

New nasal methicillin-resistant *Staphylococcus aureus* colonization during hospitalization in children: a prospective observational study from Iran

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Abstract

Background

Nasal carriage of methicillin-resistant *Staphylococcus aureus* (MRSA) may increase the risk of subsequent infection and facilitate transmission in healthcare settings. However, data on MRSA acquisition during hospitalization among children in Iran are limited. We aimed to determine the frequency of new nasal MRSA colonization and identify associated clinical and healthcare-related factors.

Methods

In this prospective observational study, children aged ≤ 18 years admitted to five clinical units at Mofid Children's Hospital, Tehran, Iran, were enrolled between December 2025 and January 2026. Nasal swabs were obtained within 48 hours of admission and repeated at discharge and every 10 days during prolonged hospitalization. New MRSA colonization was defined as a positive follow-up culture after a negative baseline culture. Demographic, clinical, antibiotic exposure, and healthcare-related factors were evaluated. Antimicrobial susceptibility and Panton–Valentine leukocidin (PVL) gene status were assessed in newly acquired MRSA isolates.

Results

Among 313 children screened at baseline, 164 met the criteria for the final analysis. New nasal MRSA colonization occurred in 10 children (6.1%), with a mean time to detection of 8.1 ± 5.1 days. Most children with new MRSA colonization had an underlying disease (80.0%), including malignancy in 50.0%. Female sex (90.0% vs 37.7%, $p = 0.002$), sulfonamide exposure (30.0% vs 5.8%, $p = 0.027$), corticosteroid use (70.0% vs 36.4%, $p = 0.046$), and clinical unit ($p = 0.047$) were associated with MRSA acquisition. Nasogastric tube insertion showed a borderline association ($p = 0.054$). All isolates were susceptible to linezolid and rifampin, while none carried the PVL gene.

Conclusions

New nasal MRSA colonization occurred in 6.1% of hospitalized children who completed follow-up, particularly among those with underlying diseases. Female sex, sulfonamide and corticosteroid exposure, and clinical unit were associated with acquisition. Given the small number of cases, these findings should be considered exploratory and confirmed in larger multicenter studies.

Background

Methicillin-resistant *Staphylococcus aureus* (MRSA) remains an important healthcare-associated pathogen in children and is associated with substantial morbidity, mortality, and healthcare costs [1]. Nasal colonization is particularly important because the nose is a major reservoir of *S. aureus*, and colonized patients may contribute to transmission within healthcare settings [1, 2]. Moreover, MRSA colonization is associated with an increased risk of subsequent infection [3], and nasal screening may help guide appropriate infection-control strategies and empirical anti-MRSA therapy, and reduce unnecessary antibiotic exposure [4, 5].

Acquisition of MRSA during hospitalization is influenced by both patient-related and healthcare-related factors, including underlying illness, prolonged hospitalization, antibiotic exposure, invasive devices, and the level of care provided in different hospital units. These factors may result in varying risks of MRSA acquisition across clinical settings, particularly in units caring for children with more severe illness or requiring more intensive interventions [2, 3].

Characterizing colonizing MRSA isolates can provide additional epidemiological information. Antimicrobial susceptibility patterns provide an overview of their resistance phenotypes [6, 7], while investigation of virulence factors, including Panton–Valentine leukocidin (PVL), can provide complementary information on the molecular characteristics [6]. PVL is a bicomponent leukocidin encoded by the *lukS-PV* and *lukF-PV* genes and has been of particular interest in several *S. aureus* lineages, especially certain community-associated MRSA lineages [8]. Although the presence of PVL alone is insufficient to determine the origin of a strain or predict disease severity, investigating this gene in MRSA isolates acquired during hospitalization may contribute to a more precise characterization of their molecular features [8].

Despite the clinical and infection-control importance of MRSA, data on new nasal MRSA colonization among hospitalized children in Iran remain limited [7]. Therefore, we conducted a prospective study to determine the frequency of new nasal MRSA colonization among hospitalized children. We further evaluated clinical and healthcare-related factors associated with colonization and characterized the antimicrobial susceptibility patterns and PVL gene status of the colonizing MRSA isolates.

Methods

Study design and setting

This prospective observational study was conducted at Mofid Children’s Hospital, Tehran, Iran. Patients were enrolled over a one-month period between December 2025 and January 2026, with follow-up continuing until hospital discharge. All patients admitted to five inpatient units (infectious diseases, surgery, pediatric intensive care unit (PICU), hematology, and pulmonary) were screened for eligibility.

