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# *Escherichia albertii* isolated from the bloodstream of a patient with liver cirrhosis in China: A case report

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# ABSTRACT

A rare case of bacteremia caused by *Escherichia albertii*, in a 50-year-old male with liver cirrhosis was reported. Clear, colorless, and circular colonies were recovered on blood agar after 24 h of aerobic incubation at 37 °C. The isolate was identified as *E. albertii* using MALDI-TOF/MS and confirmed by the diagnostic triplex-PCR targeting *clpX*, *lysP*, and *mdh* genes. The administration of piperacillin/tazobactam intravenously (4.5g every 8 hours) for 3 days was effective. This study suggested that specific strains of *E. albertii* have been implicated in causing extraintestinal infections in humans, similar to extraintestinal pathogenic *E. coli* (ExPEC). However, a comprehensive understanding of the underlying pathogenic mechanisms requires further exploration.

# 1. Introduction

*Escherichia albertii* is an emerging enteric pathogen associated with sporadic episodes of infectious diarrhea and gastroenteric outbreaks in humans [1]. It was first described as atypical *eae*-positive *Hafnia alvei* from a diarrheic infant in Bangladesh in 1991, and was later confirmed as a new species within the genus *Escherichia* in 2003 [2]. The locus of enterocyte effacement (LEE), cytolethal-distending toxin (CDT), and Shiga toxin 2 variants (Stx2a, Stx2f) played a significant role in the virulence of *E. albertii*, contributing to clinical manifestations [1]. It was generally believed that the serotype of strains provided valuable information for identifying pathogenic clonal groups, especially for public health surveillance. Currently, 43 *E. albertii* O-antigen genotypes (EAOg) and 4 *E. albertii* H-antigen genotypes (EAHg) were defined in *E. albertii* strains [3–6].

*E. albertii* has been widely detected in poultry, birds, and raccoons [7]. Infection in humans could occur due to contact with these animals or the consumption of contaminated food. It has implicated gastrointestinal disease and several urinary tract infections (UTI) [8–10]. The incidence of bacteremia caused by *E. albertii* is generally uncommon and rare, with only one reported case in the literature [11]. Herein, we reported the first case of a male with liver cirrhosis presenting bacteremia caused by *E. albertii* in China.

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#### 2. Case presentation

A 50-year-old male with liver cirrhosis (>2 years) presented on June 20th, 2022 with chief complaints of abdominal distension, fatigue, and poor appetite for 10 days. He has a history of smoking for 20 years and alcoholism for 10 years. Laboratory findings on admission were as follows: serum albumin (ALB), 29.6 (reference, 40-60) g/L; albumin/globulin (A/G), 0.82 (reference, 1.2–2.5); total carbon dioxide 17.5 (reference, 22–29) mmol/L; total bilirubin, 43.6 (reference, 5.1–19) µmol/L; direct bilirubin, 29.1 (reference, 0–6) µmol/L; total bile acid 144.5 (reference: 0–10) µmol/L; alanine aminnotransferase, 51 (reference: 0–40) U/L; aspartate transaminase, 44 (reference: 0–40) U/L; alkaline phosphatase, 162 (reference: 45–125) U/L; cholinesterase, 1462.0 (reference: 4500–13000) U/L; hemoglobin (Hb), 63 (reference: 120–165) g/L; red blood cell (RBC) count, 2.75 (reference: 4.3–5.8) × 10<sup>12</sup>/L; neutrophil percentage, 77 (reference: 55–70) %; absolute lymphocyte count, 0.74 (reference: 1.1–3.2) × 10<sup>9</sup>/L; lymphocyte percentage, 13.3 (reference: 20–50) %, platelet count, 75 (reference: 125–350) × 10<sup>9</sup>/L. The physical examination revealed an appearance consistent with chronic liver disease, including yellowing of the skin and sclera, dilation of cheek capillaries, spider web-like blood vessels in the chest, as well as redness in the palms. Additionally, the abdominal magnetic resonance imaging (MRI) examination indicated hepatomegaly, splenomegaly, cholecystitis with inflammatory deposits, small cysts in both kidneys, and an accessory spleen. Rivaltas test of ascites fluid was positive. The diagnosis on admission was multiple comorbidities, including decompensated cirrhosis, chronic liver failure, ascites, pleural effusion, hypoproteinemia, gallstones, and renal cysts. The initial treatment was intravenous injection of glutathione and polyene phosphatidylcholine. On June 30, his Hb level was only 62 g/L, and as a result, RBC suspension was initiated.

