

Abstract

Human respiratory syncytial virus (HRSV) is the major cause of acute lower respiratory infection in infancy, causing annual epidemics together with repeated infections of individuals. Severe HRSV pneumonia was also found in immuno-compromised hosts with neoplastic disease or bone marrow transplantation patients. HRSV infection is also a very common and important disease in Taiwan. Various antigenic types and genotypes of HRSV have been reported in other countries. There is no clear data showed the antigenic and genotypes of HRSV circulated in Taiwan. In order to understanding the strain variations of HRSV in Taiwan, virus strains isolated in 2004 were collected for analysis. The subgrouping and antigenic typing of HRSV are determined by immunofluorescence stain with monoclonal antibodies. The N and G gene typing are identified by RT-PCR and partial nucleotide sequencing. The results showed that 65% (13/20) of HRSV isolated in 2004 was belonged as subgroup A and 35% (7/20) of isolates were grouped as subgroup B. Based on antigenic analysis, 92.3% of subgroup A was further identified as A3 and 7.7% was as A5. In subgroup B, six of 7 strains (85.7%) was identified as B3 and only one strain was as B1 (14.3%). By N gene typing, NP2 (45.5%), NP3 (18.1%) and NP4 (36.4%) was identified in subgroup A, whereas all 7 strains of subgroup B was NP3 (100%). Two clusters of subgroup A was found by phylogenetic analysis. The results can provide pictures of molecular epidemiology of HRSV in Taiwan.

Keywords : Respiratory syncytial virus ; antigenic type ; genotype ; molecular epidemiology