Type: Poster Presentation

Final Abstract Number: 58.005
Session: Bacterial Infections
Date: Saturday, April 5, 2014
Time: 12:45-14:15
Room: Ballroom

Molecular identification of pathogenic bacteria in eschars from acute febrile patients, Senegal

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Background: Fever caused by Rickettsia felis was recently shown to play an important role in infectious diseases morbidity in sub-Saharan Africa. Eschar biopsy has been repeatedly shown to be very useful for the detection of rickettsial DNA in patients. To evade the biopsy, a good alternative may be the examination of swabs from skin lesions in rickettsiosis patients. Rickettsial DNA may be present in the crusts and fluids of the eschars, even after the initiation of treatment and in cases for which serum (even convalescent) remains negative against rickettsial antigens To clarify the clinical symptoms of R. felis infection, we collected 68 cotton swabs from fever-associated eschars in four different regions of Senegal.

Methods & Materials: The criteria for inclusion in the study were as follows: (1) the presence of fever (axillary temperature >37.5 °C) as the primary symptom, and (2) the presence of eschar(s) on the skin of the patient. Eschars (tache noire) in our patients were identified as single or several (grouped) local skin lesions coated by a coagulated crust or slough that developed without anterior anamnestically evident trauma. The DNA extracted from these samples, as well as DNA from negative controls (healthy skin swabs from Senegal and France), was tested for the presence of pathogenic bacteria.

Results: In 5/68 of eschar samples (7.4%), we have identified DNA from R. felis. In 49/68 (72.1%), we found DNA from Staphylococcus aureus; in 35/68 (51.5%), Streptococcus pyogenes; and in 4/68 (5.9%), Streptococcus pneumoniae. In 34 cases, S. aureus was found together with S. pyogenes. DNA from R. felis was also found in swabs from the skin of the healthy Senegalese villagers (3/60, 5%), but not from French urbanites.

Conclusion: The presence of DNA from S. aureus and S. pyogenes was significantly associated with the presence of eschars in febrile patients compared to the healthy skin from the control group. When the two negative control groups were compared, only the presence of S. aureus DNA was significantly higher in Senegalese villagers. Finally, we confirmed that Senegal is an endemic region for R. felis, which is found in both eschars and healthy skin swabs.

http://dx.doi.org/10.1016/j.ijid.2014.03.1111

Type: Poster Presentation

Final Abstract Number: 58.006
Session: Bacterial Infections
Date: Saturday, April 5, 2014
Time: 12:45-14:15
Room: Ballroom

Three new *Bartonella* species from rodents in Senegal

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Background: Bartonella is the monotypic genus of the family Bartonellaceae, Alpha-proteobacteria. TMany Bartonella species are associated with human diseases. Rodent-associated species, such as B. elizabethae, B. grahamii and B. vinsonii are human pathogens. To date, no studies investigating the presence of Bartonella spp. in rodents from Senegal were carried out and the only West African country where it was performed is Nigeria.

Methods & Materials: The aim of this study was to investigate the presence of Bartonella spp. in commensal rodents in Sine-Saloum region of Senegal where rodents and are reservoirs rodent-associated soft ticks are vectors of relapsing fever caused by Borrelia crocidurae. Rodents and insectivores were captured alive in February 2013 in two sites (Dielmo and Ndiop) using wire mesh traps baited with peanut butter or onions. Trapped rodents and insectivores were anaesthetized and opened in sterile conditions. Blood was inoculated on Columbia agar plates (5% sheep blood). The gltA, rpoB, 16S rRNA, ftsZ genes and ITS were amplified and sequenced from recovered Bartonella isolates.

Results: In total, during the period of 6 days 119 small mammals were captured: 116 rodents and 3 shrews (Crocidura cf. olivieri). Rodents were identified morphologically: 5 Arvicantis niloticus, 56 Gerbilliscus gambianus, 49 Mastomys erythroleucus, 5 Mus musculus and 1 Praomys daltoni. 30 isolates of Bartonella spp. were recovered from the blood of rodents. None of the isolated belonged to already described species of Bartonella. Phylogenetic analysis showed that the isolated bartonellae form three separate clusters within the genus Bartonella. Comparison of gltA genes of recovered isolated with those of officially recognized species allowed to conclude that three clusters may present three separate new species of Bartonella. Candidatus "Bartonella raoultii" (1 isolate) and Candidatus "Bartonella mastomydis" (21 isolates) were recovered only from Mastomys erythroleucus, Candidatus "Bartonella saheliensis" (8 isolates) were recovered only from Gerbilliscus gambianus.

Conclusion: Rodents in Senegal are not only reservoirs of the agent of relapsing fever, but also of three new Bartonella species. The pathogenicity for humans of these isolates is yet to be investigated. Unlike other African countries, each genetic cluster of bartonellae from Senegalese rodents is associated with a specific rodent species.

http://dx.doi.org/10.1016/j.ijid.2014.03.1112