PREDICTION OF HIGH-CONSERVED, SOLVENT-EXPOSED REGIONS IN ROTAVIRUS(G9) VP4 AND VP7 FOR THE RATIONAL DEVELOPMENT OF VACCINES.

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Rotavirus is the major causative of acute gastroenteritis in children younger then five years old. This disease is responsible for expressive mortality and morbidity, mainly in countries in development. Rotavirus outer capsid is formed by two proteins (VP4 and VP7). VP4 is known to be essential for the host cell contact, while VP7 is probably involved in the very first steps of virus penetration into host cells. VP4 and VP7 exert a pivotal role in type-specific antibody induction, being important targets for vaccines. In this work, we performed multiple alignment analysis with VP4 and VP7 sequences from rotavirus type G9, extracted from NCBI data bank, as well as determined the aminoacids solvent exposure, and hydrophobicity, in order to predict solvent-exposed high-conserved (SEHC) regions in these proteins. VP4 and VP7 solvent-exposed regions may lie on the virus surface and should be important both for antibody induction and for virus attachment and penetration into host cells. We have found two SEHC regions in VP4 and three in VP7. Prediction of secondary structure and molecular modeling of such regions have confirmed that they may be solvent-exposed non-structured loops. We believe that, in further works, those regions could be used for the rational production of antigenic molecules for future development of rotavirus vaccines.

Supported by FAPESB.