

Molecular Epidemiology of Circulating Adenovirus Types in Acute Conjunctivitis Cases in Chandigarh, North India

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Abstract : Introduction: Human adenovirus is the most common agent involved in viral conjunctivitis. The clinical manifestations vary with different serotypes. The identification of the circulating strains followed by phylogenetic analysis can be helpful in understanding the origin and transmission of the disease. The present study aimed to carry out molecular epidemiology of the adenovirus types in the patients with conjunctivitis presenting to the eye centre of a tertiary care hospital in North India. Materials and Methods: The conjunctival swabs were collected from 23 suspected adenoviral conjunctivitis patients between April-August, 2014 and transported in viral transport media. The samples were subjected to nested PCR targeting hexon gene of human adenovirus. The band size of 956bp was eluted and 8 representative positive samples were subjected to sequencing. The sequences were analyzed by using CLUSTALX2.1 and MEGA 5.1 software. Results: The male: female ratio was found to be 3.6:1. The mean age of presenting patients was 43.95 years (+17.2). Approximately 52.1% (12/23) of patients presented with bilateral involvement while 47.8% (11/23) with unilateral involvement of the eye. Human adenovirus DNA could be detected in 65.2% (15/23) of the patients. The phylogenetic analysis revealed presence of serotype 8 in 7 patients and serotype 4 in one patient. The serotype 8 sequences showed 99-100% identity with Tunisian, Indian and Japanese strains. The adenovirus serotype 4 strains had 100% identity with strains from Tunisia, China and USA. Conclusion: Human adenovirus was found to be an important etiological agent for conjunctivitis in our set up. The phylogenetic analysis showed that the predominant circulating strains in our epidemic keratoconjunctivitis were serotypes 8 and 4.

Keywords : conjunctivitis, human adenovirus, molecular epidemiology, phylogenetics

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