V 1 Population biology of the Lyme borreliosis group of spirochaetes

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In memory of Klaus Kurtenbach

A fundamental question in infectious disease research is how vector-borne zoonotic diseases spread. To understand dispersal of these agents, one needs to understand their contemporary population structure and migration patterns. A pre-requisite for such studies are appropriate typing tools being able to capture the evolutionary and demographic processes that shape such pattern in space and time. Another pre-requisite is a 'model' organism that covers a broad ecological scope, such as Lyme borreliosis (LB) group of spirochaetes.

Borrelia burgdorferi, the causative agent of LB, was discovered only 30 years ago. Using molecular typing methods, it soon became apparent that *B. burgdorferi* represented a highly diverse group of bacteria, now consisting of 18 named species known as *B. burgdorferi* sensu lato species complex or the LB group of spirochaetes. LB species are found in the Holarctic region, but species and genotypes are not evenly distributed across the distribution range. The development of methods for species identification and utilization of transmission experiments resulted in the concept of host associations. The remarkable ecological niche diversity of LB group of spirochaetes, i.e. that different spirochaete species vary in the degree of specialism for hosts and vectors, is well documented. This makes it a very useful model to study the impact of ecological adaptations on the population biology of tick-borne zoonotic disease agents.

In this talk, we shall give a brief overview of the ecology of the LB group of spirochaetes, present an outline of molecular typing tools including multi locus sequence typing, their benefits and pitfalls for population studies, and the impact of host associations on population dynamics of species using examples from Europe and North America. We will discuss the data in view of recent range expansions of vector ticks.