

Detection of porcine-like G4P[6] and human-porcine multiple-reassortant G4P[8] rotavirus strains in Ghanaian children: evidence for interspecies transmission and reassortment

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Background

Group A rotavirus (RVA) is a leading cause of acute gastroenteritis in infants and young children worldwide. RVA is generally considered a species-specific pathogen with few reports of interspecies transmission. Rotavirus G4P[6] strains, though detected sporadically in humans, are highly prevalent in pigs in Asia and Europe. In contrast, rotavirus G4P[8] strains are globally common in humans.

Methods

As part of rotavirus surveillance post-vaccine introduction in Ghana, stool samples were collected from diarrhoeic children < 5 years old reporting at selected health facilities, and screened for rotavirus. Total nucleic acid extracts of two rotavirus EIA-positive samples displaying long electropherotypes, and bearing G4P[6] and G4P[8] specificities (Northern Ghana, 2015 and Southern Ghana, 2013 respectively), were subjected to whole genome sequence characterization by Illumina MiSeq Next Generation Sequencing. Identified de novo assembled RVA genes were genotyped using the Viral Pathogen Database and Analysis Resource (ViPR). Phylogenetic analyses of the 11 gene segments was carried out using MEGA v7.026.

Results

The G4P[6] strain possessed a typical porcine genotype constellation G4-P[6]-I1-R1C1-M1-A8-N1-T7-E1-H1. On the contrary, the G4P[8] strain displayed a typical Wa-like genotype constellation G4-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1. Phylogenetic analyses confirmed the porcine origin of all 11 genes for the G4P[6] strain, indicative of interspecies transmission. However, the G4P[8] strain was a multiple human-porcine interspecies reassortant, with the VP1, VP2, VP7, NSP1, NSP2 and NSP3 genes confirmed to be of porcine-origin. Interestingly, the genes of porcine origin in both strains appeared to be distantly related, suggesting the existence of variants.

Conclusion

The existence of these porcine-like RVA variants ultimately contributes to the wide diversity of rotavirus strains. This may have implications for long-term rotavirus vaccine efficacy in Ghana.