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Care Trajectory, Microbiological Ecology, and System-Level Determinants of Tracheitis in Tracheostomized Children

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Abstract

Purpose

To evaluate the determinants of tracheitis in tracheostomized pediatric patients by integrating microbiological, clinical, and system-level factors, with particular emphasis on the role of care environment.

Methods

This retrospective observational study included pediatric patients with tracheostomy followed at a tertiary care center from 2020 to 2024. Data on demographics, comorbidities, functional status, and tracheal aspirate microbiology were extracted from medical records. Tracheitis was analyzed as global, PICU-specific, and post-PICU outcomes. Multivariable logistic regression and generalized estimating equations were used to assess patient-level and environment-level effects.

Results

Ninety-six patients were included. Tracheitis occurrence was strongly influenced by care environment, with lower odds in post-PICU settings than in the PICU (OR 0.40, 95% CI 0.24 to 0.68; $p < 0.001$). Gram-negative microorganisms were independently associated with tracheitis (OR 2.25, 95% CI 1.35 to 3.75; $p = 0.002$), and prematurity also emerged as a significant predictor (OR 2.49, 95% CI 1.40 to 4.42; $p = 0.002$). Neurological comorbidity showed a borderline association (OR 1.69; $p = 0.096$). Model discrimination was moderate (AUC 0.725 to 0.749).

Conclusion

Tracheitis in tracheostomized children reflects a dynamic interaction between care environment, microbial ecology, and host vulnerability. Gram-negative profiles and prematurity are key determinants, while the PICU setting represents a high-risk ecological context.

What is Known – What is New

- What is Known: Tracheostomized children are highly vulnerable to airway colonization and recurrent respiratory infection.
- What is Known: The oral cavity and oropharynx can seed lower-airway infection through microaspiration.
- What is New: In this cohort, PICU environment, Gram-negative microbial profile, and prematurity were the main determinants of tracheitis.

- What is New: Risk patterns shifted after PICU discharge, supporting environment-specific prevention strategies.

Introduction

Respiratory tract infections remain a major source of morbidity and healthcare burden in pediatric populations, particularly among critically ill children requiring advanced airway support. Among these, tracheitis represents a clinically significant and potentially severe condition, characterized by airway inflammation and bacterial colonization that may progress to lower respiratory tract infections and prolonged hospitalization [1–3]. In children with tracheostomy, this risk is amplified due to disruption of natural airway defenses, chronic exposure to healthcare environments, and the presence of indwelling devices that facilitate microbial colonization [4–6].

The pathophysiology of tracheitis in this population is complex and multifactorial. Traditional perspectives have emphasized the role of nosocomial pathogens, particularly Gram-negative organisms, in driving airway infections in hospitalized patients [7–9]. However, emerging evidence suggests that the respiratory tract cannot be understood in isolation. Increasing attention has been directed toward the oral cavity and oropharynx as dynamic microbial reservoirs capable of seeding lower airway infections, especially in mechanically ventilated or tracheostomized patients [10–12]. The oral microbiome is now recognized as a key component of the respiratory microecosystem, with bidirectional interactions influencing both colonization and disease processes [13–15].

This ecological perspective is supported by studies demonstrating overlap between pathogens identified in oral biofilms and those recovered from tracheal aspirates, reinforcing the concept of microaspiration as a central mechanism in respiratory infections [16, 17]. In critically ill patients, impaired swallowing, sialorrhea, and reduced airway clearance further increase the likelihood of aspiration, linking functional impairment to infection risk [18, 19]. Interventions targeting oral microbial load, such as chlorhexidine decontamination, have shown reductions in ventilator-associated pneumonia, highlighting the clinical relevance of this oral–lung axis [20–23].

Despite these advances, important gaps remain. First, most studies have focused either on microbiological profiles or clinical outcomes, without integrating both within a unified analytical framework. Second, the temporal and environmental dynamics of tracheitis—particularly the transition from pediatric intensive care unit (PICU) to ward and home settings—are poorly characterized. This is especially relevant in tracheostomized children, who experience continuous care across multiple environments, each with distinct ecological and clinical pressures. Third, the relative contribution of host factors, such as comorbidities and functional impairment, versus microbial factors remains incompletely understood.

