An infant case of cervical purulent lymphadenitis caused by ST834 community-acquired methicillin-resistant *Staphylococcus aureus* with SCC*mec*-IVc in Japan

Satoshi Hirakawa and Toshihiko Mori
Department of Pediatrics, NTT EC Sapporo Medical Center, Sapporo, Japan
Yasuo Ohkoshi
Department of Microbial Laboratory, NTT EC Sapporo Medical Center, Sapporo, Japan
Meiji Soe Aung and Nobumichi Kobayashi
Department of Hygiene, Sapporo Medical University School of Medicine, Sapporo, Japan

Keywords: Infant, lymphadenitis, ST834, *Staphylococcus aureus*, SCC*mec*-IVc
Original Submission: 7 June 2022; **Accepted:** 13 June 2022
Article published online: 16 June 2022

Corresponding author. Department of Hygiene, Sapporo Medical University School of Medicine, S-1 W-17, Chuo-ku, Sapporo 060-8556, Japan.
E-mail: nkobayas@sapmed.ac.jp

Dear Editor,

Community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has been increasingly recognized as a cause of serious and invasive infections in children. CA-MRSA typically carries SCC*mec*-IV or V, often associated with production of Panton-Valentine leukocidin (PVL). In Japan, ST5 and ST764 (clonal complex (CC) 5), ST8, ST30, ST59 have been commonly described for genotypes of CA-MRSA [1]. However, we experienced a severe lymphadenitis case caused by CA-MRSA belonging to ST834, which is a rare genotype, in Hokkaido, northern main island of Japan.

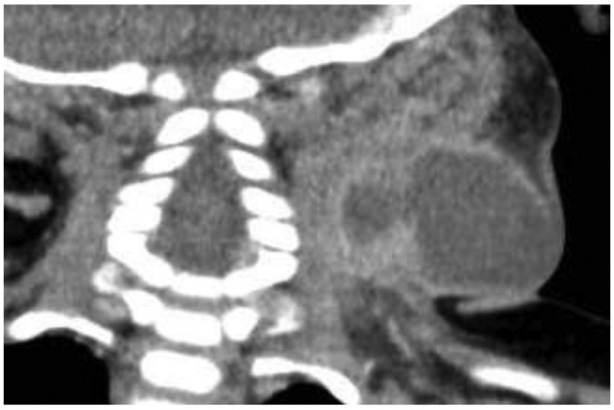
A previously healthy 4-month-old boy was admitted to our hospital with a four-day history of left cervical swelling with erythema which did not improve despite antibiotics treatment with oral faropenem. On admission, he was febrile (37.3°C), having pulse rate of 122/min, and respiratory rate of 36/min with an O_2 saturation of 97 % on room air. Physical examination revealed redness of pharynx and erythema and swelling of the left cervical lesion with 3 × 4 cm diameter. The rest of the physical examination results were unremarkable. Laboratory tests revealed a white blood cell (WBC) count of 25,300/μL with a differential of 69.4% neutrophils, erythrocyte sedimentation rate of 96 mm/h, C-reactive protein (CRP) level of 2.20 mg/dL. Renal and liver function tests, serum electrolytes, and urine analysis were normal. His past medical history and family history were insignificant. He was diagnosed cervical purulent lymphadenitis and was administered cefotaxime (118 mg/kg/day) as empiric therapy. However, after 2 days, he had cervical swelling grew large to 5 × 6 cm diameter. We performed an enhanced cervical computed tomography (CT) (Fig. 1) and referred to otolaryngology. His left cervical purulent lymphadenitis spontaneously self-destructed and drained. The next day, MRSA was isolated from a pharyngeal swab culture on admission and CRP increased to 5.01 mg/dl. We changed antibiotics from cefotaxime to vancomycin (39mg/kg/day). At day 13, we also detected MRSA in purulent matter culture, but blood culture was negative. He made an uneventful recovery with normalized CRP and was discharged on day 14.

Genetic analysis revealed that the isolated MRSA (ID: DY046) carried SCC*mec*-IVc, and belonged to ST834 (MLST), *spa*-t9624 (*spa* type), *agr*-I (*agr* type), and *coa*-VIIa (coagulase genotype). The isolate DY046 harbored hemolysin genes (*hla*, *hlb*, *hld*, *hlg*), enterotoxin (-like) genes (*sec*, *seh*, *sei*, *sel*, *selx*, *selw*), and toxic shock syndrome toxin-1 gene (*tst-1*), while PVL and exfoliative toxin genes were not detected. In addition to adhesin genes commonly found in *S. aureus*, *bap* (biofilm associated protein), *sak* (staphylokinase), and *chp* (chemotaxis inhibiting protein) were detected. Isolate DY046 was resistant to penicillins, cephalosporins, carbapenems, gentamicin, and erythromycin, harboring *blaZ*, *tet(K)*, *erm(A)*, and *msrA*, while susceptible to vancomycin, teicoplanin, linezolid, and levofloxacin.

