ABSTRACT

Rotavirus Group A (RVA) is the most important cause of severe dehydrating acute gastroenteritis (AGE) in young children. Up to 128, 500 deaths of children < 5-year-old were attributed to RVA infection in 2016 worldwide. Despite the introduction of the RVA vaccination in many countries, RVA continues to be a major cause of child hospitalization due to a variety of factors including imperfect protection from host immune responses and existing RVA genetic and antigenic diversity. Several RVA genotypes occur in nature that infects humans, some common others uncommon depending on geographic region and season e.g. as exemplified by G9P[8] and G8P[4] fluctuating prevalence patterns in recent coastal Kenya studies. The transmission patterns, genetic relatedness and full genotype constellation of these genotypes (G8P[4] and G9P[8]) detected in the pre-post vaccine era in coastal Kenya remains unknown. Such inferences will give insights on the genomic epidemiology of these RVA genotypes, important for continued optimization and, design of future optimal control strategies. Sequence data is available for all genes (11 segments) from samples positive for RVA, G8P[4] (n=47) and G9P[8] (n=14) collected at Kilifi County Hospital (KCH) from January 2010 to December 2019. The sequence data is yet to be analysed to investigate full genotype constellation, transmission and evolutionary patterns, genetic relatedness and, potential sources of introductions. Phylogenetic analyses will be conducted to investigate the genetic diversity of RVA genotypes G8P[4] and G9P[8]. Intra and inter-seasonal diversity of genotypes G8P[4] and G9P[8] will also be investigated. Phylogenetic analysis will be carried out to investigate the global phylogenetic context of the Kilifi G8P[4] and G9P[8] strains using state-of-the-art phylogenetic and bioinformatic approaches to provide insights into their genomic epidemiology and evolution pre-post introduction of rotavirus vaccination in Kenya.