

Whole-Genome Analysis of *Paenibacillus campinasensis* from Blood of a Hand-Foot-Mouth Patient

Xiaoling Yu¹, Jun Lin², Wenqian Jiang², Tianzhu Zhu², Xiao Lin³, Xiaolong Liu⁴, Yongyi Zeng⁵

¹Department of Pharmacy, Mengchao Hepatobiliary Hospital of Fujian Medical University, Fuzhou, People's Republic of China; ²Institute of Applied Genomics, Fuzhou University, Fuzhou, People's Republic of China; ³Department of Critical Care Medicine, the First Affiliated Hospital of Fujian Medical University, Fuzhou, People's Republic of China; ⁴The United Innovation of Mengchao Hepatobiliary Technology Key Laboratory of Fujian Province, Mengchao Hepatobiliary Hospital of Fujian Medical University, Fuzhou, People's Republic of China; ⁵Department of Hepatobiliary Surgery, Mengchao Hepatobiliary Hospital of Fujian Medical University, Fuzhou, People's Republic of China

Correspondence: Xiaolong Liu, The United Innovation of Mengchao Hepatobiliary Technology Key Laboratory of Fujian Province, Mengchao Hepatobiliary Hospital of Fujian Medical University, No. 312 Xihong Road, Gulou District, Fuzhou, 350025, Fujian Province, Email xiaoloong.liu@gmail.com, Yongyi Zeng, Department of Hepatobiliary Surgery, Mengchao Hepatobiliary Hospital of Fujian Medical University, No. 66 Jintang Road, Cangshan District, Fuzhou, 350001, Fujian Province, Email lamp197311@126.com

Purpose: This study aims to investigate the antibiotic resistance and virulence factors of *Paenibacillus campinasensis*, an understudied opportunistic pathogen, through whole-genome sequencing and resistance genes. The findings will contribute to the development of effective clinical strategies for infection control.

Patients and Methods: A 1-year and 3-month-old boy presenting with fever and rash was admitted to the hospital and clinically diagnosed with hand-foot-mouth disease. A blood culture was obtained, and the pathogen was preliminarily identified as belonging to the genus *Paenibacillus* using MALDI-TOF-MS. Subsequent 16S rDNA PCR product Sanger sequencing confirmed the isolate as *Paenibacillus campinasensis*. Whole-genome sequencing and bioinformatics analysis were performed to evaluate the antibiotic resistance and virulence factors of the strain.

Results: Whole-genome sequencing and bioinformatics analysis identified 18 resistance genes in the *Paenibacillus campinasensis* strain, spanning multiple antibiotic categories. These findings suggest the potential for multidrug resistance in this bacterium, despite its isolation from blood without associated clinical infection in the patient.

Conclusion: The identification of resistance genes in *Paenibacillus campinasensis* underscores the challenges in clinical treatment and emphasizes the critical role of whole-genome analysis in pathogen detection and characterization. These findings are vital for informing effective clinical strategies to address infections, particularly given the potential for antibiotic resistance to hinder treatment outcomes, even in the absence of direct disease causation by the bacterium.

Keywords: antibiotic resistance, whole-genome sequencing, multidrug resistance, bioinformatics analysis, virulence factors

Introduction

Paenibacillus campinasensis (*P. campinasensis*) is a Gram-variable bacillus, first isolated from soil in Brazil by Yoon et al in 1998.¹ Since its discovery, it has been generally utilized in the industrial production of β -cyclodextrin glucanotransferase, xylanase, and cellulase.^{1–3} There is only one report of its isolation from the prostatic fluid of a patient with chronic prostatitis, with no literature on clinical infections caused by *P. campinasensis*.⁴

A 1-year and 3-month-old male patient presented to our hospital with a chief complaint of “fever with rash for 1 day”. The patient’s examination results were as follows: weight 10 kg; body temperature 36.8°C; scattered, medium-sized, red maculopapular rashes on both hands, elbows, knees, feet, and buttocks without petechiae; multiple granulated herpes on the oral cavity; heart rate 130 beats/min; respiratory rate 28 breaths/min; blood pressure 117/70 mm Hg; enterovirus universal type tested positive. Initial complete blood count showed the following: white blood cell counts $12.77 \times 10^9/L$

