Infection and Drug Resistance

Dovepress
Taylor & Francis Group

Open Access Full Text Article

ORIGINAL RESEARCH

Clinical Characteristics and Antimicrobial Susceptibility of *Lautropia mirabilis* Isolated from Patients with Lower Respiratory Tract Infection in China

Huicang Liang[1–3,*], Kaiyi Qin[1–3,*], Chunlan Huang[1–3], Yuyuan Xue[4], Liuchun Luo[1–3], Renli Qin[1–3], Qiuhong Xu[1–3], Tingting Zhou[1–3], Dan Qiao[5]

[1]Department of Laboratory Medicine, Liuzhou People's Hospital, Liu Zhou, People's Republic of China; [2]Key Laboratory of Precision Medicine for Viral Diseases, Liuzhou People's Hospital, Liu Zhou, People's Republic of China; [3]Guangxi Health Commission Key Laboratory of Clinical Biotechnology, Liuzhou People's Hospital, Liu Zhou, People's Republic of China; [4]Department of Dermatology, Huashan Hospital, Fudan University, Shanghai, People's Republic of China; [5]Department of Laboratory Medicine, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, People's Republic of China

*These authors contributed equally to this work

Correspondence: Dan Qiao, Department of Laboratory Medicine, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, People's Republic of China, Email qiaodan840924@163.com

Objective: *Lautropia mirabilis* is a rare Gram-negative opportunistic pathogen, with limited clinical understanding of the infectious diseases it causes. This study aims to provide reliable experimental data for epidemiological analysis, monitor in vitro antibiotic susceptibility, and guide clinical treatment through the identification of this bacterium and in vitro drug susceptibility testing, along with an analysis of patient clinical data.

Methods: From March to August 2024, sputum or bronchoalveolar lavage specimens from patients in Shanghai and Guangxi were collected and cultured, resulting in the isolation of 38 strains of *L. mirabilis*. The demographic characteristics, clinical manifestations, imaging, and microbiological data of the patients were analyzed. Identification of the strains was performed using 16S rRNA polymerase sequencing and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), and in vitro drug susceptibility tests were conducted to study the microbiological characteristics of *L. mirabilis*. Cluster analysis was performed using mass spectrometry, and molecular phylogenetic tree analysis was conducted to evaluate the differences among strains from different regions.

Results: A total of 38 patients infected with *L. mirabilis* were collected, and the majority of these patients had underlying diseases. All infected patients received antibacterial treatment during hospitalization and were discharged after recovery. The identification accuracy of the strains at the species and genus levels using 16S rRNA polymerase chain reaction sequencing and MALDI-TOF MS was 100%. Cluster and phylogenetic tree analyses revealed no significant differences among different regions and strains.

Conclusion: *L. mirabilis* poses a higher susceptibility risk in elderly patients with underlying diseases or weakened immunity. This bacterium is fully sensitive to cephalosporins, aminoglycosides, and carbapenem antibiotics, while the resistance rate to fluoroquinolone antibiotics exceeds 50%. This study provides a more comprehensive understanding of this bacterium and offers a more thorough reference for clinical treatment of such diseases.

Keywords: *Lautropia mirabilis*, infection, drug resistance, risk factors

Introduction

Lautropia mirabilis is a motile, facultatively anaerobic, gram-negative coccoid bacterium from the *Burkholderiaceae family.*[1] *L. mirabilis* was described in 1994 by P. Gerner-Smidt et al.[1] Both Orskov and Gerner-Smidt et al isolated the organism from oral or upper respiratory sites. Subsequently, it has been isolated as the predominant microorganism from

https://doi.org/10.2147/IDR.S573707
Received: 29 October 2025
Accepted: 16 January 2026
Published: 27 January 2026

the sputum of one Australian patient with cystic fibrosis.[2] The organism is gram negative, facultatively anaerobic, and oxidase positive, with cell morphology varying from coccobacilli 1 µm in diameter to spheroblast-like forms more than 10 µm in diameter. The colonies are pleomorphic. Coronavirus disease 2019 (COVID-19) has emerged as a global concern due to its high prevalence, resulting in hundreds of millions of deaths and overwhelming healthcare systems worldwide. Evidence has clearly indicated that the incidence of infections caused by opportunistic pathogens has increased in association with the COVID-19 pandemic.[3,4] With the increasing aging population and the rise of immunocompromised individuals, the incidence of opportunistic pathogen infections in humans is rising annually. *L. mirabilis* frequently infects patients with compromised immune systems, leading to subacute or chronic, localized or disseminated, suppurative or granulomatous diseases in the lungs.[5–7]Currently, there are few research reports on this bacterium. It has been previously reported that this bacterium is sensitive to cephalosporins and aminoglycoside antibiotics;[1,6] however, studies on its related drug sensitivity are relatively scarce. Consequently, this study analyzes the microbiological morphology, in vitro drug sensitivity, and clinical infection characteristics of *L. mirabilis* to provide a scientific basis for laboratory identification as well as clinical diagnosis and treatment of *L. mirabilis* infections.

