Discovery and Validation of Biomarkers to Guide Clinical Management of Pneumonia in African Children

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Background. Pneumonia is the leading cause of death in children globally. Clinical algorithms remain suboptimal for distinguishing severe pneumonia from other causes of respiratory distress such as malaria or distinguishing bacterial pneumonia and pneumonia from other causes, such as viruses. Molecular tools could improve diagnosis and management.

Methods. We conducted a mass spectrometry–based proteomic study to identify and validate markers of severity in 390 Gambian children with pneumonia (n = 204) and age-, sex-, and neighborhood-matched controls (n = 186). Independent validation was conducted in 293 Kenyan children with respiratory distress (238 with pneumonia, 41 with Plasmodium falciparum malaria, and 14 with both). Predictive value was estimated by the area under the receiver operating characteristic curve (AUC).

Results. Lipocalin 2 (Lpc-2) was the best protein biomarker of severe pneumonia (AUC, 0.71 [95% confidence interval, 0.64–0.79]) and highly predictive of bacteremia (78% [64–92%]), pneumococcal bacteremia (84% [71–98%]), and “probable bacterial etiology” (91% [84–98%]). These results were validated in Kenyan children with severe malaria and respiratory distress who also met the World Health Organization definition of pneumonia. The combination of Lpc-2 and haptoglobin distinguished bacterial versus malaria origin of respiratory distress with high sensitivity and specificity in Gambian children (AUC, 99% [95% confidence interval, 99–100%]) and Kenyan children (82% [74–91%]).

Conclusions. Lpc-2 and haptoglobin can help discriminate the etiology of clinically defined pneumonia and could be used to improve clinical management. These biomarkers should be further evaluated in prospective clinical studies.

Keywords. pneumonia; malaria; lipocalin-2/NGAL; respiratory infection; biomarkers.

Pneumonia is the leading cause of death in young children globally, accounting for almost 2 million deaths every year, mainly in developing countries [1–4]. In The Gambia, acute lower respiratory tract infection, principally pneumonia, is a leading cause of death in young children [5, 6].

To reach and push beyond the United Nations’ Millennium Development Goal 4 for child survival, the number of deaths caused by pneumonia must be reduced. This will require a combination of effective preventive measures and improved clinical management [7–10]. Previous studies have shown that delayed referral is one of the most important risk factors for death in children with pneumonia [11]. Therefore, current clinical algorithms to refer patients with pneumonia to hospital are commonly based on diagnostic sensitivity rather than specificity. Consequently, over-referral of pneumonia cases has been a significant problem with the World Health Organization (WHO) case management strategy in some settings [12].
Importantly, clinical criteria do not distinguish bacterial causes of pneumonia from other causes such as viruses that do not require antibiotic treatment.

The analysis of biofluids (eg, plasma) using mass spectrometry–based methods has been widely adopted for biomarker discovery [13–15]. Once identified and validated, proteins of clinical value could be incorporated into rapid, point-of-care tests.

In African children, pneumonia is not the only cause of respiratory distress in children. In malaria endemic areas, *Plasmodium falciparum* infection may cause respiratory distress and the overlap of these conditions frequently compromises the diagnosis and management of these patients [16–18]. In acute pediatric admissions, the clinical syndrome of severe pneumonia overlapped in 39% of severe malaria cases [19].

We conducted a study to describe the plasma proteomic signature in samples from Gambian children with severe pneumonia and nonsevere pneumonia and controls. We identified and validated biomarkers to (1) predict disease severity in children with pneumonia, (2) predict blood culture positivity, (3) predict probable bacterial etiology of children with pneumonia, (4) evaluate biomarker performance to discriminate respiratory distress caused by pneumonia or by severe malaria, and (5) provide an independent validation for the diagnostic performance of these markers in Kenyan children.

**METHODS**

**Study Sites and Populations Studied**

The study participants were infants and children from the Greater Banjul and Basse areas aged 2–59 months taking part in a case-control study of childhood pneumonia and children admitted at the Kilifi District Hospital with a diagnosis of lower respiratory tract infection (Table 1). The sites, populations studied, and clinical definitions are described in detail in the Supplementary Methods and Supplementary Table 1.