On July 2nd, 2022, he developed an undetermined fever accompanied by mild cough, with peak body temperature of 38.8 °C. Subsequent laboratory findings were as follows: ALB, 28.8 g/L; Hb, 84 g/L; neutrophil percentage, 83.9%; hypersensitive C-reactive protein, 9.3 (reference: <5) mg/L. Blood culture collected during febrile episodes over a 24-h resulted in isolating a Gram-negative bacterium. A secondary diagnosis was bacteremia. The patient was then treated with piperacillin/tazobactam intravenously (4.5 g every 8 hours) for 3 days. His health condition improved, and the subsequent blood culture was negative. Afterward, the patient was discharged from the hospital, and there was no relapse of bacteremia after 6 months of follow-up.

# 3. Identification

The strain (ESA303) isolated from the bloodstream of the patient displayed clear, colorless, and circular colonies on the MacConkey agar. The strain was non-motile in a semisolid agar medium. Later, matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF/MS, Bruker Daltonics, Germany) was performed in clinical laboratory, which displayed presumptive identification of *E. albertii* (score 2.44). Subsequently, the isolate was transferred to Zigong Center for Disease Control and Prevention, and was confirmed as *E. albertii* by the diagnostic triplex-PCR targeting *clpX*, *lysP*, and *mdh* genes, as previously described [12]. Then, the antimicrobial susceptibility was evaluated using VITEK2 Compact (bioMérieux, Lyon, France) and strain ESA303 was sensitive to all antibiotics, including ampicillin, amikacin, aztreonam, ciprofloxacin, cefotetan, ertapenem, cefepime, gentamicin, levofloxacin, cotrimoxazole, tobramycin, piperacillin/tazobactam, ampicillin/sulbactam, ceftriaxone, imipenem, ceftazidime, amoxicillin/clavulanate, cefuroxime, cefzolin, meropenem, and cefoperazone/sulbactam.

The genomic DNA of strain ESA303 was extracted using the Wizard Genomic DNA purification kit (Promega, WI, USA). Fragment libraries of the genomic DNA were generated using the Universal DNAseq Library Prep Kit (KAITAI-BIO, Hangzhou, China) and were sequenced using the Illumina HiSeq 2000 platform (Illumina, San Diego, CA, USA). Then, Unicycler v0.4.8 and QUAST v5.2.0 were used for *de novo* assembly and genomic quality check as previously described [13]. The draft genome sequence of strain ESA303 had a total length of 4,856,921 bp, comprising 87 scaffolds, with a GC content of 49.5% and N50 value of 237,302, similar to the previously reported [14]. Based on the whole genome sequencing (WGS) analysis, the isolate carried *eae*- $\alpha$ 10 subtype, and harbored both *cdtB*-I and *cdtB*-II, but was negative for *stx2* gene. The EAOg and EAHg of the isolate were determined as EAOg13 and EAHg1, respectively. In addition, strain ESA303 harbored *papA/C/D/H* (P fimbriae structural subunit and assembly), *ibeA/B/C* (invasion of brain endothelial cells), *chuA/S/T/U/W/X/Y/Z* (heme uptake), *vat* (vacuolating autotransporter gene), which were important virulence markers of extraintestinal pathogenic *E. coli* (EXPEC) [15]. Notably, *faeC/D/E/F/H/I* (K88/F4 fimbriae) genes were also detected in strain ESA303, which was the most common colonization factor associated with intestinal infection of enterotoxigenic *E. coli* (ETEC) [16].