[reference range: $3.5\text{--}9.5 \times 10^9/\text{L}$]; lymphocyte percentage 64.8% [reference range: 20–50%]; neutrophil percentage 28.6% [reference range: 40–75%]; interleukin-6: 47.8 pg/mL [reference range: 0–7 pg/mL]. Routine biochemical test results showed the following: alkaline phosphatase 283 U/L [reference range: 35–100 U/L]; lactate dehydrogenase 409 U/L [reference range: 120–250 U/L]. Abdominal ultrasound showed hepatomegaly and coarse liver echo. After admission, the patient was treated with methylprednisolone to counteract inflammatory cytokine responses, omeprazole to protect the gastric mucosa, pediatric amino acid support therapy, Jinlian liquid for oral spray to clear heat and detoxify, and *Bifidobacterium bifidum* and *Lactobacillus bulgaricus* granules to regulate intestinal flora. The rash and oral granulated herpes subsided, and the patient's condition improved. Clinically, there was no specific anti-infection treatment for *P. campinasensis*, and the patient was discharged with the doctor's consent.

Materials and Methods

Bacterial Identification and Genome Sequencing

Blood culture results indicated microbial growth, which was preliminarily identified as *Pantoea* spp. using MALDI-TOF-MS (VITEK MS, BioMerieux SA, BioMerieux Inc., France). Species-level identification was achieved through Sanger sequencing (ABI 3730xl DNA Sequencer) following bacterial genome extraction with a one-step genomic extraction kit (Weiyin, China) and 16S rDNA PCR amplification (universal primers: 27F: 5' AGAGTTTGATCCTGGCTCAG 3', 1492: 5' TACGGYTACCTTGTTACGACTT 3'). NCBI Blast analysis confirmed the isolate as *P. campinasensis* (16S rRNA gene sequence data are provided in [Table S1](#)), not *Pantoea* spp. A next-generation sequencing (NGS) library was constructed using the Illumina NextEra XT DNA Library Preparation Kit, and metagenomic next-generation sequencing was performed on the Illumina NextSeq platform.

Bioinformatics Analysis of High-Throughput Sequencing Data

Following the acquisition of preliminary high-throughput sequencing data, a rigorous quality assessment of the raw sequencing data was performed using bioinformatics tools such as seqkit, fastqc, and multiqc.^{5,6} Subsequently, trim_galore software was employed to further refine sequence quality. Clean sequences obtained after quality control were aligned to *P. campinasensis* reference genome using bwa software to validate sequencing accuracy and consistency.⁷ Genome assembly was conducted using SOAPDenovo2 (version 2.40) with optimized parameters: “-K 63” (kmer size), “-p 64” (activation of 64 CPU cores), “-d 0” (retention of low-frequency kmers), “-D 1” (elimination of low-coverage edges), “-M 1” (merging intensity of similar sequences), and “-L 65” (shortest contig length for scaffolding).⁸ Additional configuration parameters included “max_rd_len=150” (maximum read length), “avg_ins=350” (average insert fragment length), “reverse_seq=0” (no reverse-complementary operation), “asm_flags=3” (assembly markers), “rd_len_cut-off=150” (read length cutoff), and “rank=1” (data priority). These parameters collectively ensured successful genome assembly. For comprehensive analysis of antibiotic resistance and virulence factors of *P. campinasensis*, gene annotation was performed using ABRicate 1.0.1 with the following parameters: “-minid 50” (minimum 50% sequence similarity), “-mincov 50” (minimum 50% coverage of target genes), and “-threads 8” (8 BLAST+ threads for stable parallel processing). Annotation accuracy was further enhanced by integrating multiple databases, including NCBI AMRFinderPlus, CARD, ARG-ANNOT, Resfinder, MEGARES, EcOH, PlasmidFinder, Ecoli_VF, and VFDB.^{9–16}

Gene annotation was further performed using Prokka 1.14.6. Among its key “Matching” parameters, “-evalue” was set to the default value of “1e - 09”. This extremely low e-value was used to meticulously filter out highly similar and reliable sequences, ensuring the precision of the annotation. The “-coverage” parameter was set to the default “80”, stipulating that the coverage of the aligned protein sequence over the target protein must be at least 80%, guaranteeing the comprehensiveness and credibility of the annotation results. The “-cpus 8” parameter specified the use of 8 CPU cores for computation, striking a balance between computing resources and time expenditures to accelerate the annotation process and provide efficient and high-quality data support for subsequent in-depth gene function analyses.

