Structural Analysis of the Ectodomain of HIV Gp41 and Implication on the Gp41 Assisted Membrane Fusion

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An ectodomain of gp41, the transmembrane fusion protein of HIV, without the fusion peptide region was expressed using pET system in *E. coli*. The expressed protein, gp41core, was isolated as inclusion body and was purified by ion-exchange chromatography after solubilized in 6M urea. The purified denatured protein was renaturated and the folded domain of gp41core was identified by the presence of the proteolysis resistence domain and a high content of α-helical secondary structure. Matrix associated laser desorption ionization (MALDI) analysis, N-terminal sequencing and CD analysis showed that the trypsin resistent domain (TRD) represented the C-terminal region of gp41core consisted with 51 amino acids and consisted of α-helix. Gel filtration and chemical cross-linking analysis of gp41core and TRD suggest that they present in solution dominantly as dimer, although the apparent sizes were bigger than 300kDa. High content of α-helical structure in TRD, dimeric nature and coiled coil sequence suggested that it forms dimeric unit by coiled coil formation. The N-terminal half of gp41 ectodomain contained less amount of α-helical structure and sensitive to proteolytic digestion which indicated that this region was extended form. A model of tertiary structure of gp41 and its possible strucutral change during fusion process was suggested based on the obtained results.