Addressing these gaps requires a system-level approach that integrates patient-level characteristics, microbiological ecology, and care environment into a single analytical framework. Observational studies

designed under rigorous reporting standards, such as those recommended by the STROBE initiative [24, 25], are particularly suited to explore these complex interactions in real-world clinical settings.

Therefore, the aim of this study was to evaluate the determinants of tracheitis in tracheostomized pediatric patients by integrating demographic, clinical, microbiological, and environmental factors. Specifically, we sought to (1) characterize the microbiological profile of tracheal aspirates, (2) assess the role of functional and comorbidity-related factors, and (3) investigate how the care environment—particularly the transition from PICU to post-PICU settings—influences the occurrence of tracheitis using both patient-level and system-level analytical models.

Methods

Study design and reporting framework

This retrospective observational cohort study was based on a review of medical records of pediatric patients who underwent tracheostomy during hospitalization in a public referral PICU. The study was designed and reported in accordance with the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement [24, 25] to enhance clarity, transparency, and reproducibility.

The primary objective was to investigate the relationship between tracheitis and airway-associated microbiological profiles in tracheostomized children, with particular attention to clinical conditions related to secretion management and aspiration. A secondary objective was to determine whether the determinants of tracheitis differed across care environments, namely the PICU, the ward, and the home setting.

Study setting

The study was conducted at the Pediatric Intensive Care Unit of Hospital Materno-Infantil de Brasília Dr. Antônio Lisboa (HMIB), a public referral hospital in the Federal District, Brazil. The study period extended from January 2020 to December 2024. This institution receives pediatric patients with complex clinical conditions, including neurological disorders, congenital anomalies, chronic respiratory insufficiency, and prolonged ventilatory dependence, making it an appropriate setting in which to investigate tracheostomy-associated respiratory complications.

Participants

The source population consisted of pediatric patients hospitalized in the PICU who underwent tracheostomy during the study period. Patients were eligible if they were admitted to the PICU during the study period, underwent tracheostomy during hospitalization, and had sufficient information in the medical record to allow assessment of tracheitis and the main clinical and microbiological variables of interest. Patients were excluded if they had not undergone tracheostomy, had undergone tracheostomy at another institution, or had records insufficient for outcome assessment. After application of these criteria, 96 pediatric patients were included in the final analysis.

Data sources and data collection

Data were obtained through retrospective chart review using the electronic medical record system (TrackCare) of the Federal District State Health Secretariat. Data extraction was performed manually by a single trained investigator using a structured data collection form developed for the study. To preserve confidentiality, all data were anonymized before analysis, and no directly identifying information was retained in the analytical dataset.

The following domains were extracted: demographic characteristics, hospitalization history, tracheostomy-related variables, clinical outcomes, microbiological findings from tracheal aspirates, and selected information regarding bedside dental care and oral health management. Because the study relied on routine clinical documentation, no intervention or prospective follow-up was performed.

Study variables

Demographic variables included age at tracheostomy and sex. Clinical variables included dysphagia, sialorrhea, and history of multiple PICU admissions. Comorbidities included neurological disease, cardiac disease, prematurity, genetic syndromes, and immunocompromised status. Microbiological variables comprised tracheal aspirate culture results, including the identification of specific microorganisms.

The primary outcome was the occurrence of tracheitis. Tracheitis diagnosed during PICU admission was considered to have occurred in situ. For ward and home settings, tracheitis was defined according to diagnosis made during hospital evaluation, without certainty regarding the exact environment of onset. Accordingly, tracheitis was analyzed at three levels: global tracheitis (occurrence in any setting), PICU tracheitis (events diagnosed during the PICU stay), and post-PICU tracheitis (events diagnosed after PICU discharge, with ward and home combined).

Microorganisms identified in tracheal aspirates were recorded at species level and subsequently grouped into ecological categories. Gram-negative organisms included Pseudomonas aeruginosa, Serratia marcescens, Klebsiella pneumoniae, Enterobacter cloacae, Acinetobacter baumannii, Escherichia coli, Proteus mirabilis, Morganella morganii, Stenotrophomonas maltophilia, and Haemophilus influenzae. Gram-positive organisms included Staphylococcus aureus, Staphylococcus haemolyticus, and Streptococcus mitis/oralis. Fungal organisms included Candida albicans. Derived variables included the presence of any Gram-negative organism, any Gram-positive organism, any fungal organism, and the total number of pathogens per patient.

