hotline accessible to all providers across the community, Spectrum Health prioritized the professional development of healthcare workers as well as their psychosocial well-being during the pandemic.

Frontline healthcare staff are not only experiencing a rapid increase in the volume and intensity of their work but are also facing additional challenges such as unfamiliar working environments, changing protocols, and unprecedented exposure to COVID-19 with little opportunity for orientation and training.[4] It is widely recognized that healthcare professionals need evidence-based support initiatives to mitigate the effects of COVID-19 on their current and future well-being.[4] Spectrum Health's COVID-19 Provider Resource Work Group is an example of a successful and crucial support initiative in closing the knowledge gap and having a positive impact on the providers, emphasizing the need for support resources during these tumultuous times. Similar support initiatives and resources should be made available for clinicians during any other healthcare emergency or outbreak that has a public health impact.

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References

1. Cucinoto D, Vanelli M. WHO declares COVID-19 a pandemic. *Acta Biomed* 2020;91:157–160.
2. Pfefferbaum B, North CS. Mental health and the COVID-19 pandemic. *N Engl J Med* 2020;383:510–512.
3. Emmanuel A. COVID-19: the physician's response in the first phase. *Clin Med (Lond)* 2020;20:237.
4. Kinman G, Teoh K, Harriss A. Supporting the well-being of healthcare workers during and after COVID-19. *Occupat Med* 2020;70:294–296.

Regional outbreak of methicillin-resistant *Staphylococcus aureus* ST2725-t1784 in rural Japan

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To the Editor—Novel strains of methicillin-resistant *Staphylococcus aureus* (MRSA) continue to be discovered,[1] and understanding the trends of these strains in each region is important because MRSA genotype affects clinical outcomes.[2] Despite the introduction of various interventions, the prevalence of MRSA infection in Japanese hospitals remains relatively high.[3] Although MRSA USA300, which causes severe infectious disease with high mortality, is not common in Japan,[4] other SCCmec type IV MRSA strains have become widespread.[5]

Akiha Ward has 3 hospitals serving a population of ~80,000. The local incidence of MRSA bacteremia was ~10 per 100,000 person years in 2017–2018, which is considered high.[6] Therefore, to clarify the main route of MRSA transmission, we surveyed clinical isolates of MRSA from Akiha Ward using whole-genomic sequencing (WGS).

We collected clinical isolates of MRSA from 2 hospitals, namely, Kaetsu Hospital and Niitsu Medical Center Hospital, from April to September 2018. All clinics and a psychiatric hospital were excluded because they performed a relatively low number of bacterial tests. Despite these exclusions, our data covered most bacterial tests performed in Akiha Ward and thus can be considered to reflect the local epidemiology of MRSA infection. WGS analyses were performed at the Department of Microbiology, Niigata University of Pharmacy and Applied Life Sciences (NUPALS). The protocol was approved by the institutional review boards of NUPALS (no. H30-05), Kaetsu Hospital (approval # 2018-2), and Niitsu Medical Center Hospital (no. 2018-2). All clinically characterized MRSA isolates, including redundant ones, were further confirmed using MRSAII selective agar (Eiken-Chemical, Japan) and WGS. Additional isolates from the same patient with the same multilocus sequence typing profile were considered to be redundant samples and were therefore excluded, leaving 120 individual strains from 102 patients for further analysis.

Total DNA samples were prepared from each isolate by DNeasy Ultraclean Microbial kit (Qiagen, Germany), and WGS was performed using NexteraXT and Miseq Reagent kit v2 (500 cycles) or v3 (600 cycles) (Illumina, USA). All read sequences were deposited in the DDBJ/EMBL/GenBank database (accession nos. DRA010434–DRA010440). Multilocus sequence typing (MLST) analysis was performed using nullarbor v.2.0.20180819 (https://github.com/tseemann/nullarbor) with SPAdes v.3.12.0 as the assembler.[7] A k-mer–based tool, stringMLST, was also used for MLST analysis when the above software failed to define the sequence type.[8] SCC*mec* and *spa* typing were performed by

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Table 1. SCC*mec* and *spa* Types Determined by Whole-Genome Analysis in All MRSA Isolates

