

## Background

*Staphylococcus aureus* (*S. aureus*) colonization is an essential risk factor for development of infection. The current evidence suggests long-term carriage leads to a higher bacterial load compared to intermittent carriage, potentially associated with a higher risk of transmission<sup>1</sup>.

## Objectives

- To document colonization of methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) in nasal samples of community-dwelling individuals without an active infection.
- To identify temporal patterns of colonization with MSSA and MRSA.

## Methods

Community-dwelling participants were recruited in Hong Kong during 2020-2022. Nasal samples were collected from the participants to isolate MSSA and MRSA, and the antibiotic susceptibility of the isolates were determined by the CLSI and EUCAST guidelines. Follow-up sample were provided by some participants 3-6 months after the initial sample collection. We included those who provided at least two samples in the analysis and the prevalence of MRSA and MSSA in all samples was calculated. Participants with MRSA detected in  $\geq 2$  consecutive samples were classified as persistent carriers while others with only sporadic detection(s) were intermittent carriers. Temporal detections of these participants were used to characterise the carriage status and the frequency of colonization categories were determined.

## Results

In total 436 participants provided two or more samples, leading to 1,157 samples included in our analysis. Among these samples, the prevalence of MRSA and MSSA was 7.8% (90/1,157) and 19.4% (224/1,157), respectively. Seventy-two (16.5%) participants tested positive for MRSA colonization at least once, including 14 (3.2%) were persistent carriers. Around 43% (6/14) of MRSA persistent carriers were aged 65 years or above. Over a median follow-up time of 8 months (range 2-26 months), there were in total 539 defined events of colonization conversion. Transition from one colonization status to another was common (170/539, 31.5% Table 2), including 27 events (5.0%) from MSSA to MRSA, 21 (3.9%) from MRSA to MSSA, 16 (3.0%) from MRSA to no detection of *S. aureus*, 49 (9.1%) from no detection of *S. aureus* to MSSA, and 40 (7.4%) MSSA to no detection of *S. aureus*.