Materials and Methods

Strain Source

Between March and August 2024, we collected a total of 38 strains of rare *L. mirabilis*. All strains were isolated from sputum or bronchoalveolar lavage specimens, and only those strains that were cultured and isolated from the same patient at least twice were included in the study. Among these, 27 strains were from patients treated in Shanghai, and 11 strains were from patients treated in Liuzhou, Guangxi.

DNA Extraction, Amplification and Sequencing

Strains cultured on blood plates in an aerobic incubator at 35°C for 72 hours were used to extract genomic DNA using the TianGen kit. The extracted DNA was sent to Shanghai Saiyin Biological Sequencing Co. Ltd. for polymerase chain reaction (PCR) amplification of the bacterial 16S rRNA gene, utilizing the general primers 341F 5′-CCTAYGGGRBGCASCAG-3′ and 806R 5′-GGACTACHVGGGTWTCTAAT-3′.

Alignment and Phylogenetic Reconstruction

For phylogenetic reconstruction at various sites, first obtain suitable reference sequences from GenBank and manually review and correct the results. Utilize the MAFFT software for multiple sequence alignment, followed by the use of trimAl for sequence trimming to eliminate low-quality alignment sites. This process includes the removal of homologous regions or sites that are inaccurately inferred during the multiple sequence alignment (MSA) process, as well as regions characterized by a high frequency of insertions or deletions. Finally, the 38 sequences of 16S rRNA were merged into a FASTA format and imported into PhyloSuite (v1.2.3). The evolutionary tree was constructed using the maximum likelihood method with the FastTree software.

MALDI-TOF MS Identification

The strains isolated from clinical samples were subcultured on blood agar plates and incubated in an aerobic incubator at 35°C. After 48 hours, pure colonies were collected and identified using the formic acid direct coating method. Spectrum acquisition was conducted with the EXS3000 instrument utilizing version 3.1.2.4 software (Zybio, China). The instrument's ion source settings included a target high voltage of 19.13 kV and a lens high voltage of 1330 V, among others, with a mass range spanning from 2000 to 20000. Bacterial identification is conducted using the EXS3000 database version 3.1.2.4. An identification score of ≥2.00 indicates identification at the species level, while a score of ≥1.70 indicates identification at the genus level. Scores below 1.70 are deemed unreliable. For each sample, three protein fingerprints are generated; when all three parallel tests align with the sequencing results, the identification at the highest scoring level is regarded as correct. In this study, the identification scores of the 38 strains were all greater than 2.00, successfully identifying the species level for all strains.

Antimicrobial Susceptibility Test

L. mirabilis is a clinically uncommon Gram-negative bacterium. This study follows the interpretive criteria for antimicrobial susceptibility testing as outlined by the Clinical and Laboratory Standards Institute. Nine antimicrobial agents were selected, including ampicillin (0.064–256 μg/mL), cefuroxime (0.016–256 μg/mL), cefotaxime (0.016–-256 μg/mL), ciprofloxacin (0.002–32 μg/mL), levofloxacin (0.002–32 μg/mL), meropenem (0.008–32 μg/mL), amikacin (0.032–512 μg/mL), tetracycline (0.064–256 μg/mL), and aztreonam (0.064–256 μg/mL). The E-test method was employed to conduct in vitro susceptibility testing on the strains. The E-test strips utilized for this study were procured from Wenzhou Kangtai Technology Co., Ltd. The quality control strains utilized are *Escherichia coli* ATCC25922 and *Staphylococcus aureus* ATCC29213. Pre-experiments indicated that colonies grown on NH agar plates are easier to emulsify than those cultivated on blood agar plates. A single colony from the blood agar plate should be picked and subcultured onto an NH agar plate for 48 hours. Following this incubation, a pure colony was used to prepare a bacterial suspension with a turbidity of 0.5 McFarland, which was then evenly spread across the surface of a sheep blood agar plate. After allowing the plate to stand for 10 minutes, sterile forceps were employed to place the E-test strip onto the sheep blood agar. The plates were subsequently incubated in an aerobic incubator for 48 hours, after which the results were recorded. If the bacterial growth was insufficient, the observation period was extended to 72 hours.

