Investigation of secretor status and rotavirus VP4 genotypes in cases of diarrhoea in South African children

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Background
Secretor status can affect host-genetic susceptibility to enteric infections, and influences strain-specific susceptibility to norovirus. Proportions of non-secretors are higher in African populations, and this could explain increased P[6] rotavirus strain circulation in Africa. The study evaluated secretor status in children <5 years of age hospitalized with rotavirus diarrhoea.

Methods
A subset of 500 children from the South African Rotavirus Sentinel Surveillance Program (2009 – 2017) were randomly selected for analysis; rotavirus EIA screening results (and genotyping of positive EIAs) was completed, and each participant had a dried-blood spot (DBS) specimen. The subset had 250 rotavirus-positive cases, including prevalent P-genotypes (VP4) namely P[8] (n=120), P[6] (n=90) and P[4] (n=40), and 250 rotavirus-negative controls. DNA was extracted from DBS specimens using the QIAamp DNA Mini kit, and secretor status determined using the TaqMan® (G428A) SNP Genotyping assay. Sanger sequencing will be conducted for 10% of specimens.

Results
Rotavirus-positive cases comprised 183 secretors (73%) and 67 non-secretors (27%), while controls comprised 145 secretors (58%) and 107 non-secretors (42%; p=0.003). Susceptibility to rotavirus appeared to be genotype-specific: rotavirus P[8] infections (78% secretors and 22% non-secretors), P[4] infections (76% secretors and 24% non-secretors), and P[6] infections (53% secretors and 47% non-secretors). P[8] and P[4] infections had significantly different ratios of secretors as compared to P[6] infections (p=0.001).

Conclusions
These results suggest that secretors are significantly more susceptible to rotavirus infections compared to non-secretors overall. Secretors were significantly more susceptible to P[8] and P[4] infections, while non-secretors showed a natural resistance to these strains, and were more susceptible to P[6] strains. This may provide an explanation for the observed higher frequency of P[6] rotavirus infections in African populations.