**Biomarker Discovery and Validation Studies**

Plasma samples from Gambian infants and children aged 2–59 months were used for mass spectrometry–based proteomic studies (see Supplementary Methods for details). The concentrations of selected proteins (C-reactive protein [CRP], von Willebrand factor [vWF], lipocalin 2 [Lp-2] and haptoglobin) were measured with enzyme-linked immunosorbent assay (R&D Systems), according to the manufacturer’s instructions.

**Data Management and Statistical Analyses**

Clinical data were collected on standardized forms and double entered. Univariate and multiple logistic regression models were fitted for all clinical variables using disease severity and probable bacterial etiology as dependent variables. The interaction of independent variables was checked using the likelihood ratio test. Data were analyzed with Stata 11 software (StataCorp).

**Diagnostic Performance and Selection of Clinical Variables for Multivariate Models**

The area under the receiver operating characteristic curve (AUC) was used to compare the sensitivity and specificity of selected markers. Cutoff values were chosen based on highest sensitivity and specificity to predict outcome using the roctab/detail function (Stata 11.0). When the diagnostic performance was assessed for >1 variable, the estimates were derived from a logistic regression model using the selected markers or clinical features as independent variables and the condition to diagnose as the dependent variable. These analyses were carried out using the lroc, lstat, and roctab/graph functions in Stata. The positive and negative likelihood ratios have been calculated for the biomarker concentrations with the highest sensitivity and specificity for predicting severe pneumonia.

Clinical variables and/or molecular markers were included in the multivariate models if (1) the variable showed a statistically significant association ($P < .05$) in the univariate model and (2) the variable had not been used as a criterion for a priori classification. For example, respiratory rate was combined with molecular markers to compare nonsevere and severe pneumonia because this variable was not used as a criterion to separate the 2 conditions. Ordinal univariate logistic regression models using disease severity coded as 0–3 (from control [0] to very severe [3]) as the dependent variable were used to evaluate the significance of the association between biomarker concentration and clinical outcome.

**Ethical Approval**

Written informed consent was given by the parent or guardian of each participant. Joint Gambia Government/Medical Research Council (MRC) Ethical Committee approval was obtained for both the pneumonia study (SCC/EC 1062) and the severe malaria study (SCC/EC 630 and 670). The use of the archived plasma samples from Kenya was approved by the Kenya Medical Research Institute (KEMRI) Ethics Review Committee (SSC 2280).

**RESULTS**

**Diagnostic Performance of Clinical Features and Protein Biomarkers to Discriminate Severe Pneumonia and Nonsevere Pneumonia**

The proteomic analysis identified 238 proteins in children with severe pneumonia, 316 in children with nonsevere pneumonia, and 268 in healthy controls. The difference in protein numbers across different groups and batches was not significantly different (analysis of variance, $P = .35$). We identified 23 differentially regulated proteins (>1.5 fold) that were present in ≥2 of 3 batches.
when severe and nonsevere cases were compared and 19 when
nonsevere cases and controls were compared (Supplementary
Figure 2). Of these 42 proteins, only 8 (19%) indicated a progres-
sion pattern, namely, increasing concentration from controls to
mild to severe cases. Based on the number of peptides used to
identify these proteins and their biological relevance, Lpc-2,
CRP, and vWF were selected for further validation (Table 2).

Lpc-2, CRP, and vWF levels were significantly higher in
children with severe pneumonia than in those with nonsevere
pneumonia (Supplementary Figure 3). Lpc-2 was the best pre-
dictor of severe pneumonia, with a sensitivity of 72.3% and a
specificity of 70.1% (AUC, 0.71 [95% confidence interval [CI],
64.7–79]; Table 3). In children with Lpc-2 levels >118 ng/mL,
the odds of having severe disease increased by nearly 3-fold
(odds ratio [OR], 2.69 [95% CI, 1.08–6.69]. A CRP concentra-
tion >157 µg/mL was associated with increased disease severity
(OR, 3.55 [95% CI, 1.41–8.93]), but despite its good sensitivity
to predict disease severity (70.8%), its specificity was low
(56.2%). Similarly, plasma vWF concentrations >648 mU/mL
were associated with a 5-fold increase in the odds of severe
pneumonia (OR, 5.26 [95% CI, 2.42–11.4]), with good sensitiv-
ity (87.0%) but poor specificity (41.7%; Figure 1).

