Colonization Density of the Upper Respiratory Tract as a Predictor of Pneumonia—Haemophilus influenzae, Moraxella catarrhalis, Staphylococcus aureus, and Pneumocystis jirovecii

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Background. There is limited information on the association between colonization density of upper respiratory tract colonizers and pathogen-specific pneumonia. We assessed this association for Haemophilus influenzae, Moraxella catarrhalis, Staphylococcus aureus, and Pneumocystis jirovecii.

Methods. In 7 low- and middle-income countries, nasopharyngeal/oropharyngeal swabs from children with severe pneumonia and age-frequency matched community controls were tested using quantitative polymerase chain reaction (PCR). Differences in median colonization density were evaluated using the Wilcoxon rank-sum test. Density cutoffs were determined using receiver operating characteristic curves. Cases with a pathogen identified from lung aspirate culture or PCR, pleural fluid culture or PCR, blood and age-frequency matched community controls were tested using quantitative polymerase chain reaction (PCR). Differences in colonization density cutoff for...
Many pneumonia pathogens can also be upper respiratory tract (URT) colonizers, including Streptococcus pneumoniae, Haemophilus influenzae, Staphylococcus aureus, Moraxella catarrhalis, and Pneumocystis jirovecii [1–6]. Obtaining specimens from the site of infection remains challenging, as direct lung aspiration is rarely done, and blood cultures are insensitive and often unavailable in areas of highest pneumonia burden [7, 8]. In many settings, the high frequency of URT colonization with these potential pathogens in healthy children undermines the application of qualitative diagnostic tests, such as polymerase chain reaction (PCR), to ascribe etiology [9].

Previous studies have suggested that children with pneumonia may have higher pathogen density in the URT compared to children without pneumonia, though there is heterogeneity by study and pathogen [1, 4, 10–19]. We set out to determine if density of URT colonizers predicted pathogen-specific infections among pneumonia cases in the Pneumonia Etiology Research for Child Health (PERCH) study. Provided differences in densities between cases and controls, we evaluated whether pathogen densities offer any value in pneumonia diagnostic algorithms, or provide information beyond presence or absence of positivity alone in analytic models such as the PERCH integrated analysis [20]. The density evaluation for S. pneumoniae is reported elsewhere [21].

**METHODS**

The PERCH study is a multicountry, standardized evaluation of the etiologic agents causing severe and very severe pneumonia among children in sites in 7 low- and middle-income countries: Dhaka and Matlab, Bangladesh; Basse, The Gambia; Kilifi, Kenya; Bamako, Mali; Soweto, South Africa; Nakhon Phanom and Sa Kaeo, Thailand; and Lusaka, Zambia. *Haemophilus influenzae* type b vaccine was used routinely at all sites except Thailand, while South Africa, The Gambia, Mali, and Kenya used pneumococcal conjugate vaccine throughout the duration of the study [22]. PERCH followed a standardized protocol for enrollment, specimen collection, and laboratory testing [23].

**Case and Community Control Selection and Clinical Evaluation**

Identification and selection of cases and controls have been described previously [24]. In brief, we enrolled hospitalized patients aged 1–59 months with World Health Organization (WHO)–defined severe or very severe pneumonia and age-frequency matched community controls. Severe pneumonia was defined as having cough or difficulty breathing and lower chest wall indrawing; very severe pneumonia was defined as cough or difficulty breathing and at least 1 of the following: central cyanosis, difficulty breastfeeding/drinking, vomiting everything, convulsions, lethargy, unconsciousness, or head nodding [25]. Within this case definition we further defined radiographic pneumonia as consolidation or any other infiltrate on chest radiograph (CXR positive) as interpreted by a panel of trained CXR readers [26, 27]. Microbiologically confirmed cases were those with identification of the respective pathogen by PCR from lung aspirate or pleural fluid; bacterial culture from lung aspirate, pleural fluid, or blood; or *P. jirovecii* by induced sputum, pleural fluid, or lung aspirate immunofluorescence or toluidine blue staining [28]. Antibiotic pretreatment was defined by having either positive serum bioassay or clinician report of antibiotics administered prior to specimen collection on the day of admission.