Comorbidities were initially extracted as free-text entries from clinical records and subsequently structured into predefined categories through automated parsing followed by manual validation. Neurological comorbidity included conditions affecting the central or peripheral nervous system, such as encephalopathy, epilepsy, hydrocephalus, and structural brain abnormalities. Cardiac comorbidity included congenital or acquired heart disease, including septal defects, valvular abnormalities, and

pulmonary hypertension. Prematurity was defined according to documentation of preterm birth or related neonatal conditions. Immunocompromised status included primary immunodeficiency, malignancy, or immunosuppressive therapy. Genetic syndrome included clinically documented syndromic conditions or genetic diagnoses recorded in the chart, such as trisomies, Moebius syndrome, CHARGE syndrome, Pena-Shokeir syndrome, craniofacial syndromes associated with dysmorphism or craniosynostosis, and documented chromosomal deletions or duplications.

Aspiration risk was defined as the presence of either dysphagia or sialorrhea. Post-PICU environment was defined as ward and home settings combined. Trajectory patterns were defined according to the occurrence of tracheitis across care environments.

Statistical analysis

Continuous variables were summarized as means and standard deviations or medians and interquartile ranges, as appropriate. Categorical variables were reported as frequencies and percentages. Associations between predictors and tracheitis were initially explored using bivariate analyses. Odds ratios were estimated, and Fisher's exact test was used when appropriate because of small cell counts.

Multivariable logistic regression models were constructed to evaluate independent predictors of tracheitis. A hierarchical modeling strategy was applied, sequentially incorporating demographic variables, microbiological variables, functional variables, and comorbidities. Model performance was assessed using the area under the receiver operating characteristic curve (AUC).

For analyses involving individual microorganisms with low frequency, Firth penalized logistic regression was applied to reduce small-sample bias and address separation issues. To account for repeated measures across care environments, generalized estimating equations (GEE) with a binomial distribution and exchangeable correlation structure were used. This approach allowed simultaneous evaluation of patient-level and environment-level effects.

Predictive performance was evaluated using AUC, sensitivity, specificity, positive predictive value, negative predictive value, and F1 score. Optimal classification thresholds were determined with the Youden index. All statistical analyses were performed using Python version 3.10 (Python Software Foundation, Wilmington, DE, USA). Data handling and preprocessing were conducted with pandas; multivariable logistic regression and GEE models were fitted with statsmodels; performance metrics and ROC analyses were computed with scikit-learn; and graphical outputs were generated with matplotlib.

Ethical considerations

This study was performed in accordance with the principles of the Declaration of Helsinki and was approved by the Research Ethics Committee of Faculdade São Leopoldo Mandic, Brazil (CAAE 85964625.1.0000.5374; approval no. 7.390.867). Because this was a retrospective review of medical records, the requirement for informed consent was waived by the ethics committee.

Results

Study population

A total of 96 tracheostomized pediatric patients with complete data were included in the final analysis. The cohort was predominantly composed of young children, with a median age of 5 months (IQR 3–31.8) and a mean age of 23.8 ± 35.4 months. Males accounted for 53.6% of the sample.

The population exhibited a high burden of clinical complexity. Neurological comorbidities were present in 42.7% of patients, cardiac comorbidities in 45.8%, and genetic syndromes in 40.6%. Prematurity was identified in 25.0% of cases, while immunocompromising conditions were uncommon (6.3%).

Functional impairment was frequent, with dysphagia observed in 48.5% and sialorrhea in 70.1% of patients, resulting in a high prevalence of aspiration risk (Table 1).

