Epidemiology of the four human coronaviruses 229E, HKU1, NL63 and OC43 detected over 30 months in the Singapore military

C.W.J. Liaw 1−∗, A.S.E. Lim 1, W.H.V. Koh 1, J.P. Loh 1, C. Kan 1, K.W. Chan 1, P.J. Ting 1, S.H. Ng 1, S.W.J. Chew 1, A. Dua 1, C.H. Tan 2, Q.H.C. Gao 2, H.P.V. Ho 2, V. lee 2, B.H. Tan 1

1 DSO NATIONAL LABORATORIES, Singapore, Singapore
2 Ministry of Defence, Singapore, Singapore

Background: Human coronaviruses (HCoVs) are common etiological agents of acute respiratory tract infections. However their prevalence and clinical presentations are less well studied.

Methods: Here in Singapore, we conducted acute respiratory infection surveillance in selected military camps to investigate the epidemiology of such infections and pathogens involved. Nasal washes were done for patients that meet the case criteria along with a survey questionnaire. Nucleic acids were then extracted from the nasal washes and subjected to molecular testing for presence of various pathogens, including human coronaviruses.

Results: The results presented will focus on the four human coronaviruses 229E, HKU1, NL63 and OC43 detected over a 2 ½ year period of surveillance.

Conclusion: The epidemiology of the four human coronaviruses 229E, HKU1, NL63 and OC43 over the 2 ½ year period and how they compare with that of other published studies will be discussed.

Epidemiology of the four human coronaviruses 229E, HKU1, NL63 and OC43 detected over 30 months in the Singapore military

C.W.J. Liaw 1−∗, A.S.E. Lim 1, W.H.V. Koh 1, J.P. Loh 1, C. Kan 1, K.W. Chan 1, P.J. Ting 1, S.H. Ng 1, S.W.J. Chew 1, A. Dua 1, C.H. Tan 2, Q.H.C. Gao 2, H.P.V. Ho 2, V. lee 2, B.H. Tan 1

1 DSO NATIONAL LABORATORIES, Singapore, Singapore
2 Ministry of Defence, Singapore, Singapore

Background: Human coronaviruses (HCoVs) are common etiological agents of acute respiratory tract infections. However their prevalence and clinical presentations are less well studied.

Methods: Here in Singapore, we conducted acute respiratory infection surveillance in selected military camps to investigate the epidemiology of such infections and pathogens involved. Nasal washes were done for patients that meet the case criteria along with a survey questionnaire. Nucleic acids were then extracted from the nasal washes and subjected to molecular testing for presence of various pathogens, including human coronaviruses.

Results: The results presented will focus on the four human coronaviruses 229E, HKU1, NL63 and OC43 detected over a 2 ½ year period of surveillance.

Conclusion: The epidemiology of the four human coronaviruses 229E, HKU1, NL63 and OC43 over the 2 ½ year period and how they compare with that of other published studies will be discussed.

http://dx.doi.org/10.1016/j.ijid.2012.05.306

Type: Poster Presentation

Final Abstract Number: 41.031
Session: Infectious Disease Surveillance
Date: Thursday, June 14, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Rapid differentiation of Vibrio cholerae strains using MLVA and creation of a public MLVA database for epidemiological investigations

J.P. Loh 1−∗, W.H.V. Koh 2

1 DSO NATIONAL LABORATORIES, Singapore, Singapore
2 DSO National Laboratories, Singapore, Singapore

Background: Vibrio cholerae is a globally important pathogen endemic in many areas of the world and causes up to 5 million reported cases of cholera every year. Strain-typing is thus important for epidemiological surveillance purposes as well as determining source of infections for more targeted preventive measures. Multilocus variable-number tandem-repeat (VNTR) analysis (MLVA) is one method that has been proven useful for differentiating between strains that would be indistinguishable by other techniques such as PFGE and phage-typing.

Methods: Here we present a rapid method for strain-typing of Vibrio cholerae using MLVA which does not require the use of a sequencer for analysis but give better resolution compared to conventional gel electrophoresis.

Results: We are also in the process of generating a public MLVA database for Vibrio cholerae and compiling information from various sources and collaborators so as to build a useful database...