Result

Clinical Characteristics

The study included 38 patients, comprising 19 males and 19 females. The age range of the participants was from 19 to 89 years, with those aged 60 years or older accounting for 60.6%. All patients exhibited clinical symptoms of bacterial infection and were diagnosed with this infection after two or more lower respiratory tract specimens were cultured, resulting in the isolation of the unusual *L. mirabilis*. The majority of patients presented with underlying health conditions and low immune function. Specifically, there were 7 cases of diabetes, 12 cases of hypertension, 11 cases following tumor surgery, 7 cases of cerebral infarction, 6 cases of coronary heart disease, and 5 cases of blood system diseases. Among the patients, 24 exhibited significant signs of inflammatory infection in the lungs (Table 1). Fourteen patients exhibited mild infection symptoms and were able to recover independently without the need for clinical intervention.

Table 1 Clinical Data of 24 Patients with *L. mirabilis* with More Severe Infection Symptoms

No.	Gender	Age	Underlying Diseases	Clinical Features	Treatment
N1	M	66	Diabetes mellitus, coronary artery heart disease	Interstitial pneumonia, cough, expectoration	Norfloxacin
N2	M	77	Hypertension, myelodysplastic syndrome	Pneumonia	Cefoperazone
N3	M	77	Cerebral infarction, Hypertension, diabetes mellitus	Cough, fever	Imipenem, cefoperazone
N4	M	66	Coronary artery heart disease	Pneumonia, Cough, Expectoration, fever	Meropenem, cefoperazone
N5	M	71	Cough, fever	Emphysema, pneumonia, cough, Expectoration, fever	Biapenem
N6	M	56	Right temporal parietal astrocytoma.	Pneumonia, Cough, expectoration	Cefmetazole
N7	F	70	Diabetes mellitus, Hypertension, chronic pyelonephritis	Pneumonia, cough, fever	Piperacillin
N8	M	66	Diabetes mellitus, coronary artery heart disease	Pneumonia, Cough, expectoration	Norfloxacin, biapenem
N9	M	61	Lung cancer, Post-gastrectomy.	Pneumonia, Cough, expectoration	Cefotaxime

(*Continued*)

https://doi.org/10.2147/IDR.S573707

Table 1 (Continued).

No.	Gender	Age	Underlying Diseases	Clinical Features	Treatment
N10	M	83	Hypertension, cerebral infarction	Pneumonia, Cough, expectoration	cefoperazone
N11	F	80	Cerebral infarction	Fever	Cefotaxime
N12	F	59	Hypertension	Pneumonia, Cough, expectoration	Meropenem
N13	F	64	Hypertension, Post-thyroidectomy for carcinoma of thyroid	Fever, Cough, expectoration	Cefmetazole, meropenem
N14	M	71	Chronic obstructive pulmonary diseases, Bronchiectasis, chronic cholecystitis	Cough, Expectoration, Fever, pneumonia	Levofloxacin, meropenem
N15	M	77	Coronary artery heart disease, Hypertension, rectal cancer, carcinoma of prostate	Cough, expectoration pneumonia	Piperacillin
N16	F	59	Recurrent headaches and dizziness for 40 years	Cough expectoration, pneumonia	Moxifloxacin
N17	M	19	Acute myelogenous leukemia M4 Type	Fever, Cough, pneumonia	Cefoperazone, meropenem,
N18	M	53	Myelodysplastic syndrome, osteomyelitis of jaw	Dental pyorrhea, fever	Piperacillin, imipenem
N19	F	79	Chronic obstructive pulmonary disease, cerebral infarction, Hypertension, coronary artery heart disease	Cough, Expectoration, Fever, pneumonia	Cefoperazone
N20	F	56	Lymphoma, bone marrow transplantation	Fever, cough, pneumonia	Meropenem
N21	F	49	Acute leukemia	Fever, Cough, pneumonia	Meropenem
N22	F	57	Lymphoma	Fever, Cough, Expectoration, pneumonia	Piperacillin
N23	F	48	Diffuse large B cell lymphoma	Cough, expectoration	Meropenem
N24	F	50	Lung cancer	Pneumonia, Cough, expectoration	Piperacillin