To comprehensively uncover the antibiotic resistance and virulence factors of *P. campinasensis*, we employed the ABRicate software to conduct a comparative analysis of the assembled scaffolds, and the results were compared with nine authoritative databases, namely NCBI AMRFinderPlus, CARD, ARG-ANNOT, Resfinder, MEGARES, EcOH,

PlasmidFinder, Ecoli_VF, and VFDB. Different databases vary in data sources, coverage scopes, and annotation standards, which may lead to similarities and differences in the detection results. For instance, there might be a high overlap between NCBI AMRFinderPlus and Resfinder in the inclusion of common β -lactam resistance genes, which will strengthen our confidence in the detection results of such resistance genes. On the other hand, MEGARES may detect unique resistance genes that are not covered by other databases. Through this analysis, we can more accurately evaluate the reliability of the results, thereby enhancing our confidence in the research findings.

Results

Figure 1A presents the coverage of sequences after quality control by Trim_galore software when aligned with the reference sequence of *Paenibacillus campinasensis* (GCF_002272015.1) using BWA software across various genomes (only the top 30 genomes in terms of length are shown in the figure). This figure is presented in the form of a bar chart. The red part visually represents the full length of each genome, while the green part accurately indicates the length of the covered region. The text above each bar represents the average sequencing depth. From the data in the figure, it can be seen that most genes not only exhibit extremely high coverage but also possess a considerably high sequencing depth.

Figure 1B shows the base quality distribution. Through a detailed analysis of this figure, it can be clearly observed that both the Q20 and Q30 quality indicators of the obtained sequences significantly exceed 90%. Taken together, the information reflected in **Figures 1A** and **B** fully demonstrates that the sequencing data obtained in this study, in terms of both quantity and quality, have reached the ideal standards for scientific research. This has laid an extremely solid foundation for the subsequent in-depth bioinformatics analysis work, ensuring that follow-up research can conduct precise and reliable analyses and investigations based on high-quality data resources.

The quality-controlled sequences were aligned to the *P. campinasensis* reference genome using BWA software. Alignment results demonstrated an 88.20% match rate (15,053,371/17,067,368), indicating high sequences purity and reliability. Based on these data, de novo assembly was performed using SOAPDenovo2 software to identify potential key gene differences between this strain and the reference genome. This approach aimed to uncover potential biological characteristics and functional variations unique to this bacterial strain.

The genome assembly results were evaluated using QUAST software, as summarized in **Table 1**.¹⁷ The assembly produced a total of 766 scaffolds, with lengths ranging from 100 bp to 278,860 bp, an average length of approximately 7,242.3 bp, and an N50 of 109.4 kbp.

Based on the QUAST assessment results, the current genome assembly has shown positive outcomes, particularly with the maximum contig length reaching 278,860 base pairs (bp), which indicates the effective formation of longer continuous sequences during the assembly process. As can be seen from the Nx length distribution graph of sample MC2017006996 (**Figure 2**), the N50 value exceeded 100,000 bp, suggesting that most of the genomic information is integrated into longer contigs. This is not only conducive to subsequent gene annotation and functional analysis but also

