





# **10th Tick and Tick-Borne** Pathogen Conference

### 29 August-2 September 2022 Murighiol, Danube Delta, Romania

Abstracts



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Platinum





Gold



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Silver



#### Bronze



FULLER









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## Symposium "Diversity of symbiotic interactions in ticks" (SY1.1-SY1.6)

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#### SY1.2 *Rickettsia lusitaniae*, a widespread maternally inherited symbiont of *Ornithodoros* soft ticks

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*Rickettsia* are obligate intracellular bacteria best known as pathogens of vertebrates and transmitted by blood-feeding arthropods, mainly ticks. However, new Rickettsia species and strains with no apparent pathogenicity are continually uncovering from a variety of arthropod groups as ladybirds. spiders, wasps, book lice and even ticks. These *Rickettsia* are endosymbionts which live exclusively within arthropod cells and typically undergo high efficiency maternal (transovarial) transmission to offspring. In this context, the recent discovery of *R. lusitaniae* in several soft tick species belonging to the genus Ornithodoros is worthy of interest. R. lusitaniae is closely related to the causative agent of flea-borne spotted fever, R. felis. It can successfully infect cell lines in lab conditions but was only reported once in organs of a bat in China. In our study, we have investigated on the mechanisms used by R. lusitaniae to spread and persist in Ornithodoros species. We have first characterized important variations of prevalence (from 0 to 100%) between natural populations and laboratory colonies for six Ornithodoros species: O. maritimus, O. sonrai, O. capensis, O. costalis, O. moubata and O. erraticus. Multilocus genetic typing and complete genome sequencing further revealed a low level of genetic differentiation between multiple strains of R. lusitaniae across the Old and New Worlds: all R. *lusitaniae* strains cluster in a robust phylogenetic clade well distinct to other species (including *R*. felis, R. asembonensis and R. hoogstraalii) of the Rickettsia transitional phylogenetic group. We further examined the tissue tropism of *R. lusitaniae* using real-time quantitative PCR and Fluorescence in situ Hybridization (FISH): we found this bacterium highly abundant in Malpighian tubules and ovaries, and less abundant in salivary glands and gut. Subsequent surveys of tick progeny revealed a high level of maternal transmission in several Ornithodoros species: from 83 to 100% of larvae from an infected mother are themselves infected. Experimental investigations lastly showed that O. erraticus does not transmit *R. lusitaniae* to mice on which they have feed. Examination of several mices' organs (skin, heart, spleen and blood) through real-time quantitative PCR assays revealed absence infection. While current view in rickettsiology has a strong anthropocentric bias and tends to describe novel Rickettsia species as pathogenic forms, our observations rather establish that R. lusitaniae is a common endosymbiont of Ornithodoros ticks that largely relies on maternal inheritance to spread and persist in tick populations.