled with Unicycler v0.4.7, and coding sequences were annotated using Prokka v1.14.5. Acquired antimicrobial resistance (AMR) genes were identified using ResFinder 4.1 (https://cge.cbs.dtu.dk/services/ResFinder/), and virulence genes were identified using the Virulence factor database (VFDB) (http://www.mgc.ac.cn/). PlasmidFinder (https://cge.cbs.dtu.dk/services/PlasmidFinder/) was used to characterize plasmid types present in the genome sequence. The genetic context of $bla_{IMP-1-like}$, bla_{OXA-1}, and bla_{VIM-2} were visualized with Easyfig 2.3 (http://mjsull.github.io/Easyfig/files.html). Analysis of the plasmid from *P. juntendi* L4326 was performed by BLAST Ring Image Generator (BRIG) (http://sourceforge.net/projects/brig/). Maximum likelihood phylogenetic analysis of gene and protein sequences was performed using MEGAX (version 10.1.7), following ClustalW alignment of sequences, and the resulting tree was visualized using the Interactive Tree of Life (iTOL, https://itol.embl.de).

The average nucleotide identity based on BLAST (ANIb)

Analysis of *P. juntendi* L4326 taxonomy by ANIb was performed using pyani stools (v. 0.2.3) [21]. Whole-genome alignments were generated by nucleotide BLAST (BLASTN) [22]. After pairwise alignment, the percent nucleotide identity of all genomes was subject to hierarchical clustering by a Euclidean distance metric. A

heatmap was generated including *P. juntendi* L4326 and nine reference strains, where the color scale bar indicates ANI percentages from 75% (blue) to 100% (red), and 95% identity was considered the threshold of a species boundary.

Maximum likelihood phylogenetic analysis

Phylogenetic analysis was performed using a General Time Reversible model and the Maximum Likelihood method. The evolutionary relationship between each taxon was discerned from a consensus tree derived from 1000 bootstrap replicates. MEGA11 [23] was used to generate an initial tree using BioNJ and Neighbor-Joining algorithms from a matrix of pairwise distances. The tree topology was refined using the superior log likelihood value through the Maximum Composite Likelihood approach [24]. Model evolutionary rate differences between sites (5 categories; +G, parameter = 0.0500) were estimated by discrete Gamma distribution.

Conjugation experiments

E. coli J53 was used as a recipient strain for conjugation experiments as previously described [25]. Briefly, 200 mg/L sodium azide (NaN_3) and 2 mg/L meropenem were dissolved in MH broth (OXOID, Hampshire, UK). The broth was subsequently inoculated with *P. juntendi* L4326 and the recipient strain, before culturing until the logarithmic growth phase. Plasmid conjugation was determined using a PCR-based method.

Results

Isolation and identification of *Pseudomonas juntendi* L4326

Fresh fecal samples were plated on MacConkey Agar Medium supplemented with meropenem. Multiple resulting colonies were present after 18 h growth at 37 °C. MALDI-TOF/MS analysis revealed that one of these strains belonged to the genus *Pseudomonas*. ANIb analysis (Fig. 1) subsequently revealed high degrees of similarity between this isolate and *P. juntendi* PP 2463 SAMN24966705. Conversely, the ANIb percentage identity of our isolate with other strains within the *Pseudomonas* genus was low. We therefore named this strain *Pseudomonas juntendi* L4326.

AST of this strain indicated a multidrug-resistant phenotype (Table 1), with detected resistance to piperacillin/tazobactam, ceftazidime, cefepime, imipenem, meropenem, ceftazidime/avibactam, aztreonam, polymyxin B, gentamicin, levofloxacin, and ciprofloxacin. This strain was however sensitive to amikacin.

Genomics features of *P. juntendi* L4326 and comparison to other *P. juntendi* strains

P. juntendi L4326 consists of a 5,403,450 bp chromosome and a 501,858 bp large plasmid, with a total GC content of 61.7%. Interestingly, we detected no similarity of this large plasmid to other plasmids in public databases (Fig. 2). Both a novel 250 kbp-length drug resistance gene named $bla_{IMP-1-like}$ and a known drug resistance gene named bla_{OXA-1} were located on this giant plasmid. As expected, horizontal transfer of the large plasmid was undetected using our conjugation assay.

Comparison of L4326 to 40 previously described *P. juntendi* strains worldwide, revealed high degrees of similarity to *P. juntendi* strain SAMN30525517, which was isolated in America and may represent a source of transmission (Fig. 3).

Genetic context of the *IMP-1-like* gene

To further verify the novel *IMP* allele detected in strain L4326, we analyzed both the genomic sequence and protein structure of *IMP* 1-100 (http://bldb.eu/BLDB.php?prot=B1#IMP). The protein structure of L4326-IMP was the same as *IMP-1* (Fig. 4A). By comparing the SNP differences, we found that the protein SNPs of *IMP-1-like* and *IMP-1* are identical, but its gene sequence is closest to *IMP-79* and *IMP-98*, with 3 SNP differences. The gene sequence revealed that L4326-IMP was a novel antibiotic resistance gene with high degrees of gene homology to *IMP*-79 and *IMP*-98 (Fig. 4B). Together, this indicates that we have identified a new mutant gene named *IMP-1-like* encoded on a novel megaplasmid.