The best combination of clinical and molecular markers to
predict severe pneumonia included respiratory rate, crackles,
Lpc-2, and CRP. The addition of molecular markers to the clinical
features had no impact on sensitivity but increased specific-
ity from 68.0% to 82.0% (Figure 1), and the effect was superior to
radiological changes (end point consolidation), crackles, and
positive blood culture combined (Supplementary Figure 6). The
sensitivity of this combination of markers increased to 94.7%
(95% CI, 88.4%–100%) in children enrolled during the dry sea-
son, possibly owing to the absence of malaria cases (Supple-
mentary Figure 4). Only 3 children of 204 (1.5%) identified as
having pneumonia had a positive malaria slide. These children
all had nonsevere pneumonia (2 enrolled during the dry season
and 1 during the rainy season).

**Association of Lpc-2 With Probable Bacterial Pneumonia**

Bacterial cultures were performed on 198 of 200 patients with
pneumonia (99%). Of these, 12 of 198 (6%) were positive for
true pathogens, namely *Streptococcus pneumoniae* (n = 10),
*Staphylococcus aureus* (n = 1), and *Streptococcus pyogenes*
(n = 1). The contamination rate was 6%. None of the clinical
variables were associated with a positive blood culture (Supple-
mentary Table 6), but children with a concentration of Lpc-2
>163 ng/mL had 9 times the odds of having a positive blood
culture with a clinically significant isolate (OR, 9.03 [95% CI,
1.91–42.6]; Supplementary Figure 11). The plasma concentra-
tions of Lpc-2, CRP, and vWF in children with a positive
blood culture or with “end point” consolidation on their chest
radiograph (probable bacterial pneumonia) were significantly
higher than in children with no consolidation and a low
white blood cell count (P < .01; Table 4). Lpc-2 concentrations
were strongly associated with pneumonia of probable bacterial
origin (Figure 2). The diagnostic performance of Lpc-2 was su-
perior to that of vWF or CRP. Lpc-2 showed good sensitivity
(77% [95% CI, 65.6%–89.9%]) and very high specificity
(94.4% [95% CI, 86.8%–100%]) for identifying children with
probable bacterial pneumonia. Similar results were obtained
when patients with a positive blood culture were excluded from
the analysis (OR, 22.5 [95% CI, 6.77–74.7]).

**Haptoglobin in Discriminating Between Pneumonia and Malaria-
Associated Respiratory Distress in Gambian Children**

Lpc-2 concentrations in children with pneumonia did not differ
significantly from those in children with severe malaria and respi-
ratory distress (Figure 3A). We reasoned that a marker of hemo-
lysis such as haptoglobin could discriminate respiratory distress

![Figure 1](cidimage.png)

**Figure 1.** Diagnostic performance of clinical and molecular markers to predict severe pneumonia (vs nonsevere pneumonia) in Gambian children. Only clinical features that were not used to distinguish the 2 groups were introduced in the model (see Methods). Odds ratios (with 95% confidence intervals [CIs]) indicate odds of severe pneumonia for cutoff values with the highest sensitivity and specificity. Abbreviations: CRP, C-reactive protein; Lpc-2, lipocalin 2; NPV, negative predictive value; PPV, positive predictive value.
caused by pneumonia from that caused by severe malaria because haptoglobin levels increase with pneumonia severity and decrease with malaria severity owing to erythrocyte destruction. The median (interquartile range) plasma haptoglobin concentration in children with severe malaria and respiratory distress (10,406 [5,267–38,597] ng/mL) was 2 orders of magnitude lower than that in children with severe pneumonia (2,618,150 [1,800,000–4,400,000] ng/mL; \( P < .001 \); Supplementary Figure 7). The sensitivity and specificity of haptoglobin (>1.1 mg/mL) in discriminating respiratory distress caused by pneumonia from that caused by malaria were 92.8% and 99.2%, respectively (Figure 3B). Children with probable bacterial pneumonia presented with the highest concentrations of haptoglobin and Lpc-2 (Supplementary Figure 3C). The combination of Lpc-2 and haptoglobin were effective in discriminating between pneumonia and severe malaria with respiratory distress (Figure 3C and 3D). Only 2 of 307 patients (0.65%) presented with the hemoglobin S mutation of the \( \beta \)-globin chain (SS genotype). The haptoglobin concentrations did not differ significantly between patients with AS or SS genotype and those with AA phenotype.