The inclusion criteria were age ≤ 18 years, hospitalization for at least 48 hours, and informed consent from parents or legal guardians. The exclusion criteria were a positive baseline MRSA culture, hospitalization for less than 48 hours, transfer to a unit outside the five study units during

hospitalization, or failure to obtain a discharge sample. Children discharged against medical advice, or discharged without parental consent for a second nasal sampling, and were therefore excluded. This was not related to clinical deterioration or transfer to the intensive care unit.

Data collection and study outcome

Demographic, clinical, hospitalization, and microbiological data were collected using a standardized data collection form. For patients with repeated follow-up samples, the timing and results of each culture were recorded. The primary outcome was new nasal MRSA colonization during hospitalization (hospital-acquired MRSA, HA-MRSA), defined as a positive MRSA culture in any follow-up nasal swab after a negative baseline culture obtained within the first 48 hours of hospitalization. Positive baseline cultures were classified as community-acquired (CA-MRSA or CA-MSSA), and new colonization with methicillin-susceptible *S. aureus* (HA-MSSA) was considered a secondary microbiological finding.

In-hospital antibiotic exposure was recorded up to the time point of the follow-up sample at which MRSA colonization was detected (or up to discharge for non-colonized patients); therefore, no patient had received an antibiotic as a consequence of a positive MRSA culture result, supporting the interpretation of antibiotic exposure as an association preceding, rather than resulting from, colonization.

Sampling

A baseline nasal swab specimen was obtained from each eligible child within the first 48 hours of hospitalization. Nasal swabbing was repeated at discharge and every 10 days during prolonged hospital stay, when applicable.

Microbiological procedures

Nasal swab specimens were collected from both anterior nares using sterile cotton swabs and were inoculated directly onto blood agar plates at the patient's bedside. Plates were incubated aerobically at 37°C for 24 hours. Suspected *S. aureus* colonies were identified based on Gram staining, catalase, coagulase, and mannitol fermentation tests. Methicillin resistance was screened using cefoxitin disk diffusion. MRSA isolates were then tested for susceptibility to azithromycin, ciprofloxacin, clindamycin, erythromycin, gentamicin, linezolid, rifampin, doxycycline, and penicillin, according to the Clinical and Laboratory Standards Institute (CLSI) guidelines [9].

Vancomycin susceptibility was not assessed, as its accurate determination requires quantitative minimum inhibitory concentration (MIC)-based methods; disk diffusion is not considered a reliable method for vancomycin susceptibility testing of *S. aureus*.

Molecular detection of the PVL gene

For detection of the PVL gene, bacterial DNA was extracted from confirmed isolates using a DNA extraction kit. DNA adequacy was verified by amplification of the 16S rRNA gene. The PVL gene was then detected by conventional PCR using primers targeting the lukS-PV/lukF-PV region, as previously described by Johnsson et al. [10]. The expected amplicon size was 421 bp. PCR products were analyzed by agarose gel electrophoresis using positive and negative controls.

Statistical analysis

All statistical analyses were conducted using IBM SPSS Statistics version 27.0. Categorical data were expressed as frequencies and percentages, whereas continuous variables were reported as mean $\pm$ standard deviation (SD). Differences between groups were assessed using Fisher's exact test, chi-square test, and independent-samples t test, as appropriate. Given the small number of newly colonized HA-MRSA cases, multivariable logistic regression was not performed to avoid model overfitting and unstable estimates. Univariable analyses were therefore used to identify factors associated with HA-MRSA colonization. A two-sided p value < 0.05 was considered statistically significant.

Results

Patient flow

During the enrollment period, 313 children underwent baseline sampling. Of these, 149 were excluded for the reasons detailed in Fig. 1, and 164 were included in the final analysis. The most common reason for exclusion was the absence of a discharge nasal sample ($n = 60$, 40.3% of exclusion).

S. aureus and MRSA prevalence at baseline and follow-up

At baseline testing, 66 of 313 (21.1%) patients were positive for *S. aureus*, including 52 (16.6%) CA-MSSA and 14 (4.5%) CA-MRSA patients. During follow-up, 27 of 164 (16.5%) children had *S. aureus* detected, comprising 17 (10.4%) with HA-MSSA and 10 (6.1%) with HA-MRSA colonization.

