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CASE REPORT

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A case of a renal abscess caused by *Salmonella* bareilly in a previously healthy boy

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Abstract

Background: Renal abscesses are relatively uncommon in children, and usually due to Gram-negative rods or *Staphylococcus aureus*, whereas abscesses caused by *Salmonella* are very rare.

Case presentation: We present the case of a previously healthy 10-year-old boy who had a renal abscess due to *Salmonella* bareilly. He responded well to treatment with antibiotics, and computed tomography (CT)-guided drainage of the abscess. His blood, urine and abscess aspirate cultures were sterile, but a broad-range 16S rDNA polymerase chain reaction (PCR) assay of the aspirate followed by analysis of four *Salmonella* genes (*fliC*, *fliD*, *sopE2*, and *spaO*) identified *S.* bareilly as the causative agent.

Conclusion: To the best of our knowledge, this is the first report of renal abscess caused by *S.* bareilly.

Keywords: *Salmonella* bareilly, Renal abscess, Broad-range 16S rDNA PCR, Single-nucleotide polymorphism

Background

Nontyphoidal salmonellae are foodborne and waterborne [1] pathogens that cause gastroenteritis, bacteraemia, and focal infection. Endovascular infection and deep bone or visceral abscesses are severe complications that may be difficult to treat [2]. However, renal abscess is a rare consequence of *Salmonella* bacteraemia, and the presence of a urogenital abnormality or compromised host immunity may predispose patients to complications even in cases of transient bacteraemia. *S.* bareilly, a group C1 serovar first identified in India in 1928 [3] is one of the most common *Salmonella* found in water [1] that can cause food poisoning. There was previously a worldwide foodborne outbreak of *S.* bareilly [4]. *S.* bareilly is less invasive than other nontyphoidal *salmonella* serovars [5] and has not, to our knowledge, been associated with renal abscesses.

Microbiological culture is an essential procedure for diagnosis of bacteraemia and sepsis, but prior use of antibiotics before sampling frequently reduces the detection rate of bacteria in culture studies. In these cases, molecular methods may be useful to identify the causative agent [6]. Here, we describe a case of renal abscess in a 10-year-old previously healthy boy who had no urogenital abnormality. The patient was previously treated with antibiotics, and thus, no bacterial growth was observed in the drainage culture. The application of a broad-range bacterial polymerase chain reaction (PCR) of 16S rDNA technology coupled with sequencing of four *Salmonella* genes identified *S.* bareilly as the causative agent of the infection.

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Case presentation

A 10-year-old previously healthy boy living in Japan presented with a 6-week history of fever, appetite loss, and weight loss of 2 kg. He had met normal developmental milestones and had received routine childhood vaccinations. He had no history of urinary tract infection or allergies. The family history was unremarkable. These symptoms began approximately 2 weeks after his return from Guam, where he had travelled for a 6-day vacation with his parents and brother. He enjoyed swimming at a pool in a "3-star resort hotel", and frequently dived into the water. He received no typhoid vaccination or prophylactic therapy prior to his travel. He had no abdominal pain or diarrhoea but had precordial discomfort, difficulty swallowing, some nausea, and anorexia. Two weeks before admission, examination by a home doctor or otolaryngologist was unremarkable, except for tonsillar hypertrophy. One week before admission, he was found to have low-grade fever. Four days before admission, he was treated by a home doctor with azithromycin (10 mg/kg/day) for 3 days, but his symptoms did not improve. Physical examination on admission at the paediatric centre was unremarkable except for fever (38.5 °C) and right-sided flank tenderness. Pertinent laboratory findings included a total white blood cell (WBC) count of 8.35 (normal value, 3.5–8.5) $\times 10^9$/L, with 64% neutrophils. C-reactive protein (CRP) was 88.4 (normal value, 0.0–3.0) mg/L. Renal function tests revealed normal blood urea nitrogen (10.1 mg/dL) and serum creatinine (0.37 mg/dL). Urinalysis was normal. No organism was isolated from urine or blood culture. The test for human immunodeficiency virus was negative. Ultrasound examination showed that the right kidney was normal in size (9.8 × 4.2 cm) but had a cystic lesion (4.58 × 3.63 × 3.36 cm). The left kidney showed no evidence of disease. There was no abnormality in the urinary tract. Computed tomography (CT) revealed a cystic mass with ring enhancement in the right kidney (Fig. 1). Based on these results, we tentatively diagnosed his illness as a right renal abscess and treated him with ceftriaxone 2 g (80 mg/kg/day) by the intravenous route in two divided doses for 3 days. Because there was no clinical improvement, the treatment was changed to meropenem trihydrate (120 mg/kg/day), which was administered three times a day for 3 days. Thereafter, vancomycin (45 mg/kg/day) was added three times a day for 3 days because of increased fever (38.9 °C) and CRP (114.8 mg/L). However, because there was still no clinical improvement despite a 10-day treatment with antibiotics, he was transferred to our hospital, where under local anaesthesia, a CT-guided percutaneous puncture of the renal abscess was performed, and 10 mL of creamy pus was drained. He became afebrile soon after, and the flank tenderness also subsided, but he was continued on the antibiotic regimen of intravenous meropenem and vancomycin for an additional 15 days. The duration of hospitalization was a total of 31 days. He was thereafter discharged, and remained asymptomatic for more than 1 year.