**Lpc-2 and Haptoglobin in Discriminating Between Pneumonia and Malaria-Associated Respiratory Distress in Kenyan Children**

The diagnostic performance of Lpc-2 and haptoglobin in discriminating respiratory distress caused by pneumonia or malaria was evaluated in an independent population of 293 Kenyan children (Table 5). The same cutoff values derived from the Gambian data set were applied (Figure 3D). In children admitted to the hospital who had a plasma haptoglobin concentration >1.1 mg/mL, respiratory distress was 14.8 times more likely to be caused by pneumonia than by malaria (OR, 14.8 [95% CI, 7.05–31.2]). The diagnostic performance based on sensitivity and specificity was high but expectedly lower than that observed in Gambian children (AUC, 0.82 [95% CI, 0.73–0.91]). The proportion of children with severe malaria and a high haptoglobin concentration (11 of 41 [27%]) was the major difference observed between the Kenyan and the Gambian study. We observed a bimodal distribution in haptoglobin concentrations (above and below 5 × 10⁶ ng/mL) in children with malaria and respiratory distress and in children with both pneumonia and malaria (Supplementary Figure 8).

The odds of a positive bacterial culture with a significant bacterial isolate were significantly higher in children with higher plasma concentrations of Lpc-2 (OR, 5.62 [95% CI, 1.60–19.6]). However, the diagnostic performance of Lpc-2 in predicting bacteremia was lower than in Gambian children (AUC, 0.67 [95% CI, 0.54–0.79]). In Kenyan children, nutritional status, measured with the height-for-age z score and weight for age, was inversely correlated with Lpc-2 concentration (\( r = -0.13 \) [\( P = .02 \)] and \( r = -0.12 \) [\( P = .03 \)]. These differences were not observed in Gambian children. We therefore reasoned that differences in the proportion of malnourished children in the

<table>
<thead>
<tr>
<th>Lpc-2</th>
<th>vWF</th>
<th>CRP</th>
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<tbody>
<tr>
<td>Sensitivity (95% CI)</td>
<td>77.7 (65.6–89.9)</td>
<td>80 (68.3–91.6)</td>
</tr>
<tr>
<td>Specificity (95% CI)</td>
<td>90.4 (86.8–100)</td>
<td>73.5 (60.1–86.8)</td>
</tr>
<tr>
<td>PPV (95% CI)</td>
<td>89.7 (80.8–98.5)</td>
<td>80 (68.3–91.6)</td>
</tr>
<tr>
<td>NPV (95% CI)</td>
<td>79.1 (66.8–91.3)</td>
<td>73.5 (60.1–86.7)</td>
</tr>
</tbody>
</table>

Figure 2. Diagnostic performance of lipocalin 2 (Lpc-2), von Willebrand factor (vWF) and C-reactive protein (CRP) in predicting probable bacterial infection. Abbreviations: AUC, area under the receiver operating characteristic curve; CI, confidence interval; LR, likelihood ratio; NPV, negative predictive value; PPV, positive predictive value; ROC, receiving operating characteristic.
Kenyan and Gambian populations may account for differences in the diagnostic performance of Lpc-2. Indeed, the proportion of children with stunting (measured with the height-for-age z score) was higher in Kenyan children than in Gambian children. The height-for-age z score (but not other measures of nutritional status) and the presence of oral candidiasis were independently associated with bacteremia. The diagnostic performance of Lpc-2 in predicting blood stream infection increased to an AUC of 78.7% (95% CI, 60%–86%) after adjustment for these 2 variables (Supplementary Figure 10). The human immunodeficiency virus (HIV) status was available for 163 of 293 patients (55.6%) and was positive in 30 patients (18.4%). Of 12 patients with oral candidiasis, 7 were HIV negative (58.3%). HIV was not associated with blood stream infection in the population studied (OR, 1.53 [95% CI, 0.38–6.03]). The diagnostic performance of Lpc-2 in predicting bacteremia was higher in younger children (aged <13.9 months) after adjustment for stunting (AUC, 86%), whereas haptoglobin performed better in older children (>13.9 months) regardless of nutritional status (Supplementary Figure 9).

**DISCUSSION**

This study shows that Lpc-2 is a biomarker associated with severe pneumonia, specifically with blood culture positivity and pneumonia designated as being of probable bacterial origin based on radiological and other criteria. Furthermore, the
combination of Lpc-2 with haptoglobin discriminates between pneumonia and malaria-associated respiratory distress.

