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Editorial

Inaugural meeting of the international babesiosis research community, 2018: A glimpse into the future of an emerging research field

April 12, 2018, 6:00 AM. The quiet of an early New England, USA, morning was broken by the soft steps and chatting of 50 jet-lagged scientists assembled in the lobby of the New Haven Hotel. As anxious as children on the first day of school, they were readying to board an awaiting bus to take them to the Yale West Campus. They had arrived the night before from China, France, Japan, South Africa, the United Kingdom and various corners of the United States, excited to meet colleagues and exchange ideas. After a 15 min journey to the conference hall, they were served breakfast, listened to a few introductory remarks and moved to the Grace Murray Hopper auditorium to hear the first oral presentation of the inaugural Human Babesiosis Meeting.

Babesiosis infections are caused by apicomplexan parasites of the genus *Babesia*. They include several pathogens of humans such as *Babesia microti*, *Babesia duncani* and *Babesia divergens*, as well as important pathogens of veterinary importance such as *Babesia bovis*, *Babesia bigemina* and *Babesia equi*. A recent report by Paules et al. (2019) in the New England Journal of Medicine highlighted the overall emergence of tick-borne diseases worldwide. This emergence is fueled largely by changes in the climate and anthropogenic factors affecting the geographical distribution of the tick vectors and mammalian reservoirs. With the urgent need for advanced epidemiological, molecular and genetic tools to understand the physiology, transmission and pathogenesis of these parasites, the inaugural conference provided a unique opportunity for scientists to meet, establish collaborations, design plans for development and sharing of tools and resources, and to discuss bold ideas that will shape the future of this field. Prior to the organization of this meeting, a venue focused on interactions among those working specifically with *Babesia* parasites and diseases was not available.

The keynote lecture of the conference was given by Dr. Samuel R. Telford III, Tufts University, USA. Dr. Telford provided a short history of the discovery of *Babesia* parasites from 1890 with the discovery of *B. bigemina* (originally named *Pyrosoma bigeminum*) by Drs. Smith and Kilborne (1893), to the discovery of the white footed mouse as the reservoir and the deer tick as the vector of *B. microti* by Dr. Spielman et al. (1979). He further discussed the global epidemiology of babesiosis, and the evolution and diversity of *Babesia* parasites. He called for a need for rigorous approaches to classification of *Babesia* spp. and understanding their mode of transmission.

The scientific meeting included sessions focused on clinical presentations of babesiosis infection in humans and animals, *Babesia* epidemiology, vectors and transmission, pathogenesis and host immune responses to infection, genomics and proteomics analyses, and diagnosis and therapy. Dr. Omar Harb from EupathDB, USA, highlighted the importance of community-based efforts in advancing babesiosis research and enhancing the quality of data (parasite and host genomic data and responses) available to the scientific community. Dr. Robert Molestina from BEI Resources, USA, presented data on resources available to the community.

The meeting ended with an open discussion on the future of babesiosis research and initiatives to be taken to create an International Society for Babesia Research (ISBR). Other topics discussed included community efforts to develop and share tools and resources to advance our understanding of the biology, transmission, diagnosis, and therapy of *Babesia* parasites, as well as training of students and postdoctoral fellows in this field. Several of the talks were provided by graduate students and postdoctoral fellows, reflecting the movement of young scientists into this field.

This Special Issue of the *International Journal for Parasitology*, dedicated to the Human Babesiosis 2018 conference, comprises five original articles and five invited reviews. Original articles include studies on the discovery of the tick vector and mammalian reservoir of *B. duncani* (Swei et al., 2019); annotation of the apicoplast and mitochondrial genomes of *B. duncani* (Virji et al., 2019); the *B. microti* proteome in infected red blood cells using a combination of nanotechnology and mass spectrometry (Magni et al., 2019); identification of cell surface and secreted proteins of *B. microti* for diagnostics discovery and reverse vaccinology (Elton et al., 2019); and the association of SBP2t11 protein expression levels with *B. bovis* cytoadhesion and virulence phenotypes (Gallego-Lopez et al., 2019). Review articles covered investigation of disease severity in an animal model of concurrent babesiosis and Lyme disease (Bhanot and Parveen, 2019); genetic tools to advance discovery and target identification in *Babesia* parasites (Keroack et al., 2019); human babesiosis (Krause, 2019); vaccination against babesiosis using recombinant GPI-anchored proteins (Wieser et al., 2019); and pathogenesis of bovine babesiosis (Suarez et al., 2019).

The 2nd International Babesiosis Meeting- so renamed to recognize the scope of the meeting- will be held at Yale University, USA on April 17–18, 2019. More information about the meeting and program agenda can be found at www.internationalbabesiosismeeting.com.

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