Molecular epidemiology of rubella virus isolated in São Paulo during 1997-2004


Rubella is an acute infectious disease with normally a mild clinical course. However, infections during pregnancy, especially before week 12 of gestation (WG), can cause severe birth defects known as congenital rubella syndrome (CRS). Genetic characterization of wild-type rubella virus is based on sequence analysis of a hypervariable region of the glycoprotein E1 gene.

This study presents the first molecular characterization of isolates from São Paulo, Brazil. Samples (blood, urine, oropharyngeal swab, explanted liver, product of conception and cerebrospinal fluid) were collected between 1997 and 2004 from patients with clinical symptoms of rubella. The rubella virus E1 gene coding region was amplified by reverse transcriptase polymerase chain reaction directly from clinical specimens and isolates and the resulting DNA fragments were sequenced.

Sequences were assigned to genotypes by phylogenetic analysis with rubella virus reference sequences. Twenty-nine isolates were obtained, including isolates from acute liver failure, encephalitis and congenital infections. Phylogenetic analysis showed that 19 out of 29 isolated in the São Paulo strains of rubella virus belonged to genotype 1a and 10 strains to genotype 1G.

This work demonstrated two genotypes of RV circulated simultaneously between years 1997 and 2004 in the state of São Paulo. The information reported in this paper may be useful for contributes to understand better the molecular epidemiology of RV in São Paulo, Brazil.