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Special molecular typing and epidemiological studies of viruses of animal origin with special interest of zoonotic ones

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Molecular genotyping tools use for the characterization of pathogens has become a standard component of infectious disease surveillance and outbreak investigations. Molecular epidemiology of infectious diseases combines traditional epidemiological methods with analysis of genome of pathogens over time, place and person across human populations and relevant reservoirs, to study host–pathogen interactions and infer hypotheses about host-to-host or source-to-host transmission. Identification by different molecular techniques has been extensively exploited to identify isolates and localize disease outbreaks. Often, phenotypic assays do not reflect underlying genealogical information. The multi-locus sequence typing (MLST) scheme played a major role in investigating the extent of genetic structure in bacterial populations and rapidly became the cornerstone technique for molecular typing of pathogenic microorganisms. MLST approach provides an accurate assessment of species and sometimes even strains and has the added advantage of also providing population genetic insights into levels and directionality of gene flow. This genetic based species diagnosis is much more accurate than performing conventional immunological assays to determine species and strain. But given the recent advances in sequencing technologies, the question naturally arises: what is the future of the MLST scheme in the genomic era? The sequence variation of viruses provides more suitable data for phylogenetic analysis. The study of Reo viruses and especially of rotaviruses is used to illustrate how phylogenetic analyses provide information on the origin, spread and maintenance of infections. Identification of rotaviruses genotypes by using multiplex PCR assays found that bovine rotaviruses genotype was (23%) lower than equine rotaviruses genotype was (14%) and human rotaviruses (28%) by using specific cocktail primer the main prevalent biovar all over Egypt. RVs diversify and evolve mainly through two mechanisms. Point mutations generate genetic lineage and lead to the emergence of antibody escape mutants. Genetic shift results in exchange of genetic material through gene re-assortment and occurs during dual infection of a single cell. Also, zoonotic transmission and gene re-assortment between human and animal RV contribute to the generation of diversity of RVs infecting humans. Development of sensitive methods to detect rotaviruses in foals, enabling surveillance of the genotypes present in various horse, bovine and human populations were found. However, there has been limited epidemiological investigation into the significance of these circulating genotypes, their correlation with disease and the use of vaccination in these animal populations.

Biography

G S Gamil Zeedan obtained PhD in Virology, from Cairo University, Egypt, MVSCs Virology, Cairo University, BVSCs, Cairo University. Currently he is Researcher at National Research Center (NRC), Cairo, Egypt. From 2010-2013, he was Assistant Professor in the Department of Microbiology and Virology at Collage of Medicine and Applied Medical sciences, Northern Border University(NBU) Saudi Arabia in teaching the following courses Medical Microbiology and Virology, Diagnostic Microbiology, Clinical Rotation of Microbiology and Clinical Rotation Immunology & Virology. Title of supervised projects: Development of a Therapeutic Vaccine against Hepatitis B Virus - Incidence of hepatitis A, B, C, D and E in Saudi Arabia -The laboratory diagnosis of hepatitis B virus-Human immunodeficiency virus (HIV) infection testing technologies & strategies -Hepatitis C virus virological studies and diagnosis of liver diseases. His research focuses on the molecular epidemiology of animals and human diseases, immune and inflammatory responses.

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