## 4. Discussion

Bacteremia is a serious complication in patients with liver cirrhosis, affecting 4–21% of patients [17]. The major causative organisms are Gram-negative bacteria, e.g., *E. coli, Klebsiella* spp., and *Enterobacter* spp [17]. To our knowledge, there was only one reported case of bacteremia caused by *E. albertii*. That case involved a 76-year-old female with multiple comorbidities: a recent pelvic fracture, a dysplastic polyp of the gastric fundus with carcinoma-in-situ, hypothyroidism due to a previous thyroidectomy for papillary carcinoma, epilepsy, and hypertension [11]. Here we reported the first case of *E. albertii* bacteremia in China, which involves a patient with liver cirrhosis. Similarly, to the former case, this male was also elderly, with various chronic diseases, but displayed no clinical features of gastrointestinal infection. The presence of multiple comorbidities might compromise the patient's immune system, and hamper effective bacterial clearance, hence resulting in a high risk of pathogen invasion and bacteremia in the elderly.

In previous surveillance, *E. albertii* was typically found in poultry feces/intestinal contents and poultry meat, wild birds, and raccoons [7,12,18,19]. People might be infected through contact with these animals or by consuming contaminated water, vegetables, and meat [20]. In this case, the infected patient resided in a rural area, and his neighbor fed chickens and ducks in the backyard. Therefore, we speculated that this infection was more likely transmitted through animals. This case further proved that *E. albertii*, an

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emerging diarrheagenic pathogen, could invade human blood and cause bacteremia. It emphasized the need for more attention to *E. albertii* as a potential threat to human health. Fortunately, the patient experienced a transient bacteremia and was effectively managed after antibiotic treatment.

Pathogenic *E. coli*, including intestinal pathogenic *E. coli* (IPEC) and extraintestinal pathogenic *E. coli* (ExPEC), can acquire virulence factors associated with increased pathogenicity, causing intestinal or extraintestinal infections. ExPEC has many virulenceassociated factors, typically encoded on pathogenicity islands (PAIs), plasmids, and other mobile genetic elements [15]. In this study, the isolates simultaneous possession of papA/C/D/H, ibeA/B/C, chuA/S/T/U/W/X/Y/Z, and *vat* genes might explain the extraintestinal infection. Moreover, strain ESA303 harbored the F4 fimbriae-related genes, which could have contributed to the pathogenicity of the isolate [21]. Therefore, it is possible that certain *E. albertii* strains acquired specific virulence factors, enabling them to settle in different niches and causing extraintestinal infections, similar to ExPEC. Nevertheless, further investigation is required for this mechanism.

# 5. Conclusion

This case report described a rare case of bacteremia caused by *Escherichia albertii*, in a 50-year-old male with liver cirrhosis. The administration of piperacillin/tazobactam intravenously (4.5g every 8 hours) for 3 days was effective. This report implied that some certain *E. albertii*, can cause human extraintestinal infection, similar to ExPEC, and the underlying pathogenic mechanism needs further study.

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#### **Ethics statement**

We have obtained written informed consent from the patient for the publication of the data. All investigations in this case report were approved by the Research Ethics Committee of Zigong Center for Disease Control and Prevention (No. 2021004).

# Data availability statement

The genome of strain ESA303 was submitted to GenBank under the accession number JAUGZJ000000000.

## Additional information

No additional information is available for this paper.

