

# **Rotavirus strains detected in Dr George Mukhari academic hospital and Oukasi primary healthcare, Pretoria from 2015-2016**

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## **Introduction**

South Africa became the first African country to introduce Rotarix™ rotavirus vaccine. Since the introduction, rotavirus mortality and morbidity has reduced. Rotavirus strain surveillance remains essential to monitor the impact of vaccine on the circulating strains. The aim of this study was to detect and phylogenetically analyse rotavirus strains.

## **Material and Methods**

This was a cross-sectional study comprising of 246 diarrhoeal stool samples collected in OPHC and DGMAH (2015-2016). Stool samples were tested for RVA using ProSpecT™ EIA. RNA was extracted using QIAmp® Viral RNA kit and VP4 and VP7 genes were subjected to multiplex genotyping PCR targeting common strains. Phylogenetic trees were constructed in MEGA v7 and BEAST v1.8.4. VP7 major antigenic regions A-C & F were mapped.

## **Results**

16.2% of the diarrhoeal samples were positive for RVA and the detected genotypes were: G1P[8], G2P[4], G8P[4], G9P[8], G9P[6], G3P[4], G3P[X] and GXP[8]. An uncommon G3P[4] rotavirus combination was detected, it has not been detected before in South Africa. G9P[8] strains formed a cluster unrelated to any known G9 lineages (confirmed with Bayesian analysis). Compared to GenBank sequences they shared 98-99% aa similarity with strains isolated from sewage water and <95% aa similarity with strains belonging to G9 lineages. Mutation Y144H was observed only in the studied G9P[8] strains.

## **Discussion and Conclusion**

During 2015-2016 G9P[8] and G3P[4] were the dominant strains. The detection of G9P[8] harbouring unique Y144H might be maintaining the spread and continued circulation of G9P[8] as a new lineage in this population. Their relation to strains isolated in sewage water emphasises the risk of rotavirus-contaminated water and need for improved sanitation. The detection of uncommon G3P[4] might have been as a result of genetic exchange with previously circulating G2P[4] in the same population. The findings provides more evidence for evolution of rotavirus. Whole genome analysis is necessary for the detected uncommon G3P[4] and G9P[8] to understand the mechanism of evolution.