

Group A rotavirus infection in Tunisia: comparison between children and adults molecular epidemiology

Fodha Imene, Bennour Haifa, Bouazizi Asma, Jerbi Amira, Lakhel Samia, Ben Hadj Fredj Mouna, Ben Hamida-Rebai Meriem, Boujaafar Noureddine, Trabelsi Abdelhalim
LR14SP02, Laboratory of Microbiology, Sahloul University Hospital, Sousse, Tunisia

Background

Group A Rotaviruses (RVA) are the most important etiologic agents of acute gastroenteritis in infants worldwide. Due to immunity acquired in childhood, most adults are not susceptible to RVA, however they can become infected by exposure to children with RVA gastroenteritis. The aim of the present study was to compare the epidemiology of RVA infections in Tunisia between adults and children.

Methods

Stool specimens were collected from young children (under five years of age), older children (5–15 years) and adults (≥ 15 years) hospitalized or consulting for gastroenteritis in Tunisia between 2015 and 2017. All samples were screened by reverse transcription-polymerase chain reaction (RT-PCR) for the detection of VP6 gene specific of RVA. RVA-positive samples were further analyzed for VP7/VP4-genotyping by semi-nested multiplex RT-PCR.

Results

The total number of samples screened for RVA was 1371, with 454 (33.1%) stools collected from young children, 316 (23.0%) from older children and 601 (43.9%) from adults. Specimens were positive for RVA in 15.9%, 6.3% and 12.1% of cases among young children, older children and adults, respectively. A statistically significant male predominance among RVA infected patients was observed in all age groups ($p < 0.05$). RVA disease most commonly occurred during the coolest season among young children, whereas it was detected continuously throughout the entire period of study for older patients. Concerning G/P genotypes of circulating strains, seven different G/P combinations were found to co-circulate in young children: G1P[8] widely predominated (41.7%), followed by G9P[8] (32.8%), G2P[4] (7.5%), G12P[8] (7.5%), G1P[6] (3.0%), G2P[8] (1.5%) and G3P[8] (1.5%). Surprisingly, in patients older than 5 years, the most frequent genotype was G9P[8] (51.9%) followed by G2P[4] (13.9%), with G1P[8] strains detected only in third position (12.6%).

Conclusion

Adults are a significant source of RVA transmission to infants, highlighting the importance of monitoring the epidemiology of these viruses in this particular population.