The genetic context of *IMP-1-like* and *VIM-2* was predicted through comparison of related *IMP-1* (Fig. 5A) and *VIM-2* (Fig. 5B) genes in the NCBI database. *IMP-1-like* (L4326-IMP) shared sequence similarity with *Pseudomonas sp*. NY11382 plasmid pNY11382-IMP (CP097104), *Pseudomonas putida* strain NY5709 plasmid pNY5709-IMP (MN961670), and *Pseudomonas putida* strain ZXPA-20 plasmid pZXPA-20-602k (CP061724). Among these, we considered that the

Table 1 AST results of *Pseudomonas Juntendi* L4326

Classification	Subclassification	Antimicrobials	MIC values	R/S
β-lactamases	Penicillins	Piperacillin/Tazobactam	64/4	R
	Cephalosporins	Ceftazidime	32	R
		Cefepime	64	R
	carbapenems	Imipenem	> 32	R
		Meropenem	> 32	R
	β-Lactamaseinhibitors	Ceftazidime/avibactam	8/4	I
	monobactams	Aztreonam	64	R
polypeptides	polypeptides	Polymixin B	1	I
aminoglycosides	aminoglycosides	Amikacin	4	S
		Gentamicin	64	R
Synthetic antibacterial agents	quinolones	Levofloxacin	16	R
		Ciprofloxacin	8	R

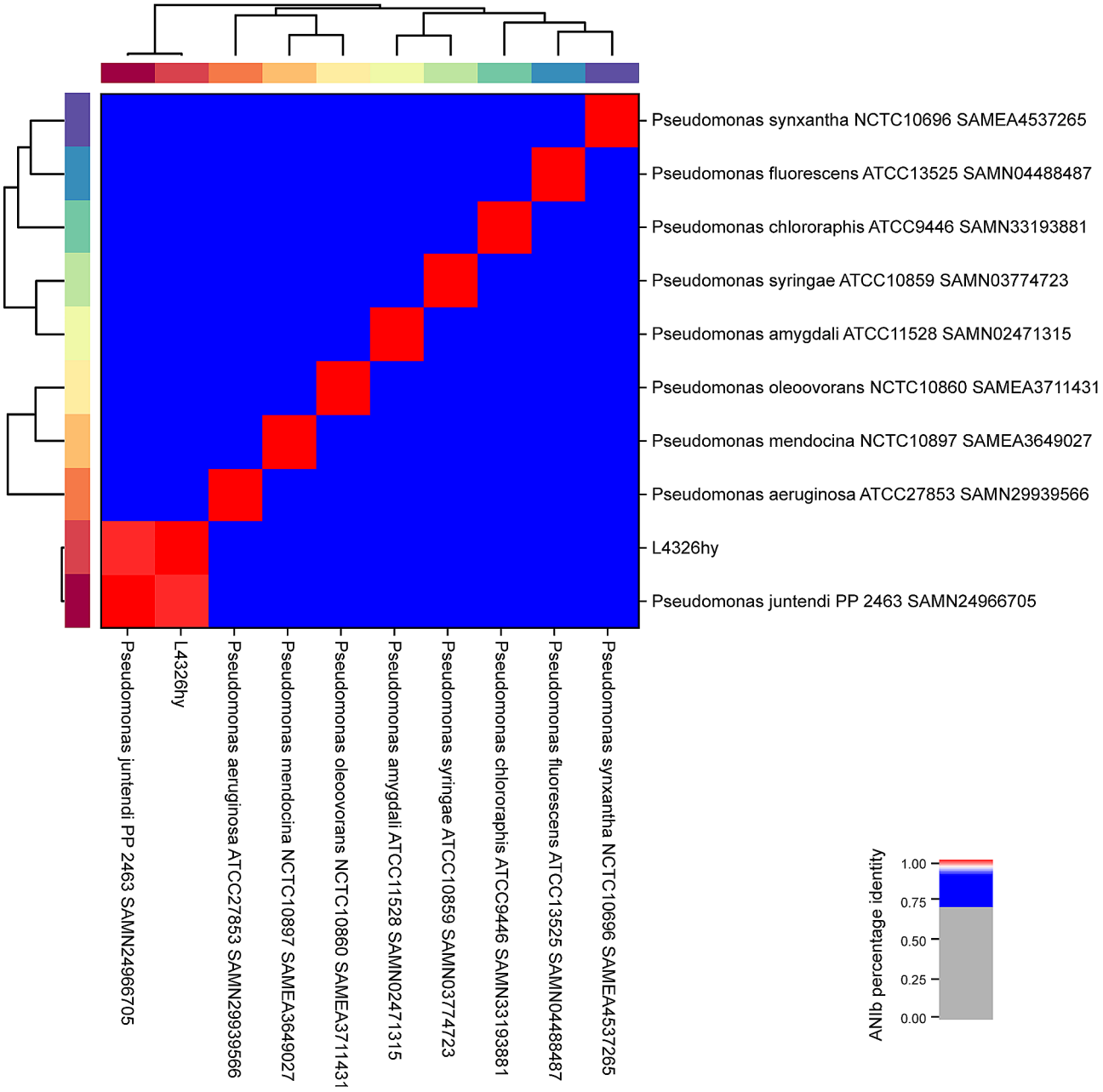

Fig. 1 A heatmap displaying ANIb scores between *P. juntendi* L4326 and eight reference strains of the genus *Pseudomonas*. ANIb percentage identities below 0.7 are gray, while a gradient of blue to red indicates values from 0.7 to 1

genetic organization of "*TnAs1-xerC-bla*$_{\text{IMP-1-like}}$*-aacA4-bla*$_{\text{OXA-1}}$*-ant1-emrE*" may have arisen from "*TnAs1-xerC-bla*$_{\text{IMP-34}}$*-emrE*" through insertion of the antibiotic resistance gene "*bla*$_{\text{OXA-1}}$" via an integrating mobile element exploiting the *xerC* site and Xer (IMEX) recombination [26]. EmrE belongs to the Small Multidrug Resistance (SMR) transporter family, which may promote further drug resistance [27]. In addition, *VIM-2* (L4326-VIM) had a comparable genetic context to that of *Pseudomonas putida* strain NY5709 plasmid pNY5709-IMP (MN961670), *Pseudomonas fulva* strain ZDHY316 plasmid pVIM-24-ZDHY316 (CP064945), and *Pseudomonas* sp. NY11382 plasmid pNY11382-IMP (CP097104).