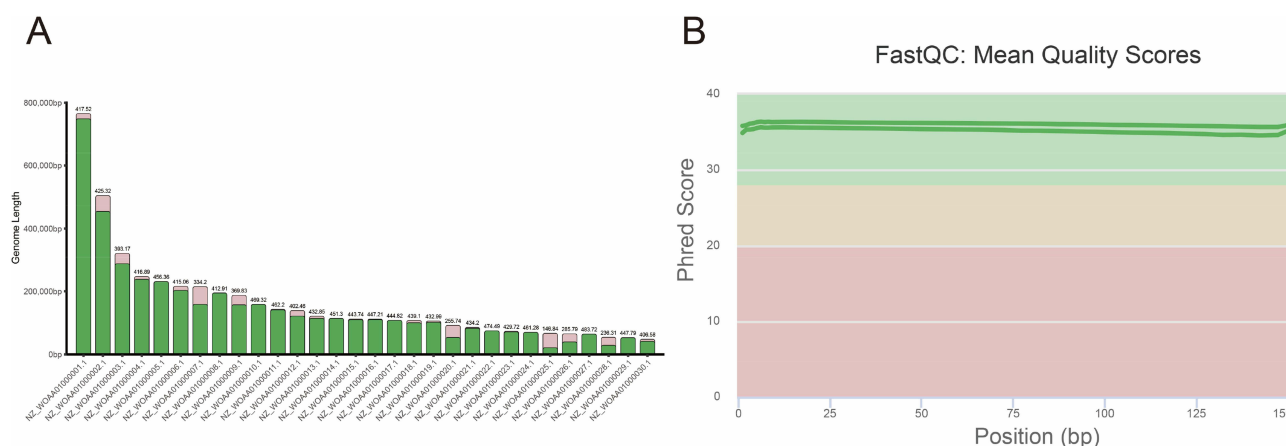


Figure 1 Quality Check of the Sequences After Quality Control. **(A)** Mean Coverage of Genome Mapping; **(B)** Base Quality Distribution After Quality Control.

Table 1 *P. Campinasensis* Genome Assembly Contig and Scaffold Statistics

Statistics	<i>P. campinasensis</i>
Contigs	110
Contigs (≥ 0 bp)	766
Contigs (≥ 1000 bp)	101
Contigs (≥ 5000 bp)	75
Contigs (≥ 10000 bp)	69
Contigs (≥ 25000 bp)	54
Contigs (≥ 50000 bp)	40
Largest contig	278,860
Total length	5,461,980
Total length (≥ 0 bp)	5,547,630
Total length (≥ 1000 bp)	5,455,752
Total length (≥ 5000 bp)	5,391,393
Total length (≥ 10000 bp)	5,347,054
Total length (≥ 25000 bp)	5,098,522
Total length (≥ 50000 bp)	4,581,050
N50	109,457
N90	34,886
auN	121,347
L50	17
L90	49
GC (%)	52.08

Abbreviations: Contigs, Total number of assembled contigs; bp, base pairs; N50, Length such that half of the genome's bases are in contigs of this length or longer; N90, Length such that 90% of the genome's bases are in contigs of this length or longer; auN, Average of the lengths of the largest N contigs; L50, Number of contigs at which 50% of the total number of contigs is reached; L90, Number of contigs at which 90% of the total number of contigs is reached; GC%, Percentage of guanine and cytosine nucleotides.

demonstrates the high continuity of the assembly results. The total length is close to the total length after removing contigs of zero length, indicating that the assembly results cover most of the genomic sequences, providing a solid foundation for the integrity of the genome. In addition, the GC content is within a reasonable range, which helps to maintain the stability of the genome and provides favorable conditions for subsequent research. In summary, the assembly process has successfully reconstructed the genomic structure of *P. campinasensis*, providing a more complete sequence framework for subsequent drug resistance analysis.

