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level and this predictable relationship may be exploited for vaccine design and evaluation. These approaches can be enhanced by also incorporating phylogenetic analysis. Specifically the relationship between HLA alleles and HIV polymorphism in chronically infected patients may be used to predict protective responses to a preventative vaccine in a population with similar HLA diversity exposed to a similar range of HIV diversity. Importantly, the innate advantage provided by intense human HLA diversity can then be exploited to ameliorate problems posed by HIV diversity. Analyses of real and theoretical candidate vaccines suggest that polyvalent and more specifically “polyalleric” vaccines will most effectively exploit known regional HLA diversity to cover HIV diversity.

K5 Nucleic acid amplification tests for detection of respiratory viruses

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Background and Aim: We aimed to introduce respiratory virus nucleic acid amplification tests (NATs) into routine diagnostics and assess the impact on laboratory work-flow and costs.

Methods: Polymerase chain reaction (PCR) and nucleic acid sequence based amplification (NASBA) were utilised for identification of influenza (IFV) A and B, parainfluenza (PIV) 1–4, respiratory syncytial virus (RSV), adenovirus (ADV) and human metapneumovirus (hMPV). Nucleic acid extraction was automated (bioMérieux). In a two phase process, NATs were first used to replace DFA and culture for lower respiratory specimens and then to replace culture for DFA negative nasopharyngeal samples. The impact of these changes was assessed over a period of one year with more than 10,000 specimens analysed.

Results: NATs identified a significant proportion of mixed infections and picked up IFV, PIV and RSV positives missed by DFA. NATs identified hMPV and ADV as a probable cause of respiratory symptoms in a wider range of patients than previously appreciated. hMPV was also found to be associated with outbreaks of respiratory infection in the elderly. The feasibility of direct amplification, typing and sequence analysis of influenza A from clinical specimens (without prior culture) was confirmed.

Discussion and Conclusions: NATs for respiratory viruses can be incorporated into a routine diagnostic laboratory. Direct analysis of respiratory specimens (without prior culture) is feasible and real-time provision of influenza A subtyping, strain drift and antiviral resistance data will have a positive impact on outbreak management and pandemic preparedness.

K6 The Gardner lecture: New respiratory viruses: from viral RNA to symptomatic patients

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Respiratory viruses are a major cause of morbidity and mortality worldwide. These viruses can be classified in one of five viral families including DNA viruses (Adenoviridae) and most commonly RNA viruses (Orthomyxoviridae, Paramyxoviridae, Picornaviridae and Coronaviridae). Five new viral agents associated with respiratory symptoms have been discovered since 2001: The human metapneumovirus (hMPV) belonging to the pneumovirinae subfamily in the Paramyxoviridae family, the SARS-coronavirus as well as two other members of the Coronaviridae family i.e. coronavirus-NL and -HKU1 and finally parechovirus type 3 which belongs to the Picornaviridae family. Most of these new respiratory viruses with the exception of SARS-coronavirus are probably old pathogens whose pathogenicity has increased because of changes in conventional public health practices.

This presentation will primarily review the virological, epidemiological and clinical features of emerging respiratory viruses such as hMPV, the new coronaviruses and parechovirus type 3. Also, in the case of hMPV infections, the potential therapeutic and prophylactic modalities will be discussed. Human metapneumovirus infects virtually all children by the age of 5–10 years and is associated with upper respiratory tract infections (URTI), bronchiolitis and pneumonia like those caused by human respiratory syncytial virus. Viral inhibition has been reported with ribavirin and intravenous immunoglobulins and live-attenuated vaccines generated by the reverse genetics technology are currently under development and evaluation. The SARS-coronavirus was responsible for about 800 cases of severe acute respiratory syndromes worldwide in 2003 with a 10% fatality rate. Coronavirus NL has been associated mainly with upper and lower respiratory tract infections as well as with Kawasaki’s disease in some studies. Coronavirus HKU1 seems to be a rare cause of URTI and pneumonia in studies from Hong Kong, Europe and North America. It has also been recently detected in stool samples of symptomatic children. Finally, parechovirus type 3 has been detected in a variety of clinical samples of neonates presenting with sepsis-like syndromes with or without respiratory symptoms.

The development of sensitive molecular methods has allowed the detection of these emerging viral pathogens in many parts of the world. Careful prospective studies are now needed to fully describe the clinical burden associated with these new respiratory viral agents. Furthermore, the development of new therapeutic modalities as well as effective and safe vaccines constitutes another important research priority.