	CC1, No. (%)			CC5, No. (%)				CC8, No. (%)
SCC*mec*/*spa* Type	ST1	ST81	ST2725	ST5	ST764	ST2581	NT	ST8
Type-II								
t002	0	0	0	4 (3)	10 (8)	1 (1)	1 (1)	0
t856	0	0	0	1 (1)	0	0	0	0
t1062	0	0	0	0	2 (2)	0	0	0
t3794	0	0	0	1 (1)	0	0	0	0
Type-IVa								
t179	0	0	0	1 (1)	0	0	0	0
t1784	2 (2)	0	82 (68)	0	0	0	0	0
t2207	0	0	3 (3)	0	0	0	0	0
t4494	3 (3)	0	0	0	0	0	0	0
Untypeable	0	0	1 (1)	0	0	0	0	0
Non-type-IV								
t008	0	0	0	0	0	0	0	1 (1)
t1581	0	0	0	0	0	0	0	1 (1)
t7167	0	0	0	0	0	0	0	4 (3)
Untypeable	0	0	0	0	0	0	0	1 (1)
Type-IVg								
t127	0	1 (1)	0	0	0	0	0	0

Note. MRSA, methicillin-resistant *Staphylococcus aureus*; CC, clonal complex; ST, sequence type.

SCC*mec*Finder v.1.2 and *spa*Typer (http://spatyper.fortinbras.us/), respectively.[9] In addition, the presence of the cytotoxin Panthon–Valentine Leucocidin (accession no. AB006796.1) was determined by searching for assembled sequences with BLASTN (US National Library of Medicine).

Among the 102 patients, median age was 87 years (range, 1–100) and 68% were men. MRSA isolates were obtained from sputum (n = 91, 76%), urine (n = 12, 10%), skin and soft tissue (n = 9, 8%), blood (n = 4, 3%), and stool (n = 4, 3%). Table 1 shows the SCC*mec* and spa types determined by WGS analyses of all MRSA isolates. The most common type of MRSA was SCC*mec* type-IVa, which was detected in 92 (77%) isolates, followed by type II, type IV, and type IVg, which were detected in 20 (17%), 7 (6%), and 1 (1%) isolate(s), respectively. All isolates were negative for Panthon–Valentine Leucocidin. Surprisingly, 82 isolates (68%) were identified as SCC*mec* type-IVa MRSA ST2725-t1784. In addition, MRSA ST2725-t1784 was detected not only in inpatients but also in 37% of outpatients, including a 1-year-old child with low medical exposure.

MRSA ST2725-t1784 was observed at a high detection ratio in this study; thus, it may be easily transmissible at healthcare facilities and in the community. Moreover, 3 of 4 blood cultures tested positive for MRSA ST2725-t1784, indicating that it might be the predominate MRSA strain causing infectious disease in the area. MRSA ST2725-t1784 accounted for 44% of all MRSA strains in neonatal intensive care units in Shizuoka, which is >400 km from Niigata.[10] Therefore, an epidemic of MRSA ST2725-t1784 is of concern in Japan.

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References

1. Lakhundi S, Zhang K. Methicillin-resistant *Staphylococcus aureus*: molecular characterization, evolution, and epidemiology. *Clin Microbiol Rev* 2018;31(4):e00020–e00018.
2. Iwata Y, Satou K, Furuichi K, *et al.* Collagen adhesion gene is associated with bloodstream infections caused by methicillin-resistant *Staphylococcus aureus*. *Int J Infect Dis* 2020;91:22–31.
3. Mizuno S, Iwami M, Kunisawa S, *et al.* Comparison of national strategies to reduce meticillin-resistant *Staphylococcus aureus* infections in Japan and England. *J Hosp Infect* 2018;100:280–298.
4. Takadama S, Nakaminami H, Sato A, Shoshi M, Fujii T, Noguchi N. Dissemination of Panton-Valentine leukocidin–positive methicillin-resistant Staphylococcus aureus USA300 clone in multiple hospitals in Tokyo, Japan. *Clin Microbiol Infect* 2018;24:1211.e1–1211.e7.
5. Nakaminami H, Takadama S, Ito A, *et al.* Characterization of sccmec type IV methicillin-resistant *Staphylococcus aureus* clones increased in Japanese hospitals. *J Med Microbiol* 2018;67:769–774.