To reduce the number of deaths caused by pneumonia, early diagnosis is critical for pneumonia cases due to bacterial infection or likely to become severe, so appropriate treatment can be administered promptly. However, the diagnosis of bacterial pneumonia is usually compromised by the lack of specificity of respiratory symptoms, which are commonly shared with other conditions that cause respiratory distress in children, many associated with high case fatality rates. In sub-Saharan Africa P. falciparum malaria and bacterial blood stream infections are frequent causes of respiratory distress in children and possibly pathogenically linked [20]. For a biomarker to be helpful in this clinical context, its diagnostic performance must be sufficient to guide clinical management.

The WHO definition of pneumonia severity used in our study is an operational clinical algorithm rather than a “gold standard.” This definition aims to reduce mortality by improving referral practices and thus prioritizes sensitivity over specificity. The WHO has recently proposed a more specific definition [21]. The starting hypothesis of our study was that the addition of molecular markers could increase the specificity of the clinical definition of severe pneumonia. In this context, we have reported 3 potential plasma biomarkers that alone or in association with clinical features could be used to improve clinical management by identifying pneumonia with high disease severity or probable bacterial etiology.

Our results indicate that CRP and Lpc-2 can correctly distinguish most patients with severe pneumonia from those with nonsevere pneumonia and probable bacterial from probable nonbacterial causes. The sensitivity of these markers combined increased to 94.7% when the analysis was performed exclusively in children with pneumonia recruited during the dry season. The specificity of this panel of markers decreased from 82% to 77% when the analysis was performed in children enrolled during the rainy season (Supplementary Figure 4). Owing to the high seasonality of malaria transmission in The Gambia

Table 1. Demographic and Clinical Characteristics of the Study Participants by Outcome Group

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Control (n = 186)</th>
<th>Nonsevere (n = 96)</th>
<th>Severe (n = 76)</th>
<th>Very Severe (n = 32)</th>
<th>P Valuea</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, median (IQR), mo</td>
<td>15 (8–24)</td>
<td>15 (8–24)</td>
<td>15 (8–24)</td>
<td>12 (6–17)</td>
<td>.10</td>
</tr>
<tr>
<td>Male sex, %</td>
<td>54.4</td>
<td>54.7</td>
<td>54.0</td>
<td>50.9</td>
<td>.95</td>
</tr>
<tr>
<td>Weight-for-age z score, mean (95% CI)</td>
<td>−0.93 (−1.01 to −0.86)</td>
<td>−1.26 (−1.38 to −1.13)</td>
<td>−1.46 (−1.59 to −1.32)</td>
<td>−1.41 (−1.79 to −1.03)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Respiratory rate, mean (SD), respirations/min</td>
<td>34 (6.66)</td>
<td>57 (10.1)</td>
<td>64 (12.1)</td>
<td>69 (14.0)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Oxygen saturation, mean (SD), %</td>
<td>98.3 (1.59)</td>
<td>96.5 (1.81)</td>
<td>95.2 (3.09)</td>
<td>84.6 (7.56)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Positive bacterial culture, No. (%)</td>
<td>. . .</td>
<td>6 (6.25)</td>
<td>3 (3.95)</td>
<td>2 (6.25)</td>
<td>.17</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; IQR, interquartile range; SD, standard deviation.

a P values were obtained using Kruskal-Wallis or χ² test for quantitative or discrete variables, respectively.

Table 2. Molecular Marker Concentrations by Outcome Group

<table>
<thead>
<tr>
<th>Molecular Marker</th>
<th>Control</th>
<th>Mild</th>
<th>Severe</th>
<th>Very Severe</th>
<th>P Valuea</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lpc-2, ng/mL</td>
<td>59.8 (44.3–78.4) [174]</td>
<td>92.0 (51.6–144) [77]</td>
<td>152 (87.6–283) [73]</td>
<td>224 (139–455) [32]</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Haptoglobin, mg/mL</td>
<td>1.22 (0.8–1.94) [160]</td>
<td>1.9 (1.2–2.8) [79]</td>
<td>2.6 (1.8–4.4) [76]</td>
<td>3.8 (2.5–4.9) [32]</td>
<td>&lt;.001</td>
</tr>
</tbody>
</table>