**Specimen Collection**

A flocked nasopharyngeal (NP) swab (flexible minitip, Copan) and a rayon oropharyngeal (OP) swab (Fisher Scientific), transported in universal transport media (Copan) and processed within 24 hours of collection were used for URT pathogen detection by PCR. Blood was collected for culture. Pleural fluid specimens were collected as clinically indicated. Lung aspirates were collected from a subset of cases in The Gambia, South Africa, Mali, and Bangladesh.

**Laboratory Testing**

PERCH employed conventional and molecular diagnostic techniques for the identification of potential pathogens, as described elsewhere [8, 28–31]. In brief, total nucleic acid extraction was performed on respiratory specimens using the NucliSens easyMAG system (bioMérieux, Marcy l’Etoile, France). Four hundred microliters of each respiratory specimen was eluted to a final volume of 60–110 μL nucleic acid.

Respiratory specimens (including lung aspirate and pleural fluid specimens) were evaluated using the Fast Track Diagnostics Respiratory Pathogens 33 test (FTD Resp-33) (Fast-track Diagnostics, Sliema, Malta), a 33-target, 8-multiplex real-time quantitative PCR platform for the detection of selected viruses and the following bacteria and fungi: *P. jirovecii; Mycoplasma pneumoniae; Chlamydia pneumoniae; S. pneumoniae; H. influenzae type b; H. influenzae species; S. aureus; M. catarrhalis; Bordetella pertussis; Klebsiella pneumoniae; and Salmonella* species. Standard curves for quantification were generated using 10-fold serial dilutions of plasmid standards provided by FTD approximately every 3 months and were used to calculate pathogen density (log$_{10}$ copies/mL) from the sample cycle threshold values; standards were only available for the linear range of detection of the assay from 4.0 to 8.0 log$_{10}$ copies/mL. Additionally, induced sputum, pleural fluid, and lung aspirate specimens were tested for *P. jirovecii* by immunofluorescence (South Africa) and toluidine blue staining (Zambia).

Blood cultures were incubated using automated systems (BacT/ALERT in South Africa, Thailand, and Bangladesh; BACTEC at all other sites). Organisms were identified according to standard microbiological methods.
Statistical Analysis
We made comparisons between community controls and both microbiologically confirmed pneumonia cases and radiographic pneumonia cases. Microbiologically confirmed cases were not restricted to children with abnormal findings on CXR in order to include children who died before a radiograph was taken or had not developed a positive finding at time of initial radiograph. Human immunodeficiency virus (HIV)–infected cases were included in a supplemental analysis for P. jirovecii but excluded from all other analyses.

Among children positive for each organism, mean and median colonization densities were compared using Wilcoxon rank-sum tests. Potential covariates of colonization density were evaluated, including site, age, sex, vaccination status, and prior antibiotic administration [32]. Total bacterial load (across all bacteria tested for by FTD Resp-33) was compared between cases and controls, in addition to proportional pathogen densities comparing proportional contributions of a given organism to the total bacterial load. Receiver operating characteristic (ROC) curves and the corresponding area under the curve (AUC) were generated to investigate the performance of absolute density in determining case status among microbiologically confirmed cases and community controls including children without detection of the given pathogen in the URT by PCR, and also between radiographic pneumonia cases and community controls positive for each organism in the URT by PCR. The Youden index was calculated to determine the best-performing cutoffs to differentiate cases and community controls [33]. To guard against bias in the estimates of sensitivity due to having a small number of confirmed cases for each potential pathogen, the Youden index was calculated using leave-one-out cross-validation when sample sizes were sufficient [34]. Positive and negative predictive values associated with each cutoff were calculated comparing microbiologically confirmed cases as the gold standard against all HIV-uninfected cases.

All analyses were performed using SAS software version 9.4 (SAS Institute, Cary, North Carolina) and R Statistical Software 3.2.1 (R Foundation for Statistical Computing, Vienna, Austria). P values are 2 sided.

Ethical Considerations
The PERCH study protocol was approved by the institutional review board or ethical review committee at each of the study site institutions and at the Johns Hopkins Bloomberg School of Public Health. Parents or guardians of all participants provided written informed consent.

