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Modern Methods of Microorganisms in Molecular Epidemiology

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DESCRIPTION

Incorporating molecular biology with epidemiological research led to the development of the field is Molecular Epidemiology (ME). The authors try to discuss the methods used by Molecular Epidemiology research to identify the origins and pathogenesis of infectious diseases as well as the sources, reservoirs, circulation patterns, transmission orders, and probabilities of transmission of various infectious agents. In order to identify the aetiology of disease and facilitate intervention, the field of medicine known as molecular epidemiology combines modern laboratory techniques with epidemiology. It is increasingly being used to explain interactions between genetic, environmental, and other factors as well as to pinpoint vulnerable communities and individuals. This course will explore theoretical and methodological challenges in molecular epidemiology, including the use of biomarkers to investigate disease causation, risk assessment, and prevention.

The traditional methods for distinguishing strains serotyping, bio-typing, identifying patterns of antibiotic sensitivity, and bacteriophage typing rely on phenotypic variations. The ability of bacteria to change the expression of the trait being evaluated in unpredictable ways limits the effectiveness of such systems. As a result, the phenotypes of different isolates of the same strain can differ. Bacitracin and bacteriophage typing phage typing has been the backbone of strain discrimination across bacterial species, such as *Salmonella* species, for which a number of lytic bacteriophages (i.e., viruses capable of infecting and lysing bacterial cells) have been found. By assessing an isolate's susceptibility to or resistance to lytic each bacteriophage on a panel, a method is used to classify the isolate. Phage typing is only available in reference laboratories since it is necessary to keep stocks of physiologically active phage's and control strains.

In the study of infectious diseases, the field of molecular epidemiology has become a well-established central issue. In this field, patterns of disease transmission are monitored using specific markers that identify various populations of the disease-causing agent.

Knowledge gained from such an approach enhances comprehension of viral emergence and spread and prevent disease. The creation and implementation of more complex and sensitive viral typing techniques have been made possible over the past few decades by a number of technological advancements, particularly in the tools used for genomic characterization of viruses. This chapter will summarize the knowledge gained by applying such methods to rabies and the rabies-related viruses that constitute the *Lyssavirus* genus.

Immunoblotting and electrophoretic protein characterization. Number of techniques can be used to identify variations in the structure of bacterial proteins. By isolating whole cell or cell surface proteins, separating them using SDS-PAGE, and staining the gel to reveal the resultant pattern, electrophoretic protein typing is carried out. As an alternative, the proteins can be radiolabeled while being isolated, and the pattern can be found autoradiography. Transferring the separated bacterial products to a nitrocellulose membrane is the first step in the immunoblotting procedure. Then, antisera to particular strains of the bacteria or pooled human sera as a source of broadly reactive antibodies are used to detect the bacteria.

Since mycobacteria only have one ribosomal operon, ribo typing can only reliably identify one or two bands in these organisms, which limits its applicability. The capacity of the approach is constrained in general, ribotypes are a highly stable trait within a species and occasionally exhibit the same pattern in isolates from epidemiologically distant populations.