Biophysical and molecular docking insight into interaction mechanism and thermal stability of human serum albumin isoforms with a semi-synthetic water-soluble camptothecin analog irinotecan hydrochloride.

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Abstract:

In the present work, we have examined the binding parameters, thermodynamics and stability of human serum albumin (HSA) isoforms at pH 7.4 and 9.0, using spectroscopic, calorimetric and molecular docking methods in the presence of water soluble camptothecin analog irinotecan hydrochloride (CPT-11). We observed that CPT-11 binds to HSA through a static quenching procedure of ground-state complex formation with N-isoform and B-isoform. Hydrogen-bond and hydrophobic interactions are the major governing forces that participating in the formation of protein-drug complex. To determine the binding site of CPT-11 within HSA molecules we also have perform molecular docking experiments. We explored the CPT-11 mediated stability and modulation of HSA by performing dynamic light scattering (DLS) and differential scanning calorimetry (DSC) experiments. DLS and DSC techniques are used to determine the size and the melting point (Tm) of HSA, which was decreased in the presence of CPT-11. Therefore, CPT-11 plays an important role in HSA stability and protein-ligand interactions. The present study provides valuable information in the field of pharmaco-kinetics pharmaco-dynamics and drug discovery.

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