Abstract

OBJECTIVE: To assess the risk of aerosol transmission in severe acute respiratory syndrome (SARS) patients admitted to Hospital through testing the air samples.

METHODS: Air samples were collected from 7 wards and 1 balcony of the Hospital, 3 times a day for 3 continuous days, using bioaerosol sampler type FA-2. Bioaerosol particles were then washed down from the samples by serum-free Dulbecco's Modified Eagle Medium (DMEM) culture medium. Nested-reverse transcription-polymerase chain reaction (RT-PCR) was used to amplify the N protein gene of the SARS associated coronavirus (SARS-CoV) from these washing solutions. The residual solutions were inoculated into prepared cell cultures to isolate live virus. The positive samples were then identified by indirect immunofluorescence assay and sequence analysis of the PCR products.

RESULTS: Positive rates of RT-PCR test on air samples were 29.03% in the wards and 20.0% in balcony respectively. Results from sequential analysis showed that the homology of amplified cDNA fragments to previously known SARS-CoV stains was 98%. A strain of live pathogen was isolated from one of the 36 samples. The isolate could cause typical cytopathic effects, similar to those SARS-CoV on Vero-E6 cells and the effects could be stably passed. Indirect immunofluorescence assay showed positive from serum of a SARS patient.

CONCLUSION: SARS-CoV existed in the air hospital, where SARS patients were admitted to, but the activity of SARS-CoV in air samples was rather low. SARS patients could still shed SARS-CoV even during the recovery phase. Potential possibility of aerosol transmission might exist within 1 meter square area around SARS patients.