## IX ENCONTRO DO INSTITUTO ADOLFO LUTZ I SIMPÓSIO INTERNACIONAL DE VIGILÂNCIA E RESPOSTA RÁPIDA

## M-023-22 **RELATIONSHIP BETWEEN ELECTROPHORETIC PROFILES AND VP7-VP4 GENOTYPES OF ROTAVIRUSES DETECTED IN SÃO PAULO STATE, BRAZIL**

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## Resumo

Group-A rotavirus (RV-A) is the one most important agents of acute gastroenteritis in infants and young children. In developing countries, more than 125 million cases of rotavirus infection have been estimated to occur annually. Analysis of mobility of the 11 segments of the rotavirus RNA genome by polyacrylamide gel electrophoresis yields a pattern which is characteristic for each strain and has often been used as an indicator of the diversity rotavirus isolated. The aim of present study was to determine the frequency of rotavirus infection and to characterize their diversity of dsRNA genomic electrophoretic from patients with acute diarrhea in São Paulo state, from January 2011 to May 2012. Stool samples from 1,277 patients were tested by ELISA and polyacrylamide gel electrophoresis (PAGE) for detection of RV-A. A total of 140 (11.0%) stool samples were positive for the presence of RV-A. Of these, 106 (75.7%) were positive by PAGE. Among RV-A strains, infant cases accounted for 51 cases (36.4%), children aged 1-5 years for 80 cases (57.1%), 6-15 years, for 5 cases (3.6%), and 3 cases (2.1%) for =15 years. Based on migration pattern of RNA segments (10 and 11) of RV-A visualized (n=93), two distinct groups of electrophoretypes were identified: 83 long profile strains (89.2%) and 11 short profile strains (11.8%). Rotaviruses with a long profile were correlated with G3P[8], G9P[8], G12P[8], G3P[3], and G12P[9] genotypes; whereas short profile rotaviruses were correlated with G2P[4], G3P[6] and G12P[6] types. The long profiles showed a high incidence during the studied period. Recent studies have demonstrated a reduction rate of rotavirus among population. In addition, there is a need for further detailed analysis of the migration patterns of the 11 RNA segments of RVA, which would have important contributions to the knowledge of the epidemiology of rotaviruses and evaluation of vaccine programs.