Discussion

We have isolated and characterized a novel strain of *Pseudomonas juntendi* carrying a giant plasmid coharboring *bla*$_{\text{IMP-1-like}}$ and *bla*$_{\text{OXA-1}}$ and a chromosomal copy of *bla*$_{\text{VIM-2}}$. In addition to the first isolation of a *P. juntendi* strain from a clinical sample in southern China, we also identified *IMP-1-like*, a novel resistance gene.

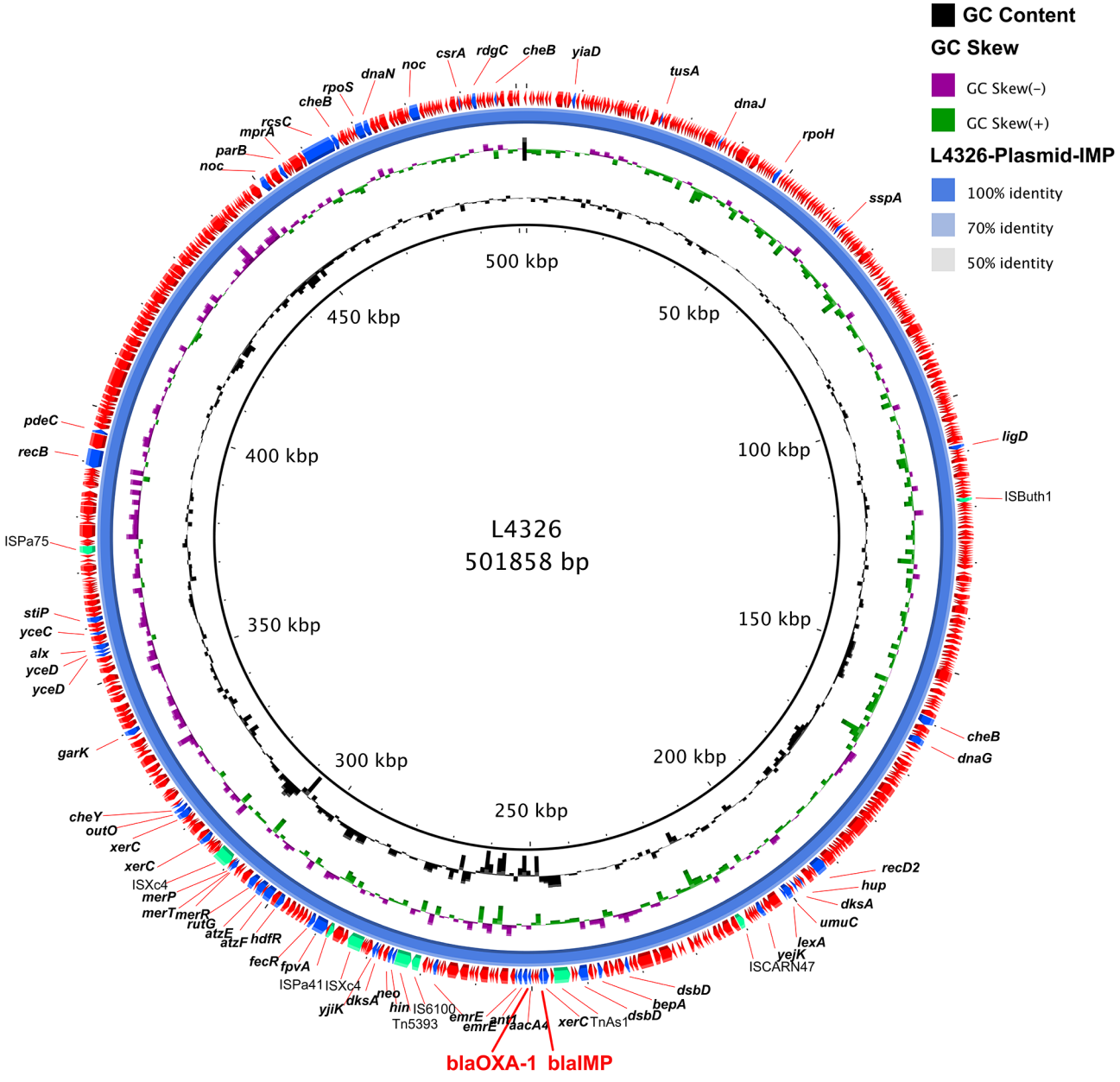

Fig. 2 Map of the megaplasmid from *P. juntendi* L4326 coharboring $bla_{IMP-1-like}$ and bla_{OXA-1} genes. The two inner circles indicate the GC content and skew, while the outer circle represents key genes. Red represents hypothetical proteins, green represents mobile elements, and blue represents AMR and other genes

The genus *Pseudomonas* are not typically considered constituents of the healthy gut microbiome [28], and are associated with intestinal infection and intestinal barrier dysfunction [29]. 79% of *Pseudomonas* strains from humans in a previous study from Ethiopia were MDR [30]. Within the genus, *P. juntendi* are not a commonly isolated species in the clinic. Tohya M et al. [31]. first identified and officially named *P. juntendi* in 2019. The first clinical isolate of *P. juntendi* was isolated in northern China in 2022 [4]. We have subsequently identified *P. juntendi* strain L4326 in southern China carrying a large plasmid encoding the $bla_{IMP-1-like}$ gene. There are currently 40 described strains of *P. juntendi* worldwide, seven of which were isolated in China. *P. juntendi* L4236, however, shows high degrees of sequence similarity with *P. juntendi* SAMN30525517, which was isolated in America, indicating that our strain may have been introduced to China through migration. The *P. juntendi* L4326 plasmid is larger than previously described plasmids, and notably encoded multiple antibiotic resistances genes including $bla_{IMP-1-like}$ and bla_{OXA-1}. The World Health Organization (WHO) has indicated that critically