RESULTS
Of the 4232 cases enrolled in the PERCH study, 4139 cases had available NP/OP PCR results; of those, 239 additional cases

Table 1. Characteristics of Children Included in Analysis of Quantification*  

| Characteristic | Microbiologically Confirmed Casesb (n = 52) | CXR-Positive Casesc (n = 1700) | Controls (n = 4986) |
|---------------|---------------------------------------------|---------------------------------|---------------------|
| Site          |                                             |                                 |                     |
| Kenya         | 4 (7.7)                                     | 278 (16.4)                      | 855 (17.1)          |
| The Gambia    | 8 (15.4)                                    | 267 (15.7)                      | 624 (12.5)          |
| Mali          | 14 (26.9)                                   | 229 (13.5)                      | 724 (14.5)          |
| Zambia        | 11 (21.2)                                   | 185 (10.9)                      | 535 (10.7)          |
| South Africa  | 13 (25.0)                                   | 425 (25.0)                      | 823 (16.5)          |
| Thailand      | 2 (3.8)                                     | 97 (5.7)                        | 657 (13.2)          |
| Bangladesh    | 0 (0)                                       | 219 (12.6)                      | 768 (15.4)          |
| Age           |                                             |                                 |                     |
| 1-5 mo        | 24 (46.2)                                   | 667 (39.2)                      | 1555 (31.2)         |
| 6-11 mo       | 11 (21.2)                                   | 409 (24.1)                      | 1187 (23.8)         |
| 12-23 mo      | 11 (21.2)                                   | 414 (24.4)                      | 1235 (24.8)         |
| 24-59 mo      | 6 (11.5)                                    | 210 (12.4)                      | 1009 (20.2)         |
| Sex           |                                             |                                 |                     |
| Female        | 32 (61.5)                                   | 736 (43.3)                      | 2477 (49.7)         |
| Antibioticsd  |                                             |                                 |                     |
| Prior to NP/OP swab collection | 22 (42.3)                  | 791 (46.5)                      | 84 (1.7)            |
| No. of bacteria detectede |                                  |                                 |                     |
| 0             |                                             |                                 |                     |
| 1             | 2 (3.8)                                     | 197 (11.6)                      | 486 (9.7)           |
| 2             | 9 (17.3)                                    | 376 (22.1)                      | 1141 (22.9)         |
| ≥3            | 40 (76.9)                                   | 1033 (60.8)                     | 3195 (64.1)         |

*P value <.05 for case-control group comparisons of overall site, overall age, sex, prior antibiotics, and number of bacteria detected, obtained from χ² test.

Data are presented as No. (%).

Abbreviations: CXR, chest radiograph; NP/OP, nasopharyngeal/oropharyngeal.

*aChildren with available NP/OP polymerase chain reaction results.

*bMicrobiologically confirmed for Haemophilus influenzae, Moraxella catarrhalis, Staphylococcus aureus, or Pneumocystis jiroveci.

*cCXR-positive defined as having radiographic evidence of pneumonia (consolidation and/or other infiltrate), excluding microbiologically confirmed cases of H. influenzae, M. catarrhalis, S. aureus, or P. jiroveci.

*dAdministered antibiotics at the study facility prior to the collection of specimens (cases only), positive serum bioassay (cases and controls), received antibiotics at a referral facility (cases only), or received routine cotrimoxazole prophylaxis (cases and controls).

*eIncluding Bordetella pertussis, Chlamydia pneumoniae, H. influenzae, M. catarrhalis, Mycoplasma pneumoniae, P. jiroveci, S. aureus, Salmonella species, and Streptococcus pneumoniae.
among controls than CXR-positive cases, even after adjusting for feed. All Sites
Cases, Non–Microbiologically Confirmed Radiographic Pneumonia Cases, Cases Microbiologically Confirmed for Another Pathogen, and Controls—
Table 2. Detection Prevalence and Median Pathogen Density (Copies/mL) From Nasopharyngeal/Oropharyngeal Swabs for Microbiologically Confirmed Cases, Non–Microbiologically Confirmed Radiographic Pneumonia Cases, Cases Microbiologically Confirmed for Another Pathogen, and Controls—All Sites

