34.004
Arconobacterium pyogenes associated with pulmonary and submandibular lymph node abscessation in white tailed deer (Odocoileus virginianus)

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Background: Thin, lactating and uncoordinated female white-tailed deer was submitted for necropsy as part of a surveillance program for chronic wasting disease (CWD). Laboratory tests for CWD and rabies were negative. Post-mortem examination revealed pulmonary and submandibular lymph node abscesses associated with Arcanobacterium pyogenes and Pasteurella. The overall presentation suggests that the infections may have been associated with chronic stress.

Methods: Brain tissues were removed aseptically and transferred to Virginia’s Department of Game and Inland Fisheries for analysis for CWD and rabies virus, and Brain culture swabs were sent to the Virginia-Maryland Regional College of Veterinary Medicine for aerobic and anaerobic bacterial cultures, including Listeria monocytogenes culture. Lung and lymph node samples were taken aseptically for aerobic culture, including culture for Mycoplasma and Salmonella. Lung and lymph node were plated onto Blood Agar, MacConkey Agar and Columbia CAN Agar. Culture swabs of lung tissue were plated onto Chocolate agar, TSA and CAN agar. Chocolate Agar plates were incubated in 5% CO2 incubated at 37 °C with no CO2 analysis.

Results: Arcanobacterium pyogenes was isolated from lung and submandibular lymph node, and identified using bioMérieux API Coryne strips. Pasteurella spp. was isolated from the same lymph node, and identified using bioMérieux API 20 NE strip. Laboratory tests for rabies, CWD, Listeria, Mycoplasma, Mycobacterium and Salmonella were all negative. Histopathologic examination was performed on lung, brain, spleen, lymph node, intestine, heart and liver. The lung had multiple discrete nodules of coagulative necrosis containing neutrophils and macrophages (figure 1). A rim of neutrophilic inflammation surrounded the necrosis; peripheral to this was a layer of fibroplasia and fibrosis.

Conclusion: In conclusion, even though it was not isolated from the lung, Pasteurella was the primary cause of infection in the lung and from there it spread to the lymph node. A. pyogenes was considered to be a secondary infection in the lungs where pneumonia was already present. The final diagnosis was pulmonary and lymph node abscesses due to A pyogenes and fibrinopurulent and necrotizing broncho-pneumonia due to a mixed Pasteurella and A. pyogenes.

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34.005
Phylogenetic analysis of sporadic hepatitis E virus in Eastern China

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Background: Recently, evidence for the existence of hepatitis E virus (HEV) was reported all over the mainland of China. The number of acute sporadic hepatitis E cases increased annually and small outbreaks happened more frequently, probably due to food-borne transmission. The phylogenetic characteristics of the circulating HEV worth further understanding.

Methods: A total of 413 serum samples were collected from acute sporadic hepatitis E patients in 14 hospitals in Eastern China from 2005 to 2008 under informed consent. All the samples were detected with a nested RT-PCR assay for HEV RNA, and a 150-nt fragment within HEV ORF2 region was sequenced for phylogenetic analysis using Neighbor-Joining method with reference HEV sequences from the GenBank.

Results: The ratio of male to female was 1.75: 1 among all the patients. The majority (61.5%) of them was 40-69 years old, with an average age of 50 ± 16 years old. 140 out of 413 (34.0%) sera were positive in HEV RNA, and all the isolates were sequenced subsequently. Phylogenetic analysis revealed that all these isolates belonged to genotype-IV with much high similarities, sharing 77.9%-88.3%, 80.8%-90.6%, 73.4%-85.2% and 91.0%-95.4% nucleotide identities with prototype I (D10330, Burma; D11092, China; X98292, India; AY230202, Morocco; AY204877, Chad), II (M74506, Mexico), III (AB089824, AB189070, Japan; AY119488, Canada) and IV (AB097812, AY994199, AB108537, China) HEV strains, respectively. Those isolates could be further divided into six clusters within genotype IV, but no obvious geographical difference was observed among the clusters.

Conclusion: It is evident that genotype-IV HEV had been the principle causative agent of acute sporadic HEV infection for human in Eastern China.

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34.006
Molecular characterization of VP1-3 and NSP1-3 genes of porcine group A rotavirus G12 strain RU172: Evidence for porcine origin of human G12 strains

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Background: Group A rotavirus is an important cause of infantile diarrhea in humans, and classified into 23 G and 31 P genotypes. Among them, G12 has been regarded as an important emerging genotype of human strains, world-