Biophysical and molecular docking insight into the interaction of cytosine -D arabinofuranoside with human serum albumin.

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Abstract:

Interaction of pharmacologically important anticancer drug cytosine -D arabinofuranoside with human serum albumin (HSA) at physiological pH 7.4 has been studied by utilizing various spectroscopic and molecular docking strategies. Fluorescence results revealed that cytosine -D arabinofuranoside interacts with HSA through static quenching mechanism with binding affinity of 2.4×103 M1. The average binding distance between drug and Trp214 of HSA was found to be 2.23 nm on the basis of the theory of Förster's energy transfer. Synchronous fluorescence data indicated that interaction of drug with HSA changed the microenvironment around the tryptophan residue. UVvisible spectroscopy and circular dichroism results deciphered the complex formation and conformational alterations in the HSA respectively. Dynamic light scattering was utilized to understand the topology of protein in absence and presence of drug. Thermodynamic parameters obtained from isothermal titration calorimetry (H=26.01 kJ mol1 and TS=6.5 kJ mol1) suggested the involvement of van der Waal interaction and hydrogen bonding. Molecular docking and displacement study with site specific markers suggested that cytosine -D arabinofuranoside binds to subdomain IB of HSA which is also known as the hemin binding site. This study will be helpful to understand the binding mechanism of cytosine -D arabinofuranoside with HSA and associated alterations.

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