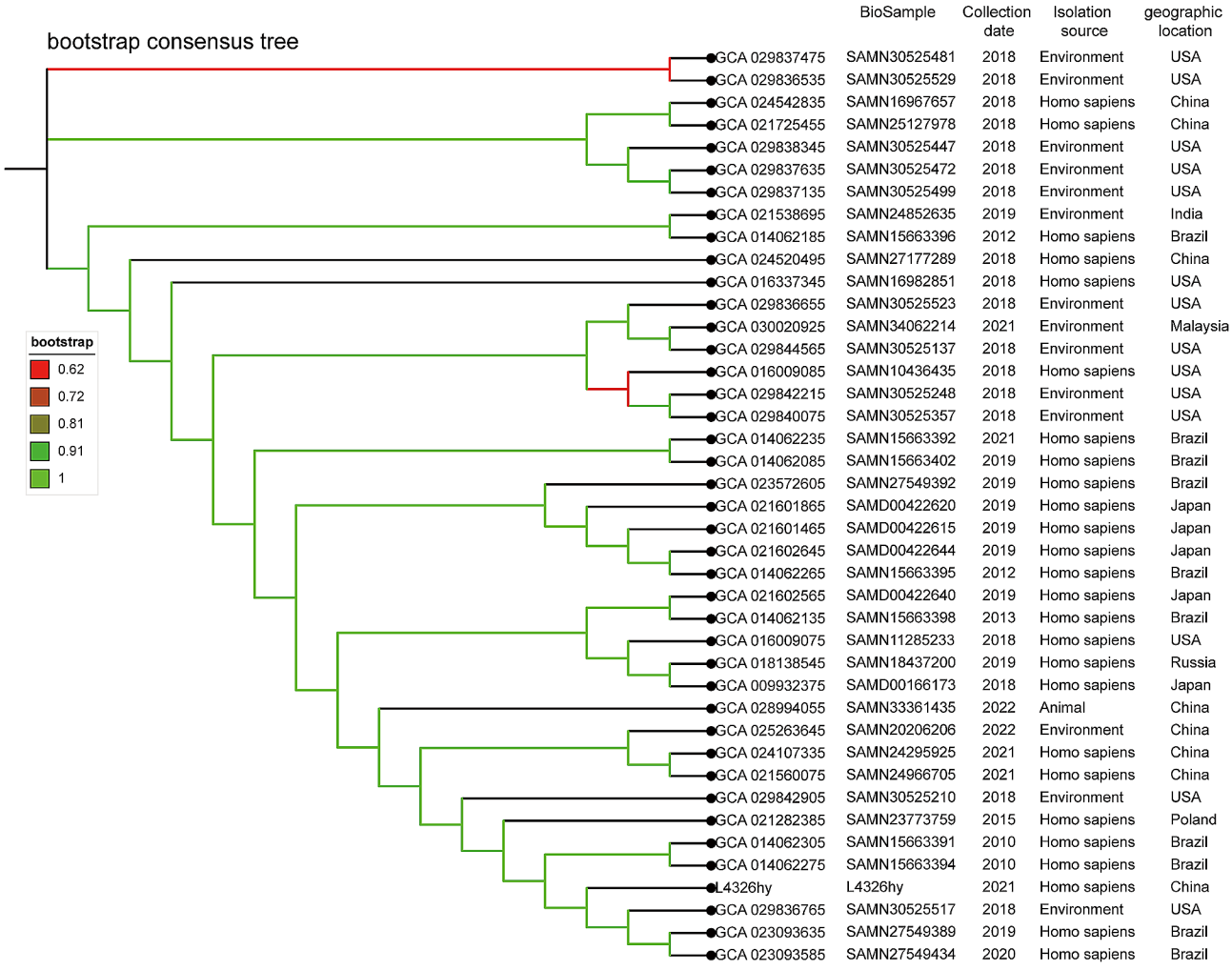

Fig. 3 Maximum-likelihood phylogenetic tree of *P. juntendi* L4326 and 40 other *P. juntendi* isolates. The tree was discerned from an alignment generated using Roary. Branches are colored based on bootstrap support values from red (0.62) to green [1] using the Maximum Composite Likelihood approach. Sample type, collection date, isolation source, and geographic location are indicated

important pathogens such as those of the genus *Pseudomonas* are often isolated from clinical infections and display resistance to last-resort antibiotics including colistin [32]. Drug resistance is an enormous burden on public health and government financial expenditure [33]. While *P. juntendi* L4326 showed resistance to multiple antibiotics, this strain remained susceptible to amikacin.

P. juntendi is considered a potential hazard due to expression of bla_{IMP} and bla_{VIM} which promote carbapenem resistance [4]. Since its earliest detection in a strain of *Pseudomonas aeruginosa* in Japan [34], up to 100 *IMP-1* variants have been described. Expression of the *IMP-1* metallo-β-lactamase is a major determinant of decreased antibiotic sensitivity [35]. Compared with *IMP 1-100*, IMP-1-like protein of *P. juntendi* L4326 is the same as IMP-1 protein, while *IMP-1-like* gene of *P. juntendi* L4326 is similar as *IMP-1* gene, which manifested the fact that *IMP-1-like* might be shifted from *IMP-1*. Drug-resistance genes are prone to the accumulation of mutations under antibiotic selection pressure. The continuing emergence of novel drug-resistance genes is a further reminder that we should consider the rational use of antibiotics.

P. juntendi L4326 encodes not only *IMP-1-like*, but also *VIM-2*. The existence of $bla_{\mathrm{VIM-2}}$ in *P. juntendi* L4326 indicate that *P. putida* G complex serves as a reservoir for $bla_{\mathrm{VIM-2}}$ which may spread to other clinically relevant pathogens [15].

