

Role of Molecular Epidemiology in Infectious Disease Surveillance

Abstract

Molecular epidemiology is progressively a vast area of research and now molecular biology techniques have become increasingly integrated into the practice of infectious disease epidemiology. By definition molecular epidemiology is molecular strain-typing or we can say fingerprinting techniques regardless any epidemiologic application. Molecular is basically the use of the techniques of molecular biology and the epidemiology is the study of the distribution and determinants of disease occurrence in human populations. The benefits and challenges of applying these techniques to disease and their affected host is the core which gets served by molecular epidemiologist.

Keywords: Amplification techniques; Automation; Infectious diseases; Molecular methods

Case Report

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Introduction

The science of epidemiology helps in understanding the distribution of diseases in populations. And molecular epidemiology provides new opportunities for epidemiologist for disease prevention and treatment in a better way and technological progress has continued to spark enthusiasm about future prospects. Traditional typing systems based on phenotypes, such as serotype, biotype, phage-type, or antibiogram, have been used for many years. However, more recent methods that examine the relatedness of isolates at a molecular level have revolutionized our ability to differentiate among very close bacterial strains [1]. Epidemiologic methods with modern molecular methods are now integrated into the practice of medicine for applications, such as surveillance of disease, investigating outbreaks and for finding modes of transmission including risk factors by means of Collection, analysis and interpretation of data. In addition typing methods for discriminating different bacterial isolates of the same species are essential epidemiological tools in infection prevention and control [2,3].

Bring together genome and epidemiology

Most genetic and molecular epidemiology studies collect little information on environmental exposures and few address even simple analyses where both genetic variables and environmental exposures are considerable. It makes sense that disease risk is shaped by the interplay of both genetic and environmental factors. Genetic and molecular studies should aim to incorporate more measurements on non-genetic exposures [2].

Pathogen detection, pathogen discovery, and genomic profiling

As mechanisms of microbial pathogenicity, acquisition of virulence, and drug resistance are revealed, pathogen detection, strain identification, and pathogen discovery assume increasing importance in the practice of clinical infectious diseases. It is already

apparent that studies of microbial pathogenicity at the molecular level have made substantial contributions to our understanding of the epidemiology, clinical manifestations, diagnosis, treatment, and immunoprophylaxis of infectious diseases. Infectious disease epidemiology hinges on a clear definition of the clinical problem under study and, moreover, precise identification of the etiologic agent [3-6]. Molecular techniques provide for the sensitive and specific detection of putative pathogens and supply a means for establishing relationships among multiple isolates of the same species. As a result, seemingly unrelated cases occurring during an outbreak have been connected; similarly, geographically or temporally distinct outbreaks have been linked to the same pathogenic clone.

Molecular techniques have been used in other epidemiologic investigations to study transmission mechanisms and the role of avirulent microbial variants in the spread of disease [3-7]. Molecular strain typing data some- times provide the only clue that a group of cases are related, that is, that an outbreak of disease has occurred. Morphologic and metabolic features often fail to indicate the important genetic diversity found within strains. Nucleic acid amplification techniques have had a far-reaching impact on study of microbial pathogenesis and the diagnosis of infectious diseases.

Molecular epidemiology infectious diseases

For Measles, meningitis, dengue, and other viral infection molecular epidemiology are used to be significance. The findings from genetic fingerprinting help classify a case as endemic or imported which is valuable information not only for the purposes of surveillance but for case management as well. When virus genotype of laboratory-confirmed cases is known, the case can be classified as endemic or imported depending on whether the genotype detected belongs to the endemic genotypes or not [8,9].

By using molecular techniques, such as the polymerase chain reaction (PCR), detection and typing of the infectious agent can

be achieved in less than 2 hours, significantly improving case confirmation and disease surveillance [8].

Consequently, the molecular methods used for diagnosis do not have to be characterized by the same high sensitivity that is required for the methods used for asymptomatic individual screening [9]. PCR, reverse transcription PCR (RT-PCR), real-time RT-PCR and nucleic acid amplification tests (NAT) are some of the molecular methods used for identification of viruses, depending on the requirements. Circulation of the virus in a given area usually precedes the onset of an outbreak by a year or more, and the detection of a specific viral strain in space and time helps the instigation of an efficient infection surveillance system [5].

Seroepidemiologic surveillance of dengue is performed mainly by the detection of specific IgM antibodies, while the detection of circulating serotypes is done traditionally by viral isolation and identification. But now reverse transcriptase-polymerase chain reaction assays have been used for the Identification of serotypes in supernatants of infected cells and in clinical specimens [6].

Future prospects

Today, the human population globally faces continuous threat with respect to emergence and reemergence of infectious diseases. Molecular data today are widely used in epidemiological studies to evaluate the transmission dynamics, to characterize the biology and diversity of the pathogens. And these can be dealt with accurate surveillance, evolving newer control and preventive strategies to contain the global spread of infectious microorganisms. Molecular epidemiology of population studies gives better prospective to all the clinicians and researchers.

Conclusion

Without doubt, molecular epidemiology not only improves our understanding of disease pathogenesis by providing

clues regarding specific mechanisms, molecules and genes that influence the risk of developing a disease but also assists epidemiological disease surveillance by providing reliable data with high sensitivity and specificity. Additionally, with the results of molecular techniques it is possible to identify the origin of a disease, the route of transmission or spread, and to assess the effectiveness of preventive measures.

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