Babesiosis

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KEYWORDS

• Babesiosis • *Babesia microti* • Protozoan • Apicomplexa • Erythrocyte • Tick • Transfusion

KEY POINTS

- Human babesiosis is an emerging infectious disease caused by hemoprotozoan parasites that are transmitted by tick vectors and less frequently through blood transfusion or transplacentally.
- *Babesia microti*, the most frequent cause of human babesiosis, is endemic in the northeastern and upper midwestern United States and is sporadic throughout the rest of the world.
- The clinical presentation most commonly consists of a viral-like illness but ranges from asymptomatic infection to severe illness that may result in complications or death.
- Diagnosis is confirmed by identification of babesia organisms on blood smear, detection of babesia DNA by PCR, or a four-fold rise in babesia antibody titers in acute and convalescent sera.
- Treatment with atovaquone plus azithromycin is used for mild to moderate babesiosis, whereas clindamycin plus quinine is recommended for severe disease.

INTRODUCTION

Babesiosis is caused by intraerythrocytic protozoan parasites that are transmitted by ticks, or less commonly through blood transfusion or transplacentally. The microorganisms that are now recognized as babesia were first described by Victor Babes

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in 1888 when he investigated the cause of hemoglobinuria in febrile cattle. Five years later, Smith and Kilbourne identified a tick as the vector for *Babesia bigemina* that caused Texas cattle fever, thereby establishing for the first time transmission of an infectious agent by an arthropod vector. Human babesiosis was first recognized in a splenectomized patient in Europe but most cases have been reported from the northeastern and upper midwestern United States in people with an intact spleen and no history of immune impairment.[1–3] Cases also are reported in Asia, Africa, Australia, Europe, and South America.[2] Babesiosis shares many clinical features with malaria and can be fatal, particularly in the elderly and the immunocompromised.

EPIDEMIOLOGY

The Pathogens

Babesia species belong to the phylum Apicomplexa, which is comprised of several important human pathogens, such as species of Plasmodium, Toxoplasma, and Cryptosporidium. Of the large number of babesia species that infect wild and domestic animals, only a few are known to cause disease in humans, including *Babesia microti* and *B microti*–like organisms, *Babesia duncani* and *B duncani*-type organisms, *Babesia divergens* and *B divergens*–like organisms, and *Babesia venatorum*.[2,4] The genome of *B microti* recently has been sequenced.[5,6] Phylogenetic analyses indicate that the *B microti* group is distant from all other species of Babesidae and Theileridae and should constitute a new genus in the Apicomplexa phylum.[5–9] *B microti* has the smallest genome among all Apicomplexan parasites sequenced to date with approximately 3500 genes. In addition to the four nuclear chromosomes, the parasite harbors two organellar genomes, one in the mitochrondia and one in the apicoplast. Sequencing of the *B microti* genome has helped gain further understanding about the biology and phylogenetics of the parasite and has identified several targets for the development of novel therapies for human babesiosis.

Transmission

Ixodes ticks are the primary mode of transmission of babesia species to vertebrates, including humans (**Fig. 1**). Babesia species are maintained in a wide range of vertebrate reservoirs; humans are incidental and terminal hosts. The primary reservoir for *B microti* in the northeastern and upper midwestern United States is the white-footed mouse (*Peromyscus leucopus*), but the parasite also has been found in other hosts.[4] The primary vector is *Ixodes scapularis*, which also transmits *Borrelia burgdorferi* (the etiologic agent of Lyme disease), *Anaplasma phagocytophilum*, *Borrelia miyamotoi*, *Ehrlichia muris*–like agent, and Powassan virus.[4,10,11] Humans can be infected with two or more of these pathogens. The prevalence of *B microti* infection in nymphal *I scapularis* ticks ranges from 1% in newly endemic areas to 20% in some well-established endemic areas.[11] Initially identified on the coastal islands of southern New England, *B microti* has spread north, west, and south to encompass much of the northeastern United States. This geographic expansion mimics that of Lyme disease but has proceeded more slowly. The reported incidence of human babesiosis is lower than that of Lyme disease because of a more restricted geographic range, lower tick infection rate, greater proportion of asymptomatic infection, insufficient physician awareness, and greater difficulty in diagnosis.[2,11] Carefully designed epidemiologic studies have shown that differences in the incidence of babesiosis and Lyme disease are small at certain sites that have long been endemic for both diseases.[11,12]

Each of the three active stages in the life cycle of *I scapularis* (larva, nymph, and adult) takes a blood meal from a vertebrate host to mature to the next stage