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Pneumonia in the tropics: Report from the Task Force on tropical diseases by the World Federation of Societies of Intensive and Critical Care Medicine

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ABSTRACT

The aetiology of community acquired pneumonia varies according to the region in which it is acquired. This review discusses those causes of CAP that occur in the tropics and might not be readily recognizable when transplanted to other sites. Various forms of pneumonia including the viral causes such as influenza (seasonal and avian varieties), the coronaviruses and the Hantavirus as well as bacterial causes, specifically the pneumonic form of *Yersinia pestis* and melioidosis are discussed.

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1. Introduction

In general, community acquired pneumonia (CAP) is caused by pathogens that are common to all geographical areas; *S. pneumoniae*, viruses, chlamydia, mycoplasma, legionella and less commonly *S. aureus* and *K. pneumoniae*. However some organisms are endemic to specific regions and early recognition and awareness of these is critical to the diagnosis and to a favourable outcome. This is no less the case in residents of or travellers to tropical regions. This review discusses those that are most prevalent and which can cause potentially lethal infections.

2. Viral infections

In adults, respiratory viruses account for 10% to 40% of CAP and the most common of these are influenza, parainfluenza, adenovirus and respiratory syncytial viruses (RSV) [1,2]. Influenza viruses which are classified by their core proteins (i.e. A, B or C) and belong to the family orthomyxoviridae, cause predominantly respiratory disease in humans. Influenza type A and B account for >50% of viral pneumonia in adults whereas influenza C infections generally cause mild respiratory disease and are not thought to cause epidemics [3]. The close contact between humans and animals in tropical areas may enhance the genetic reassortment of influenza viruses which when disseminated into the human population may result in pandemics [4]. Other important respiratory viruses in the tropics that can cause severe pneumonia are Influenza A H1N1, avian influenza viruses (H5N1, H7N9), Severe Acute Respiratory Syndrome associated Coronavirus (SARS-CoV) and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) [5,6]. Standard, droplet and contact precautions are recommended for these selected acute respiratory infections and whenever possible patients should be placed in airborne infection isolation rooms.

3. Influenza viruses

Influenza viruses have been associated with annual epidemics and intermittent pandemics throughout the world. Despite the absence of a winter season in the tropics, consistent seasons of infection have nevertheless been observed. The composition of the antigenic surface glycoproteins of the influenza virus, hemagglutinin (H) and neuraminidase (N) are used for subtyping, resulting in names like H3N2 and H1N1. Antigenic drift represents the minor changes of H and N side chains and is responsible for seasonal epidemics. Influenza pandemics occur less frequently and these result from major changes in antigenic structure in the envelope glycoproteins (antigenic shift) resulting from reassortment of various viruses such as swine, equine and human varieties. Contemporary geographic distributions show that East, South and Southeast Asia influence unduly the evolution of seasonal influenza A (H3N2), exporting most of the evolutionarily strains that ultimately spread globally. The obvious role of Asia in H3N2's evolution has been ascribed to the seasonal nature of influenza in temperate climates [7].

Seasonal influenza is an acute respiratory illness caused by influenza A or B viruses. Given that these infections including the pandemic variety H1N1 now occur in all parts of the world they will not be discussed in any detail in this treatise.

3.1. Avian influenza viruses

Avian influenza viruses (e.g. H5N1 and H7N9) have emerged relatively recently and cause disease in humans and currently remain a potential threat, particularly in the Southeast Asia [5,8].

3.1.1. Avian influenza H5N1

The first association of avian influenza H5N1 with clinical respiratory disease was in 1997 in Hong Kong, as a human infection transmitted from birds. Later H5N1 re-emerged in humans in 2003 as a highly pathogenic virus resulting from antigenic drift to which a larger number of species were vulnerable and conferring resistance to adamantine antivirals [9]. As yet, human to human transmission is rare and the vast majority of cases are related to contact with birds. Travellers who have a history of recent exposure to birds in affected areas and who present with otherwise unexplained ARDS should be screened. H5N1 has been reported from 16 countries and is currently most prevalent in Egypt [9]. As of August 2017, from 859 laboratory confirmed cases of influenza A H5N1, 453 (53%) patients have died [10].

3.1.1.1. Clinical. Following exposure, the incubation period is seven days or less. Clinical characteristics include fever, respiratory illness, pneumonia, diarrhoea and encephalopathy. Laboratory abnormalities may include leukopenia, lymphopenia, thrombocytopenia and elevated serum aminotransferases. Complications include multi-organ failure, pulmonary haemorrhage, pneumothorax and pancytopenia. Radiographic findings include diffuse or patchy infiltrates and segmental or lobar consolidation. Progression to respiratory failure is associated with diffuse bilateral ground-glass infiltrates.

3.1.1.2. Diagnosis. A comprehensive travel and epidemiological history is critical in suspected cases. Patients who meet clinical and epidemiological criteria should be tested for H5N1 avian influenza infection. Diagnosis can be established by rRT-PCR or viral culture of respiratory specimens. Serological testing is not helpful in the acute setting but useful for retrospective diagnosis [11].

3.1.2. Avian influenza H7N9

3.1.2.1. Introduction. Another avian influenza virus, H7N9, derived from reassortment of at least four avian influenza viruses, has caused severe pneumonia in some patients. It emerged in 2013 and originated from Eastern China [12]. Additional cases have been detected in mainland China, Hong Kong, Macao, Taiwan and Malaysia. Similar to H5N1 this virus occurs primarily in bird handlers or following recent exposure to live poultry or potentially contaminated environments. To date, there is no evidence of sustained human-to-human transmission. The incubation period has been estimated to be from 3 to 7 days, but can be as long as 10 days.

3.1.2.2. Clinical. Presenting signs and symptoms may include fever, cough, dyspnoea, headache, myalgia and malaise. Patients present with LRTI which may progress rapidly to pneumonia and potentially acute respiratory failure, ARDS, septic shock, multi-organ failure, rhabdomyolysis and encephalopathy. Severe illness and fatal outcome have been frequently observed in pregnant women, older persons and