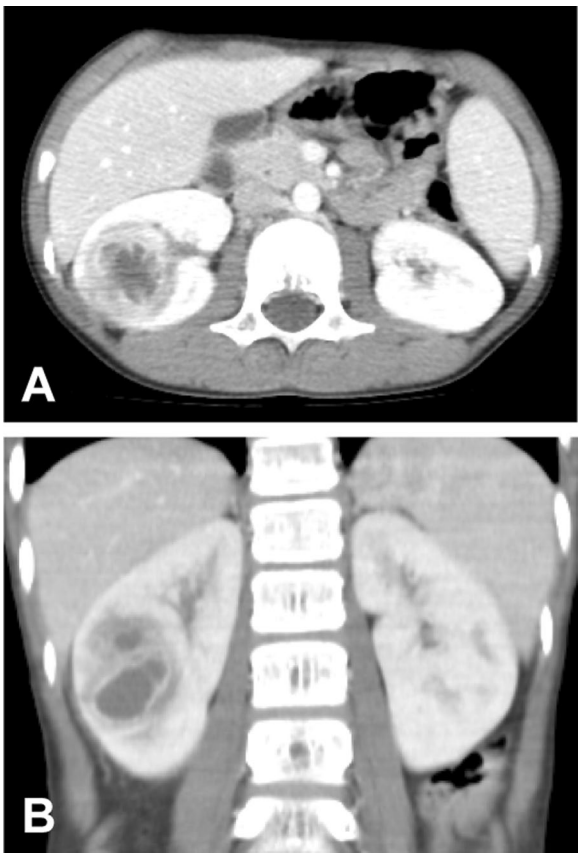

Fig. 1 Abdominal contrast-enhanced computed tomography of the patient, **A** horizontal and **B** vertical slices

Gram staining of the aspirate revealed only WBCs, and its culture was sterile. Therefore, broad-range 16S rDNA PCR amplification and sequencing were performed using PCR primers 8UA (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1485B (5′-TACGGTTACCTTGTTACGAC-3′) [7] and DNA extracted from the aspirate. The sequence (Fig. 2) was 99.9% identical (1465/1466) to several *Salmonella enterica* strains.

To identify the serovar of *Salmonella*, we examined single-nucleotide polymorphisms (SNPs) located on three *Salmonella* genes, *fliD* (STM1960), *sopE2* (STM1855), and *spaO* (STM2891) [8], and found SNPs identical to *S.* bareilly or *S.* paratyphi B variant Java (Table 1). Next, we examined the *fliC* gene of *S.* bareilly and *S.* paratyphi B variant Java by comparison with that of *S.* typhimurium (STM1959). Further PCR amplification and sequencing were also performed to analyse the *fliC* gene using

