Background
Group A rotavirus is the leading cause of acute gastroenteritis in children. Serotypes G1, G2, G3 and G4 are mainly responsible for human infections. Strain characterization and serotype distribution of rotavirus in a country is an important determinant of future vaccine strategy. Information in this regard is scarce in Sri Lanka.

Objectives
To determine the prevalence, severity and molecular epidemiology of rotavirus diarrhoea among children hospitalized with diarrhoea in Sri Lanka.

Design, setting and method
A prospective hospital-based study was conducted in the paediatric units of the North Colombo Teaching Hospital from April 2005-February 2006. Stool samples of children admitted with diarrhoea were analyzed for Group A rotavirus antigen by enzyme linked immunosorbent assay (ELISA) (Rotaclone). Samples positive for rotavirus were characterized electropherotyping (PAGE) and serotyping (reverse transcription-polymerase chain reaction (RT-PCR)) respectively. Severity of diarrhoea was assessed by the Vesikari severity score.

Results
A total of 341 children [204 males mean age 25.7 months (range 1-144)] were studied. Sixty seven (19.6%) had rotavirus diarrhoea. RT-PCR and PAGE were done on 58 rotavirus positive samples. Thirty one were PAGE positive with 6 different electropherotypes. RT-PCR revealed the presence of serotypes G1, G2, G3, G4 and G9 in 7 (12.1%), 16 (27.6%), 2 (3.4%), 2 (3.4%), and 11 (19.0%) samples respectively. Twenty (34.5%) were untypable. Severity score, assessed in 326 patients, revealed a mean score of 13.3 and 11.4 in rotavirus positive and negative patients respectively (p=0.05). Presence frequency and duration of vomiting and duration of diarrhoea were significantly higher in rotavirus diarrhoea (p<0.05).

Conclusions
• Rotavirus is an important agent of severe paediatric diarrhoea in Sri Lanka.
• Molecular analysis indicates genetic diversity among group A rotavirus in Sri Lanka.
• This study reports for the first time of G9 type rotavirus infection in Sri Lanka.