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6. Tong SYC, Davis JS, Eichenberger E, Holland TL, Fowler VG. *Staphylococcus aureus* infections: epidemiology, pathophysiology, clinical manifestations, and management. *Clin Microbiol Rev* 2015;28:603–661.
7. Nurk S, Bankevich A, Antipov D, *et al.* Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. *J Comput Biol* 2013; 20:714–737.
8. Gupta A, Jordan IK, Rishishwar L. stringMLST: a fast k-mer based tool for multilocus sequence typing. *Bioinformatics* 2017;33:119–121.
9. Kaya H, Hasman H, Larsen J, *et al.* SCCmecFinder, a web-based tool for typing of staphylococcal cassette chromosome *mec* in *Staphylococcus aureus* using whole-genome sequence data. *mSphere* 2018;3(1). doi: 10.1128/mSphere.00612-17.
10. Tsujiwaki A, Hisata K, Tohyama Y, *et al.* Epidemiology of methicillin-resistant *Staphylococcus aureus* in a Japanese NICU. *Pediatr Int* 2020;62: 911–919.

A simple way to minimize cross infection from tear droplets during noncontact air-puff tonometry

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To the Editor—Noncontact air-puff tonometry (NCT) is a routine ophthalmological examination used to measure intraocular pressure (IOP). During NCT, tears might be scattered after the pulse of pressurized air on the cornea.[1] It has been reported that severe acute respiratory coronavirus virus 2 (SARS-CoV-2) can be identified in the tears of patients with coronavirus disease 2019 (COVID-19).[2,3] Considering the risk of cross infection through tear droplets, we investigated the contamination during NCT. In addition, we describe an effective protective measure to reduce cross infection.

The experimental procedure was performed using a volunteer with normal IOP and tear secretion. After applying 0.4% fluorescence sodium, the volunteer received the IOP measurement. Thereafter, the NCT machine was photographed to screen the droplets under a blue LED light. Next, we employed a protective measure and investigated its ability to prevent contamination from tear droplets. A transparent plastic shield was installed between the chin rest and forehead rest and the main mobile unit, and a home-made paper funnel was installed on the sensor (Fig. 1A). The IOP measurement and droplets screening were repeated using the same volunteer with the protective measure.

Many scattered droplets were found on the NCT instrument after IOP measurement, including the main mobile main unit (Supplementary Fig. 1A–D online) and the sensor (Supplementary Fig. 1E online). We also detected some small droplets at the base of main unit and on the column of the chin and forehead rest (data not shown). The findings indicate that the NCT machine would have been contaminated widely if the IOP measurement was performed on an infected individual and that routine examinations posed a great risk for virus transmission from tears.

However, when we performed the IOP measurement with the shield, the droplets were dispersed on the shield instead of the main unit (Fig. 1C). Although the shield reduced the contamination of the main unit, it could not prevent the contamination of sensor, base, and column. Thus, a potential risk of cross infection remained, even with the shield.

Therefore, we designed and added a paper funnel to the sensor (Fig. 1A). The funnel could cover the examinee's eye when performing the IOP measurement (Fig. 1B). As shown in Fig. 1D, droplets were only observed on the sensor, with no obvious dye found on the other parts of the machine.

We have demonstrated that tears could be dispersed during NCT in the absence of any protective barrier. Moreover, the scattered droplets were widely distributed on the surface of the tonometry equipment, even on the margin of the main unit and the column of chin rest, which would be touched by examiners frequently. Our findings reinforce the necessity of wearing protective equipment and of disinfecting tonometry equipment totally when performing NCT on people with infectious diseases such as COVID-19.

Considering the medical supply shortage and the difficulty of complete disinfection, we adopted an easy protective measure on NCT and demonstrated that it could reduce the number of infectious scattered droplets reaching the machine and could minimize the dispersal distance and area. With the shield only, droplet dispersion was limited to the shield and sensor. With the shield and paper funnel, droplet dispersion was limited to the sensor. Although such a barrier could not prevent the dispersion of tears completely, it would simplify the workflow of disinfection greatly. Additionally, the disposable paper funnel should be changed after each examination to avoid potential cross infection between patients.

Collectively, such a protective measure during air-puff tonometry should be recommended to minimize the risk of cross infection and to protect frontline ophthalmologists during the ongoing COVID-19 pandemic.

Supplementary material. To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2020.1232

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