

Abstract

Three outbreaks of adenovirus (Ad) respiratory infection were found during Nov. 1999 to Dec. 2001 in southern Taiwan via a surveillance program. To elucidate the serotypes and their molecular epidemiology as well as their association with the clinical features, a total of 526 virus strains were randomly selected from 1064 strains isolated during 1981-2001 and were studied using restriction fragment length polymorphism (RFLP) and Polymerase chain reaction (PCR) -RFLP. The major subgenus found was subgenus B (45.1%), followed by subgenus E (29.3%) and C (25.5%). Ad3 and Ad7 were the major types found during the 1st outbreak from Nov. 1999 to March 2000, while Ad4 was found mainly in the 2nd and 3rd outbreaks in October 2000 and September 2001. Ad7 and Ad4 emerged in 1999 and 2000 and declined in 2001, respectively. Ad3 was constantly isolated during the surveillance, however it declined drastically from more than 36% to only 2% in 2001. Genotype analysis showed that Ad7a was found in 1983, however, only Ad7b was found in 1999-2000. The clinical features of 218 patients were analysed during the 1999-2000 outbreak. About 79% of total cases, their age were less than 7 years old. The ratio of male to female was 2:1. Severe infections, such as pneumonia and acute bronchitis, account for nearly half of the cases (42.6%). The results reveal the reemerging, shifting of serotypes and the clinical association of respiratory adenovirus infections as well as the molecular epidemiology of Ad7 genotypes in southern Taiwan during recent two decades.

Keywords: Adenovirus, Molecular Epidemiology and RFLP