| Colonizer          | Measure                     | A. Confirmed Cases* | B. CXR-Positive Cases (n = 1687) | C. Cases Confirmed for Other Pathogen* | D. All Controls (n = 4986) | Difference in Median Densities, P Valuea |
|--------------------|-----------------------------|---------------------|----------------------------------|---------------------------------------|---------------------------|------------------------------------------|
|                    |                              |                     |                                  |                                       |                           |                                          |
| Haemophilus influenza | NP/OP+, No. (%)b            | 21/21 (100)         | 949 (57.3)                       | 76/121 (62.8)                        | 2562 (51.5)               |                                          |
|                    | Median density (IQR)c        | 6.77 (6.00–7.12)    | 5.90 (5.00–6.66)                 | 6.39 (5.53–7.08)                     | 5.71 (4.89–6.35)          | .19 < .001 < .001                       |
| Moraxella catarrhalis | NP/OP+, No. (%)b            | 6/7 (85.7)          | 1091 (65.8)                     | 92/135 (68.1)                       | 3694 (74.3)               |                                          |
|                    | Median density (IQR)c        | 6.01 (5.00–6.73)    | 5.50 (4.65–6.26)                 | 6.15 (5.09–6.78)                    | 5.59 (4.87–6.20)          | .88 .44 .07                             |
| Pneumocystis jiroveci | NP/OP+, No. (%)b            | 1/2 (50.0)          | 149 (9.0)                       | 10/140 (7.1)                        | 382 (7.7)                 |                                          |
|                    | Median density (IQR)c        | 4.01 (NA)           | 3.92 (3.08–4.73)                 | 4.00 (2.14–5.95)                    | 3.56 (3.02–4.10)          | ... .44 < .001                          |
| Staphylococcus aureus | NP/OP+, No. (%)b            | 15/23 (65.2)      | 342 (20.6)                      | 29/119 (24.5)                      | 940 (18.9)                |                                          |
|                    | Median density (IQR)c        | 4.87 (3.87–5.64)    | 4.48 (3.43–5.53)                 | 5.14 (4.48–5.85)                    | 4.29 (3.42–5.17)          | .43 .13 .05                             |

Abbreviations: CXR, chest radiograph; IQR, interquartile range; NA, not applicable; NP/OP, nasopharyngeal/oropharyngeal.

*Microbiologically confirmed case for any other bacteria or virus.

Comparing median densities using Wilcoxon rank-sum test.

No. (%) positive in the NP/OP for organism among those with available results for that target.

Log_{10} copies/mL, among all confirmed case positives including NP/OP PCR negatives counted as zero densities.

Among those positive on NP/OP PCR.
tended to be higher in *H. influenzae*–confirmed cases (41.6%) and CXR-positive cases (7.2%) compared with controls (1.2%). Conversely, median proportional densities of *M. catarrhalis* were higher in controls compared to CXR-positive cases (14.3% vs 5.0%). Among 100 randomly selected controls, 24% had *M. catarrhalis*–dominated proportional densities (≥ 50%) compared with 14%–16% of non–*M. catarrhalis* confirmed cases (Supplementary Figure 6). However, there was substantial overlap in the range of proportional densities between microbiologically confirmed cases, CXR-positive cases, and controls.

**Determination of Density Cutoffs**

Using density in log_{10} copies/mL in microbiologically confirmed cases compared to controls, the ROC curve best-performing cutoff of 5.9 log_{10} copies/mL was identified for *H. influenzae* with a sensitivity of 86% and specificity of 77% (Figure 2 and Table 3). Though the *S. aureus* cutoff (3.0 log_{10} copies/mL) was moderately sensitive and specific, the *S. aureus* cutoff did not significantly improve sensitivity and specificity over qualitative analysis using simply presence or absence of specific organisms.

Given the limited numbers of NP/OP-positive microbiologically confirmed *P. jirovecii* (n = 1) and *M. catarrhalis* (n = 6) cases, we explored the use of NP/OP positive, CXR-positive cases and controls to identify potential cutoffs for *P. jirovecii* (4.0 log_{10} copies/mL) and *M. catarrhalis* (5.0 log_{10} copies/mL) (Supplementary Figure 5). Densities among the limited number of microbiologically confirmed cases were consistent with these cutoffs, as 5 of 6 microbiologically confirmed *M. catarrhalis* cases were above the thresholds. The *P. jirovecii* cutoff demonstrated 48% sensitivity and 72% specificity for identifying *P. jirovecii*–positive CXR-positive cases (AUC = 0.58), among cases and controls positive for *P. jirovecii* (98% specificity)
Colonization density of the Upper Respiratory Tract

including negatives). Moraxella catarrhalis cutoffs did not help differentiate CXR-positive cases from controls (AUC = 0.50).

