Horse Exposition to Coxiella burnetii in France: Antibody Dynamics in Serum, Environmental Risk Assessment and Potential Links with Symptomatology

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Abstract : Q fever is a worldwide zoonosis caused by the bacterium Coxiella burnetii. It may infect a broad range of host species, including horses. Although the role of horses in C. burnetii infections remains unknown, their use as sentinel species may be interesting to better assess the human risk exposure. Thus, we aimed to assess the C. burnetii horse exposition in a French endemic area by describing the antibody dynamics detected in serum; investigating the pathogen circulation in the horse environment, and exploring potential links with unexplained syndromes. Blood samples were collected in 2015 and 2016 on 338 and 294 horses, respectively and analyzed by ELISA. Ticks collected on horses were identified, and C. burnetii DNA detection was performed by qPCR targeting the IS1111 gene. Blood sample analyses revealed a significant increase of the seroprevalence in horses between both years, from 11% [7.67; 14.43] to 25% [20.06; 29.94]. On 36 seropositive horses in 2015 and 73 in 2016, 5 and four respectively showed clinical signs compatible with a C. burnetii infection (i.e., chronic fever or respiratory disorders, unfitness and unexplained weight loss). DNA was detected in almost 40% of ticks (n=59/148 in 2015 and n=103/305 in 2016) and exceptionally in dust samples (n=2/46 in 2015 and n=1/14 in 2016) every year. The C. burnetti detection in both the serum and the environment of horses confirm their exposure to the bacterium. Therefore, consideration should be given to target a relevant sentinel species to better assess the Q fever surveillance depending on the epidemiological context.

Keywords : ELISA, Q fever, qPCR, syndromic surveillance
Conference Title : ICEID 2017 : International Conference on Epidemiology and Infectious Diseases
Conference Location : Boston, United States
Conference Dates : April 24-25, 2017