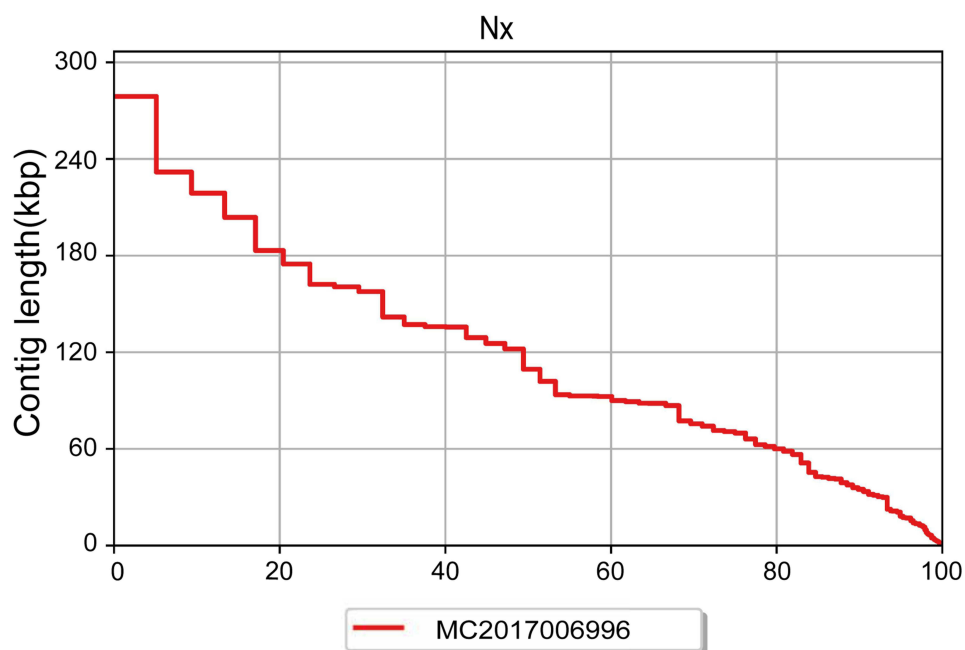


Figure 2 Nx Length Distribution Curve.

To identify potential functional regions associated with drug resistance that may be contained in the assembled scaffolds, Prokka was employed to annotate and predict the functional regions of 766 scaffolds with a total of 5,547,630 bp of base pairs.¹⁸ The results presented in Figure 3, include the annotation of over 5,000 protein-coding regions, among which are proteins and systems associated with drug resistance. These annotations primarily focus on the mechanisms of antibiotic resistance in bacteria. They include: 1) Multidrug resistance proteins: Multidrug resistance ABC transporter ATP-binding/permease protein BmrA, Multidrug resistance protein 3, Multidrug resistance protein MdtA, Multidrug resistance protein MdtG, Multidrug resistance protein MdtK, Multidrug resistance protein NorM; 2) Antibiotic-specific resistance: Tetracycline resistance protein, class C, Daunorubicin/doxorubicin resistance ABC transporter permease protein DrrB, Daunorubicin/doxorubicin resistance ATP-binding protein DrrA; 3) Regulatory proteins

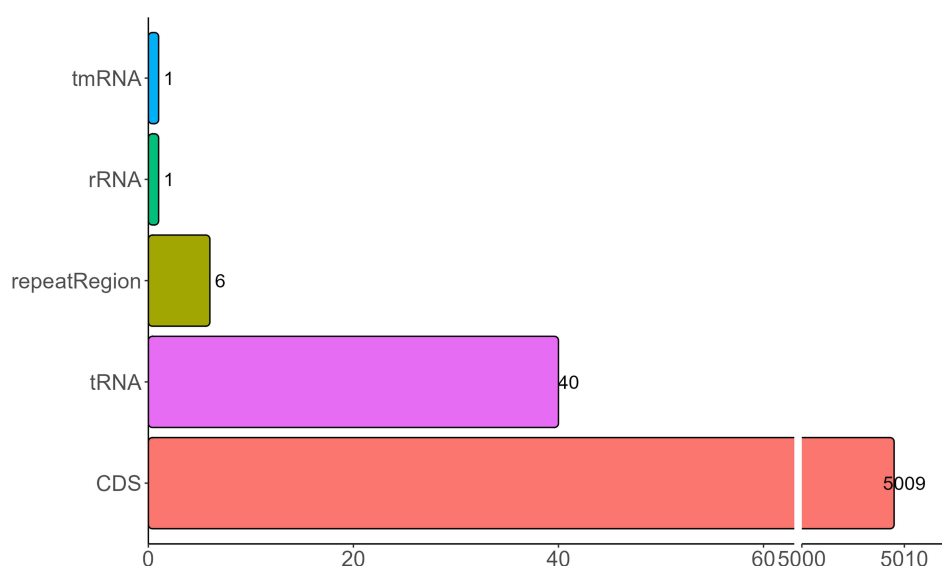


Figure 3 Prokka Annotation of Functional Regions.

for drug resistance: Transcriptional regulatory protein CusR, Transcriptional regulatory protein CymR, Transcriptional regulatory protein QacR.

These proteins and systems play a key role in the formation of bacterial drug resistance. They can help bacteria resist the effects of antibiotics through various mechanisms, such as pumping out antibiotics, altering the target structure of antibiotics, producing enzymes to destroy antibiotics, or changing the cell wall structure to reduce the entry of antibiotics.