Strain Identification and Morphological Characteristics

The strain was isolated from sputum or bronchial lavage fluid submitted for clinical examination. The specimens were inoculated onto blood agar plates, chocolate agar plates, and MacConkey agar plates. After being cultured in an aerobic incubator at 35°C for 24 to 72 hours, colonies of varying sizes, ranging from white to light yellow, exhibited a rough texture, were non-hemolytic, and displayed a dry "biting agar" phenomenon on the blood agar plates (Figure 1A–C). After performing direct smearing of the original specimen and conducting Gram staining, the morphology observed under the oil immersion microscope does not resemble that of typical bacteria. Instead, it exhibits larger spherical cells (Figure 1D). Following acid-fast staining, the bacteria are stained blue, indicating a negative result for acid-fastness.

Drug Susceptibility

The drug susceptibility test results for 38 strains indicated that the sensitivities to ampicillin, cefuroxime, ceftazidime, meropenem, amikacin, tetracycline, and aztreonam were all 100%. However, resistance was observed for ciprofloxacin and levofloxacin, with a resistance rate of 52.6%. No significant difference in drug sensitivity was found between strains from Shanghai and Guangxi (Table 2).

Evolutionary Tree and Mass Spectrometry Clustering Analysis

DNA was extracted from 38 strains, followed by polymerase chain reaction (PCR) amplification of the 16S rRNA gene of the bacteria. For phylogenetic reconstruction of various loci, the FastTree software was utilized to construct an evolutionary tree (Figure 2). The evolutionary tree diagram indicates that the 38 strains can be categorized into

 https://doi.org/10.2147/IDR.S573707

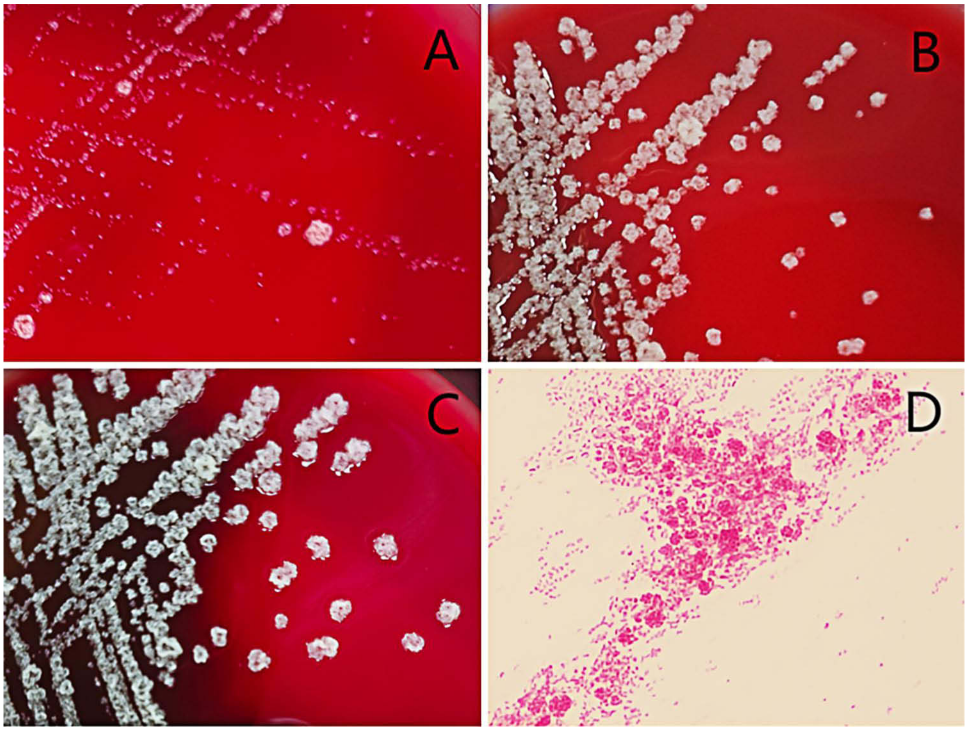

Figure 1 Morphology of *L. mirabilis*. (**A**) Columbia blood agar plate culture for 24 hours and the colony morphology; (**B**) Columbia blood agar plate culture for 48 hours and the colony morphology; (**C**) Columbia blood agar plate culture for 72 hours and the colony morphology; (**D**) Gram stain, magnification × 1000.

three clusters, with no significant differences observed among the strains from various regions. The strain samples were prepared following the standard operating procedure for the formic acid extraction method. All strains were identified as *L. mirabilis* using the MALDI-TOF mass spectrometer (Zybio, China). The cluster dendrogram of the *L. mirabilis* species complex was generated using EX-Smartspec V1 software (Figure 3). The cluster dendrogram indicates that the 38 strains can be categorized into three clusters, with no significant differences observed among strains from different regions. By comparing the evolutionary tree with the cluster tree, we found no notable regional differences among the 38 strains.