Positive and Negative Predictive Values Using Dichotomous Positivity and Density Cutoffs

Positive predictive values (PPVs) for identifying microbiologically confirmed cases from all cases using dichotomous URT positivity were low and improved marginally when density cutoffs were applied to H. influenzae (1.01% to 1.75%), S. aureus (1.81% to 2.14%), and P. jirovecii (0.89% to 1.67%), though the PPV is limited by lack of sensitivity in identifying microbiologically confirmed cases. Conversely, negative predictive values for identifying H. influenzae, S. aureus, and P. jirovecii microbiologically confirmed cases remained >99% for any detection in the URT and when utilizing the density cutoff.

Clinical Characteristics Associated With Being Above Versus Below Optimized Cutoffs

Densities above the cutoffs (compared to low densities and negatives) were associated with hypoxemia (adjusted odds ratio [AOR], 1.22; 95% confidence interval [CI], 1.02–1.47), any CXR abnormality (AOR, 1.23; 95% CI, 1.05–1.45), and primary endpoint consolidation (AOR, 1.57; 95% CI, 1.28–1.92) for H. influenzae, adjusted for site, age, sex, and prior antibiotic use. Additionally, having a density above the cutoff was associated with case fatality for P. jirovecii (AOR, 4.5; 95% CI, 2.6–7.5).

DISCUSSION

Colonization density of the URT with H. influenzae was significantly higher in microbiologically confirmed cases compared with community controls. Given the high prevalence of H. influenzae as a common colonizer, the improved specificity provided by the optimized cutoff of 5.9 log_{10} copies/mL helped delineate between common colonization and H. influenzae-mediated pneumonia. However, the overlapping density distributions between all case and control groups, and the low PPV limit the utility of density in individuals for clinical diagnosis. Our findings are similar to results from a study in adult patients in Denmark that yielded 90% sensitivity and 65% specificity using a cutoff at 5.0 log copies/mL [17]. Another study in Vietnamese children did not find an association between NP H. influenzae density and radiographic pneumonia; however, findings may have been limited by lack of a confirmed case group [12].

Colonization density of P. jirovecii may provide information toward differentiating carriage and pathogen-mediated pneumonia, although our evaluation was limited by a lack of microbiologically confirmed pneumocystis pneumonia (PCP) cases. A potential cutoff at 4.0 log_{10} copies/mL conferred 50% sensitivity and 72% specificity for radiographic pneumonia; however, the proportion of radiographic pneumonia cases with PCP-mediated pneumonia is unknown, and the PERCH process for identifying CXR abnormality may have been less sensitive for detecting radiographic features uniquely associated with PCP. The potential density cutoff is in line with other studies that have identified cutoffs between approximately 3 and 4.5 log copies/mL using clinically confirmed PCP patients, though we have not standardized the quantitative standards across these different studies [14–16]. Utilizing P. jirovecii detection from induced sputum PCR is widely accepted in clinical practice and would have expanded our sample of microbiologically

Figure 2. Receiver operating characteristic (ROC) curve and Youden index analysis for Haemophilus influenzae and Staphylococcus aureus confirmed cases compared with controls.
confirmed cases [35, 36]. However, these diagnostic tests are typically carried out when pneumocystis pneumonia is clinically suspected; findings from the PERCH study complicated the utility of induced sputum PCR as a confirmatory diagnostic tool in settings where nearly all cases had an induced sputum specimen collected [37].

Previous studies have failed to identify an association between density and pathogen-confirmed pneumonia for M. catarrhalis and S. aureus [1]. While the optimized S. aureus cutoff was specific, the relatively high proportion of NP/OP negatives among the microbiologically confirmed cases precludes the identification of a highly sensitive and specific cutoff. It has been suggested that Moraxella and Corynebacterium/Dolosigranulum-dominated microbiota profiles confer stability and are protective against respiratory disease, while Streptococcus- and Haemophilus-dominated microbiota profiles enhance susceptibility to respiratory infections [38, 39]. The protective effect of M. catarrhalis is supported by our finding of both higher prevalence, proportional density, and absolute density in controls compared to radiographic pneumonia cases.