Together, our findings clearly highlight that both the rapid spread of *P. juntendi* in China, and the emergence of antibiotic resistance gene mutations under selection pressure warrant careful monitoring.

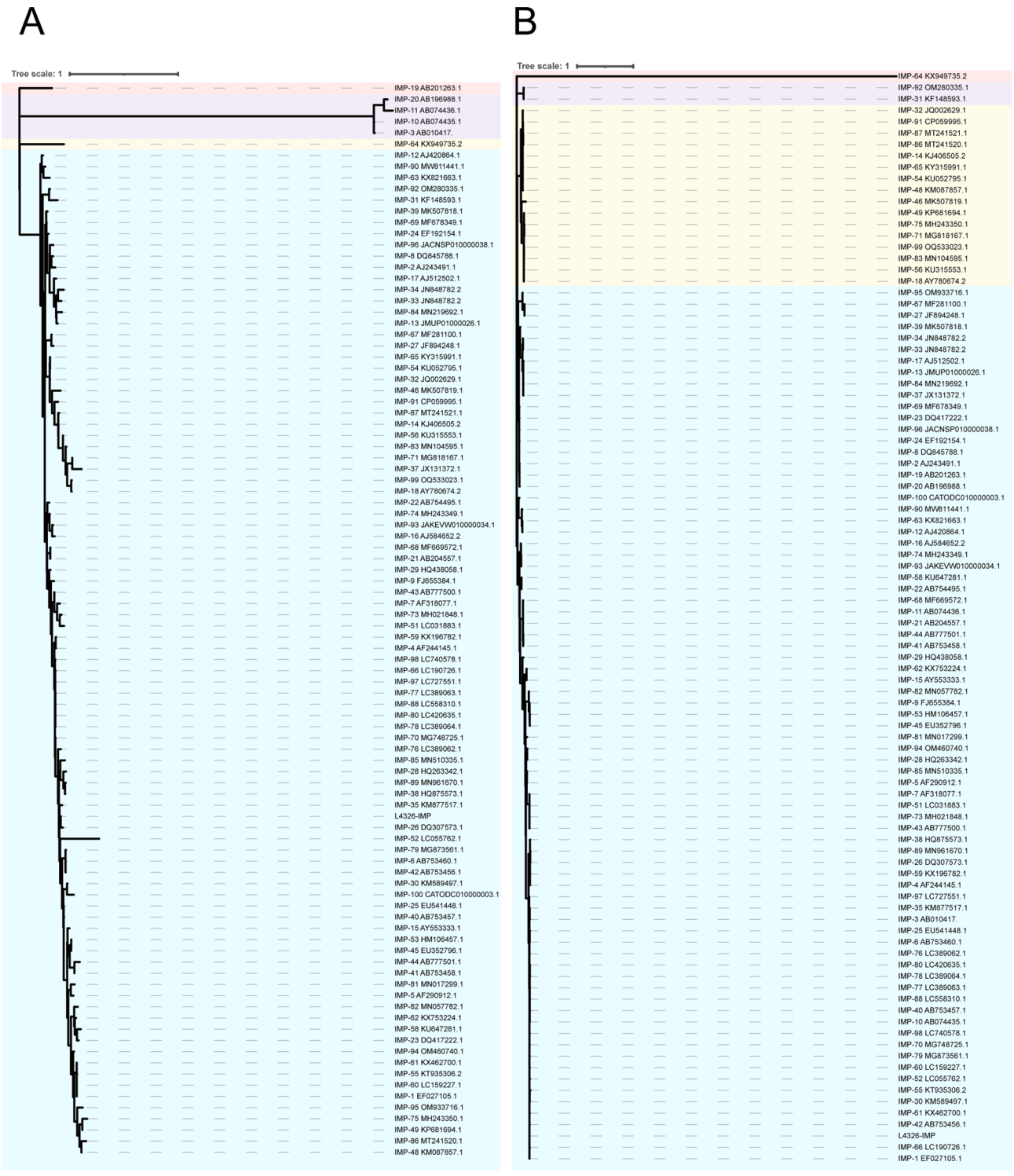

Fig. 4 Phylogenetic tree of IMP protein (A) and gene (B) sequences visualized using Interactive Tree of Life. The protein and gene sequences of IMP 1-100 and L4326-IMP were subject to BLAST analysis, and different colors indicate branch regions of interest. The location and origin of L4326-IMP are shown

Conclusion

We isolated a strain of *P. juntendi* encoding a novel *IMP-1-like* gene from a patient in southern China. This strain contains both a 501,858 bp megaplasmid coharboring $bla_{\text{IMP-1-like}}$ and $bla_{\text{OXA-1}}$, and a chromosomal copy of $bla_{\text{VIM-2}}$. These findings indicate the rapid transmission of *P. juntendi* in China, and highlight the need to monitor emergence of novel drug-resistance mutations.

