

Postvaccination rotavirus surveillance in Hungary, 2007-2011

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Vaccination is the main strategy to control severe dehydrating gastroenteritis caused by rotaviruses in early childhood. The introduction of new generation rotavirus vaccines, Rotarix[®] and RotaTeq[®], has resulted in an intensification of strain surveillance worldwide to monitor strain prevalence across countries. An international strain surveillance network (EuroRotaNet) was launched in 2007 in Europe with the participation of Hungary. In the present study, the geographical and temporal distribution of human rotavirus G and P types and the impact of vaccine use on strain prevalence and diversity in Hungary is reported.

Rotavirus positive stool samples were collected from patients, mostly children <5 years of age with gastroenteritis in 8 geographic areas of Hungary between 2007-2011. Viral RNA was amplified by multiplex genotyping RT-PCR assay, targeting the medically most important G and P types. Sequencing of the VP4 and VP7 genes was performed to monitor the genetic relatedness of rotavirus strains.

In total, 2380 strains were genotyped. During the five-year surveillance 17 different antigen combinations were identified with the dominating prevalence of genotype G1P[8] (44,9%) strains, followed by G4P[8] (23,4%), G2P[4] (14,8%) and G9P[8] (6,8%). The prevalence of common G3P[8] strain remained below 1% in our country. Additional rare genotypes were identified in a low percentage of samples (4.12%): G1P[4], G1P[6], G2P[6], G2P[8], G3P[4], G3P[9], G4P[6], G6P[9], G9P[4], G9P[6], G12P[6] és G12P[8]. The prevalence of common strains fluctuated both in the consecutive years and between geographical regions in the same rotavirus season. Sequence and phylogenetic analyses revealed evidence for the imported G9P[6] strains from India and some primer mistyping in our PCR assay (G6 and G12 strains). The sequence determination and comparison of VP4 and VP7 genes of selected field strains and vaccine strains did not prove direct genetic relatedness between them. However, G1 and P[8] types closely related but not identical with Rotarix[®] parental strain were determined, their vaccine origin was unlikely. Rotarix[®] was purchased more often, but the nationwide vaccine coverage among infants remained low (~ 18%).

Our data indicates that the antigen specificities of medically important rotavirus strains identified in our country are represented in the vaccines available in the pharmaceutical private market in Hungary. The intensification of vaccine use in the forthcoming years may help to decrease the socio-economic burden of rotavirus infections.

Kulcsszavak: rotavírus, vakcináció, surveillance, EuroRotaNet

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