Screening for functional peptide based SsGPRC6A to recognize L-amino acids specifically by molecular docking and dynamics simulation

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One of the most important function of G protein-coupled receptors family C subtype 6A (GPRC6A) recognizes and responds to L-amino acids as its principal physiological ligand. In this study, homology modeling, molecular docking and molecular dynamics simulation were performed to explore structural features and binding mechanism of L-amino acids on SsGPRC6A of *Sus scrofa*, and to construct model containing the binding domain of the ligands for searching functional and special polypeptide to recognize the L-amino acids respectively. The homology model of SsGPRC6A was constructed using the crystal structure of the extracellular region of the group II metabotropic glutamate receptor (2E4U) at 2.35 Å resolution as template. The homological models for SsGPRC6A were constructed by the method of Swiss model and EasyModeller4.0. The constructed models were evaluated and docked by using the online servers and Discovery studio 2.5. Twenty L-amino acids were docked in the active site of the obtained model by autodock program. The results indicating the quality of all the models generated by Swiss model is higher than that of the models generated by EasyModeller4.0 by 45.1%, the model is better than that of the models were minimized of free energy. After docking, the constructed model and the favorite ligands complex were put into a TIP3P water box, a 20 ns molecular dynamics (MD) simulation was performed on the whole system. The model with a high-affinity binding site in active pocket interact with broad-spectrum amino acids by hydrogen bond as well as hydrophobic interaction. And the model have binding preference and stability for basic and aromatic amino acids. Thus, the findings from this study will be helpful for predicting and elucidating the binding pattern of SsGPRC6A to L-amnio acids.

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