Table 1
Integrated summary of predictors, clinical characteristics, and model performance

Domain	Variable	Prevalence (%)	OR	95% CI	p-value	Interpretation
Demographics	Age (months)	—	—	—	—	Non-linear effect suggested (ML)
	Male sex	53.6	NS	—	> 0.05	No independent association
Comorbidities	Neurological	42.7	1.69	0.91–3.14	0.096	Borderline (post-PICU signal)
	Cardiac	45.8	1.45	0.79–2.66	0.233	Not independently associated
	Prematurity	25.0	**2.49**	1.40–4.42	**0.0019**	Strong independent predictor
	Genetic syndrome	40.6	0.86	0.48–1.51	0.592	No association
	Immunocompromised	6.3	—	—	—	Low frequency
Functional variables	Dysphagia	48.5	0.76	0.42–1.38	0.36	No independent effect
	Sialorrhea	70.1	1.61	0.85–3.07	0.146	Suggestive (post-PICU)
Microbiology (aggregated)	Gram-negative	41.2	**2.25**	1.35–3.75	**0.0018**	Strong independent predictor
	Gram-positive	18.6	—	—	—	Not independently tested
	Fungal	7.2	—	—	—	Low contribution
Microbiology (specific)	*Staphylococcus aureus*	—	2.92	0.95–8.96	0.061	Borderline

This table summarizes demographic, clinical, and microbiological variables and their associations with tracheitis in tracheostomized pediatric patients. Values are presented as prevalence (%) and odds ratios (OR) with 95% confidence intervals (CI) and p-values from multivariable logistic regression and generalized estimating equations (GEE). Abbreviations: OR, odds ratio; CI, confidence interval; GEE, generalized estimating equations; PICU, pediatric intensive care unit.

Domain	Variable	Prevalence (%)	OR	95% CI	p-value	Interpretation
System-level (GEE)	Post-PICU vs PICU	—	**0.40**	0.24–0.68	**0.0007**	Protective outside PICU

This table summarizes demographic, clinical, and microbiological variables and their associations with tracheitis in tracheostomized pediatric patients. Values are presented as prevalence (%) and odds ratios (OR) with 95% confidence intervals (CI) and p-values from multivariable logistic regression and generalized estimating equations (GEE). Abbreviations: OR, odds ratio; CI, confidence interval; GEE, generalized estimating equations; PICU, pediatric intensive care unit.

Microbiological profile

Microbiological analysis of tracheal aspirates revealed a predominance of opportunistic pathogens typically associated with healthcare environments. The most frequently identified microorganisms were *Staphylococcus aureus, Pseudomonas aeruginosa*, and *Serratia marcescens*, followed by *Candida albicans, Enterobacter cloacae, and Acinetobacter baumannii.*

The overall microbial profile was characterized by a predominance of Gram-negative organisms, consistent with hospital-acquired respiratory colonization patterns.

At the species level, no individual microorganism demonstrated a robust independent association with tracheitis after correction for sparse data using Firth penalized logistic regression. However, Staphylococcus aureus showed a borderline association with PICU tracheitis (OR 2.92; 95% CI 0.95–8.96; p = 0.061), while several Gram-negative organisms, including Klebsiella pneumoniae and Serratia marcescens, demonstrated positive but imprecise associations.

These findings indicate that the microbiological signal is more strongly expressed at the ecological level (Gram-negative profile) rather than at the level of individual species (Table 1).

Occurrence of tracheitis across care environments

Tracheitis occurred in a substantial proportion of patients, both during PICU stay and after transition to lower levels of care. The distribution of events across environments supported the presence of distinct clinical contexts influencing disease occurrence.

Bivariate analysis

In unadjusted analyses, Gram-negative organisms and prematurity were consistently associated with tracheitis. In contrast, functional variables and comorbidities did not demonstrate strong independent associations in the global model.

However, stratified analyses suggested a differential pattern across care environments. In PICU, microbiological factors predominated, whereas in post-PICU settings, neurological comorbidity and

functional impairment showed stronger, although not statistically definitive, associations with the outcome (Table 1).

Multivariable analysis

Global tracheitis

Model discrimination improved progressively with the addition of clinical variables, reaching an AUC of 0.749 in the fully adjusted model.

In the final model, Gram-negative organisms and prematurity remained independently associated with tracheitis. Comorbidity variables, including neurological and cardiac conditions, were not independently associated after adjustment.

PICU tracheitis

The fully adjusted model demonstrated good discrimination (AUC 0.737). Gram-negative organisms and prematurity remained the only independent predictors of tracheitis in the PICU setting.