# CRediT authorship contribution statement

Qian Liu: Writing – original draft, Software, Methodology, Formal analysis, Data curation. Hong Wang: Writing – original draft, Resources, Investigation, Funding acquisition, Data curation. Suchuan Zhang: Writing – original draft, Software, Resources, Investigation, Data curation. Guodong Yan: Writing – review & editing, Software, Formal analysis. Xi Yang: Writing – review & editing, Software, Formal analysis. Jianping Deng: Writing – review & editing, Resources, Investigation. Xi Chen: Writing – review & editing, Resources, Investigation. Ling Zhang: Writing – review & editing, Resources, Investigation. Jie Zhang: Writing – review & editing, Resources, Investigation. Bin Wang: Writing – review & editing, Resources, Investigation. Nianli Zou: Writing – review & editing, Resources, Investigation. Yanwen Xiong: Writing – review & editing, Supervision, Funding acquisition. Zhengdong Zhang: Writing – review & editing, Validation, Project administration.

#### Declaration of competing interest

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 paper.

# References

- T.A.T. Gomes, T. Ooka, R.T. Hernandes, D. Yamamoto, T. Hayashi, M.S. Donnenberg, *Escherichia albertii* pathogenesis, EcoSal Plus 9 (2020), https://doi.org/ 10.1128/ecosalplus.ESP-0015-2019.
- [2] G. Huys, M. Cnockaert, J.M. Janda, J. Swings, Escherichia albertii sp. nov., a diarrhoeagenic species isolated from stool specimens of Bangladeshi children, Int. J. Syst. Evol. Microbiol. 53 (2003) 807–810, https://doi.org/10.1099/ijs.0.02475-0.
- [3] O.I. Naumenko, H. Zheng, A.S. Shashkov, Y. Sun, S.N. Senchenkova, L. Bai, et al., *Escherichia albertii* EA046 (O9) harbors two polysaccharide gene clusters for synthesis of the O-antigen by the Wzx/Wzy-dependent pathway and a mannan shared by *Escherichia coli* O8 by the Wzm/Wzt-dependent pathway, Int. J. Biol. Macromol. 142 (2020) 609–614, https://doi.org/10.1016/j.ijbiomac.2019.09.135.
- [4] H. Wang, H. Zheng, Q. Li, Y. Xu, J. Wang, P. Du, et al., Defining the genetic features of O-antigen biosynthesis gene cluster and performance of an O-antigen serotyping scheme for *Escherichia albertii*, Front. Microbiol. 8 (2017) 1857, https://doi.org/10.3389/fmicb.2017.01857.