Table 2 In vitro MIC of 38 *L. mirabilis* Strains by E-Test Method

Antifungal Agent	Number of Strains MIC/(μg/mL)												
	0.008	**0.016**	**0.032**	**0.064**	**0.125**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**
Ampicillin	5	6	6	9	10	1	1						
Cefuroxime				1	10	6	7	11	2			1	
Cefotaxime		5	15	11	4	1	1	1					
Ciprofloxacin			1	10	6		1					1	19
Levofloxacin					16	1		1				1	19
Meropenem	3	11	10	8	4	1	1						
Amikacin					3	13	15	6	1				
Tetracycline					4	18	12	4					
Aztreonam				37	1								

https://doi.org/10.2147/IDR.S573707

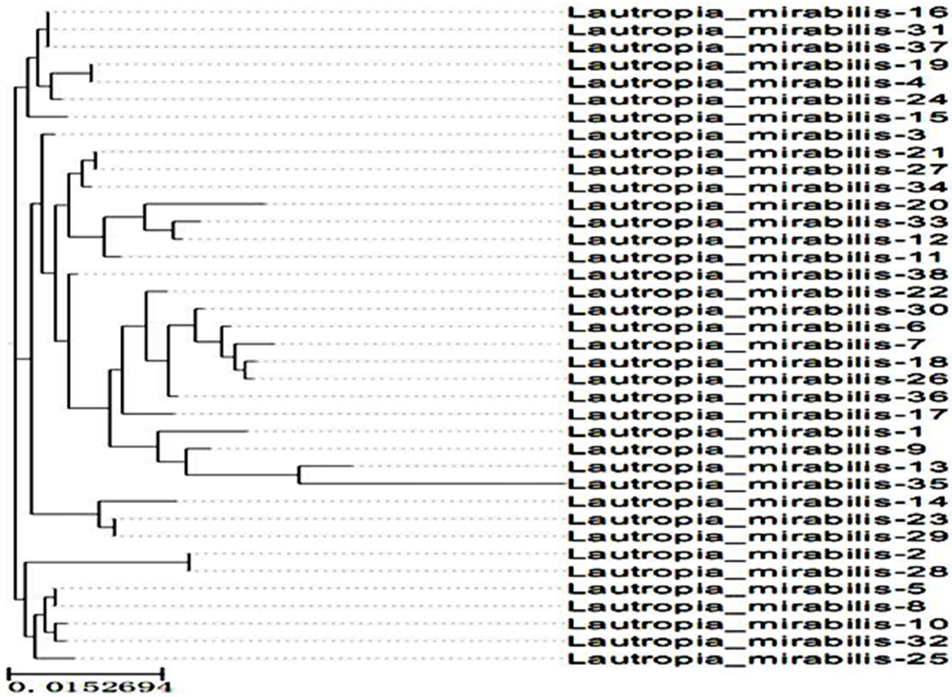

Figure 2 Molecular evolution tree of 38 *L. mirabilis* strains.