As mentioned earlier, to assess the drug resistance of *P. campinasensis*, we conducted a comprehensive genomic analysis. On this basis, we compared the assembled scaffolds with multiple drug resistance gene databases to identify potential drug resistance genes. Through this process, we identified a total of 18 drug resistance genes, as shown in Table 2. These genes are involved in various categories of antibiotics, including macrolides, rifampicin, streptomycin, lincosamides, and tetracyclines, indicating that the bacterial strain may have multiple-drug resistance. For example, the coverage and identity percentages of the *VatI* gene are 99.05% and 75.92%, respectively, which suggests a high correlation with known streptomycin resistance. In addition, the *rphB* gene is not only resistant to rifampicin but is

Table 2 ABRicate Drug Resistance Database Annotation Results

Gene	Coverage (%)	Identity (%)	Database	Product	Resistance
(MLS) <i>vat(A)</i>	66.06	68.61	Argannot	(MLS) <i>vat(A)</i>	Macrolide-Lincosamide-Streptogramin
(Rif) <i>rphD</i>	99.31	73.35	Argannot	(Rif) <i>rphD</i>	Rifampin
(MLS) <i>msr(D)</i>	80.33	65.24	Argannot	(MLS) <i>msr(D)</i>	Macrolide-Lincosamide-Streptogramin
<i>VatI</i>	99.05	75.92	Card	Streptogramin A acetyltransferase found in <i>Paenibacillus</i> sp. LC231 isolated from Lechuguilla Cave NM USA. Confers resistance to streptogramin A antibiotics. Described by Pawlowski et al 2016.	streptogramin
<i>rphB</i>	99.13	79.74	Card	<i>rphB</i> is a rifampin phosphotransferase protein found in <i>Paenibacillus</i> sp. LC231 a strain of <i>Paenibacillus</i> isolated from Lechuguilla Cave NM USA. Confers resistance to rifamycin antibiotics specifically rifampin through rifampin inactivation. Described by Pawlowski et al 2016.	rifamycin
<i>TaeA</i>	98.82	77.72	Card	Pleuromutilin (Tiamulin) ABC efflux pump found in <i>Paenibacillus</i> sp. LC231 a strain of <i>Paenibacillus</i> isolated from Lechuguilla Cave NM USA. Confers resistance to pleuromutilin antibiotics. Described by Pawlowski et al 2016.	pleuromutilin
<i>LlmA_23S_ribosomal_RNA_methyltransferase</i>	99.42	80.14	Card	Lincosamide (Clindamycin) resistant (putative) ribosomal methyltransferase related to the RlmK 23S rRNA methyltransferase COG family. Detected in <i>Paenibacillus</i> sp. LC231 an isolated strain of <i>Paenibacillus</i> found in Lechuguilla Cave NM USA. Described by Pawlowski et al 2016.	lincosamide
<i>VATI</i>	99.05	75.92	Megares	Drugs: MLS: Streptogramin_A_O-acetyltransferase: VATI	Macrolide-Lincosamide-Streptogramin

(Continued)

Table 2 (Continued).

Gene	Coverage (%)	Identity (%)	Database	Product	Resistance
<i>RPH</i>	99.13	79.74	Megares	Drugs: Rifampin; Rifampin_phosphotransferase: RPH	Rifampin
<i>MSRD</i>	80.12	65.83	Megares	Drugs: MLS: MLS_resistance_ABC_efflux_pumps: MSRD	Macrolide- Lincosamide- Streptogramin
<i>TAEA</i>	98.82	77.72	Megares	Drugs: Multi-drug_resistance: Multi- drug_ABC_efflux_pumps: TAEA; The TAEA group of genes confer resistance to Drug and biocide resistance through the mechanism, Drug and biocide ABC efflux pump.	TIAMULIN
<i>LLMA</i>	99.42	80.14	Megares	Drugs: MLS:23S_rRNA_methyltransferases: LLMA	Macrolide- Lincosamide- Streptogramin
<i>vat(I)</i>	99.05	75.92	ncbi	Streptogramin A O-acetyltransferase Vat(I)	STREPTOGRAMIN
<i>rphC</i>	99.39	75.19	ncbi	Rifamycin-inactivating phosphotransferase RphC	RIFAMYCIN
<i>msr(D)</i>	80.12	65.83	ncbi	ABC-F type ribosomal protection protein Msr(D)	MACROLIDE
<i>taeA</i>	98.82	77.72	ncbi	ABC-F type ribosomal protection protein TaeA	TIAMULIN
<i>vat(H)_I</i>	71.43	69.02	Resfinder	<i>vat(H)</i>	Dalfopristin; Pristinamycin_IIA; Virginiamycin_M
<i>msr(D)_3</i>	80.12	65.83	Resfinder	<i>msr(D)</i>	Erythromycin; Azithromycin; Telithromycin; Quinupristin; Pristinamycin_IA; Virginiamycin_S