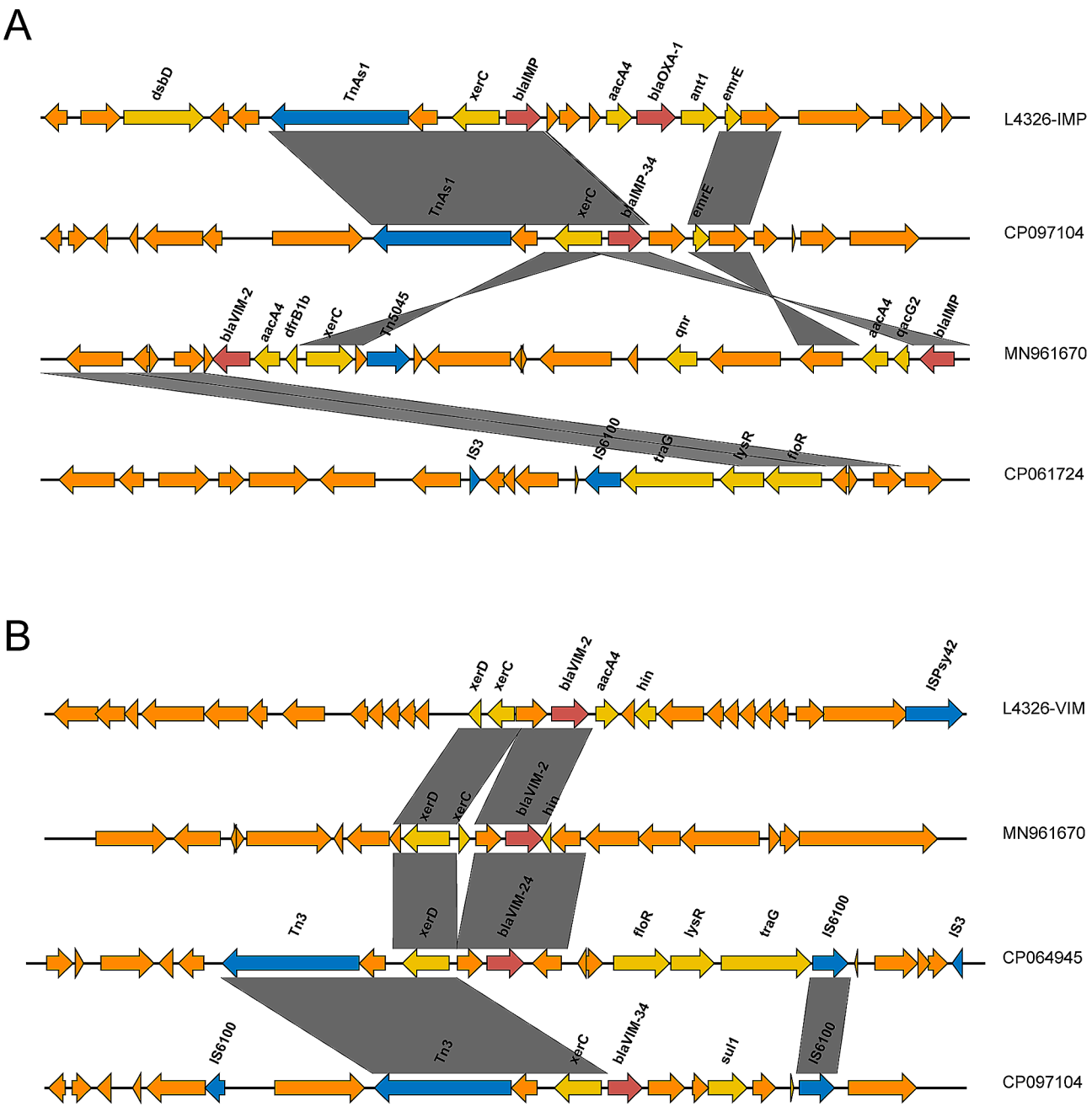

Fig. 5 The genetic context of $bla_{IMP-1-like}$ (**A**) and bla_{VIM-2} (**B**) compared with three similar plasmids. Red arrows indicate bla_{IMP-1} and bla_{VIM-2}, while blue arrows indicate insertion sequences (IS) and transposons (Tn). Gray shading represents a high degree of homology among these plasmids

Abbreviations

AMR	Acquired antimicrobial resistance
ANIb	Average Nucleotide Identity based on BLAST
AST	Antimicrobial susceptibility testing
BLAST	Basic Local Alignment Search Tool
BRIG	BLAST Ring Image Generator
CLSI	Clinical and Laboratory Standards Institute
EUCAST	European Committee on Antimicrobial Susceptibility Testing
IMEX	Integrating mobile element exploiting Xer
MALDI-TOF-MS	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
MBLs	Metallo-β-lactamases
MCL	Maximum Composite Likelihood
MDR	Multi-drug resistance
MH	Mueller-Hinton
MICs	Minimum inhibitory concentrations
MPPP	MBL-producing P. putida
NaN_3	Sodium azide
SMR	Small Multidrug Resistance
VFDB	Virulence factor database
WHO	World Health Organization

Acknowledgements
We are grateful to the reviewers who helped to improve this paper.

Author contributions
SMJ and YLL did conceptualization, methodology, experiment execution, and writing; KFB prepared statistical analysis, reviewing and editing; SSY, HX, SJL, and HC prapred editing; LJL is responsible for funding acquisition and supervision. All authors read and gave permission for the manuscript.

Funding
This work was supported by the Fundamental Research Funds for the Central Universities, grant No. 2022ZFJH003.

Data availability
Sequencing data of Pseudomonas juntendi L4326 are available from the NCBI database under sample accession number SAMN37524096.

Declarations

Ethical approval
All experimental protocols were approved by Ethics Committee of the First Affiliated Hospital, Zhejiang University School of Medicine (Issuing number: IIT20200594A). Informed consent was waived by Ethics Committee of the First Affiliated Hospital of Zhejiang University School of Medicine due to the study's observational nature mainly focused on bacteria and did no interventions to patients, additionally, patient information was anonymized. All experiments were performed in compliance with the relevant laws and institutional guidelines in accordance with the ethical standards of the Declaration of Helsinki.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

Received: 28 March 2024 / Accepted: 5 August 2024
Published online: 08 August 2024