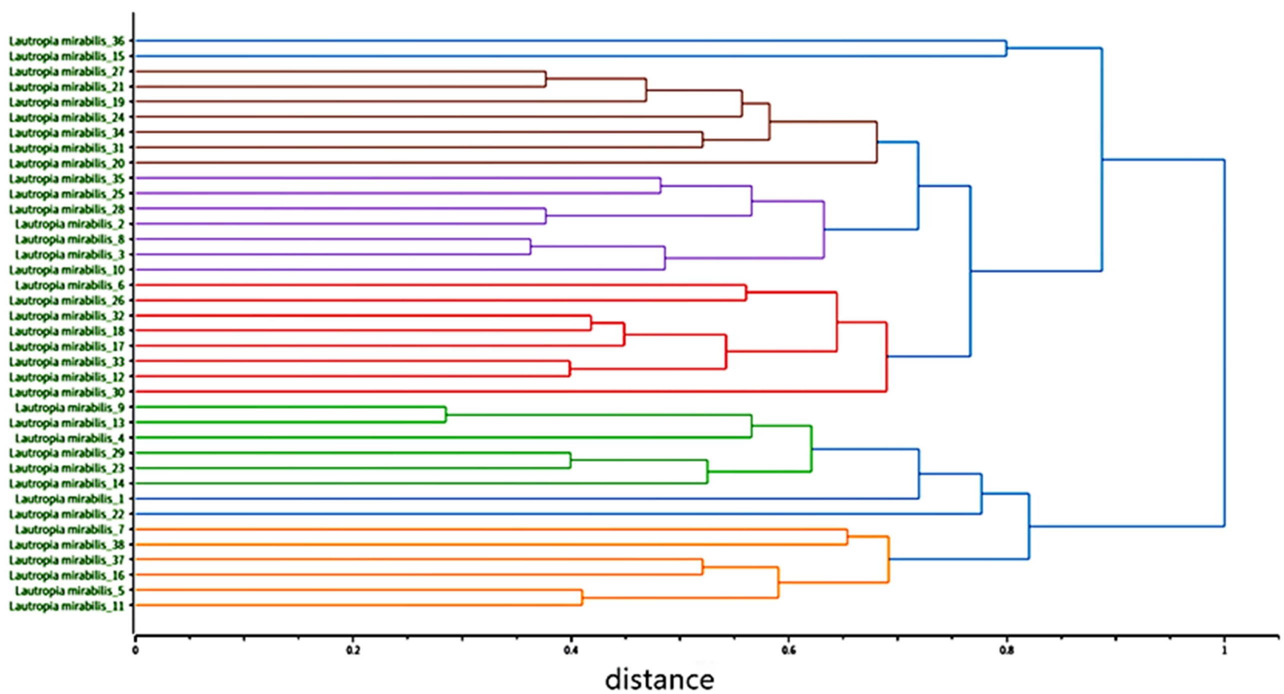

Figure 3 Cluster dendrogra of 38 *L. mirabilis* strains.

Discussion

L. mirabilis was initially described by Gerner-Smidt et al in 1994.[8] This organism is a motile, facultatively anaerobic, gram-negative coccus that is capable of fermenting glucose, fructose, sucrose, and mannitol. It can reduce both nitrate and nitrite and typically gives positive results for oxidase and urease tests, with occasional weak positivity for catalase. The cell morphology of *L. mirabilis* is highly polymorphic, exhibiting diameters that vary from 1 to over 10 μm. Phylogenetic analysis based on the 16S rRNA gene sequence positions this species within a distinct branch of the beta-subclass of Proteobacteria, where it is most closely associated with the genus Burkholderia.[9] While *L. mirabilis* has been isolated from a variety of human sources, its potential to cause disease remains poorly understood. It was first identified from samples taken from oral and upper respiratory regsm in the sputum of a cystic fibrosis patient[10] and from the oral cavities of children infected with the human immunodeficiency virus.[11]

L. mirabilis is a facultative anaerobic bacterium that exhibits optimal growth under aerobic conditions without the requirement for CO2. Its preferred growth temperature ranges from 30°C to 44°C.[12] This bacterium can thrive on various enriched media, including blood agar, chocolate agar, MacConkey agar, and MH agar. On blood agar, it displays slow growth with no hemolytic activity. In the initial stages of culture, the colonies appear flat, dry, and round. However, with prolonged culture time, they enlarge and develop a wrinkled, brittle texture reminiscent of volcanic craters. The colonies typically adhere to the substrate, resulting in a "biting agar" phenomenon.[13] Gram staining reveals that it is Gram-negative, and it forms larger spherical aggregates that are difficult to emulsify and prone to aggregation, often leading to misidentification as impurities due to their morphology.[14] The identification results of MALDI-TOF MS for 38 isolates were compared with the sequence data obtained from 16S RNA sequencing. Utilizing a cut-off score of ≥2.0, all isolates (100%, n = 38) were successfully identified at the species level. In the cluster dendrogram of the 38 strains analyzed, along with the molecular evolutionary tree constructed from 16S RNA sequencing, we observed no significant differences between different geographical locations and strains of *L. mirabilis*. However, due to the limited sample size collected, further studies are necessary to confirm this observation.

