

Genetic variability of human metapneumovirus isolated from Chilean children, 2003-2004

Escobar, Carola

Luchsinger, Vivian

De Oliveira, Danielle Bruna

Durigon, Edison

Chnaiderman, Jonás

Avendaño, Luis F.

Human metapneumovirus (hMPV) is a significant cause of acute lower respiratory tract infection in all age groups, particularly in children. Two genetic groups and four subgroups of hMPV have been described. They co-circulate during an epidemic in variable proportions. The aims were to characterize the genotypes of hMPV recovered from children hospitalized for acute lower respiratory tract infection and to establish the molecular epidemiology of strains circulating in Santiago of Chile during a 2-year period. The detection of the N gene by reverse-transcription polymerase chain reaction was carried out for screening 545 infants hospitalized for acute lower respiratory tract infection in Santiago during 2003-2004. The genetic typing of hMPV was performed by analyzing the fusion gene sequences. hMPV was detected in 10.2% (56/545 cases). Phylogenetic analysis of F gene sequences from 39 Chilean hMPV strains identified the two groups and four subgroups previously described. Strains cluster