References

1. Girard L, Lood C, Hofte M, Vandamme P, Rokni-Zadeh H, van Noort V, et al. The ever-expanding Pseudomonas Genus: description of 43 new species and partition of the Pseudomonas putida group. Microorganisms. 2021;9(8). https://doi.org/10.3390/microorganisms9081766. Epub 2021/08/28.
2. Passarelli-Araujo H, Jacobs SH, Franco GR, Venancio TM. Phylogenetic analysis and population structure of Pseudomonas Alloputida. Genomics. 2021;113(6):3762–73. https://doi.org/10.1016/j.ygeno.2021.09.008. Epub 2021/09/17.
3. Alberto-Lei F, Nodari CS, Streling AP, Bessa-Neto FO, Siqueira AV, Cayo R, et al. Characterization of a Carbapenem-resistant BKC-1-producing clinical isolate belonging to the Pseudomonas putida group from Brazil. Antimicrob Agents Chemother. 2022;66(12):e0083922. https://doi.org/10.1128/aac.00839-22. Epub 2022/11/16.
4. Zheng L, Zhang X, Zhu L, Lu G, Guan J, Liu M, et al. A clinical Pseudomonas juntendi strain with bla (IMP-1) carried by an integrative and conjugative element in China. Front Microbiol. 2022;13:929800. https://doi.org/10.3389/fmicb.2022.929800. Epub 2022/08/16.
5. Yang J, Zeng Z, Hu J, Liu Z, Gu J, Chen X, et al. Emergence of the resistance-nodulation-division efflux pump tmexCD3-toprJ3 gene confers resistance to tigecycline in Pseudomonas Juntendi and Proteus terrae isolated from a pig farm in China. Vet Med Sci. 2022;8(6):2460–5. https://doi.org/10.1002/vms3.950. Epub 2022/09/22.
6. Urbanowicz P, Izdebski R, Biedrzycka M, Literacka E, Hryniewicz W, Gniadkowski M. Genomic epidemiology of MBL-producing Pseudomonas putida group isolates in Poland. Infect Dis Ther. 2022;11(4):1725–40. https://doi.org/10.1007/s40121-022-00659-z. Epub 2022/06/11.
7. Karampatakis T, Antachopoulos C, Tsakris A, Roilides E. Molecular epidemiology of carbapenem-resistant Pseudomonas aeruginosa in an endemic area: comparison with global data. Eur J Clin Microbiol Infect Dis. 2018;37(7):1211–20. https://doi.org/10.1007/s10096-018-3244-4. Epub 2018/04/13.
8. Taggar G, Attiq Rheman M, Boerlin P, Diarra MS. Molecular epidemiology of carbapenemases in enterobacteriales from humans, animals, food and the environment. Antibiot (Basel). 2020;9(10). https://doi.org/10.3390/antibiotics9100693. PubMed PMID: 33066205; PubMed Central PMCID: PMCPMC7602032. Epub 2020/10/18.
9. Fortunato G, Vaz-Moreira I, Gajic I, Manaia CM. Insight into phylogenomic bias of bla(VIM-2) or bla(NDM-1) dissemination amongst carbapenem-resistant Pseudomonas aeruginosa. Int J Antimicrob Agents. 2023;61(5):106788. https://doi.org/10.1016/j.ijantimicag.2023.106788. Epub 2023/03/17.
10. Zhao WH, Hu ZQ. IMP-type metallo-beta-lactamases in Gram-negative bacilli: distribution, phylogeny, and association with integrons. Crit Rev Microbiol. 2011;37(3):214–26. 2011.559944. PubMed PMID: 21707466.
11. Senda K, Arakawa Y, Nakashima K, Ito H, Ichiyama S, Shimokata K, et al. Multifocal outbreaks of metallo-beta-lactamase-producing Pseudomonas aeruginosa resistant to broad-spectrum beta-lactams, including carbapenems. Antimicrob Agents Chemother. 1996;40(2):349–53. PubMed PMID: 8834878; PubMed Central PMCID: PMCPMC163114.
12. Cheung CHP, Alorabi M, Hamilton F, Takebayashi Y, Mounsey O, Heesom KJ, et al. Trade-offs between antibacterial resistance and fitness cost in the production of metallo-beta-lactamases by enteric bacteria manifest as sporadic emergence of carbapenem resistance in a clinical setting. Antimicrob Agents Chemother. 2021;65(8):e0241220. https://doi.org/10.1128/AAC.02412-20. Epub 2021/05/12.
13. Lopez C, Ayala JA, Bonomo RA, Gonzalez LJ, Vila AJ. Protein determinants of dissemination and host specificity of metallo-beta-lactamases. Nat Commun. 2019;10(1):3617. https://doi.org/10.1038/s41467-019-11615-w. Epub 2019/08/11.
14. Walsh TR. The emergence and implications of metallo-beta-lactamases in Gram-negative bacteria. Clin Microbiol Infect. 2005;11(Suppl 6):2–9. https://doi.org/10.1111/j.1469-0691.2005.01264. Epub 2005/10/08.
15. Brovedan MA, Marchiaro PM, Diaz MS, Faccone D, Corso A, Pasteran F, et al. Pseudomonas putida group species as reservoirs of mobilizable Tn402-like class 1 integrons carrying bla(VIM-2) metallo-beta-lactamase genes. Infect Genet Evol. 2021;96:105131. https://doi.org/10.1016/j.meegid.2021.105131. Epub 2021/11/09.
16. Meng L, Liu Z, Liu C, Li C, Shen H, Cao X. The distribution characteristics of global blaOXA-carrying Klebsiella pneumoniae. BMC Infect Dis. 2023;23(1):182. https://doi.org/10.1186/s12879-023-08156-5. Epub 2023/03/30.
17. Naas T, Nordmann P. OXA-type beta-lactamases. Curr Pharm Des. 1999;5(11):865–79. Epub 1999/12/14. PubMed PMID: 10539993.
18. Walsh TR. Combinatorial genetic evolution of multiresistance. Curr Opin Microbiol. 2006;9(5):476–82. https://doi.org/10.1016/j.mib.2006.08.009. Epub 2006/09/01.
19. Qiao J, Chen Y, Ge H, Xu H, Guo X, Liu R, et al. Coexistence of bla(IMP-4), bla(NDM-1) and bla(OXA-1) in bla(KPC-2)-producing Citrobacter freundii of clinical origin in China. Front Microbiol. 2023;14:1074612. https://doi.org/10.3389/fmicb.2023.1074612. Epub 2023/06/28.
20. Liu R, Xu H, Zhao J, Hu X, Wu L, Qiao J, et al. Emergence of mcr-8.2-harboring hypervirulent ST412 Klebsiella pneumoniae strain from pediatric sepsis: a comparative genomic survey. Virulence. 2023;14(1):233–45. PubMed PMID: 36529894; PubMed Central PMCID: PMCPMC9794005.
21. Widada J, Damayanti E, Mustofa M, Dinoto A, Febriansah R, Hertiani T. Marine-derived streptomyces sennicomposti gmy01 with anti-plasmodial and anticancer activities: genome analysis, in vitro bioassay, metabolite profiling, and molecular docking. Microorganisms. 2023;11(8). https://doi.org/10.3390/microorganisms11081930. PubMed PMID: 37630491; PubMed Central PMCID: PMCPMC10458361. Epub 2023/08/26.
22. Yang Y, Yang X, Zhang Y, Ren Z, Zhong J, Hu Q et al. First report of Fusarium cugenangense causing root rot of tea plants (Camellia sinensis) in China. Plant Dis. 2023. Epub 2023/09/20. https://doi.org/10.1094/PDIS-06-23-1172-PDN. PubMed PMID: 37729648.
23. Tamura K, Stecher G, Kumar S. MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol. 2021;38(7):3022–7. https://doi.org/10.1093/molbev/msab120. Epub 2021/04/24.
24. Jiang Q, Wei Y, Huang Y, Jiang H, Guo Y, Lan G, et al. The complete mitochondrial genome and phylogenetic analysis of the Debao pony (Equus caballus). Mol Biol Rep. 2011;38(1):593–9. https://doi.org/10.1007/s11033-010-0145-8. Epub 2010/04/15.
25. Ge H, Qiao J, Zheng J, Xu H, Liu R, Zhao J, et al. Emergence and clonal dissemination of KPC-3-producing Pseudomonas aeruginosa in China with an IncP-2 megaplasmid. Ann Clin Microbiol Antimicrob. 2023;22(1):31. https://doi.org/10.1186/s12941-023-00577-z. Epub 2023/04/30.

