An *in silico* investigation into possible structural constraints during reassortment of rotavirus segment 9, encoding VP7

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Background
Reassortment of genome segments during mixed infections is a major distinguishing feature of rotavirus genetics and one of the reasons for strain diversity which is thought to contribute to the lower vaccine efficacy in Africa. Intergenogroup reassortment of rotavirus strains has been observed during post vaccine introduction. Protein-protein interactions, involving VP2, VP6, VP7 and VP4, play a major role in rotavirus reassortment. In order to understand possible structural constraints during reassortment, an *in silico* investigation into the protein-protein interactions between one of the outer layer proteins, VP7 and the middle-layer viral capsid protein, VP6, was carried out using docked protein structures and molecular dynamics (MD).

Method
A VP6-VP7 protein complex from the RRV-G3P[2] rotavirus genogroup (entry:4V7Q) were obtained from the PDB. The structure was altered to produce individual SA11-N5-G3P[2] VP7 and VP6 proteins. Amino acid sequence alignments were performed to identify conserved as well as variable regions amongst the different genogroups and specific amino acid alterations were made to the VP7 SA11-N5 protein structure. Protein-protein docking was used to assemble different genogroup [Wa (G1), GR10924 (G9) and 3313WC (G12)] VP7 proteins on SA11-N5 VP6. The different genogroup VP7 proteins were docked onto a SA11-N5 VP6 protein using ClusPro. Protein-protein interactions and structure compatibility were analysed by means of 100ns MD simulations on the High Performance Cluster at the University of the Free State.

Result
Structural alignment analyses indicated that the overall VP7 protein fold of the SA11-N5, Wa, GR10924 and 3313WC genogroups are conserved. Protein-Protein docking and subsequent MD of the docked structures indicated that the VP6 H-domain loops, VP7 N-terminal arm and VP6-VP7 interface charges mediates structural compatibility and stability.

Conclusion
Here we present the key structural elements which potentially contribute to protein-protein interactions between VP6 and VP7. Finally, we discuss the possible structural constraints our results impose upon the reassortment of segment 9.