In this study, the proportion of patients over 60 years old accounted for 60.6%, all of whom had one or more underlying diseases. A total of 24 patients exhibited significant inflammatory infection manifestations in the lungs. The other 14 patients only showed mild symptoms of infection. Notably, 2 cases were associated with oral infections, indicating that *L. mirabilis* is most commonly observed in respiratory tract infections and can also lead to local or disseminated infections. These findings are consistent with previous literature reports.[15–17]This study found *L. mirabilis* infection predominantly occurs in elderly patients who have tumors, diabetes, hypertension, or exhibit low immunity due to the use of hormones or immunosuppressants. The human body primarily depends on cellular immune responses to combat bacterial infections.[10] Consequently, conditions that lead to reduced or impaired cellular immune function may increase susceptibility to *L. mirabilis*.

For in vitro drug susceptibility studies, we employed the microbroth dilution method. However, due to the poor emulsification effect and slow colony growth, the stability of the test results was compromised. Preliminary tests indicated that using E-test strips for drug susceptibility testing on sheep blood agar plates yielded more reliable results. Currently, there is no established clinical drug breakpoint for *L. mirabilis*. By referring to the drug susceptibility breakpoints for other non-Enterobacterales bacteria as outlined in CLSI M100, we determined that its sensitivities to ampicillin, cefuroxime, ceftazidime, meropenem, amikacin, tetracycline, and aztreonam were all 100%. However, it exhibited resistance to ciprofloxacin and levofloxacin, with a resistance rate of 52.6% (20/38). The patients in this study who were treated with cephalosporins, aminoglycosides, and carbapenems have all recovered. This outcome aligns with the results obtained from our bacterial in vitro drug susceptibility tests. The mechanisms of drug resistance to quinolone drugs primarily include:[18,19] mutations in the genes encoding DNA gyrase and topoisomerase IV; down-regulation of the target porin gene expression or alterations in the activity of efflux pumps, which reduce the intracellular concentration of quinolone drugs; and plasmid-mediated qnr genes that encode proteins conferring resistance to quinolone drugs.[20] Due to the constraints of this research, we were unable to detect quinolone drug resistance genes in *L. mirabilis*. Consequently, we cannot yet draw conclusions regarding the resistance mechanisms to ciprofloxacin and levofloxacin. Further research will be necessary to address this issue in the future.

Conclusion

L. mirabilis is a conditional pathogenic bacterium that can lead to opportunistic infections in humans. It is crucial to enhance our clinical understanding of this bacterium, particularly in elderly patients with compromised immune systems

 https://doi.org/10.2147/IDR.S573707

and those who have undergone extensive treatment with glycopeptides and β-lactam antibiotics. Awareness of the correlation between this bacterium and disease infections is essential. *L. mirabilis* can be identified using MALDI-TOF MS and 16S rRNA sequencing, and it can be treated symptomatically with cephalosporins, aminoglycosides, or carbapenems.

Ethical Approval

This study was approved by the Ethics Board of the Shanghai East Hospital, Shanghai, China (Approval No 2024YS-273). This study is an in vitro bacterial research and did not involve any human or animal subjects, nor did any personally identifiable information be used. The bacterial strains used were isolated from clinical samples. But the patient's personal information was permanently deleted, while only the data such as non identifying isolation sites were retained. So the samples of this study are anonymous biological materials. According to the Helsinki Declaration of the World Medical Association (Principle 1), as well as China's Ethical Review Measures for Biomedical Research Involving the Human Body (Article 3 of 2016) and Personal Information Protection Law (Article 73 of 2021), our research does not belong to "biological research involving the human body" and the data involved is anonymous. Therefore, it is not necessary to submit to the ethics committee for review and approval, nor is it necessary to obtain informed consent. Our research meets the conditions of exemption from ethical review and informed consent.

Acknowledgments

The authors thank the patients for their cooperation in the diagnostic process. Thanks Dr. Guo Jian from Shanghai East Hospital for his guidance on this study.

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.

Funding

This research received no external funding.

Disclosure

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this article.

