Is a Honeycomb Appearance on Computer Tomography Characteristic for *Burkholderia pseudomallei* Liver Abscess?

To the Editor—I read with interest the case reports by Apisarnthanarak et al. [1] in a recent issue of *Clinical Infectious Diseases*. The authors reported on the CT features of 3 patients with *Burkholderia pseudomallei* liver abscess and suggested that the “honeycomb” appearance was characteristic and that such features should prompt physicians to consider *B. pseudomallei* infection, particularly in patients from high-risk areas where *B. pseudomallei* is endemic. These findings may be useful in aiding early diagnosis. However, one wonders whether the honeycomb appearance described is actually just a part of a spectrum of liver abscess evolution from the initial solid to the later liquefied stages, regardless of the underlying organisms.

*B. pseudomallei* infection is common in certain tropical regions, particularly in Thailand and northern Australia [2], but the infection is being reported in many countries where it is not usually found. A recent review of 49 cases of liver abscess in my local region showed that *B. pseudomallei* accounted for 21.3% of cases, with infection due to *Klebsiella pneumoniae* accounting for almost 50% [3]. There were no differences in age, number of abscesses, and chest radiography and CT scan findings of liver abscess between patients with the different etiologies. Both *Klebsiella* and *B. pseudomallei* abscesses (90% and 93.3%, respectively) were significantly associated with the presence of poorly controlled diabetes mellitus that was either previously known or newly diagnosed. All of our patients had *B. pseudomallei* isolated by blood or pus culture within a few days of initiating the culture. However, species identification required at least another 48 h. The sensitivity patterns are quite distinctive, with a universal intrinsic resistance to aminoglycoside.

Although the report by Apisarnthanarak et al. [1] showed possible characteristic features, these findings were based on only 3 patients. There are other clinical and initial laboratory findings that have been reported regarding the characteristics of *B. pseudomallei* liver abscess [4]. In my local region, we always consider *B. pseudomallei* as a possible etiology in all cases of liver abscess, particularly in patients with diabetes (previously known or newly diagnosed) or any other underlying immunocompromising conditions, such as malignancies and post-chemotherapy. The standard antibiotic regimen for sepsis at my institution consists of amoxicillin and clavulanic acid (with or without metronidazole), which provides coverage for infections caused by both *B. pseudomallei* and *Klebsiella* species. Third-generation cephalosporin is added if there is a high suspicion for *B. pseudomallei* infection.

The presence of a honeycomb appearance on a CT scan may be helpful, but the absence of such findings should not detract the possibility of *B. pseudomallei* infection. Whether this CT finding is characteristic for *B. pseudomallei* liver abscess needs further evaluation using a larger sample size.

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**Vui Heng Chong**
Gastroenterology Unit, Department of Medicine, Raja Isteri Pengiran Anak Saleha Hospital, Bandar Seri Begawan, Brunei Darussalam

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**Figure 2.** Multiloculated liver abscess due to *Klebsiella pneumoniae*
The study included 170 hospitalization episodes among 163 children. Nine cases of bacteremic pneumococcal infections were detected among these patients. The clinical characteristics are shown in table 1. Respiratory viruses were detected in 7 (78%) of the 9 children (3 enteroviruses, 2 rhinoviruses, and 2 RSV). Respiratory symptoms preceded the development of more severe illness with high fever, suggesting that viral infection paved the way for pneumococcal invasion.

Our finding lends support to the epidemiologic and laboratory studies that link invasive pneumococcal disease with respiratory virus infections, in most cases with influenza virus or RSV infection [1, 5–7]. In a report published 20 years ago [8], respiratory viruses were detected in 40% of children with bacterial meningitis using serological methods (31%) and virus isolation (15%). Respiratory viruses have not been previously studied in children with invasive bacterial infection using sensitive PCR methods. Our findings suggest that rhinovirus and enterovirus infections may be important predisposing factors for invasive pneumococcal infections in children. Rhinoviruses are the most frequent cause of respiratory infections among children and adults [4, 9]. Enteroviruses are closely related to rhinoviruses, and recent studies using RT-PCR suggest that their role in respiratory infections is much more significant than previously realized [10, 11]. The association between rhinoviruses and enteroviruses and pneumococcal infections is also supported by epidemiologic data. The biphasic pattern of pneumococcal disease in children, with peaks in the autumn and spring and a decrease in the midwinter [12, 13], is remarkably similar to the seasonal pattern of rhinovirus and enterovirus infections [14].

Studies using surveillance data do not reveal the full impact of rhinoviruses and enteroviruses on the development of invasive bacterial infections, because these viruses are rarely searched for in patients with common respiratory infections using efficient RT-PCR methods. Systematic studies of these associations are needed, because it is likely that several currently unknown interactions between viral, bacterial, and host factors play important role in the pathogenesis of infectious diseases.

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**Ville Peltola,** 1 Matti Waris, 2 Timo Hyytiä, 2 and Olli Ruuskanen1

Departments of Pediatrics and Virology, University of Turku, Turku, Finland

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