Baseline demographic and clinical characteristics

The proportion of female patients was significantly higher in the HA-MRSA group (90.0% vs. 37.7%, $p = 0.002$). Cancer was also more frequent in the HA-MRSA group (50.0% vs. 20.8%, $p = 0.047$). Other clinical features are shown in Table 1. Among the 10 children with HA-MRSA colonization, 8 (80.0%) had an underlying chronic disease, including malignancy ($n = 5$), immunodeficiency ($n = 1$), congenital disorders ($n = 1$), and hepatic cirrhosis ($n = 1$). The average time from the negative baseline culture to detection of MRSA colonization was 8.1 ± 5.1 days (range 2–18 days).

Table 1

Demographic and clinical characteristics of children according to hospital-acquired MRSA colonization status

Variable	Non-HA-MRSA (N = 154)	HA-MRSA (N = 10)	Total (N = 164)	P value
Age (years), mean $\pm$ SD	5.27 $\pm$ 4.62	6.89 $\pm$ 5.89	5.37 $\pm$ 4.70	0.292
Female, n (%)	58 (37.7)	9 (90.0)	67 (40.9)	0.002
Underlying diseases, n (%)	87 (56.5)	8 (80.0)	95 (57.9)	0.194
Cancer, n (%)	32 (20.8)	5 (50.0)	37 (22.6)	0.047
Immunodeficiency, n (%)	5 (3.2)	1 (10.0)	6 (3.7)	0.319
Previous hospitalization, n (%) ^a	64 (41.6)	5 (50.0)	69 (42.1)	0.744
Pre-admission antibiotic use, n (%)	46 (29.9)	2 (20.0)	48 (29.3)	0.725

a Previous hospitalization was defined as hospitalization for > 2 days within the preceding 3 months. HA-MRSA, hospital-acquired methicillin-resistant *Staphylococcus aureus*; SD, standard deviation.

Clinical units and healthcare-associated exposures

Patients were distributed across the infectious diseases (32.9%), surgery (22.0%), pulmonary (20.1%), hematology (17.7%), and intensive care (7.3%) units, in descending order of frequency. This distribution differed significantly between groups ($p = 0.047$), with the hematology ward being the most common unit among HA-MRSA colonized patients (40.0%).

Overall, in-hospital antibiotic use was numerically more frequent in the non-HA-MRSA group. Among individual antibiotic classes, penicillins, sulfonamides, fluoroquinolones, linezolid, and colistin were used more frequently in the HA-MRSA group; however, only sulfonamide use reached statistical significance (30.0% vs 5.8%, $p = 0.027$) (Table 2).

Table 2
In-hospital antibiotic administration according to HA-MRSA colonization status

Variable, n (%)	Non-HA-MRSA (N = 154)	HA-MRSA (N = 10)	Total (N = 164)	P value
In-hospital antibiotic use	132 (85.7)	7 (70.0)	139 (84.9)	0.181
Penicillins	2 (1.3)	1 (10.0)	3 (1.8)	0.173
Cephalosporins	103 (66.9)	5 (50.0)	108 (65.9)	0.312
Carbapenems	35 (22.7)	1 (10.0)	36 (22.0)	0.467
Macrolides	12 (7.8)	0 (0.0)	12 (7.3)	1.000
Sulfonamides	9 (5.8)	3 (30.0)	12 (7.3)	0.027
Aminoglycosides	13 (8.4)	0 (0.0)	13 (7.9)	1.000
Fluoroquinolones	7 (4.5)	1 (10.0)	8 (4.9)	0.402
Vancomycin	35 (22.7)	1 (10.0)	36 (22.0)	0.693
Clindamycin	42 (27.3)	2 (20.0)	44 (26.8)	1.000
β -lactam + β -lactamase inhibitor combinations	10 (6.5)	0 (0.0)	10 (6.1)	1.000
Linezolid	2 (1.3)	1 (10.0)	3 (1.8)	0.173
Colistin	0 (0.0)	1 (10.0)	1 (0.6)	0.061

Most evaluated healthcare-associated exposures, except nebulizer use and central venous line placement, were more frequent among the HA-MRSA group, although corticosteroid use was the only factor reaching statistical significance ($p = 0.046$). Nasogastric tube insertion showed borderline statistical significance ($p = 0.054$) (Table 3).

