



Metagenomics reveals shared bacterial communities in ticks and rodents with potential interest for new epidemiological cycles affecting animals and/or humans

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OP-E04. METAGENOMICS REVEALS SHARED BACTERIAL COMMUNITIES IN TICKS AND RODENTS WITH POTENTIAL INTEREST FOR NEW EPIDEMIOLOGICAL CYCLES AFFECTING ANIMALS AND/OR HUMANS.

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In Europe, ticks are the first arthropod vectors of disease agents to humans and domestic animals and the incidence of tick-borne diseases (TBD) is increasing worldwide. Tick common habitats are woods, pastures and gardens and the main source of blood meals for larvae and nymphs are rodents, which represent one of the major reservoirs and source of tick-borne pathogens. Ticks and rodents are highly susceptible to global environmental and socio-economical changes, which in turn may lead to increased burden of tick-borne diseases. In recent years, new zoonotic bacteria carried by ticks and rodents have been described in Europe. Our study was based on the use of Next Generation Sequencing derived from bacterial metagenomics in order to generate a global picture of bacterial sequences shared by ticks and rodents. We trapped voles and ticks in the French Ardennes, a forested region on the border with Belgium, along a transect line of ~80 km. Along this transect, we sampled 6 sites in forested areas and 4 sites in fragmented habitats (i.e., hedge networks), with about 30 rodents *Myodes glareolus* and 30 ticks *Ixodes ricinus* in each site. A multiplex strategy allowed characterizing the bacterial communities within each rodent and each tick individual. Using this strategy, we have indeed identified known but unexpected bacteria as well as new or poorly known bacteria phylogenetically close to known bacteria transmissible to humans and/or animals by arthropods (*Bartonella*, *Borrelia*, *Mycoplasma*, *Neorhlichia*, *Rickettsia*, *Orientia*, *Midichloria*, *Spiroplasma*, *Spirosoma*). We also derived bacterial prevalence in ticks and rodents according to forest fragmentation, and explored bacterial co-occurrence and potential co-transmission. This study demonstrated that many still unknown bacteria are carried by both ticks and rodents and could participate to unknown epidemiological cycles potentially affecting animals and/or humans. The monitoring of these bacteria deserves to be undertaken in human and/or animal populations.