also marked as resistant to lincosamides in the megares database, further confirming the strain's multiple-drug resistance characteristics. The high coverage and identity percentages of these drug resistance genes indicate that the identified drug resistance gene sequences have a high degree of similarity to the reference sequences in the databases. The diversity of drug resistance mechanisms is also significant, including the inactivation of antibiotics (such as *rphC* and *rphD* genes), the efflux of antibiotics (such as the *TaeA* gene), and the modification of antibiotic target sites (such as the *LlmA_23S_ribosomal_RNA_methyltransferase* gene). The existence of these mechanisms suggests that *P. campinasensis* may acquire drug resistance through various pathways, which poses a challenge to clinical treatment and may require the use of a broader range of antibiotics or combination therapies to effectively treat infections.

P. campinasensis, as a microorganism with a Gram-variable staining phenotype, may exhibit resistance to antibiotics traditionally targeted against both Gram-positive and Gram-negative bacteria. This characteristic not only makes this bacterial strain a focus of attention but also suggests that it may develop resistance to a broad spectrum of antibiotics through various mechanisms. Therefore, an in-depth study of its resistance mechanisms is crucial for developing effective treatment strategies.

In the clinical setting, a wide array of antibiotics is used to treat infections caused by both Gram-negative and Gram-positive bacteria. Table 3 includes some common classes and specific drugs:

Through the results of Table 2, we have identified the resistance genes of *P. campinasensis* to the following antibiotics (the particulars are elaborated upon in Table 4):

Table 3 Antibiotics Used in Clinical Practice

Classification of Antibiotics	Targeting Gram Positive/Negative Bacteria	Antibiotics
Lincosamides	Gram positive bacteria	Lincomycin, Clindamycin
Glycopeptides	Gram positive bacteria	Vancomycin, Teicoplanin
Rifamycins	Gram positive bacteria	Rifampicin
Quinolones	Gram Positive bacteria	Ciprofloxacin, Levofloxacin, Moxifloxacin
	Gram negative bacteria	
Carbapenems	Gram negative bacteria	Meropenem, Imipenem
β -Lactamase Inhibitors	Gram negative bacteria	Clavulanate, Sulbactam
β -Lactams	Gram positive bacteria	Penicillin G, Amoxicillin, Ampicillin, Oxacillin, first-generation cephalosporins (cefazolin, cefradine, cephalosporin)
	Gram negative bacteria	Penicillin resistant to <i>Pseudomonas aeruginosa</i> (eg, piperacillin), third-generation cephalosporins (eg, ceftazidime), fourth-generation cephalosporins (eg, cefepime), and carbapenems (eg, meropenem)
Macrolides	Gram positive bacteria	Erythromycin, Azithromycin, Clarithromycin
Tetracycline Class	Gram positive bacteria	Tetracycline, Doxycycline
	Gram negative bacteria	Gentamicin, Amikacin

Table 4 Types of Antibiotics and Genes Conferring Resistance in *P. Campinasensis*

Gene Name	Classification of Antibiotics	Targeting Gram Positive/Negative Bacteria
(MLS) <i>vat(A)</i> , (MLS) <i>msr(D)</i> , <i>VAT1</i> , <i>MSRD</i> , <i>LLMA</i> , <i>msr(D)</i>	MLS	Gram positive bacteria
(Rif) <i>rphD</i> , <i>rphB</i> , <i>RPH</i> , <i>rphC</i>	Rifampicin	Gram positive bacteria
<i>TAEA</i>	Streptogramins	Gram positive bacteria
<i>LlmA_23S_ribosomal_RNA_methyltransferase</i>	Lincosamides	Gram positive
<i>vat(A)</i>	Tetracycline	Gram negative bacteria
<i>VatI</i> , <i>vat(I)</i>	Streptomycin	Gram positive/negative bacteria
<i>vat(H)_I</i> , <i>msr(D)_3</i>	Pristinamycin	Gram positive/negative bacteria