References

1. Gerner-Smidt P, KEISER-NIELSEN H, DORSCH M, et al. Lautropia mirabilis gen. nov. sp. nov. a gram-negative motile coccus with unusual morphology isolated from the human mouth. *Microbiology.* 1994;140(7):1787–1797. doi:10.1099/13500872-140-7-1787
2. Ben Dekhil SM, Peel MM, Lennox VA, et al. Isolation of Lautropia mirabilis from sputa of a cystic fibrosis patient. *J Clin Microbiol*. 1997;35(4):1024–1026. doi:10.1128/jcm.35.4.1024-1026.1997
3. Alhumaid S, Al Mutair A, Al Alawi Z, et al. Coinfections with bacteria, fungi, and respiratory viruses in patients with SARS-CoV-2: a systematic review and meta-analysis. *Pathogens*. 2021;10:809. doi:10.3390/pathogens10070809
4. Lansbury L, Lim B, Baskaran V, Lim WS. Co-infections in people with COVID-19: a systematic review and meta-analysis. *J Infect*. 2020;81:266–275. doi:10.1016/j.jinf.2020.05.046
5. Jitvaropas R, Mayuramart O, Sawaswong V, et al. Classification of salivary bacteriome in asymptomatic COVID-19 cases based on long-read nanopore sequencing. *Exp. Biol. Med*. 2022;247(21):1937–1946. doi:10.1177/15353702221118091
6. Cruz C, Sousa M, Vilela S, et al. ***Lautropia mirabilis***: an exceedingly rare cause of peritoneal dialysis-associated peritonitis. *Case Rep Nephrol Dial*.;12(2):81–84. doi:10.1159/000524494.
7. Yang I, Claussen H, Arthur RA, et al. Subgingival microbiome in pregnancy and a potential relationship to early term birth. *Front Cell Infect Microbiol*. 2022;12:873683. doi:10.3389/fcimb.2022.873683
8. Tan RYP, Tan BQ, Rao N, et al. The first case of peritoneal dialysis-associated peritonitis due to Lautropia mirabilis. *Nephrology.* 2021;26(7):634–635. doi:10.1111/nep.13866

9. Preechanukul A, Saiprom N, Rochaikun K, et al. Metabolic requirements of CD160 expressing memory-like NK cells in Gram-negative bacterial infection. *Clin. Transl. Immunol*. 2024;13(7):e1513. doi:10.1002/cti2.1513
10. Rossmann SN, Wilson PH, Hicks J, et al. Isolation of Lautropia mirabilis from oral cavities of human immunodeficiency virus-infected children. *J Clin Microbiol*. 1998;36(6):1756–1760. doi:10.1128/JCM.36.6.1756-1760.1998
11. Yang I, Arthur RA, Zhao L, et al. The oral microbiome and inflammation in mild cognitive impairment. *Exp Gerontol*. 2021;147:111273. doi:10.1016/j.exger.2021.111273
12. Baraniya D, Jain V, Lucarelli R, et al. Screening of health-associated oral bacteria for anticancer properties in vitro. *Front Cell Infect Microbiol*. 2020;10:575656. doi:10.3389/fcimb.2020.575656
13. Lim YK, Park S-N, Lee W-P, et al. Lautropia dentalis sp. nov. isolated from human dental plaque of a gingivitis lesion. *Curr. Microbiol*. 2019;76(11):1369–1373. doi:10.1007/s00284-019-01761-1
14. Muro M, Soga Y, Higuchi T, et al. Unusual oral mucosal microbiota after hematopoietic cell transplantation with glycopeptide antibiotics: potential association with pathophysiology of oral mucositis. *Folia microbiologica*. 2018;63(5):587–597. doi:10.1007/s12223-018-0596-1
15. Voronina OL, Kunda MS, Ryzhova NN, et al. On Burkholderiales order microorganisms and cystic fibrosis in Russia. *BMC Genomics*.;19(3):74. doi:10.1186/s12864-018-4472-9.
16. Colombo APV, Bennet S, Cotton SL, et al. Impact of periodontal therapy on the subgingival microbiota of severe periodontitis: comparison between good responders and individuals with refractory periodontitis using the human oral microbe identification microarray. *J. Periodontol*. 2012;83(10):1279–1287. doi:10.1902/jop.2012.110566
17. Daneshvar MI, Douglas MP, Weyant RS, et al. Cellular fatty acid composition of Lautropia mirabilis. *J Clin Microbiol*. 2001;39(11):4160–4162. doi:10.1128/JCM.39.11.4160-4162.2001
18. Chen Y, Liu LH, Wu CR, et al. Progress in the mechanism of quinolone resistance of qnr family. *Foreign Medicine*. 2021;42(4):193–203.
19. Aldred KJ, Kerns RJ, Osheroff N. Mechanism of quinolone action and resistance. *Biochemistry*. 2014;53(10):1565–1574. doi:10.1021/bi5000564
20. Vetting MW, Hegde SS, Fajardo JE, et al. Pentapeptide repeat proteins. *Biochemistry*. 2006;45(1):1–10. doi:10.1021/bi052130w