10	20	30	40	50	60
ATTGAACGCT	GGCGGCAGGC	CTAACACATG	CAAGTCGAAC	GGTAACAGGA	AGCAGCTTGC
70	80	90	100	110	120
TGCTTTGCTG	ACGAGTGGCG	GACGGGTGAG	TAATGTCTGG	GAAACTGCCT	GATGGAGGGG
130	140	150	160	170	180
GATAACTACT	GGAAACGGTG	GCTAATACCG	CATAACGTCG	CAAGACCAAA	GAGGGGGACC
190	200	210	220	230	240
TTCGGGCCTC	TTGCCATCAG	ATGTGCCCAG	ATGGGATTAG	CTTGTTGGTG	AGGTAACGGC
250	260	270	280	290	300
TCACCAAGGC	GACGATCCCT	AGCTGGTCTG	AGAGGATGAC	CAGCCACACT	GGAACTGAGA
310	320	330	340	350	360
CACGGTCCAG	ACTCCTACGG	GAGGCAGCAG	TGGGGAATAT	TGCACAATGG	GCGCAAGCCT
370	380	390	400	410	420
GATGCAGCCA	TGCCGCGTGT	ATGAAGAAGG	CCTTCGGGTT	GTAAAGTACT	TTCAGCGGGG
430	440	450	460	470	480
AGGAAGGTGT	TGTGGTTAAT	AACCGCAGCA	ATTGACGTTA	CCCGCAGAAG	AAGCACCGGC
490	500	510	520	530	540
TAACTCCGTG	CCAGCAGCCG	CGGTAATACG	GAGGGTGCAA	GCGTTAATCG	GAATTACTGG
550	560	570	580	590	600
GCGTAAAGCG	CACGCAGGCG	GTCTGTCAAG	TCGGATGTGA	AATCCCCGGG	CTCAACCTGG
610	620	630	640	650	660
GAACTGCATT	CGAAACTGGC	AGGCTTGAGT	CTTGTAGAGG	GGGGTAGAAT	TCCAGGTGTA
670	680	690	700	710	720
GCGGTGAAAT	GCGTAGAGAT	CTGGAGGAAT	ACCGGTGGCG	AAGGCGGCCC	CCTGGACAAA
730	740	750	760	770	780
GACTGACGCT	CAGGTGCGAA	AGCGTGGGGA	GCAAACAGGA	TTAGATACCC	TGGTAGTCCA
790	800	810	820	830	840
CGCCGTAAAC	GATGTCTACT	TGGAGGTTGT	GCCCTTGAGG	CGTGGCTTCC	GGAGCTAACG
850	860	870	880	890	900
CGTTAAGTAG	ACCGCCTGGG	GAGTACGGCC	GCAAGGTTAA	AACTCAAATG	AATTGACGGG
910	920	930	940	950	960
GGCCCGCACA	AGCGGTGGAG	CATGTGGTTT	AATTCGATGC	AACGCGAAGA	ACCTTACCTG
970	980	990	1000	1010	1020
GTCTTGACAT	CCACAGAAGT	TTTCAGAGAT	GAGAATGTGC	CTTCGGGAAC	CGTGAGACAG
1030	1040	1050	1060	1070	1080
GTGCTGCATG	GCTGTCGTCA	GCTCGTGTTG	TGAAATGTTG	GGTTAAGTCC	CGCAACGAGC
1090	1100	1110	1120	1130	1140
GCAACCCTTA	TCCTTTGTTG	CCAGCGGTTA	GGCCGGGAAC	TCAAAGGAGA	CTGCCAGTGA
1150	1160	1170	1180	1190	1200
TAAACTGGAG	GAAGGTGGGG	ATGACGTCAA	GTCATCATGG	CCCTTACGAC	CAGGGCTACA
1210	1220	1230	1240	1250	1260
CACGTGCTAC	AATGGCGCAT	ACAAAGAGAA	GCGACCTCGC	GAGAGCAAGC	GGACCTCATA
1270	1280	1290	1300	1310	1320
AAGTGCGTCG	TAGTCCGGAT	TGGAGTCTGC	AACTCGACTC	CATGAAGTCG	GAATCGCTAG
1330	1340	1350	1360	1370	1380
TAATCGTGGA	TCAGAATGCC	ACGGTGAATA	CGTTCCCGGG	CCTTGTACAC	ACCGCCCGTC
1390	1400	1410	1420	1430	1440
ACACCATGGG	AGTGGGTTGC	AAAAGAAGTA	GGTAGCTTAA	CCTTCGGGAG	GGCGCTTACC
1450	1460				
ACTTTGTGAT	TCATGACTGG	GGTGAA			