Though our analysis benefited from a large sample size enrolled from multiple heterogeneous study sites and comprehensive clinical and laboratory standardization, there were limitations. Despite our large overall sample size, the number of microbiologically confirmed cases was limited. However, leave-one-out cross validation and findings from comparisons of CXR-positive cases vs controls supported findings from microbiologically confirmed cases. While we were able to evaluate co-pathogen interactions and proportional densities between a select number of potential pathogens, a metagenomics or microbiome approach would be better suited to understand the contribution of individual pathogens in the context of the upper respiratory tract microbiome [40–45]. Furthermore, we were unable to establish temporality between higher densities in the NP/OP and subsequent development of pneumonia, as infection in the lung may lead to higher densities in the NP/OP. Longitudinal studies would be better suited to addressing the role of colonization density on the development of pneumonia. The study design did not control for prior antibiotic use, which was associated with lower densities for both H. influenzae and M. catarrhalis. However, because prior antibiotic use was more common among cases compared to controls, the bias was toward the null for the analyses. Staphylococcus aureus and P. jirovecii are unlikely to be significantly affected by first-line antibiotics, which was reflected in our findings [46]. Variability of density distributions by site was also observed; however, density trends between the microbiologically confirmed case, radiographic pneumonia case, and control groups within a site followed the overall trends.

While we have provided cutoffs optimized for sensitivity and specificity, the choice of a cutoff can be tailored for specific applications. Identifying a density cutoff that maximizes combined sensitivity and specificity provides additional information from the NP/OP specimen in the PERCH primary etiology analysis; however, the interpretation and application of these cutoffs may not be ideal for use as either a diagnostic or screening tool (which may prioritize specificity and sensitivity, respectively). Moreover, the PPV using the density cutoff remained low for H. influenzae, although the PPV was limited by poor sensitivity for identifying microbiologically confirmed cases and low prevalence. Regardless, it is likely impossible to identify a URT density cutoff for these colonizers that could be applied as a clinical gold standard because the densities overlap and span the PCR linear range in both cases and controls, precluding the identification of clear cutoffs that would independently guide clinical decisions.

We found evidence for the relationship between H. influenzae colonization density and H. influenzae-mediated pneumonia in children, and also a potential association between P. jirovecii colonization density and pathogen-specific pneumonia. The use of molecular diagnostics from URT specimens provides significant advantages in both sensitivity and speed over traditional culture diagnostics, but ascribing lung infection based on detection of colonization in the URT is challenging. Compared to using presence or absence of positivity, utilizing colonization density improves specificity of molecular diagnostics with small reductions in sensitivity and improves information from the URT in the context of population-level epidemiologic studies such as the PERCH integrated analysis, but remains suboptimal for use as a gold standard diagnostic in clinical settings at the individual case level.

Supplementary Data

Supplementary materials are available at Clinical Infectious Diseases online. Consisting of data provided by the author to benefit the reader, the posted materials are not copyrighted and are the sole responsibility of the author, so questions or comments should be addressed to the corresponding author.

Notes

Author contributions. D. E. P. led the analysis, interpreted results, and drafted the manuscript. Q. S. performed analyses and assisted with interpretation of results. D. R. F., H. C. B., and S. R. C. H. assisted with interpretation of results and drafting of the manuscript. O. S. L., K. L. O., D. R. F., D. R. M., M. D. K., L. L. H., H. C. B., W. A. B., S. R. C. H., K. K. L., S. A. M., J. A. G. S., D. M. T., and R. A. K. conceived and designed the study and supervised study conduct. D. A., M. A., V. L. B., A. N. D., A. J. D., W. F., C. W. G., E. O., M. H. H., A. A. M., S. M., D. P. M., S. C. M., J. W., M. M., C. P., M. M., and S. T. were involved in study conduct, data collection, and/or data management. S. Z. provided statistical guidance. All authors reviewed and approved the manuscript. D. E. P. had full access to the data and had final responsibility for the decision to submit for publication.

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