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Meet the Expert

M-I
Submitting an article to Journal of Clinical Virology
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Abstract not available at time of printing.

M-II
Quality control in a molecular virology laboratory
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The implementation of molecular diagnostics is common in most, if not all, diagnostic laboratories. Besides the use of commercial assays for an increasing number of viral targets, most diagnostic assays are home brew, simply because of the necessity to implement more tests for more targets. Furthermore, commercial tests are likely to be more expensive as home brew systems. However, both commercial and home brew assays need to fulfill requirements on quality control, summarized in guidelines like ISO15189. Although commercial assays are CE-marked in most European countries, this does not imply their usefulness for diagnostic purposes or that these assays can be implemented in routine diagnostics without further analysis. Questions related to clinical relevance still need to be answered in a number of cases, definitely as the field of molecular diagnostics is moving so fast. Issues related to quality control, validation and implementation will be addressed. Furthermore, an update will be given on the use of standardised materials or standards if available.

M-III
Laboratory diagnosis of viral gastroenteritis
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A wide range of viruses are responsible for diarrhea in humans. Rotavirus, norovirus, enteroviruses types 40 and 41, sapovirus and astrovirus are mainly responsible for diarrhea. Less frequent causes are aichivirus, coronavirus, pestivirus, torovirus etc. The causative virus is not possible to detect by clinical features of the patient or stool characteristics. It is also not possible to distinguish between viral gastroenteritis and some bacterial causes of gastroenteritis, such as enterotoxigenic strains of E. coli (ETEC). In most of the cases molecular methods have been successfully utilized to identify the virus causing diarrheal diseases. Proper diagnostic tests are essential to identify causative virus.

M-IV
Anti-viral resistance testing in hepatitis B virus infection
M. Bozdayi*, Hepatology Institute of Ankara University, Turkey
Chronic hepatitis B virus infection remains to be a major global health problem due to its high prevalence around the world. The ability of persistence of HBV in the infected cells, owing to its unique mechanism of replication, introduces a clinical challenge in the treatment of chronic HBV infection. HBV covalently closed circular DNA (HBV cccDNA), which is located in the nucleus of infected cells, acts as an intranuclear reservoir for the newly synthesized HBV due to its role in HBV replication as a template for viral mRNA transcription. Currently available antiviral therapeutics achieve the suppression of HBV replication. Therefore prolonged therapy is needed in order to prevent the relapse of viral replication that may occur after the withdrawal of antiviral therapy. The main drawback of the prolonged therapy is the arising of antiviral drug resistant HBV variants selected during the treatment. Although antivirals are very effective in the short-term therapy, both the rapid rebound of viremia after discontinuation of therapy and the emerging of resistant mutants of long term therapy remain as challenging clinical problems in the antiviral treatment.
Antiviral resistance testing is one of the main topic in the management of HBV infection. There are two main approaches for testing the resistance. One is genotypic analysis and the second one phenotypic methods.
1. Genotypic assays:
   • DNA sequencing,
     – DNA sequencing of PCR products derived from reverse transcriptase region of HBV DNA or whole genome,