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Sequence Analysis and Structural Implications of Rotavirus Capsid Proteins

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Abstract : Rotavirus is the major cause of severe gastroenteritis worldwide in children aged 5 and younger. Death rates are high particularly in developing countries. The mature rotavirus is a non-enveloped triple-layered nucleocapsid containing 11 double-stranded RNA segments. Here a global view on the sequence and structure of the three main capsid proteins, VP7, VP6, and VP2 is taken by generating a consensus sequence for each of these rotavirus proteins, for each species obtained from published data of representative rotavirus genotypes from across the world and across species. The degree of conservation between species was represented on homology models for each of the proteins. VP7 shows the highest level of variation with 14 - 45 amino acids showing conservation of less than 60%. These changes are localized to the outer surface which is exposed to antibodies alluding to a possible mechanism in evading the immune system. The middle layer, VP6 shows lower variability with only 14-32 sites having lower than 70% conservation. The inner structural layer made up of VP2 showed the lowest variability with only 1-16 sites having less than 70% conservation across species. The results correlate with proteins' multiple structural roles. Although the nucleotide sequences vary due to an error-prone replication and lack of proofreading, the corresponding amino acid sequence of VP2, 6 and 7 remains conserved. Sequence conservation maintained for the virus results in stable protein structures, fit for function. This can be exploited in drug design, molecular studies and biotechnological applications.

Keywords : amino acid sequence conservation, capsid protein, protein structure, vaccine candidate
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