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Whole genomic analysis of rotaviruses

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Rotavirus-A (RVA) are a major cause of viral diarrhea in humans, animals and birds. The RVA genome consists of 11 segments of double-stranded RNA that encode 6 structural and 6 non-structural proteins. The mechanisms of genetic diversity of RVAs include re-assortment, point mutations and rearrangement events. Whole genomic analyses of RVA strains from different host species are essential to obtain conclusive data on the complex evolutionary patterns, interspecies transmission/zoonosis, and reassortment events of rotaviruses. In 2008, the whole genome-based RVA genotyping scheme was introduced, providing researchers with a uniform platform to study the overall genetic diversity of RVAs. Since then, we have performed whole genome sequencing on several RVAs detected in humans, cattle, pigs and horses, including archival and reference strains. Analyses of these RVA whole genome sequences provided a plethora of conclusive, crucial, and/or new data on (i) emergence of novel RVA genotypes, (ii) zoonosis including the first conclusive evidence for transmission of RVAs from wildlife (simian) to humans, (iii) interspecies transmission of RVAs between farm animals, (iv) re-assortment events involving RVAs from different host species including those between human and animal RVA strains, and (v) rare inter-geno group re-assortment events. Taken together, our findings provided vital insights into the complex geno dynamics and interspecies transmission of RVAs, with implications on public health.

Biography

Souvik Ghosh is an Assistant Professor and DVM course Director of Virology at the Ross University School of Veterinary Medicine, West Indies. He holds degrees of Bachelor of Veterinary Science, Master's in Veterinary Medicine & Public Health and PhD (Virology). He is a well-known expert on rotaviruses, a major cause of diarrhea worldwide. He has published more than 60 research papers and reviews in peer reviewed international journals. He serves as the section editor of *Archives of Medical Science and Austin Journal of Virology and Retrovirology,* and acts as reviewer to more than 15 international virology/microbiology journals.

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