Table 3
Distribution of other healthcare-associated exposures according to HA-MRSA colonization status

Variable, n (%)	Non-HA-MRSA (N = 154)	HA-MRSA (N = 10)	Total (N = 164)	P value
Corticosteroids	56 (36.4)	7 (70.0)	63 (38.4)	0.046
Chemotherapy	27 (17.5)	3 (30.0)	30 (18.3)	0.392
Surgery	44 (28.6)	5 (50.0)	49 (29.9)	0.167
Urinary catheter	26 (16.9)	3 (30.0)	29 (17.7)	0.384
Nasogastric tube	22 (14.3)	4 (40.0)	26 (15.9)	0.054
Oxygen therapy	81 (52.6)	6 (60.0)	87 (53.0)	0.751
Intubation	38 (24.7)	5 (50.0)	43 (26.2)	0.130
Central venous line	26 (16.9)	1 (10.0)	27 (16.5)	1.000
Nebulizer	48 (31.2)	2 (20.0)	50 (30.5)	0.725
Bronchoscopy	11 (7.1)	2 (20.0)	13 (7.9)	0.182

Antimicrobial susceptibility and molecular characteristics of HA-MRSA isolates

All 10 HA-MRSA isolates were resistant to ceftazidime, consistent with their phenotypic identification as MRSA. High resistance rates were also observed for penicillin (90.0%), erythromycin (90.0%), and azithromycin (90.0%). Resistance to clindamycin, gentamicin, ciprofloxacin, and doxycycline was observed in 60.0%, 50.0%, 50.0%, and 40.0% of isolates, respectively. All isolates were susceptible to rifampin and linezolid. Vancomycin susceptibility was not evaluated for the reasons outlined in the Methods section. Molecular analysis revealed that none of the HA-MRSA isolates carried the PVL gene.

Univariable analysis

Univariable analysis identified female sex, cancer, sulfonamide use, corticosteroid use, and clinical unit as significantly associated with HA-MRSA nasal colonization. Nasogastric tube insertion showed a trend toward an association with HA-MRSA colonization. Detailed estimates are presented in Table 4.

Table 4
Univariable analysis of factors associated with HA-MRSA colonization

Variable	OR	95% CI	P value
Female sex	14.897	1.840–120.623	0.002
Clinical unit, overall	–	–	0.047
Sulfonamides	6.905	1.524–31.282	0.027
Corticosteroids	4.083	1.015–16.423	0.046
Nasogastric tube	4.000	1.044–15.326	0.054

OR, odds ratio; CI, confidence interval. [Add OR and 95% CI for cancer, or remove it from this table if not analyzed.]

Discussion

MRSA hospital colonization rate and its associated factors deserve close attention because colonization may precede subsequent infection and may signal ongoing transmission within a hospital. In a previous study in adults, 25% of those with MRSA colonization ultimately developed MRSA infection, compared with only 2% of patients without colonization [11]. Pediatric data have demonstrated a similarly elevated risk [12].

Most prior studies on HA-MRSA colonization come from ICU populations, with reported rates spanning 3% to 11% [13, 14]. Our colonization rate (6.1%) fell within this range, though below the higher ICU-based estimates, which likely reflects our broader inclusion of non-ICU clinical units rather than an ICU-only cohort.

One of the most notable findings was the strong association between female sex and newly detected HA-MRSA colonization (OR 14.9, 95% CI 1.84–120.6); however, this extremely wide confidence interval indicates substantial statistical uncertainty. This estimate should therefore be regarded as hypothesis-generating rather than a generalizable association. A recent meta-analysis similarly linked female sex to higher odds of MRSA colonization [15], whereas an Iranian pediatric study found the opposite, identifying male sex as the associated factor [16]. This inconsistency across studies points to a need for larger and better-powered samples.

Clinical unit was also significantly associated with HA-MRSA colonization in the overall comparison. This finding is in line with previous evidence that the hospital environment and intensity of healthcare exposure influence MRSA transmission. ICU patients, particularly, are exposed to invasive procedures, antimicrobial therapy, and frequent contact with healthcare personnel, all of which may increase opportunities for colonization [13, 17, 18].

Notably, 80% of children with HA-MRSA colonization had an underlying chronic disease, most commonly cancer, which was itself significantly more frequent in the HA-MRSA group. This is consistent with prior reports linking malignancy, associated immunosuppression, and prolonged healthcare contact to a higher risk of MRSA colonization in pediatric oncology populations [19, 20]. The average time to colonization (8.1 ± 5.1 days) also suggests that colonization risk accumulates progressively over the course of hospitalization, reinforcing the value of repeated screening in long-stay patients.

