Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Abstract No: 1769

Presentation at ESCV 2015: Oral 29

The Edinburgh microbiology archive

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Background: Understanding the epidemiology and variation of the multitude of microorganisms that infect humans requires access to large collections of clinical samples. This is especially important when a new pathogen is discovered, or when examining the relationship between known pathogens and particular patient groups. In order to obviate the need to develop prospective collections with proper ethical approval for each such pathogen or study we have developed procedures that allow us to retain samples and associated clinical information submitted to the Edinburgh Clinical Virology Laboratory as an anonymised research archive.

Methods: When all requested tests have been completed, respiratory, cerebrospinal fluid and faecal samples submitted for virological analysis at Edinburgh Royal Infirmary are relabelled with an anonymised number. Nucleic acids extracted from these samples are also retained both individually and in separately numbered pools of ten. Clinical notes associated with these samples have irreversibly scrambled but unique patient IDs. Local ethical approval was obtained for sample collection and for the retention of clinical information.

Results: The archive covers the period from 2006 to the present and consists of >70,000 respiratory, >8000 CSF and >15,000 faecal samples, together with the nucleic acid extracts from these samples and associated clinical notes. The archive has been used by us and our collaborators to study the population and temporal incidence and genetic variation of several viruses (influenza A, B and C viruses, hepatitis E virus, rhinovirus, coronavirus, enterovirus, metapneumovirus and parechovirus) and microorganisms (Mycoplasma). The archive has also been used to study associations between host genetic variation and the susceptibility to and severity of virus infections.

Conclusion: As the Edinburgh Microbiology Archive expands over the next decade it will provide a powerful resource for studying the epidemiology and evolution of human pathogens.

http://dx.doi.org/10.1016/j.jcv.2015.07.039

Abstract No: 1559

Presentation at ESCV 2015: Oral 30

Resolution of undefined aetiology of respiratory infections in lung transplant patients with unbiased metagenomic sequencing

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Background: Lung transplanted patients are a vulnerable group of immunocompromised individuals prone to respiratory infections, necessitating a tight monitoring of viral infections post-transplantation to prevent respiratory complications and allograft dysfunction. Despite routinely testing for the most common respiratory viruses, a considerable fraction of infections remains with unknown aetiology. We re-analysed respiratory samples collected from symptomatic lung transplant patients for which no viral or microbial aetiology could be found. We used an open metagenomic approach to identify potential pathogenic viruses responsible for the respiratory symptoms.

Methods: For metagenomic sequencing, virus particles were enriched from respiratory swabs, total nucleic acids extracted and randomly amplified. Sequencing libraries were prepared with NexteraXT and sequenced on a MiSeq Illumina (1×150 bp). Quality filtered reads were cleaned from non-viral reads by an in-house bioinformatics pipeline and blasted against a database containing approximately 40,000 viral genomes.

Results: Amongst the 71 participating individuals, 22 (31%) showed no respiratory symptoms up to 15 months after lung transplantation; 49 (69%) developed a total of 55 episodes of respiratory disease of which 27 were of viral and 3 of bacteriological origin. In 25 (45%) episodes of respiratory symptoms, neither a viral nor a microbial aetiology of infection was determined by conventional routine diagnostics. We analysed 13 of these undefined episodes. The metagenomic approach identified 3 cases of Rhinovirus A, Rhinovirus B and Coronavirus HKU. Of note, in two out of three cases these viruses did show evidence of late amplification in routine PCR, but did not fulfil the criteria for positivity. In 4 of the 13 samples we detected HHV-7 reads in the respiratory swabs which may have contributed to the observed disease patterns. In addition, we found Torque Teno virus and bacteriophage reads. Reads from Streptococcus phage suggested a previously not defined infection with Streptococcus species, which was supported by reads from *Streptococcus pneumoniae*.

Conclusions: Metagenomic approaches can identify microbial pathogens in a single analysis. Our study confirmed low-level infections with known respiratory viruses and additionally identified cases of HHV-7 infection. No other viruses were found in the remaining symptomatic lung transplant patients leaving the exact aetiology of infection still unclear. This study highlights the potential of metagenomic sequencing in complex diagnostic situations such as in immunocompromised hosts. Acknowledgments Funding was provided by the Clinical Research Priority Program 'Viral Infectious Diseases' of the University of Zurich. Keywords lung transplant, metagenomic sequencing, virus diagnostics

http://dx.doi.org/10.1016/j.jcv.2015.07.040

Abstract No: 1666

Presentation at ESCV 2015: Oral 31

Baseline majority and minority resistance mutations in HIV-infected MSM with acute HCV

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Background: Direct-acting antiviral (DAA) agents target hepatitis C virus proteins and are curative in combination in the majority of patients infected with HCV. Selection of DAA-resistant viral variants may hamper treatment success. Mutations that confer resistance to these agents have been reported both in vitro and in vivo.

Methods: Deep sequencing was used to detect minority variants of HCV known to confer resistance to Telaprevir, Boceprevir, Simeprevir (NS3/4a inhibitors), Daclatasvir (NS5A inhibitor)