26. Cameranesi MM, Morán-Barrio J, Limansky AS, Repizo GD, Viale AM. Site-specific recombination at XerC/D sites mediates the formation and resolution of plasmid co-integrates carrying a bla(OXA-58)- and TnaphA6-resistance module in Acinetobacter baumannii. Front Microbiol. 2018;9:66. https://doi.org/10.3389/fmicb.2018.00066. Epub 2018/02/13.
27. Shcherbakov AA, Hisao G, Mandala VS, Thomas NE, Soltani M, Salter EA, et al. Structure and dynamics of the drug-bound bacterial transporter EmrE in lipid bilayers. Nat Commun. 2021;12(1):172. https://doi.org/10.1038/s41467-020-20468-7. Epub 2021/01/10.
28. Saati-Santamaria Z, Baroncelli R, Rivas R, Garcia-Fraile P. Comparative genomics of the genus pseudomonas reveals host- and environment-specific evolution. Microbiol Spectr. 2022;10(6):e0237022. https://doi.org/10.1128/spectrum.02370-22. Epub 2022/11/11.
29. Ruiz-Roldan L, Rojo-Bezares B, de Toro M, Lopez M, Toledano P, Lozano C, et al. Antimicrobial resistance and virulence of Pseudomonas spp. among healthy animals: concern about exolysin ExlA detection. Sci Rep. 2020;10(1):11667. https://doi.org/10.1038/s41598-020-68575-1. Epub 2020/07/17.
30. Abayneh M, Zeynudin A, Tamrat R, Tadesse M, Tamirat A. Drug resistance and extended-spectrum beta-lactamase (ESBLs) - producing Enterobacteriaceae, Acinetobacter and Pseudomonas species from the views of one-health approach in Ethiopia: a systematic review and meta-analysis. One Health Outlook. 2023;5(1):12. https://doi.org/10.1186/s42522-023-00088-z. Epub 2023/09/12.
31. Tohya M, Watanabe S, Teramoto K, Shimojima M, Tada T, Kuwahara-Arai K, et al. Pseudomonas juntendi sp. nov., isolated from patients in Japan and Myanmar. Int J Syst Evol Microbiol. 2019;69(11):3377–84. https://doi.org/10.1099/ijsem.0.003623. Epub 2019/08/02.
32. Garvey M. Antimicrobial peptides demonstrate activity against resistant bacterial pathogens. Infect Dis Rep. 2023;15(4):454–69. Epub 2023/08/25. doi: 10.3390/idr15040046. PubMed PMID: 37623050; PubMed Central PMCID: PMCPMC10454446.
33. Flynn CE, Guarner J. Emerging antimicrobial resistance. Mod Pathol. 2023;36(9):100249. Epub 2023/06/24. https://doi.org/10.1016/j.modpat.2023.100249. PubMed PMID: 37353202.
34. Yano H, Miyakoshi M, Ohshima K, Tabata M, Nagata Y, Hattori M, et al. Complete nucleotide sequence of TOL plasmid pDK1 provides evidence for evolutionary history of IncP-7 catabolic plasmids. J Bacteriol. 2010;192(17):4337–47. https://doi.org/10.1128/JB.00359-10. Epub 2010/06/29.
35. Rong F, Sun Y, Li X, Zhang C. Drug resistance mechanism of enterobacteriaceae with decreased antibiotic sensitivity. Appl Bionics Biomech. 2022. https://doi.org/10.1155/2022/8285437. PubMed PMID: 36263253; PubMed Central PMCID: PMCPMC9576418. 2022:8285437. Epub 2022/10/21.

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