Sulfonamide exposure emerged as another significant association. Antibiotic administration has frequently been implicated in MRSA colonization due to alterations in normal flora and the consequent colonization of resistant organisms. As antibiotic exposure in this study was recorded only up to the time of MRSA detection, the sulfonamide association reflects exposure preceding, rather than resulting from, colonization. To our knowledge, most previous studies have examined antibiotic classes such as penicillins, cephalosporins, and fluoroquinolones [21, 22], or treated antibiotic exposure as a whole [17, 23], rather than specifically implicating sulfonamides. This association therefore merits further investigation.

Corticosteroid exposure showed a similar pattern, consistent with earlier research, occurring more frequently among children with HA-MRSA colonization [24, 25]. This association may reflect the presence and severity of underlying medical conditions rather than representing an independent associated factor. Hence, multivariable analysis would be necessary to determine whether corticosteroid use remains independently associated with HA-MRSA colonization after adjustment for relevant confounders.

Nasogastric tube insertion showed a borderline association with HA-MRSA colonization. Invasive or semi-invasive devices, including gastrostomy, central venous catheters, and mechanical ventilation, have commonly been implicated in ICU-acquired MRSA infection [23, 26, 27]. Our findings therefore support the possibility that devices might provide additional healthcare contact or disrupt normal barriers. Given the borderline p value and small number of exposed children in our study, this observation should be considered hypothesis-generating rather than conclusive.

The antimicrobial susceptibility profile of the HA-MRSA isolates revealed high rates of resistance to penicillin and macrolides. The preserved susceptibility to linezolid and rifampin, despite this broad resistance, might be clinically useful when therapeutic options are limited [28]. Although MRSA colonization does not itself require antimicrobial treatment, characterizing the susceptibility pattern of these isolates is still worthwhile, in case these patients later develop an MRSA infection that needs empirical therapy. In addition, none of the isolates carried the PVL gene, which is more commonly associated with certain CA-MRSA lineages [29, 30]. Nevertheless, the small number of cases limits the generalizability of these findings.

Strengths and limitations

The main strength of this study is its prospective design and its comprehensive assessment of associated factors, antimicrobial susceptibility patterns, and molecular characteristics of the isolates. However, the study has several limitations. Sixty children (19.2% of those screened at baseline) were excluded because no discharge sample was obtained, mostly due to discharge against medical advice or refusal of repeat sampling; their acquisition status is unknown, which may have introduced selection bias. The small number of HA-MRSA colonization events resulted in wide confidence intervals and prevented reliable multivariable modeling. The single-center, one-month design also limits the generalizability of the findings. Additionally, although all HA-MRSA isolates were PVL-negative, the lack of multilocus sequence typing (MLST) or staphylococcal cassette chromosome mec (SCCmec) typing precludes definitive conclusions about their clonal lineage or community- versus hospital-associated origin. We were also unable to evaluate vancomycin susceptibility, as this requires MIC-based methods that were not available in our laboratory. Future large multicenter studies are warranted to validate these associations and identify independent factors associated with hospital-acquired MRSA colonization.

Conclusions

Our findings demonstrated that nasal MRSA colonization occurred in 6.1% of hospitalized children, most of whom had an underlying disease such as malignancy, and developed colonization at an average of 8.1 ± 5.1 days after admission. Colonization was also associated with female sex, clinical unit, sulfonamide exposure, and corticosteroid use. Given the small number of colonization events, these findings should be interpreted cautiously and require confirmation in larger future studies. Identifying these factors may help inform infection prevention strategies and antimicrobial management in hospitalized children.

Abbreviations

CA-MRSA

Community-acquired methicillin-resistant *Staphylococcus aureus*

CA-MSSA

Community-acquired methicillin-susceptible *Staphylococcus aureus*

CI

Confidence interval

CLSI

Clinical and Laboratory Standards Institute

HA-MRSA

Hospital-acquired methicillin-resistant *Staphylococcus aureus*

HA-MSSA

Hospital-acquired methicillin-susceptible *Staphylococcus aureus*

MIC

Minimum inhibitory concentration

MLST

Multilocus sequence typing

MRSA

Methicillin-resistant *Staphylococcus aureus*

NG

Nasogastric

OR

Odds ratio

PICU

Pediatric intensive care unit

PVL

Panton–Valentine leukocidin

SCCmec

Staphylococcal cassette chromosome mec

SD

Standard deviation

Declarations

Ethics approval and consent to participate

This study was reviewed and approved by the Ethics Committee of the Research Institute for Children's Health at Shahid Beheshti University of Medical Sciences (ethical code: IR.SBMU.RICH.REC.1403.026). Informed consent was obtained from the parents or legal guardians of all participating children.