Functional variables and comorbidities did not demonstrate independent associations in this environment.

Post-PICU tracheitis

Model performance improved substantially after inclusion of functional and comorbidity variables, reaching an AUC of 0.725.

Although no individual variable reached statistical significance, neurological comorbidity, sialorrhea, and prematurity showed consistent positive associations, suggesting a clinically relevant pattern in post-PICU settings.

System-level analysis (GEE)

In the generalized estimating equation model accounting for repeated measures across care environments, the care setting was independently associated with tracheitis.

Compared with PICU, post-PICU environments were associated with significantly lower odds of tracheitis (OR 0.40; 95% CI 0.24–0.68; p = 0.0007).

Gram-negative organisms (OR 2.25; 95% CI 1.35–3.75; p = 0.0018) and prematurity (OR 2.49; 95% CI 1.40–4.42; p = 0.0019) remained independently associated with tracheitis across environments.

Neurological comorbidity showed a borderline association (OR 1.69; 95% CI 0.91–3.14; p = 0.096), while functional variables and other comorbidities were not independently associated.

Summary of findings

Across all analytical approaches, three factors consistently emerged as key determinants of tracheitis: care environment, Gram-negative microbiological profile, and prematurity.

The PICU setting was associated with a substantially higher risk of tracheitis, independent of patient-level factors. Gram-negative organisms remained a robust microbiological marker of risk, while prematurity reflected underlying vulnerability.

Although neurological comorbidity and functional impairment did not demonstrate independent effects in fully adjusted models, their consistent direction of association in post-PICU analyses suggests a potential contributory role in this setting.

Further detail on predictive values and performance metrics are shown in Table 1 and Table 2. Complementary visual data are also displayed in Fig. 1 and Fig. 2.

Table 2
Performance metrics of predictive models for tracheitis across care environments

Outcome	N	AUC	Threshold	Sensitivity	Specificity	PPV	NPV	F1 Score
Global tracheitis	96	**0.749**	optimal	0.547	0.917	**0.943**	0.541	0.688
PICU tracheitis	96	**0.737**	optimal	0.633	0.771	0.667	0.737	0.650
Post-PICU tracheitis	96	**0.725**	optimal	0.600	0.778	0.625	0.750	0.667

This table presents the performance of the fully adjusted multivariable logistic regression models for predicting tracheitis in the global cohort, PICU, and post-PICU settings. Model discrimination is reported as the area under the receiver operating characteristic curve (AUC). Classification metrics, including sensitivity (recall), specificity, positive predictive value (PPV), negative predictive value (NPV), and F1 score, were calculated using optimal probability thresholds defined by the Youden index. Post-PICU refers to ward and home environments combined. Abbreviations: AUC, area under the curve; PPV, positive predictive value; NPV, negative predictive value; PICU, pediatric intensive care unit.

Discussion

This study provides an integrated analysis of tracheitis in tracheostomized pediatric patients, combining microbiological, clinical, and system-level factors within a unified framework. Three main findings emerge. First, the care environment exerts a strong independent effect on tracheitis, with significantly higher risk during PICU stay compared with post-PICU settings. Second, Gram-negative microorganisms represent the most consistent microbiological determinant of tracheitis across analyses. Third, prematurity emerges as a robust host-related risk factor, while neurological comorbidity and functional impairment appear to play a contributory, but context-dependent, role—particularly after PICU discharge.

The most striking finding of this study is the magnitude of the system-level effect. Even after adjustment for microbiological and patient-level variables, the PICU environment remained independently associated with a substantially higher likelihood of tracheitis. This reinforces the concept that tracheitis in this population is not solely a patient-driven condition but is strongly influenced by the ecological and procedural characteristics of the care setting.

This observation aligns with previous evidence showing that critically ill children are exposed to highly selective microbial environments, invasive procedures, and frequent antibiotic pressure, all of which favor colonization by opportunistic pathogens [4–6]. In contrast, post-PICU settings represent a transition toward lower-intensity care, where these pressures are reduced, even though patients remain clinically vulnerable.