Fig. 2 DNA sequence of the 16S rDNA PCR product amplified using DNA extracted from an aspirate as a template and 8UA and 1485B primers

Table 1 Twenty-three SNPs analysed by sequencing three genes

	fliD										*sopE2*							*spaO*					
***Salmonella enterica* serovar**	**612***	**616**	**639**	**651**	**747**	**748**	**753**	**758**	**765**	**786**	**421**	**455**	**463**	**465**	**471**	**477**	**480**	**68**	**73**	**80**	**87**	**156**	**163**
S. bareilly	C	C	C	T	A	A	G	C	C	C	C	G	G	G	A	T	T	A	C	G	G	G	C
S. paratyphi B variant Java	C	C	C	T	A	A	G	C	C	C	C	G	G	G	A	T	T	A	C	G	G	G	C
Patient	C	C	C	T	A	A	G	C	C	C	C	G	G	G	A	T	T	A	C	G	G	G	C

The results of *S.* bareilly and *S.* paratyphi B variant Java are as reported [8]

*The numbers represent the nucleotide location on the coding gene

forward (5′-CGATCTGAAGCAGATCAACTCTCA-3′) and reverse (5′-CATCAATTTTAGCCAGCGGGTTT-3′) primers and DNA extracted from the aspirate. The sequence of the PCR product (Fig. 3) was 100% (753/753) identical to that of *S.* bareilly strain CFSAN000189 and 73.9% (557/753) identical to *S.* paratyphi B variant Java strain 08-00436.

We performed follow-up cultures of blood, urine, and aspirate but did not detect any bacteria. We also attempted to detect *S.* bareilly by broad-range 16S rDNA PCR using blood specimens drawn 4 days and 1 month after admission, but the results were negative.

Discussion and conclusion

Renal abscesses, potentially lethal complications of urinary tract infections or bacteraemia, are infrequently encountered in children [9–11], but the actual prevalence is still unknown [10]. Paediatric renal abscesses are most commonly small in size and less than 3 cm in diameter [10, 11]. The most common pathogens isolated in children are *Escherichia coli* and *Staphylococcus aureus* [9–11]. According to a previous report, broad-spectrum and bactericidal antibiotics, such as second- and third-generation cephalosporins, are recommended for children with renal abscesses [12]. However, pathogens are sometimes resistant to antibiotic treatment [12, 13]. Thus, for initial treatment, antibiotics, such as meropenem plus vancomycin, should be selected, considering the harmful and destructive effects of renal abscesses on the kidneys. This combination is effective against not only Gram-negative bacilli but also Gram-positive bacteria, even though they are resistant strains.

There are no definite guidelines for surgical intervention in paediatric patients [14]. In adult patients, abscesses of less than 3 cm in diameter usually resolve with antibiotic therapy for 4–6 weeks [15]. Furthermore, several recent studies on paediatric renal abscesses have reported successful effects of antibiotic therapy against abscesses of less than 3 cm in diameter

10	20	30	40	50	60
GACCCTGGGT	CTGGATACGC	TGAATGTGCA	GAAAAAATAT	GATGTTGATA	ACACGGTTGT
70	80	90	100	110	120
CACGAACCCT	AATTATGTTG	ATGGTGCAGC	GTTAAGCACT	ACGATGCCTA	CTGCGGCTGA
130	140	150	160	170	180
GATTAAAACG	GCTATTGGCA	CTGGTGCGGG	AACTCCGGCA	GTTAAAGGTA	ATGAAGTTCA
190	200	210	220	230	240
ATTTGATAAG	AGCACTGGGA	AGTATTACGT	TGAAATTGAA	GGATATTCAG	CTCCTGATGC
250	260	270	280	290	300
AGCTAAAAAC	GGCATTTATG	AAGCCAAAGT	TGCTGATGAT	GGCACAATAT	CTTTGGAGAC
310	320	330	340	350	360
TGGGACCAAA	AAAATTGGCA	CCGCAATGCC	TGCTGGTGCT	GAAGTTATTA	CTCACGTGCA
370	380	390	400	410	420
GAAAAAAGAT	CAACCAGTTG	TTGTTGATGC	CAGCGTTAAA	GATGCTCTAA	AAGCTGGTGG
430	440	450	460	470	480
GGTAGATGAT	GCAGTTGCAG	ATACCGCGCA	ATTAGTCAAA	ATGTCTTACA	CTGATAAGAA
490	500	510	520	530	540
TGGTAAAACA	ATTGAAGGCG	GTTATGCGCT	TAAAGCTGGC	GATAAGTATT	ACGCCGCAGA
550	560	570	580	590	600
TTACGATGAA	GCGACAGGAG	CAATTAAAGC	TAAAACCACA	AGTTATACTG	CTGCTGACGG
610	620	630	640	650	660
TACTACCAAA	ACAGCGGCTA	ACCAACTGGG	TGGCGTAGAC	GGCAAAACCG	AAGTTGTTAC
670	680	690	700	710	720
TATCGATGGT	AAAACCTATA	ATGCCAGCAA	AGCTGAAGGT	CACAACTTTA	AAGCACAGCC
730	740	750			
TGATCTGGCG	GAAGCAGCCG	CTAAAACCAC	CGA		