Competing interests

The authors declare that they have no competing interests.

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Author Contribution

Conceptualization: SA, LA, HK. Formal analysis: YS. Methodology: YS. Project administration: SA, HK, ShA. Writing – original draft: YS Writing – review and editing: SA, LA.

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Data Availability

The datasets used during the current study are available from the corresponding author on reasonable request.

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Figures

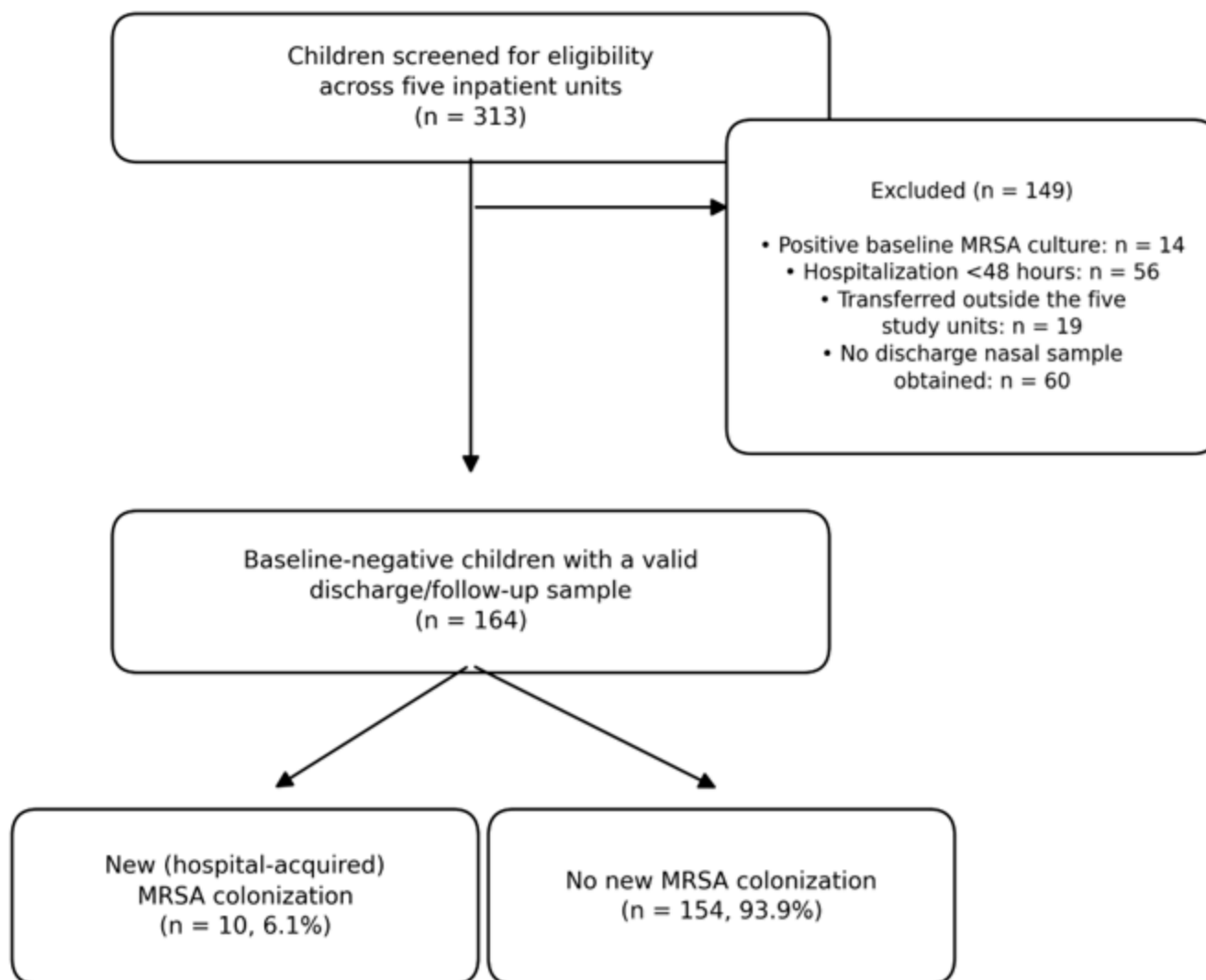


Figure 1

Flow diagram of patient inclusion for the assessment of MRSA colonization.