Importantly, this finding supports a system-awareness perspective, in which disease occurrence is interpreted within the context of care trajectories rather than as isolated events. Such an approach is particularly relevant in observational studies and is consistent with recommendations from the STROBE initiative emphasizing the need for transparent and context-aware interpretation of epidemiological data [24, 25].

The second key finding is the central role of Gram-negative organisms as predictors of tracheitis. While individual microorganisms showed variable and often imprecise associations, the aggregated Gram-negative profile consistently emerged as an independent determinant across models.

This reinforces the concept that respiratory infections in tracheostomized children are better understood at the ecological level rather than through isolated pathogen analysis. Gram-negative organisms such as Pseudomonas aeruginosa, Serratia marcescens, and Enterobacter cloacae are well-recognized components of hospital microbiota and are frequently associated with airway colonization in critically ill patients [7–9].

At the same time, the absence of strong independent effects for individual species after adjustment suggests that microbial community structure, rather than specific pathogens, may be the primary driver of disease. This interpretation is consistent with emerging concepts in microbiome research, which emphasize the role of dysbiosis and microbial interactions in disease pathogenesis [5, 22].

The observed microbiological patterns are closely aligned with the growing body of evidence supporting the oral cavity as a reservoir for respiratory pathogens. Several studies have demonstrated that microorganisms present in tracheal aspirates are also found in oral biofilms, suggesting that the oropharynx serves as a source for lower airway colonization [11, 16, 12].

This connection is mediated by microaspiration, a process that becomes particularly relevant in patients with impaired swallowing and airway protection. Functional variables such as dysphagia and sialorrhea—highly prevalent in our cohort—are known to increase aspiration risk and facilitate microbial transfer from the oral cavity to the respiratory tract [18, 19].

Although these variables did not emerge as independent predictors in fully adjusted models, their consistent directional association in post-PICU analyses suggests that they may contribute to disease in a more subtle and context-dependent manner. This interpretation is supported by studies demonstrating that oral hygiene interventions can reduce respiratory infections, further highlighting the clinical relevance of the oral–lung axis [20–23].

Among host-related factors, prematurity showed a strong and consistent association with tracheitis. This finding is biologically plausible, as premature infants often present with immature immune responses, altered airway structure, and prolonged exposure to healthcare environments, all of which increase susceptibility to infection [26–28].

Neurological comorbidity, while not reaching statistical significance in fully adjusted models, demonstrated a consistent trend toward increased risk, particularly in system-level analyses. This likely reflects the interplay between neurological impairment, reduced airway protection, and chronic aspiration risk. Together, these findings suggest that host vulnerability operates through both intrinsic (immunological) and functional (aspiration-related) pathways.

The integration of microbiological, clinical, and system-level findings has important clinical implications. First, the strong association between Gram-negative ecology and tracheitis highlights the need for targeted surveillance and antimicrobial stewardship strategies in PICU settings. Second, the role of the oral cavity as a potential reservoir for respiratory pathogens supports the incorporation of structured oral care protocols as part of preventive strategies.

Third, the differential behavior of predictors across care environments suggests that risk stratification should be context-specific. In PICU, prevention efforts may focus on infection control and microbial ecology, whereas in post-PICU settings, attention should shift toward functional rehabilitation and aspiration prevention.

This study has limitations inherent to its retrospective observational design. First, the exact timing and environment of tracheitis onset outside the PICU could not be determined, as diagnoses in ward and home settings were made during hospital evaluation. Second, microbiological data were based on tracheal aspirates, which may not fully represent lower airway infection and may be influenced by colonization. Additionally, the relatively small sample size limited the ability to detect independent effects for individual microorganisms and may have contributed to wide confidence intervals in some analyses.

Conclusion

Tracheitis in tracheostomized pediatric patients is best understood as the result of a dynamic interaction between care environment, microbial ecology, and host vulnerability. The PICU setting represents a high-risk environment characterized by Gram-negative microbial dominance, while post-PICU settings reflect a more complex interplay of functional and host-related factors. These findings support a system-level

approach to both research and clinical management, emphasizing the need to integrate environmental, biological, and patient-centered perspectives in the prevention and treatment of respiratory infections.

