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Special issue on ‘Genetic diversity and evolution of rotavirus strains: Possible impact of global immunization programs’

Krisztián Bányai,

Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary

Jon Gentsch

Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Epidemiological surveillance of rotavirus strains dates back to mid-1980s with the initial objective to describe the globally common rotavirus serotypes that could have an impact on vaccine development. With over 100,000 genotyped human rotavirus strains in the pre vaccine era worldwide and with the availability of two vaccines, the monovalent Rotarix and the pentavalent RotaTeq, the objectives of strain surveillance have changed. We have learned much about human rotavirus strain diversity and the evolutionary forces driving strain variation in nature. However questions on how rotavirus strains under vaccine induced immune pressure evolve and what the impact of vaccine use on strain prevalence in vaccinated populations is, remain open.

In the 1980s rotavirus typing protocols included monoclonal antibody based enzyme immunoassays, which were available to relatively few laboratories due to limited reagent resources. In addition, the antibodies mainly identified only four common G types. The introduction of nucleic acid based techniques (primarily multiplex RT-PCR assays) enhanced our ability to genotype both neutralizing antigen genes and advances in sequencing technology paved the way for more detailed analysis of circulating rotavirus strains. More recently, whole genome sequencing has become an alternative tool for researchers to describe the molecular epidemiology of rotaviruses. Access to high throughput sequencing technology has made molecular strain characterization an increasingly routine laboratory method without the need of cumbersome and costly pre-analytic steps, such as cloning and/or designing dozens of PCR and sequencing primers. We believe that as these technical advances mature the ultimate goals of routine surveillance in the post rotavirus vaccine era will become a reality. Strain characterization using improved methods not only allows the classification of strains into their antigenic types, but also permits whole genome based comparisons, determination of preferred genotype constellations, identification of vaccine strain derived genes in field strains, and tracking the evolution of vaccine strains.

The objectives of the special issue on rotavirus diversity have been to serve as a forum to disseminate up-to-date information about the changing epidemiology of rotaviruses. Two reviews aimed at summarizing global prevalence of rotaviruses and strain specific vaccine effectiveness (Dóro et al., 2014a; Velasquez et al., 2014). Another 17 original papers

published from low-to-high vaccine coverage countries representing each continent provide details about the epidemiology and evolution of locally circulating strains (Banga-Mingo et al., 2014; Boula et al., 2014; De Grazia et al., 2014; Donato et al., 2014a,b; Dóro et al., 2014b; Fujii et al., 2014; Gómez et al., 2014a,b,c; Ndze et al., 2014; Roy et al., 2014; Semeiko et al., 2014; Steyer et al., 2014; Tam et al., 2014; Than et al., 2014; Wu et al., 2014). With over 300 new rotavirus genomes this volume is a significant contribution to the field and doubles the available human rotavirus genome sequence data.

The guest editors are very grateful to the authors for making their valuable contributions and wholeheartedly hope that this special issue will be useful for our colleagues, students, the general reader as well as the policy makers.

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