Worldwide tracking of Neisseria meningitidis

Neisseria meningitidis is an exclusively human bacterium. Its natural habitat is the nasopharynx. Asymptomatic carriage is frequent and affects about 10% of general population. Transmission occurs through airborne salivary droplets during direct person-to-person close contact. N. meningitidis is responsible for invasive infections that occur as endemic or epidemic cases.

The development of powerful techniques for isolate characterization has improved our understanding of meningococcal epidemiology.[1] Serological typing methods were first employed to determine the antigenic formulas of isolates (serogroup:serotype:serosubtype:immunotype), which are defined by the immune specificities of the capsule, the outer membrane protein PorB, the outer membrane protein PorA, and the lipo-oligosaccharide, respectively. Five of these serogroups (A, B, C, Y, and W135) are most frequently isolated in invasive infections.

N. meningitidis is highly variable and microevolution occurs through horizontal DNA exchange between strains. Genes are randomly associated on the bacterial chromosome.[2] Capsule, PorA, PorB, and LOS are under a strong selective pressure by the host immune response. Variations of these structures reflect adaptation of Nm to its host rather than genetic relatedness between strains. Serological typing is no more adequate for tracking meningococcal strains.

Molecular characterization is now required for tracking microevolution of meningococcal strains and for analyzing the emergence of new clones. Molecular typing methods are usually based on analysis of the polymorphism of meningococcal genes.

In this issue, data described 17 cases on confirmed or probable cases of invasive meningococcal disease from Malaysia during the period 1987–2004. It is unclear how comprehensive the data are. However, this information is interesting as rare data are available from Malaysia. Five cases were owing to N. meningitidis serogroup W135. Only two cases were linked to the Hajj. A clonal outbreak of W135 meningococcal disease has occurred in the year 2000 among pilgrims returning from Saudi Arabia and their contacts.[3] The isolates belonged to the genotype ST-11/ET-37. The presence of such isolates was subsequently reported worldwide.[4] However, these isolates showed continuous diversification.[5] The presence of several local ST-11/ET-37 isolates has been reported since 1970. (Two isolates from Malaysia were isolated before 2000) incomplete sentence. Multifocal emergence of W135 ST-11/ET-37 may be suspected rather than a clonal spread of one particular clone of the ST-11/ET-37 genotype.[6] Therefore, complete characterization of invasive meningococcal isolates from Malaysia is needed, as well as the comparison of these isolates to the Hajj 2000 strain and to other W135 strains.

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References