	Participants with $\geq 2$ consecutive MRSA detections (N= 14)	Participants with single or non-consecutive MRSA detection (N= 58)	Participants with MSSA detection only (N= 91)	Participants without detection of <i>S. aureus</i> (N=273)	P-value
<b>Age</b>					
Mean (SD)	62 (17)	59 (14)	59 (12)	63 (12)	0.246
Median [Min, Max]	62 [25, 83]	62 [25, 91]	60 [29, 85]	66 [23, 89]	
<b>Age group (years)</b>					
18-49	3 (21.4%)	13 (22.4%)	17 (18.7%)	26 (9.5%)	0.00336
50-64	5 (35.7%)	23 (39.7%)	45 (49.5%)	94 (34.4%)	
65+	6 (42.9%)	22 (37.9%)	29 (31.9%)	153 (56.0%)	
<b>Gender</b>					
Female	9 (64.3%)	41 (70.7%)	66 (72.5%)	217 (79.5%)	0.356
Male	5 (35.7%)	17 (29.3%)	25 (27.5%)	56 (20.5%)	
<b>Education level</b>					
Non-tertiary	10 (71.4%)	44 (75.9%)	68 (74.7%)	207 (75.8%)	0.996
Tertiary or above	4 (28.6%)	14 (24.1%)	23 (25.3%)	66 (24.2%)	
<b>Occupation</b>					
Medical	0 (0%)	5 (8.6%)	5 (5.5%)	11 (4.0%)	0.558
Non-medical	14 (100%)	53 (91.4%)	86 (94.5%)	262 (96.0%)	
<b>Presence of chronic diseases</b>					
No	2 (14.3%)	28 (48.3%)	40 (44.0%)	99 (36.3%)	0.112
Yes	12 (85.7%)	30 (51.7%)	51 (56.0%)	174 (63.7%)	
<b>Household income level (HKD)</b>					
<\$10,000	1 (7.1%)	13 (22.4%)	16 (17.6%)	80 (29.3%)	0.268
\$10,000-\$19,999	2 (14.3%)	8 (13.8%)	11 (12.1%)	47 (17.2%)	
\$20,000-\$29,999	5 (35.7%)	10 (17.2%)	18 (19.8%)	30 (11.0%)	
\$30,000-\$49,999	0 (0%)	10 (17.2%)	12 (13.2%)	31 (11.4%)	
\$50,000+	2 (14.3%)	8 (13.8%)	16 (17.6%)	28 (10.3%)	
Unknown	4 (28.6%)	9 (15.5%)	18 (19.8%)	57 (20.9%)	
<b>No. of household members</b>					
1	3 (21.4%)	10 (17.2%)	12 (13.2%)	52 (19.0%)	0.528
2-3	10 (71.4%)	32 (55.2%)	66 (72.5%)	162 (59.3%)	
4-5	1 (7.1%)	13 (22.4%)	13 (14.3%)	52 (19.0%)	
6+	0 (0%)	3 (5.2%)	0 (0%)	7 (2.6%)	
<b>No. of household members &lt;18y</b>					
0	13 (92.9%)	48 (82.8%)	85 (93.4%)	254 (93.0%)	0.305
1-2	1 (7.1%)	10 (17.2%)	6 (6.6%)	17 (6.2%)	
3-4	0 (0%)	0 (0%)	0 (0%)	2 (0.7%)	
<b>No. of household members <math>\geq 65y</math></b>					
0	11 (78.6%)	41 (70.7%)	60 (65.9%)	171 (62.6%)	0.616
1-2	3 (21.4%)	17 (29.3%)	31 (34.1%)	102 (37.4%)	
<b>Previous antibiotic use</b>					
Never	0 (0%)	1 (1.7%)	1 (1.1%)	14 (5.1%)	0.499
0 time in the last year	8 (57.1%)	45 (77.6%)	72 (79.1%)	193 (70.7%)	
1-2 times in the last year	5 (35.7%)	11 (19.0%)	18 (19.8%)	58 (21.2%)	
3+ times in the last year	1 (7.1%)	1 (1.7%)	0 (0%)	8 (2.9%)	
<b>Any household members with occupational exposure to patients or processing raw meat</b>					
No	10 (71.4%)	44 (75.9%)	77 (84.6%)	233 (85.3%)	0.32
Yes	4 (28.6%)	14 (24.1%)	14 (15.4%)	40 (14.7%)	

Table 1. Sociodemographic characteristics of participants according to colonization status.