Fig. 3 DNA sequence of the *fliC* PCR product amplified using DNA extracted from an aspirate as a template and *fliC* forward and reverse primers

[10, 11]. Percutaneous drainage may be considered for lesions of more than 3 cm in patients with persistent fever despite treatment with appropriate antibiotics or in patients who are immunologically compromised or critically ill [9–11]. In our case, the lesion was more than 3 cm, and the abscess was refractory to antibiotic therapy, and therefore required drainage. The prompt resolution of our patient's clinical symptoms after drainage suggests that surgical intervention is helpful.

Salmonella could cause gastroenteritis, bacteraemia, and subsequent focal infections. However, invasive nontyphoidal salmonellosis rarely affects the kidneys, and there are only a small number of reports of renal abscesses caused by *Salmonella* serovars, such as *S.* virchow [16], *S.* enteritidis, *S.* typhimurium [17, 18], and *S.* oranienburg [19]. Also, some nontyphoidal *Salmonella* serovars, such as *S.* choleraesuis and *S.* dublin, can cause more invasive disease than *S.* typhimurium or *S.* bareilly [5]. Indeed, there are only a small number of reports of extraintestinal infections by *S.* bareilly [20, 21].

The route of *Salmonella* infection in our patient is unclear, although infectious agents have been reported to threaten the health of pool users in tropical countries [22–24]. Since his family members did not show gastrointestinal symptoms during and after their trip, we speculate that he may have ingested contaminated water from the pool in the hotel. Unfortunately, we could not obtain information on *Salmonella* outbreaks associated with pool water in Guam.

We were unable to isolate the microorganisms from the abscess, perhaps because he had been on antibiotics sometimes before the sample was taken for culture. The diagnosis was therefore based on the result of broad-range PCR [6, 7], which can detect a wide variety of bacteria from biological samples even after sterilization with antibiotics. However, this alone is insufficient to determine the *Salmonella* serovar, and additional examination for specific bacterial genes [8] was required.

We conclude, to the best of our knowledge, that this is the first report of a paediatric renal abscess due to *S.* bareilly, which was detected using broad-range PCR followed by DNA sequencing of specific bacterial genes. The child responded satisfactorily to treatment with antibiotics and percutaneous surgical drainage of the abscess.

Abbreviations

CT: Computed tomography; DNA: Deoxyribonucleic acid; PCR: Polymerase chain reaction; rDNA: Ribosomal DNA; WBC: White blood cell; CRP: C-reactive protein; SNP: Single-nucleotide polymorphism.

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Authors' contributions

All authors contributed both to the writing of the manuscript and to the clinical treatment of the patient. Medical treatment was performed by MO, NS, and HN. Surgical treatment was performed by YH. Molecular examination and data analysis were performed by MI, TN, MB, and ST. The first draft of the manuscript was written by TN and MO, and all authors commented on the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets generated and analysed during the current study are available in the DNA Data Bank of Japan (DDBJ) repository under the following Accession Numbers: LC687364, LC687365.

Declarations

Ethics approval and consent to participate

This study was approved by the Ethics Committee of National Hospital Organization Mie Chuo Medical Centre.

Consent for publication

Written informed consent was obtained from the parents of the patient for publication of this case report and any accompanying images.

Competing interests

No competing interests to declare.

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