- [5] T. Ooka, K. Seto, Y. Ogura, K. Nakamura, A. Iguchi, Y. Gotoh, et al., O-antigen biosynthesis gene clusters of *Escherichia albertii*: their diversity and similarity to *Escherichia coli* gene clusters and the development of an O-genotyping method, Microb. Genom. 5 (2019), https://doi.org/10.1099/mgen.0.000314.
- [6] K. Nakae, T. Ooka, K. Murakami, Y. Hara-Kudo, N. Imuta, Y. Gotoh, et al., Diversification of *Escherichia albertii* H-antigens and development of H-genotyping PCR, Front. Microbiol. (2021) 12, https://doi.org/10.3389/fmicb.2021.737979.
- [7] A. Hinenoya, K. Nagano, S.P. Awasthi, N. Hatanaka, S. Yamasaki, Prevalence of Escherichia albertii in raccoons (Procyon lotor), Japan, Emerg. Infect. Dis. 26 (2020) 1304–1307, https://doi.org/10.3201/eid2606.191436.
- [8] F. Muchaamba, K. Barmettler, A. Treier, K. Houf, R. Stephan, Microbiology and epidemiology of *Escherichia albertii* an emerging elusive foodborne pathogen, Microorganisms 10 (2022) 875, https://doi.org/10.3390/microorganisms10050875.
- [9] K. Masuda, T. Ooka, H. Akita, T. Hiratsuka, S. Takao, M. Fukada, et al., Epidemiological aspects of Escherichia albertii outbreaks in Japan and genetic
- characteristics of the causative pathogen, Foodb. Pathog. Dis. 17 (2020) 144–150, https://doi.org/10.1089/fpd.2019.2654.
  [10] M.E.S. Zaki, A.E. Eid, S.S. El-Kazzaz, A.M. El-Sabbagh, Molecular study of *Escherichia albertii* in pediatric urinary tract infections, Open Microbiol. J. 15 (2021)
- 139–144, https://doi.org/10.2174/1874285802115010139.
  [11] T.J.J. Inglis, A.J. Merritt, N. Bzdyl, S. Lansley, M.N. Urosevic, First bacteraemic human infection with *Escherichia albertii*, New Microbes New Infect. 8 (2015) 171–173, https://doi.org/10.1016/j.nmni.2015.07.003.
- [12] Q. Liu, X. Bai, X. Yang, G. Fan, K. Wu, W. Song, et al., Identification and genomic characterization of *Escherichia albertii* in migratory birds from Poyang Lake, China, Pathogens 12 (2022) 9, https://doi.org/10.3390/pathogens12010009.
- [13] M. Aswal, N. Singhal, M. Kumar, Genomic analysis of phylogroup D Escherichia coli strains using novel de-novo reference-based guided assembly, Sci. Data 10 (2023) 573, https://doi.org/10.1038/s41597-023-02444-0.
- [14] T. Ooka, Y. Ogura, K. Katsura, K. Seto, H. Kobayashi, K. Kawano, et al., Defining the genome features of *Escherichia albertii*, an emerging enteropathogen closely related to *Escherichia coli*, Genome Biol. Evol. (2015), evv211, https://doi.org/10.1093/gbe/evv211.
- [15] J. Sarowska, B. Futoma-Koloch, A. Jama-Kmiecik, M. Frej-Madrzak, M. Ksiazczyk, G. Bugla-Ploskonska, et al., Virulence factors, prevalence and potential transmission of extraintestinal pathogenic *Escherichia coli* isolated from different sources: recent reports, Gut Pathog. 11 (2019), https://doi.org/10.1186/ s13099-019-0290-0.
- [16] E. Denamur, O. Clermont, S. Bonacorsi, D. Gordon, The population genetics of pathogenic Escherichia coli, Nat. Rev. Microbiol. 19 (2021) 37–54, https://doi. org/10.1038/s41579-020-0416-x.
- [17] C. Bunchorntavakul, N. Chamroonkul, D. Chavalitdhamrong, Bacterial infections in cirrhosis: a critical review and practical guidance, World J. Hepatol. 8 (2016) 307–321, https://doi.org/10.4254/wjh.v8.i6.307.
- [18] L. Luo, H. Wang, M.J. Payne, C. Liang, L. Bai, H. Zheng, et al., Comparative genomics of Chinese and international isolates of *Escherichia albertii*: population structure and evolution of virulence and antimicrobial resistance, Microb. Genom. 7 (2021), https://doi.org/10.1099/mgen.0.000710.
- [19] H. Wang, Q. Li, X. Bai, Y. Xu, A. Zhao, H. Sun, et al., Prevalence of eae-positive, lactose non-fermenting Escherichia albertii from retail raw meat in China, Epidemiol. Infect. 144 (2016) 45–52, https://doi.org/10.1017/s0950268815001120.
- [20] T. Konno, S. Suzuki, S. Takahashi, H. Kashio, Y. Ito, Y. Kumagai, Isolation and characterization of *Escherichia albertii* from retail meats and vegetables in Akita Prefecture, Japan, Jpn. J. Food Microbiol. 38 (2021) 144–152, https://doi.org/10.5803/jsfm.38.144.
- [21] V. Michelacci, A. Maugliani, R. Tozzoli, G. Corteselli, P. Chiani, F. Minelli, et al., Characterization of a novel plasmid encoding F4-like fimbriae present in a Shiga-toxin producing enterotoxigenic *Escherichia coli* isolated during the investigation on a case of hemolytic-uremic syndrome, Int. J. Med. Microbiol. 308 (2018) 947–955, https://doi.org/10.1016/j.ijmm.2018.07.002.