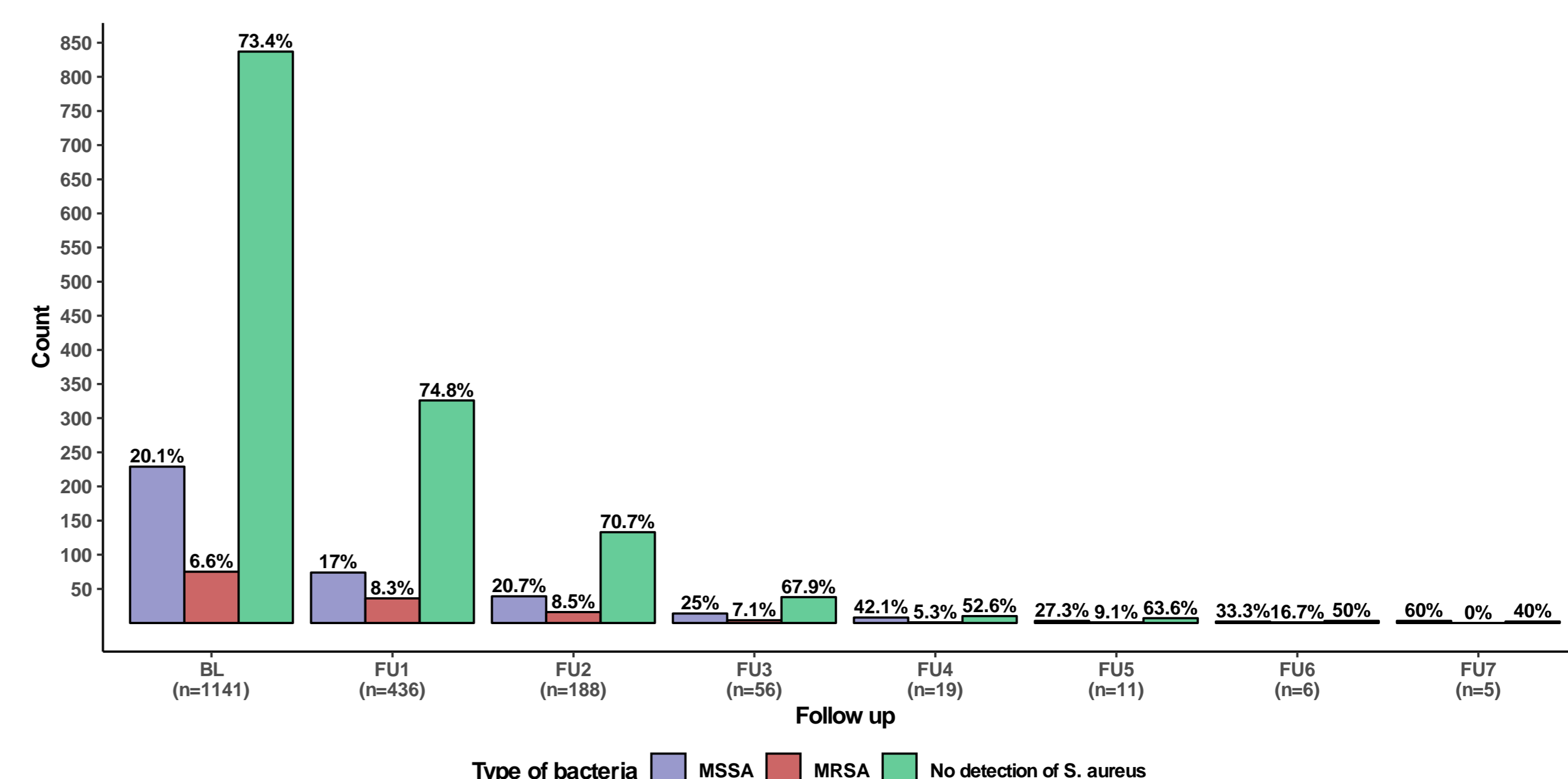


Figure 2. Number of participants with different types of *S. aureus* in each sampling period.

Temporal colonization of <i>S. aureus</i>	Number of events (n=539)
Sustained colonization of MRSA ( $\geq 2$ consecutive detections)	14 (2.6%)
Sustained colonization of MSSA ( $\geq 2$ consecutive detections)	49 (9.1%)
Sustained no colonization of <i>S. aureus</i> ( $\geq 2$ no detections consecutively)	306 (56.8%)
MSSA converted to MRSA	27 (5.0%)
MRSA converted to MSSA	21 (3.9%)
No <i>S. aureus</i> converted to MRSA	17 (3.2%)
MRSA converted to no detection of <i>S. aureus</i>	16 (3.0%)
No detection of <i>S. aureus</i> converted to MSSA	49 (9.1%)
MSSA converted to no detection of <i>S. aureus</i>	40 (7.4%)

Table 2. Number of events in all *S. aureus* conversion patterns. Events refer to as the occurrence of the above defined 9 temporal patterns among participants.

## Conclusions

This study revealed that community-dwelling individuals in Hong Kong exhibited diverse patterns of colonization of *S. aureus*, and transitions between different status of colonization appeared to be more common than persistence of certain status. Whole genome sequencing may help to better understand the dynamics of nasal colonization of commensal bacteria, and studies on factors related to patterns of colonization particularly conversions of colonization status are warranted.

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## References

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