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CONTENTS/SUMMARIES

Summary: Tuberculosis of the central nervous system (CNS) is a highly devastating form of tuberculosis, which, even in the setting of appropriate antitubercular therapy, leads to unacceptable levels of morbidity and mortality. Despite the development of promising molecular diagnostic techniques, diagnosis of CNS tuberculosis relies largely on microbiological methods that are insensitive, and as such, CNS tuberculosis remains a formidable diagnostic challenge. Insights into the basic neuropathogenesis of Mycobacterium tuberculosis and the development of an appropriate animal model are desperately needed. The optimal regimen and length of treatment are largely unknown, and with the rising incidence of multidrug-resistant strains of M. tuberculosis, the development of well-tolerated and effective antibiotics remains a continued need. While the most widely used vaccine in the world largely targets this manifestation of tuberculosis, the BCG vaccine has not fulfilled the promise of eliminating CNS tuberculosis. We put forth this review to highlight the current understanding of the neuropathogenesis of M. tuberculosis, to discuss certain epidemiological, clinical, diagnostic, and therapeutic aspects of CNS tuberculosis, and also to underscore the many unmet needs in this important field.

Summary: Nearly 2,000 ribotyping-based studies exist, ranging from epidemiology to phylogeny and taxonomy. None precisely reveals the molecular genetic basis, with many incorrectly attributing detected polymorphisms to rRNA gene sequences. Based on in silico genomics, we demonstrate that ribotype polymorphisms result from sequence variability in neutral housekeeping genes flanking rRNA operons, with rRNA gene sequences serving solely as conserved, flank-linked tags. We also reveal that from such an informatics perspective, it is readily feasible a priori to design an interpretable ribotyping scheme for a genomically sequenced microbial species, and we discuss limitations to the basic restriction fragment length polymorphism-based method as well as alternate PCR ribotyping-based schemes.

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Summary:Though several antivirals have been developed and marketed to treat influenza virus infections, the development of antiviral agents with clinical activity against other respiratory viruses has been more problematic. Here we review the epidemiology of respiratory viral infections in immunocompetent and immunocompromised hosts, examine the evidence surrounding the currently available antivirals for respiratory viral infections other than influenza, highlight those that are in the pipeline, and discuss the hurdles for development of such agents.

Summary: Human bocavirus (HBoV) is a newly identified virus tentatively assigned to the family Parvoviridae, subfamily Parvovirinae, genus Bocavirus. HBoV was first described in 2005 and has since been detected in respiratory tract secretions worldwide. Herein we review the literature on HBoV and discuss the biology and potential clinical impact of this virus. Most studies have been PCR based and performed on patients with acute respiratory symptoms, from whom HBoV was detected in 2 to 19% of the samples. HBoV-positive samples have been derived mainly from infants and young children. HBoV DNA has also been detected in the blood of patients with respiratory tract infection and in fecal samples of patients with diarrhea with or without concomitant respiratory symptoms. A characteristic feature of HBoV studies is the high frequency of coinciding detections, or codetections, with other viruses. Available data nevertheless indicate a statistical association between HBoV and acute respiratory tract disease. We present a model incorporating these somewhat contradictory findings and suggest that primary HBoV infection causes respiratory tract symptoms which can be followed by prolonged low-level virus shedding in the respiratory tract. Detection of the virus in this phase will be facilitated by other infections, either simply via increased sample cell count or via reactivation of HBoV, leading to an increased detection frequency of HBoV during other virus infections. We conclude that the majority of available HBoV studies are limited by the sole use of PCR diagnostics on respiratory tract secretions, addressing virus prevalence but not disease association. The ability to detect primary infection through the development of improved diagnostic methods will be of great importance for future studies seeking to assign a role for HBoV in causing respiratory illnesses.

Summary: A pulmonary cavity is a gas-filled area of the lung in the center of a nodule or area of consolidation and may be clinically observed by use of plain chest radiography or computed tomography. Cavities are present in a wide variety of infectious and noninfectious processes. This review discusses the differential diagnosis of pathological processes associated with lung cavities, focusing on infections associated with lung cavities. The goal is to provide the clinician and clinical microbiologist with an overview of the diseases most commonly associated with lung cavities, with attention to the epidemiology and clinical characteristics of the host.