Abbreviations: CRP, C-reactive protein; IQR, interquartile range; Lpc-2, lipocalin 2; vWF, von Willebrand factor.

a P values are derived from an ordinal univariate logistic regression model wherein the dependent variable (disease severity) is coded as 0–3 (from control [0] to very severe [3]) and the independent variables are the concentrations of the biomarkers. Differences in the number of samples tested for different biomarkers depended on sample availability and the number of tests required to measure concentration within linear range of the enzyme-linked immunosorbent assay standard.

b The sample volume available for enzyme immunoassay measurements was limited, and Lpc-2 and haptoglobin were prioritized over vWF or CRP. This accounts for the discrepancies observed in the number of samples tested for CRP and vWF.
Here we report that Lpc-2 is associated with blood culture positivity. This is particularly important because clinical features did not identify children with a positive bacterial blood culture. We did not confirm findings from some previous studies reporting an association between bacterial infection and the clinical signs of respiratory distress or high temperature (Supplementary Table 6) [24–28]. To our knowledge, we are also the first to report that Lpc-2 is associated with pneumonia of probable bacterial origin, defined by the presence of consolidation on the chest radiograph or a positive blood culture. This was true for both primary bacterial and nonbacterial pneumonia definitions. The association of Lpc-2 with positive blood cultures and pneumonia of probable bacterial origin is biologically plausible and clinically important. We also observed that the association of Lpc-2 and bacteremia in Kenyan children, although significant, was partially compromised by the patient’s nutritional status. This observation may be explained, at least in part, by the reduced ability of patients with chronic malnutrition to generate an effective immune response to infection. This limitation may be important in the design of prospective studies, and different cutoff values may be required for populations with severe stunting.

The role of Lpc-2 in innate defense against bacterial infection is well established. The transcription of the Lpc-2 gene has been shown to be up-regulated in activated macrophages through Toll-like receptor 4 ligation and to interfere with bacterial iron uptake [29, 30]. More importantly, Lpc-2 transcription is increased by 65-fold in the nasal mucosa of mice in response to S. pneumoniae and Haemophilus influenzae colonization [31].

In resource-limited settings where laboratory facilities and radiology are rarely available to help diagnose bacterial pneumonia cases, molecular markers such as Lpc-2 could be developed into a point-of-care diagnostic tool to target cases that require...
antibiotic treatment. Indeed, Lpc-2 concentrations could be used to stop antibiotic treatment in patients who show a quick clinical recovery. Similarly, for acute respiratory infections at the community level, Lpc-2 could be used to determine the indications for and guide the timing of antibiotic treatment [32–35]. The proteomic workflow used in this study could not identify proteins at concentrations below the mid–nanogram-per-milliliter range [14], such as tumor necrosis factor, interleukin 6, and procalcitonin, previously shown to be associated with blood stream infection [36].

We found that haptoglobin in combination with Lpc-2 was remarkably effective in discriminating between pneumonia and malaria in children with respiratory distress. Two major reasons account for this observation. Firstly, hemolysis is a major feature of acute malaria infection but not pneumonia [37]. During active hemolysis, free hemoglobin binds to haptoglobin, leading to a rapid depletion of this molecule from plasma [38]. Secondly, the concentration of plasma haptoglobin increased with disease severity in patients with Pneumonia.

Point-of-care diagnostics can help in making rapid clinical decisions in developing countries. Clinical efficacy and cost-effectiveness analyses indicate that studies are required to estimate the potential impact of these novel tools [39]. In malaria-endemic areas, the combination of Lpc-2 with haptoglobin should be prospectively evaluated for use in guiding the clinical management of children with respiratory distress.

Supplementary Data

Supplementary materials are available at Clinical Infectious Diseases online (http://cid.oxfordjournals.org). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyrighted. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

Notes

Acknowledgments. We would like to thank the MRC unit and the Gambian Severe Pneumonia Studies and Pneumococcal Surveillance Project field workers, nurses, laboratory staff, data staff, drivers, and administrative staff; the staff at the MRC Hospital in Fajara; the government health staff at the Royal Victoria Teaching Hospital, and the health centers at Basse, Fajikunda, Serekunda, and Brikama. Particular thanks to Simon Donkor for data management work, Nuru Adams for management of the plasma samples, and Roman Fischer and Nicola Ternette for their commitment and assistance with mass spectrometry analyses.

