and productive cough. One month earlier she developed Rhodococcus equi bacteremia. Examination did not show any source of infection. Laboratory exam, WBC of 300. Chest × ray showed right lower lobe consolidation in the lung which was confirmed on CT scan. She was started on Vancomycin and Ceftazidime. Ambisome was also added for aspergillus coverage. All the cultures remained sterile and an echo done did not show vegetations. Bone marrow aspirate and biopsy done to rule out recurrence of leukemia showed only hypocellular marrow. The cultures continued to be negative until 4 weeks after admission when the blood grew a Gram-positive weakly-acid-fast organism identified by Center for Disease Control (CDC) to be Gordonia polyisoprenivorans.

Discussion: Gordonia polyisoprenivorans is a ubiquitous environmental aerobic Actinomycetes belonging to the family of Gordoniaceae in the order Actinomycetales. Most of the 21 identified species are typically gram positive, catalase positive, weakly acid fast, thin beaded coccobacilli. G. polyisoprenivorans was first described in 1999 as a rubber-degrading bacteria isolated from stagnant water inside a deteriorated automobile tire. Extensive literature review has only identified 2 case reports of bacteremia due to this unusual organism. The 2 earlier case reports highlighted patients with hematological diseases (one with bone marrow transplant and the other with Osler-Weber-Rendu and myelodysplastic syndrome). Our patient although free from leukemia, is similar in being neutropenic. We believe that hematologically immunocompromised patients with broad-spectrum antibiotics and long term central catheters select the possibility of infection with G. polyisoprenivorans.

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49.023

Spatial-Temporal and Molecular Analyses of a DENV3 Outbreak Show the Dynamics of Dengue Infection (Viral Spread)

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Background: Dengue fever (DF) and dengue hemorrhagic fever (DHF) are important public health issues. Brazil was responsible for 60% of the worldwide dengue cases in 2006 and the virus is endemic in the country. Molecular epidemiology of dengue viruses in endemic areas, associated with spatio-temporal tracking may help to understand the dissemination patterns of viral lineages.

Methods: We followed an outbreak in the city of S.J. Rio Preto - Brazil in 2006. Blood samples from patients with DF and DHF symptoms were collected and tested by RT-PCR. Sequences of NS5 gene from viral genomic RNA were amplified and DENV-3 positive samples were sequenced and compared to other reference sequences for phylogenetic reconstruction. Phyldinamics of DENV-3 was inferred using MCMC-based Bayesian method under the assumption of the relaxed molecular clock. We also generated matrices of distances between samples to analyze the spatio-temporal dispersion pattern and applied a customized algorithm to obtain the putative spatio-temporal pattern of spread of the disease.

Results: For this analysis we generated a 399 nucleotide-long dataset with 134 taxa by aligning the 82 sequences with 52 reference sequences. DENV-3 samples were closely related to strains circulating in Martinique and in Brazil. Sixty samples formed a monophyletic group, representing lineage 1; 22 samples formed lineage 2. The basic reproductive rate (R0) was 3.765 for lineage 1 and 3.093 for lineage 2. Preliminary studies indicated that both lineages split 1 to 3 years before the last collected sample. They propagated in different regions of the city, North-Western (lineage 1) and South-Eastern (lineage 2).

Conclusion: Our results indicated that spatial analysis associated with molecular epidemiology are important tools to enhance the understanding of the viral strain spread patterns and may be paramount in monitoring an predicting the occurrence of severe forms of dengue. We plan to account in the future for other factors modulating dengue virus dispersion such as climate, adult mosquito density and biology, density of human population and socio-economical aspects.

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49.024

Synchronous Seasonal Activity of Ixodes ricinus Immature Stages in Brateiu, Sibiu County, Romania - Implications for TBE Outbreaks

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Background: The two most important tick-borne infections of humans in Europe are tick-borne encephalitis and Lyme borreliosis. While Lyme borreliosis occurs extensively throughout Europe, TBE is far more focal in its distribution suggesting that it requires more narrowly defined conditions for maintenance. In Romania the largest TBE outbreak occurred in Brateiu, Sibiu County. The aim of this study was to define those abiotic and biotic factors that could favor a TBE outbreak.

Methods: Ixodes ricinus (the main vector for TBEV) ticks were collected monthly, for two years, from six sites in Romania (including Brateiu) using the flagging method. The questing ticks’ activity was estimated by reporting the collected tick number to 100 m². Seasonal dynamics of ticks was compared between the sites. Environmental data were collected during the sampling period, including climate data like temperature, humidity, precipitations etc.

Results: Analyzing the ticks’ dynamics we noticed that in Brateiu the immature stages were synchronous for a few months, while in other sites they were not. Thus, in Brateiu approximately 75% of the immature were active during July and August, while in the other sites there was an approximately two months delay of larva peak activity to that of nymphs activity. Tick numbers were positively correlated to temperatures and humidity from the regional weather stations.

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