The Gram-variable staining characteristic of *P. campinasensis* provides a biological basis for the broad spectrum of its resistance genes, which may lead to cross-resistance to various classes of antibiotics. The identification of these resistance genes is significant for understanding the resistance mechanisms of this strain, predicting its potential response to new antibiotics, and providing targeted treatment options for clinicians facing *P. campinasensis* infections. This helps to optimize treatment plans, improve therapeutic outcomes, reduce unnecessary drug exposure, and slow the development of antibiotic resistance.

Discussion

This study introduced a case of *P. campinasensis* derived from blood culture of a child with hand-foot-mouth disease. Although *P. campinasensis* did not cause clinical infection in the patient, our detailed investigation through whole-

genome sequencing and bioinformatics analysis revealed a complex profile of antibiotic resistance genes. Specifically, we identified 18 resistance genes involving multiple antibiotic classes. This is the first study to analyze the whole genome of *P. campinasensis* and evaluate its drug resistance. The presence of numerous resistance genes within this isolate, despite the lack of active infection, poses a potential risk for the development of infections that are difficult to treat. Our findings highlight the importance of surveillance for multidrug resistance (MDR) in clinically relevant isolates, even when they do not cause immediate infections. This approach is crucial for early detection and prevention of MDR spread, which is a growing global health concern. Through genomic analysis, this study reveals that the strain has a complex profile of antibiotic resistance genes, indicating its potential to develop multidrug resistance. This finding not only emphasizes the necessity for continuous monitoring and research on the genetic determinants of bacterial resistance, especially in the face of the increasingly severe global situation of multidrug-resistant pathogens, but also highlights the application value of whole-genome sequencing and bioinformatics tools in analyzing bacterial genetic composition. This is significant for developing effective clinical treatment strategies and addressing the spread of antibiotic resistance.

Further in-depth research on the drug resistance of *P. campinasensis* is of great significance for understanding its resistance patterns to current antibiotics and predicting its potential resistance gene spectrum. This knowledge has a direct guiding role in preventing potential resistance issues in the future and formulating public health safety and disease control strategies. Against the backdrop of growing global concern over antibiotic resistance, in-depth research on the drug resistance of this strain will provide a solid scientific basis for the rational use of antibiotics, the development of new antibiotics, and the exploration of potentially effective new compounds or combination therapy regimens.

Conclusion

In summary, the study of drug resistance in *P. campinasensis* is not only of significant clinical guidance for treatment but also has far-reaching scientific value in the formulation of antibiotic management policies and the field of drug development. By identifying the resistance genes of this strain, its resistance characteristics can be more accurately grasped, thereby guiding clinical treatment, enhancing therapeutic outcomes, reducing unnecessary drug use, and effectively responding to the global challenge of antibiotic resistance.

Future research should focus on the following directions: Systematic monitoring of resistance patterns in both environmental and clinical isolates is essential to identify emerging resistance mechanisms and their potential spread. This surveillance will enable early detection of novel resistance genes and inform targeted interventions. Further studies should explore the role of horizontal gene transfer in the dissemination of resistance genes, particularly in clinical settings. Understanding the mechanisms and vectors of gene transfer will provide critical insights for developing strategies to mitigate resistance spread. Research should also focus on elucidating the environmental factors that drive the emergence and persistence of resistance genes. This includes investigating the impact of anthropogenic activities, such as antibiotic use in agriculture and wastewater management, on resistance dynamics.

Data Sharing Statement

The sequencing raw data is stored in the SRA database of NCBI, accession number PRJNA1106201.

Ethics Approval and Informed Consent

This study was reviewed and approved by the Medical Ethics Committee of Mengchao Hepatobiliary Hospital of Fujian Medical University with the approval number: 2024_049_01, dated November 10, 2023. Written informed consent has been provided by the patient's mother to have the case details published.

Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors have no conflicts of interest to declare.

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