Declarations

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Figures

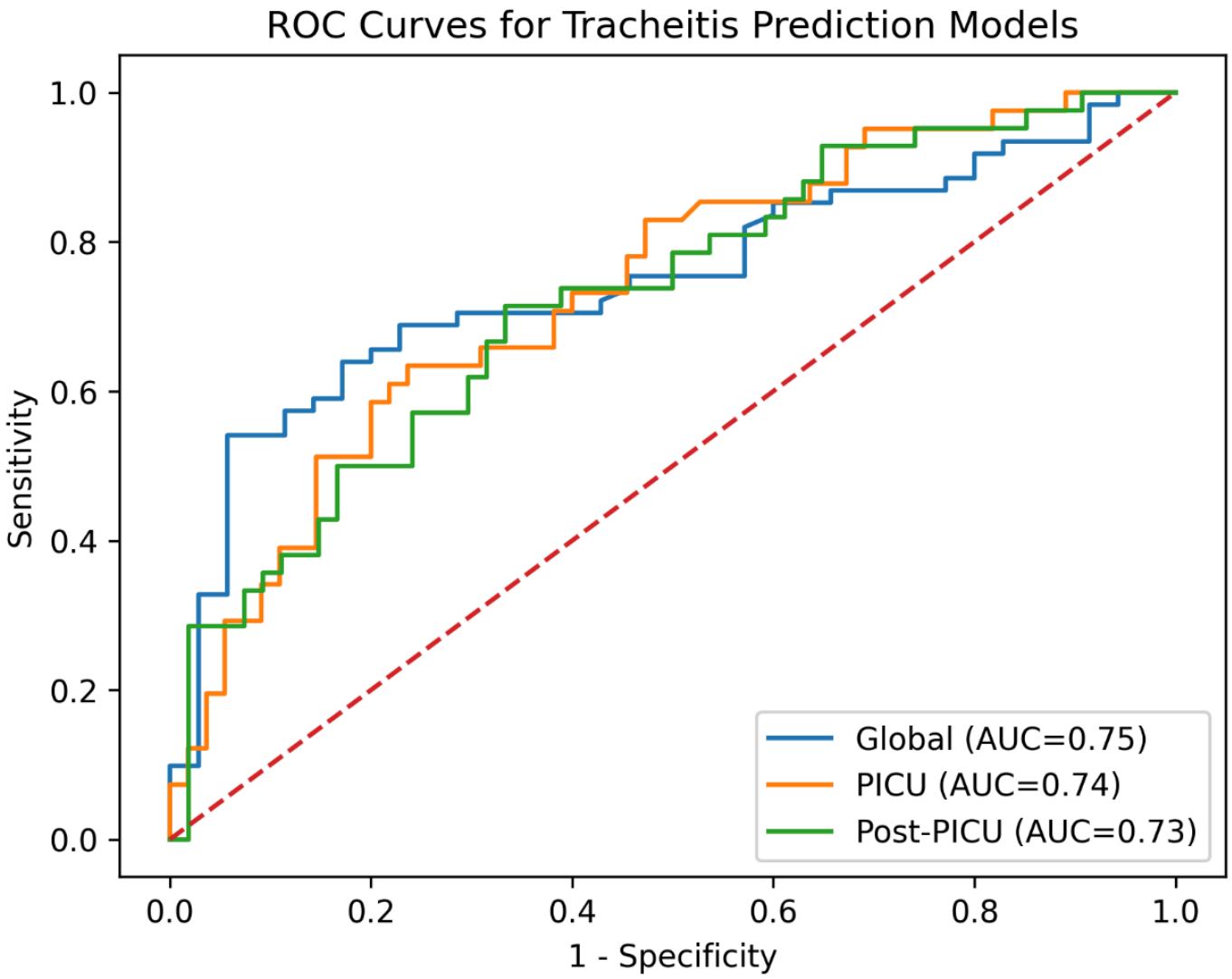


Figure 1

Receiver operating characteristic (ROC) curves for tracheitis prediction models

Receiver operating characteristic curves illustrating the discriminatory performance of the fully adjusted multivariable logistic regression models for predicting tracheitis in the global cohort, pediatric intensive care unit (PICU), and post-PICU settings. Model performance is quantified by the area under the curve (AUC). The diagonal dashed line represents the line of no discrimination.

