K.03
HPV vaccines: New opportunities for global cervical cancer prevention
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With the publication of the key short-term results of the two major Phase III trials of HPV vaccines, the perspective of tackling cervical cancer prevention with vaccination has been unambiguously open. While recognizing the limitations of the still moderate (5–6 years) follow up in a few tens of thousand young women, two vaccines to date have shown high efficacy, safety, immunogenicity, long term duration of protection and a strong suggestions of induction of immune memory.
A number of clinically relevant issues remain to be fully described, including the magnitude and the HPV spectrum included in the cross protection effect, and the long term effects of HPV vaccines on cancer-protection and safety. However, to solve these questions it is required additional follow up time and the organization of large Phase IV studies, some of which are already in place. The currently available vaccines offer HPV 16 and 18 naive women full protection from the HPV types that cause an estimated 70% of cervical cancer and a slightly lower fraction of its precursors. Once the cross protection impact is fully described and the geographical variation of the HPV types in cervical cancer is better known, these estimates will likely increase in some areas to perhaps 75–80%. HPV 16 and 18 account for a higher proportion of cervical adenocarcinomas, in the range of 80–85% of the histological subgroup that more easily escape detection by cytology-based screening practices.
In scenarios in which screening is already developed and reasonable efficient, current screening protocols will have to continue for some time because of the limitations of current HPV vaccines both in their lack of therapeutic effect (thus not protecting women with an ongoing neoplastic processes) and in their limited number of HPV types (thus leaving to evolve some 25–30% of cervical cancer cases related to HPV types other than 16 or 18). In populations without adequate screening HPV vaccines at affordable prices seem to be the only realistic option. While these arrive, more efficient screening schemes requiring fewer visits or strategies involving rapid intervention like “screen and treat” protocols, remain the only option for currently living adult women. Moreover, should polyclaval vaccines (including some 5 to 8 HPV types) result in extending protection against more than 90%+ of the oncogenic HPV types, vaccination alone would be the answer for both developing and developed countries.

K.04
Epidemiology and pathogenesis of newly discovered viruses: evaluating their threat to human health
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The development and recent spectacular success of molecular-based virus discovery methods places a series of major new demands for clinical virology laboratories. In the past 5 years, a number of human viruses with potentially or demonstrated roles in human disease have been identified in several different families, including parvoviruses, picornaviruses, paramyxoviruses, coronaviruses, polyomaviruses and anello–circoviruses. These findings add substantially to our understanding of human virus diversity and the emergence of new pathogens. However, for many a substantial amount of research into their prevalence, molecular epidemiology and transmission, and most importantly their aetiological roles in human disease is required to realistic assess their significance for the introduction of diagnostic testing in clinical virology laboratories.
The presentation will include updates on ongoing studies of molecular epidemiology, possible origins and clinical impact of a range of newly discovered viruses, and their contrasting outcomes. While current findings implicate human bocavirus as a significant cause of childhood respiratory disease, the pathogenic potential of other newly discovered parvoviruses such as PARV4, HParV5, and several human polyomaviruses is currently much less clear. The epidemiology and prevalence of human cardiovirus and another large group of newly discovered human picornaviruses will also be reviewed. Finally I will outline progress towards establishing strategic archives of diagnostic and surveillance specimens that are increasingly required for rapid and effective assessment of the pathogenic potential of both known viruses and of the likely plethora of human and animal viruses that remain to be discovered in the future.

K.05
The role of molecular diagnostics in clinical virology
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Purpose: In 2001 the Queensland Paediatric Infectious Diseases (QPID) Laboratory introduced molecular diagnosis for infectious diseases into routine practice. As a result we developed over 60 new molecular assays targeting a wide range of human pathogens. Presently, the laboratory processes approximately 120,000 specimens per year by molecular testing, with an emphasis on the detection of respiratory viruses.
Methods: The technology applied was real-time PCR using a variety of platforms, thereby increasing our capability to perform quantitative PCR and high resolution melting curve analysis. However, this technology has some significant limitations, primarily associated with sequence variation in target sites, which need special consideration in assay design.
Results: Currently, we use real-time PCR to routinely detect 11 viruses associated with acute respiratory tract infection in children, and applied these to fully characterise their prevalence rate in specimens collected over 5 years. Also, these samples were subject to investigation for new or as yet undetected viral agents, establishing the presence of the newly described human coronaviruses NL63 and HKU1, human bocavirus and the novel human polyomaviruses KI, WU and MCV in Australian children.
Conclusion: Molecular technology has significantly enhanced the level of diagnostic service delivered in our organisation, and has supplemented the research interests of the QPID laboratory, particularly in respiratory virology. This has enhanced our understanding of the role these viruses play in acute respiratory infection, and led to the discovery of new viruses associated with the human respiratory tract.

K.06
QCMD: state of the art molecular external quality assessment for sexually transmitted pathogens
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The number of clinically relevant viral and microbial pathogens continues to increase, alongside the growth in the routine use of molecular diagnostics. These changes have meant new challenges for clinical laboratories, who must continually maintain the quality of their diagnostic tests. An important part of quality control involves regular participation in External Quality Assessment (EQA) programmes. Quality Control for Molecular Diagnostics (QCMD) is at the forefront of EQA provision and offers programmes covering, amongst others, a range of sexually transmitted pathogens such as HIV, HSV, Chlamydia trachomatis and Neisseria gonorrhoeae. QCMD has continued to develop new methods for analysing and scoring EQA data in response to changes in regulatory and participant requirements both at the national and international level. These improvements allow for more informed decisions to be made about the performance of assays for the diagnosis of sexually transmitted pathogens and help support the laboratory’s annual accreditation and certification activities. The number of participants in QCMD EQA programmes for sexually transmitted pathogens has increased by 75% on average since 2004 and the use of commercial technologies increased by 20% whereas use of conventional in-house PCR assays fell by 74%. The performance of molecular diagnostics has improved on the whole but specific quality issues still remain. The key performance indicators for molecular assays are generally dependent on clinical utility and include false positive/negative results and quantitative accuracy. Given the limitations of molecular technologies, including amplification-based assays, is it reasonable to expect zero false positive results or should a low level be acceptable? The average across all EQA programmes for sexually transmitted pathogens is currently 2.2%, but there are major differences. For example the percentage of false positives on negative samples in the N. gonorrhoeae EQA programmes has been 0% for the past three years, whereas for HSV the average was 4.1%. Evolutionary changes in common pathogens have also led to the emergence of strains that are missed by current molecular diagnostic tests. For example the emergence of the Swedish variant of C. trachomatis, which is missing a portion of the cryptic plasmid, resulted in established tests reporting false negative results. This underlines the need for constant assay optimisation and