We would like to thank the Royal Victoria Teaching Hospital nurses and fieldworkers, Yaya Dibba, Anthony Mendy, and Abdoullie Camara; senior laboratory technicians, Janet Riddle-Fullah, Abdou Bah; Jalimory Njie (data entry clerk), Emmanoueli Onyewelu (clinician), Augustine Ebohny (clinician), and Haddy NJie; MRC laboratory technicians and assistants Issa Sambou, Simon Correa, Madi Njie, Omar Janha; Haddy Kanji (data supervisor) and Mamkumba Sanneh (MRC malaria program administrator); the study participants and their parents/guardians; and Kim Mulholland and Brian Greenwood for encouragement and advice.

Thanks also to the KEMRI/Wellcome Trust Research Programme clinical and nursing staff on the pediatric wards and members of the RESPIRE and pneumonia etiology study teams, and particular thanks to Anthony Scott, James Nokes, Neema Mturi, Mwanajuma Ngama, and Sidi Kazungu for their assistance. This article is published with the permission of the director of KEMRI.

Financial support. This work was supported by the Medical Research Council UK (grant G0600718), the Wellcome Trust (grants 077383/Z/05/Z, 090532/Z/09/Z, and 075491/Z/04) and the Bill & Melinda Gates Foundation, through the Foundation for the National Institutes of Health as part of the Grand Challenges in Global Health initiative. H. H., R. I., M. T., M. J., B. E., O. C., C. O., G. M., D. K., and S. H. are supported by the Medical Research Council UK. E. G., H. K., and J. B. are supported by the Wellcome Trust. D. K. is supported by the MRC, Wellcome Trust, and the Bill and

| Table 5. Population Description of Kenyan Patients With Respiratory Distress Caused by Malaria, Pneumonia, or Both |
|-------------------------------------------------|-----------------|-----------------|-----------------|-----------------|
| Characteristic                                  | Malaria (n = 41) | Pneumonia (n = 238) | Pneumonia and Malaria (n = 14) | P Value* |
| Age, median (IQR), mo                           | 21.1 (9.3–33.2)  | 12.8 (7.2–34.5)   | 30.4 (16.9–51.9) | .03 |
| Male sex, %                                     | 53.6             | 54.6             | 35.7             | .38 |
| Weight-for-age z score, mean (SD)               | –1.73 (1.48)     | –2.06 (1.45)     | –2.07 (1.43)     | .48 |
| Respiratory rate, median (IQR), respirations/min| 56.4 (12.1)      | 56 (46–64)       | 52 (42–58)       | .29 |
| Oxygen saturation, mean (SD), %                 | 99 (96–100)      | 96 (92–98)       | 97 (96–99)       | <.01 |
| WBC count, median (IQR), ×10^3/L                | 11.4 (7.9–17.1)  | 14 (9.9–20.9)    | 10.5 (6.7–21.5)  | .08 |
| Hemoglobin, mean (SD), g/dL                     | 7.35 (4.8–9)     | 9 (7.9–9.9)      | 8.1 (5.3–8.7)    | <.01 |
| Positive bacterial culture, No. (%)b           | 2 (4.88)         | 16 (6.72)        | 0 (0)            | <.01 |
| Lpc-2, median (IQR), ng/mL                      | 72.2 (44–151)    | 92.8 (51.1–159.6)| 195 (51.3–286)   | .46 |
| Haptoglobin, median (IQR), ng/mL                | 23434 (5445–1 048 424) | 3 095 352 (1 770 148–4 383 530) | 19 106 (8353–1 250 607) | <.001 |

Abbreviations: IQR, interquartile range; Lpc-2, lipocalin 2; SD, standard deviation; WBC, white blood cell.

* P values were obtained using Kruskal-Wallis or χ² for quantitative or discrete variables, respectively.

b Positive bacterial culture include the following significant microorganisms: Streptococcus pneumoniae (13 samples), Salmonella spp. (2 samples), and Staphylococcus aureus, Escherichia coli, and β-hemolytic streptococcus (1 sample each).
Melinda Gates Foundation. C. C. P. is supported by the MRC UK (Clinician Scientist Fellowship G0701885).

Potential conflicts of interest. All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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