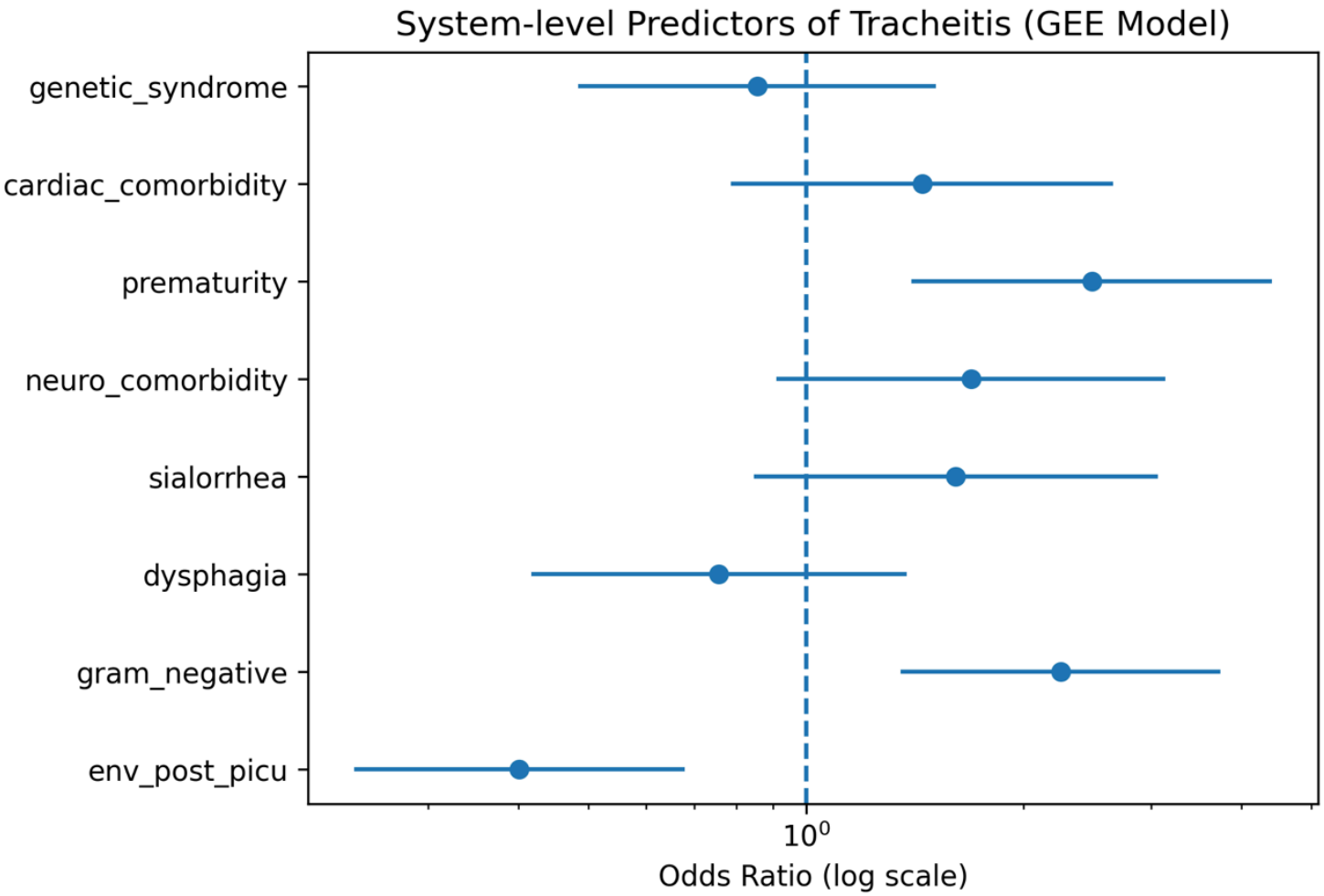


Figure 2

Forest plot of system-level predictors of tracheitis

Forest plot showing adjusted odds ratios (OR) and 95% confidence intervals (CI) for predictors of tracheitis derived from the generalized estimating equation (GEE) model accounting for repeated measures across care environments. The vertical dashed line represents the null value (OR = 1). Post-PICU refers to ward and home settings combined.