

Abstract

This study was to investigate the changes in human flu viruses in areas where unique animal flu viruses or epidemics were isolated in Taiwan and Kinmen islet. Sentinel physicians obtained throat swabs from patients presenting with flu-like illness and two-steps RT-PCR using 5 sets of primers for matrix(M) and HA2 to detect all the animal influenza viruses and then typing/subtyping for human flu viruses. Questionnaires included travel history, animal contacts, and occupations. One flu B and eight flu A H3N2 isolates were identified in the flu season of 2002-2003, including 1, 2, 2, and 3 H3N2 in Taoyuan, Yilan, Tainan and Kinmen, respectively. Amino acid sequences of HA of human isolates revealed that Pro (P) at position 227 among most of Kinmen isolates (2/3), replaced to Ser (S) in Taiwanese isolates. In addition, one mutant from Gln (Q) to His (H) at position 156 of HA gene for 5 out of 8 H3N2 Taiwan isolates. Phylogenetic analysis demonstrated that all of the H3N2 viruses were human origin (belong to the lineage of A/Fujian/411/02), with 80-90%homology in HA, NA and M gene segments of A/Swine/PingTung/ Taiwan/199.2/02 (H3N2) and 75-77% homology in HA gene segment of A/Wild Bird/Taiwan/243/02(H3) and A/Mallard Duck/Taiwan/3.3/03(H3). Up to now, all those human derived H3N2 isolates obtained from animal epidemic areas, rural pig/avian farms and migrating birds habitats have been still human origin by phylogenetic analysis. In conclusion, residents in Kinmen islet frequently traveling from China need to monitor their flu A viruses that might be different from those obtained in main Taiwan island.

Keywords : Influenza A ; Interspecies transmission ; Virological Surveillance ; Taiwan