Molecular dynamics study of the PCV-2a and PCV-2c Cap protein assembly mechanism

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The porcine circovirus 2 (PCV-2) is the principal pathogen involved in the Postweaning multisystemic wasting syndrome (PMWS) pathogenesis, that generates a huge lost in swine industry. It’s a small, non-enveloped T=1 icosahedral virus, with capsid formed by the ORF2 encoding protein Cap. Here, the capsomers formed by Cap protein from genotypes PCV-2a and PCV-2c were studied by using molecular dynamics simulations. Initially, a data set of ORF2 sequences was built and genotyped accordingly to literature. A consensus-sequence representing each of the genetic clusters were created and translated. The atomic coordinates of one capsomer (five solvated proteins and 20 sulfate ions) were selected from the crystal structure of PCV-2 capsid available in Protein Data Bank database (ID 3R0R). \textit{In silico} mutations were performed to create structural models (PCV2a and PCV2c) according to the consensus-sequence obtained previously. A water box (10.595nm x 8.049nm x 11.682nm) was constructed to simulate cell environment. The remaining space was filled with 53624 water molecules and, also, Cl\textsuperscript{-} or Na\textsuperscript{+} ions were added to obtain an electrically neutral system. After approaching a carefully energy minimization protocol, the molecular dynamics trajectories of 50 nanoseconds were calculated for this system, at 310K and pressure of 1 bar. The root mean square deviation (RMSD) with regard to the departure structure stabilized at about 0.75nm and 0.7nm for PCV2a and PCV2c, respectively. The root mean square fluctuation (RMSF) per residue was considerably more pronounced for aminoacids 75-85, 120-145 and 160-186 for both models, possibly due to their localization at 3 loop regions in Cap protein. Together, these findings are important step to get clues on how genetic differences contribute to Cap protein assembly mechanism and it’s correlation with PCV-2 pathogenicity. New in deep studies are now being pursued aiming to elucidate some others specific molecular features of Cap protein assembly.

Palavra chave: PCV-2, \textit{in silico} mutation, molecular dynamic
Patrocínio: FAPEMIG, CNPq and CAPES