

G3P[8] rotavirus strain causing diarrheal outbreak in the Kingdom of Eswatini, 2018

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Background

A large outbreak of diarrhoeal disease in children less than 5 years was reported in four surveillance sentinel sites Mbabane Government Hospital, Raleigh Fitkin Memorial Hospital, Hlathikhulu Government Hospital and Good Shepherd Hospital. Rapid increase of number diarrhoeal cases, were reported from week 34 to 41 (August to October 2018). Approximately 1,535 children presented with acute diarrhea, vomiting and dehydration.

Method

Diarrhoeal stool samples were collected from children less than 5 years of age and tested for rotavirus using enzyme immunoassay kit. A total of (n=139) were shipped to the Regional Reference Laboratory-South Africa (RRL-SA) for rotavirus detection and molecular characterization using polyacrylamide gel electrophoresis, semi nested reverse-transcription polymerase chain reaction, sequencing and phylogenetic analysis. In addition, quality control was performed to assess capacity of National Laboratories for rotavirus testing method using enzyme immunoassay kit. Negative diarrheal samples were further tested for bacteria and parasites using molecular diagnostic assays.

Results

The rotavirus positive samples were positive for group A rotavirus, by PAGE long RNA migration pattern were observed during the outbreak. The G3P[8] 59/75(78.6%) rotavirus strain were mainly associated with the outbreak. Phylogenetic analysis of the partial length VP4 P[8] associated G3 clustered together with other P[8] strains detected in Africa and distantly related to vaccine strains (Rotarix™ and RotaTeq™). Pathogens that were observed in Eswatini were *Shigella/Enteroinvasive E Coli* 18% (11/61) was frequently detected followed by *Campylobacter jejuni/coli* 13% (8/61) and *Giardia lamblia* 13% (8/61).

Conclusion

Rotavirus G3P[8] was the major cause of these outbreak. It also important to note that the G3P[8] that was circulating was the wild type stains not related to the vaccine strains. As evident from the Maximum likelihood phylogenetic tree generated, G3P[8] study strains clustered in different lineages as compared to the vaccine strains (Rotarix™ and RotaTeq™). Further studies on whole genome sequence analysis are required to determine the evolutionary relationship among the strains.