

# First report of serotype 23B *Streptococcus pneumoniae* isolated from an adult patient with invasive infection in Japan

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## Abstract

Serotype 23B *Streptococcus pneumoniae* was isolated from a 67-year-old Japanese patient with meningitis. This isolate was susceptible to penicillin G, while genotyped as gPISP with a mutation in a penicillin-binding motif in PBP2b. The 23B isolate was assigned to ST11996 that is related to CC439, a dominant group among serotype 23B. © 2017 The Author(s). Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

**Keywords:** Invasive infection, Japan, serotype 23B, *Streptococcus pneumoniae*

**Original Submission:** 1 November 2016; **Revised Submission:** 3 February 2017; **Accepted:** 28 February 2017

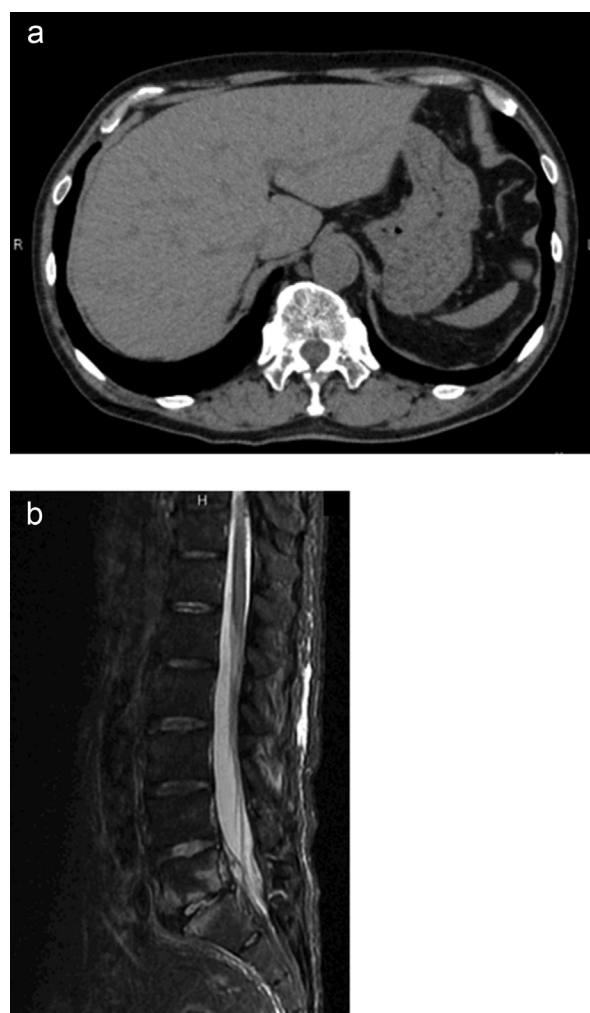
**Article published online:** 9 March 2017

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*Streptococcus pneumoniae* is a major cause of invasive infections, particularly in young children and the elderly worldwide. In Japan, a 13-valent pneumococcal conjugate vaccine (PCV13) has been used for routine immunization of children since 2013, and for adults on a voluntary basis since 2014, leading to a rapid reduction in invasive pneumococcal diseases (IPD) [1]. Since then, an increase of *S. pneumoniae* with non-vaccine serotypes has been noted for IPD as well as non-IPD [2–5]. A non-vaccine

type, 23B, has not yet been reported in Japan, although its increase was observed in Europe and the USA in the PCV13 era [6–9].

A fully ambulatory 67-year-old Japanese man with a past history of chronic kidney disease was admitted to our hospital in June 2016 for shaking chills and dysarthria without fever. He had no history of pneumococcal vaccination or recent overseas travel. On physical examination, he was lethargic with neck stiffness. Laboratory tests showed leucocytosis (18570/μL; normal range: 3500–9700/μL), elevated creatine level (6.69 mg/dL; normal range: 0.65–1.09 mg/dL), and elevated C-reactive protein level (47.59 mg/dL; normal range <0.30 mg/dL). Computed tomography (CT) revealed splenic hypoplasia without cerebral herniation (Fig. 1a). Cerebrospinal fluid analysis showed pleocytosis (cell



**FIG. 1.** Enhanced CT scan of the patient's abdomen showing splenic hypoplasia (a), T2-weighted sagittal MRI scan of the patient showing increased signal intensity at the L5–S1 level (b).

count:  $354/\text{mm}^3$ ), hypoglycorrhachia (0 mg/dL; plasma glucose level: 92 mg/dL), elevated protein (262 mg/dL; normal range: 10–40 mg/dL), and presence of Gram-positive diplococci and pneumococcal antigen. He was diagnosed with pneumococcal meningitis. Ceftriaxone (2 g twice daily) and vancomycin (1 g twice daily) with dexamethasone (10 mg four times daily) were administered intravenously. *Streptococcus pneumoniae* (MIC of penicillin G  $\leq 0.03$  mg/L) was isolated from blood and cerebrospinal fluid, and antibiotics were changed to intravenous ampicillin (3 g three times daily) on the 5th hospital day. Blood cultures turned negative from the 8th hospital day forward. On the 13th hospital day, he complained of low back pain. A T2-weighted MRI revealed increased signal intensity at the L5–S1 level, indicating osteomyelitis (Fig. 1b). Ampicillin was changed to ceftriaxone and oral rifampicin (600 mg/day). The patient was subsequently treated with intravenous antibiotics for 6 weeks, and discharged with oral amoxicillin (2 g/day) for another 2 weeks.

The *S. pneumoniae* isolate designated AT0814 was serotyped as 23B by Quellung reaction, and also by sequential multiplex PCR [10]. The *wzx* gene sequence of this isolate was identical to that of the 23B strain 1039/41, whereas it showed 81% identity to those of 23F and 23A strains. The isolate AT0814 was found to be susceptible to all the 18 antimicrobials as determined by the broth microdilution test. However, the PBP genotype was determined to be gPISP (*pbp2b*). Sequence analysis of *pbp1a*, *pbp2b* and *pbp2x* (GenBank Accession Nos KX698435–KX698437) revealed that PBP2b had an amino acid substitution in the penicillin-binding motif ( $442\text{SSNT}_{445} \rightarrow 442\text{SSNA}_{445}$ ). PCR testing revealed virulence factor genes *pspA* (Family 1, clade 1), *pspC* (Group 4), *ply*, *pavA*, *phtA*, *phtB*, *phtE*, *nanA*, *nanB* and *pcpA*, and the absence of *erm(B)*, *mefA/E* and pilus genes. AT0814 was assigned to ST11996 (allele combination 1-43-388-18-6-679-14) by multilocus sequence typing, which was not grouped into any clonal complex (CC). However, ST11996 showed similarity (four matched alleles) to ST8959 and ST11443 (CC439), both of which were reported for serotype 23B *S. pneumoniae* in Germany, Saudi Arabia and Qatar. Hence, it appears that AT0814 is genetically related to CC439, one of the dominant clones among serotype 23B [8].

This is the first report of *S. pneumoniae* serotype 23B in Japan. The isolate AT0814 was derived from IPD, and demonstrated a gPISP genotype and various virulence factors. Special attention must be paid to the prevalence and antimicrobial susceptibility of this serotype in the PCV era.

## Conflicts of Interest

None to declare.

## Acknowledgement

This study was supported by a Grant-in-Aid for Scientific Research (KAKENHI) (16K09101) from the Japan Society for Promotion of Science (JSPS).

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