Summary: To date, most Leishmania and human immunodeficiency virus (HIV) coinfection cases reported to WHO come from Southern Europe. Up to the year 2001, nearly 2,000 cases of coinfection were identified, of which 90% were from Spain, Italy, France, and Portugal. However, these figures are misleading because they do not account for the large proportion of cases in many African and Asian countries that are missed due to a lack of diagnostic facilities

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and poor reporting systems. Most cases of coinfection in the Americas are reported in Brazil, where the incidence of leishmaniasis has spread in recent years due to overlap with major areas of HIV transmission. In some areas of Africa, the number of coinfection cases has increased dramatically due to social phenomena such as mass migration and wars. In northwest Ethiopia, up to 30% of all visceral leishmaniasis patients are also infected with HIV. In Asia, coinfections are increasingly being reported in India, which also has the highest global burden of leishmaniasis and a high rate of resistance to antimonial drugs. Based on the previous experience of 20 years of coinfection in Europe, this review focuses on the management of Leishmania-HIV-coinfected patients in low-income countries where leishmaniasis is endemic.

Summary: Infection of humans with the nematode worm parasite Anisakis simplex was first described in the 1960s in association with the consumption of raw or undercooked fish. During the 1990s it was realized that even the ingestion of dead worms in food fish can cause severe hypersensitivity reactions, that these may be more prevalent than infection itself, and that this outcome could be associated with food preparations previously considered safe. Not only may allergic symptoms arise from infection by the parasites ("gastroallergic anisakiasis"), but true anaphylactic reactions can also occur following exposure to allergens from dead worms by food-borne, airborne, or skin contact routes. This review discusses A. simplex pathogenesis in humans, covering immune hypersensitivity reactions both in the context of a living infection and in terms of exposure to its allergens by other routes. Over the last 20 years, several studies have concentrated on A. simplex antigen characterization and innate as well as adaptive immune response to this parasite. Molecular characterization of Anisakis allergens and isolation of their encoding cDNAs is now an active field of research that should provide improved diagnostic tools in addition to tools with which to enhance our understanding of pathogenesis and controversial aspects of A. simplex allergy. We also discuss the potential relevance of parasite products such as allergens, proteinases, and proteinase inhibitors and the activation of basophils, eosinophils, and mast cells in the induction of A. simplex-related immune hypersensitivity states induced by exposure to the parasite, dead or alive.

Summary: Of the four species of the genus Echinococcus (Cestoda) distinguished by biological and morphological characteristics, two species, E. vogeli and E. oligarthrus, occur widely in the Neotropics. Approximately 200 cases of polycystic echinococcosis (PE) have been recorded from 12 countries in South America. Following early proliferation of E. vogeli in the human host, typically in the liver, the metacestode usually spreads in the peritoneal and pleural cavities, and numerous organs may be invaded. The clinical characteristics of PE in 81 patients with sufficient information are reviewed. Type I disease consists of polycysts in the liver and abdominal cavity (37% of the patients had this characteristic); type II is similar to type I but also includes hepatic insufficiency (26%); type III consists of cysts in liver and chest (14%); type IV consists of cysts only in the mesenteries (16%); and type V consists of cysts calcified in liver and lung (4%). The percentage of patients with polycysts in the liver was 81%, and the percentage of patients with polycysts in the chest was 14% PE is most ready diagnosed by geographic origin of the patient and by means of ultrasound or computerized tomography scanning showing cysts and calcifications. The highest mortality was for patients with type II disease, due to hepatic failure and its complications. There were five patients who died due to surgical accidents, whereas 35 cases had uncomplicated surgery. Twenty-three patients died of PE, making the total mortality 29% (23 of 78 cases). None of the 13 patients treated only with albendazole, the most efficacious treatment, was completely cured. PE represents a severe medical problem in South America. A reevaluation of the characteristics of the metacestode of E. oligarthrus indicated that it is unicystic. Only three human cases are known (two with infection in the orbit and one with infection in the heart). The metacestode of E. oligarthrus, in contrast with that of E. vogeli, consists of a spherical, fluid-filled vesicle that enlarges concentrically and is not known to undergo exogenous proliferation.