MOLECULAR CHARACTERIZATION OF *FRANCISELLA TULARENSIS* STRAIN CIRCULATING IN PORTUGAL

Isabel Lopes de Carvalho[1]; Cristina García Amil[2]; Raquel Escudero[2]; Pedro Anda[2]; Maria Sofia Núncio[1]

[1]Center for Vector and Infectious Disease Research, National Institute of Health, Portugal.[2]LEPE, Instituto de Salud Carlos III, Spain

Tularemia is a zoonosis caused by *Francisella tularensis*. In Portugal, until now, no human cases of tularemia were reported. After the occurrence of an outbreak in Spain in 1997, it's expected that the disease spread towards Portugal. A surveillance project was started in 2004 where the main goals are the epidemiologic study of this zoonosis and the evaluation of its impact in Public Health. Studied area: district of Bragança, Northern region of Portugal. Material: 26 human blood samples collected from people living in the region were analysed by PCR. 110 ticks (79 *Dermacentor reticulatus*; 1 *Ixodes ricinus*; 15 *D. marginatus*; 11 *Rhipicephalus sanguineus*; 4 *Hyalomma marginatum*) were analyzed by PCR. Two PCRs were performed, amplifying the 17 kDa lipoprotein and the SSTR9 repetitive element. A partial sequence of the 17 kDa lipoprotein was analysed BLASTn and Clustal, and a phylogenetic analysis was done using Mega2 software. This study allowed the first detection of *Francisella* DNA on biological samples. The human prevalence rate was 1,4%. Concerning the ticks, only one was found positive, with a prevalence rate of 1,3 % for *D. reticulatus* and 0,9% considering the total of ticks studied. The phylogenetic analysis showed that the strain circulating in Portugal is identical to *F. tularensis* subs. *holartica*.