

Histo-blood group antigen-expressing bacteria do not play a Role in the Infection and Replication of oral Rotavirus Vaccine in a Cohort of African infants

Ndivho P. Ndwamato¹, Mapaseka L. Seheri¹, Cliff A. Magwira¹

¹Diarrhoeal Pathogens Research Unit (DPRU), Department of Virology, Sefako Makgatho Health Science University, Pretoria, South Africa.

Background and Objectives: Rotaviruses initiate infection by first attaching themselves to the host's target intestinal epithelial cells, where they undergo a replication cycle. The attachment is said to be facilitated by histo-blood group antigens (HBGA) that are expressed by the host's mucosa surfaces in a genotype-dependent manner. This study investigated if possessing a higher abundance of HBGA-expressing bacteria was a risk factor for oral rotavirus vaccine infection.

Methods: Stool samples, collected from infants attending a routine rotavirus vaccination program at Oukasi Healthcare Clinic, Brits, north of Pretoria, were divided into vaccine shedders (n=47) and non-shedders (n=33). Quantitative real-time PCR (qPCR) was used to determine the abundance of selected HBGA-expressing bacteria namely *Enterobacter cloacae* and *Ruminococcus gauvreauii* and the expression levels (viability) of both DnaJ (for *E. cloacae*) and RC16S rRNA (*R. gauvreauii*) genes between the two study groups. Logistic regression was used to evaluate the association between the abundance of selected bacteria and vaccine-shedding status.

Results: There was no significant difference in the abundance of both *E. cloacae* and *R. gauvreauii* between shedders and non-shedders ($p = 0.98$ and 0.93 , respectively). The average expression of DnaJ (number of viable *E. cloacae*) increased 5.73-fold in vaccine shedders ($2^{(-\Delta Ct)} = 0.6365$) compared to non-shedder ($2^{(-\Delta Ct)} = 0.1516$). There was no significant difference in the expression of the 16S rDNA gene between RV vaccine non-shedders (mean of $2^{(-\Delta Ct)} = 1.2121$) versus vaccine shedders (mean of $2^{(-\Delta Ct)} = 1.6738$). Although the abundance of viable *E. cloacae* was higher in shedders, logistic regression analysis indicated no significant association with vaccine virus shedding (OR = 0.317, 95% CI = 0.0786 – 1.280), $p = 0.71$.

Conclusion: This study found no significant association between the abundance of the selected HBGA-expressing bacteria and RV vaccine shedding status, suggesting that these bacteria may not play a role in the infection and replication of the vaccine virus. Follow up studies using 16S rRNA sequencing targeting all HBGA-expressing bacteria are warranted to validate the findings.