ST834, which is represented by locus profile 3-124-1-1-1-1-40, belonging to CC1 or CC9, was first assigned for isolates in Western Australia in 2006. Thereafter, ST834 was identified as CA-MRSA having SCC*mec*-IV in only limited countries. In Cambodia, predominance of ST834 was described as colonizing MRSA in children [2]. In contrast, low prevalence of ST834-MRSA-IV was documented in Kuwait, Saudi Arabia, and Norway; isolates in Norway were described as being related to travel to Philippines [3,4]. In Japan, only one report described ST834

https://doi.org/10.1016/j.nmni.2022.100998

(a)



(b)

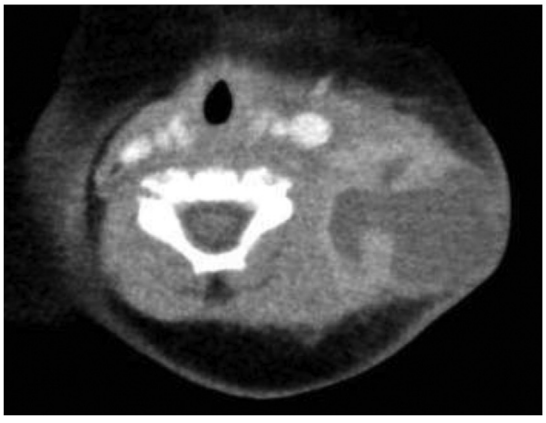


FIG. 1. Coronal (a) and axial (b) section of contrast-enhanced CT of the patient's neck, showing a cystic lesion to the left, sized 35 mm.

and its single locis variants (SLVs; ST1558, ST1566, ST2578) for CA-MRSA with SCC*mec*-IVc that caused regional outbreak of pediatric lymphadenitis in Saitama city, included in Tokyo metropolitan area, from 2011 to 2014 [5]. These strains mostly belonged to *spa*-t9624, harboring *tst-1*, *sec*, and *sel* located on a unique genomic island, which were the same genetic traits as those of DY046. Furthermore, ST834 strains in Saitama showed similar antimicrobial susceptibility profile to that of DY046, suggesting that these isolates might be the same clone. According to PubMLST database, 13 SLVs of ST834 had been registered and assigned to isolates in Japan, Taiwan, Thailand, Australia, Canada, Norway, and some African countries. Altogether, ST834 MRSA is suggested to be primarily prevalent in East and Southeast Asia, and Australia. Although ST834 has been scarcely detected in epidemiological studies of MRSA to date, this clone seems to be more related to children by unknown reason. Therefore, further epidemiological studies focusing on pediatric patients will be required to reveal its prevalence and clinical significance.

Conflicts of interest

None to declare.

References

[1] Aung MS, Kawaguchiya M, Urushibara N, Sumi A, Ito M, Kudo K, et al. Molecular characterization of methicillin-resistant *Staphylococcus aureus* from outpatients in northern Japan: increasing tendency of ST5/ST764 MRSA-IIa with arginine catabolic mobile element. Microb Drug Resist 2017;23:616–25.

[2] Nickerson EK, Wuthiekanun V, Kumar V, Amornchai P, Wongdeethai N, Chheng K, et al. Emergence of community-associated methicillin-resistant *Staphylococcus aureus* carriage in children in Cambodia. Am J Trop Med Hyg 2011;84:313–7.

[3] Udo EE, Sarkhoo E. The dissemination of ST80-SCCmec-IV community-associated methicillin resistant *Staphylococcus aureus* clone in Kuwait hospitals. Ann Clin Microbiol Antimicrob 2010;9:31.

[4] Monecke S, Aamot HV, Stieber B, Ruppelt A, Ehricht R. Characterization of PVL-positive MRSA from Norway. APMIS 2014;122:580–4.

[5] Uehara Y, Sasaki T, Baba T, Lu Y, Imajo E, Sato Y, et al. Regional outbreak of community-associated methicillin-resistant *Staphylococcus aureus* ST834 in Japanese children. BMC Infect Dis 2019;19:35.