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Binding Interactions of *β*-Lactoglobulin and Tetracycline: Spectroscopic and Calorimetric Investigations

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Abstract: Protein-drug interaction has been recognized as an important area for the design and synthesis of new drug molecules which subsequently control their therapeutic availability, efficiency and delivery. Herein, we have investigated the interactions between the protein, *β*-Lactoglobulin (*β*LG) and antibiotic tetracycline hydrochloride (TC) by steady state, time-resolved, circular dichroism spectroscopy (CD) and isothermal titration calorimetry (ITC). Intrinsic fluorescence of β-LG, due to its two tryptophan residues, has been monitored upon addition of TC for binding interaction study. The fluorescence quenching phenomenon can be explained by the well-known Stern-Volmer equation. The upward curvature of Stern-Volmer plot at higher concentrations of TC was observed. This anomaly may arise either due to the simultaneous occurrence of both static and dynamic quenching or greater extent of quenching taking place at higher concentration TC. Binding constants, thermodynamic parameters (like *ΔH*, *ΔG*, *ΔS*) and stoichiometry of the interaction has been estimated by using both steady state and ITC experiments. Life-time decay study and binding constant parameters suggested that the interaction is static in nature. Thermodynamic parameters indicate that binding interaction between drug and protein is hydrophobic type of interaction as well as thermodynamically favourable.

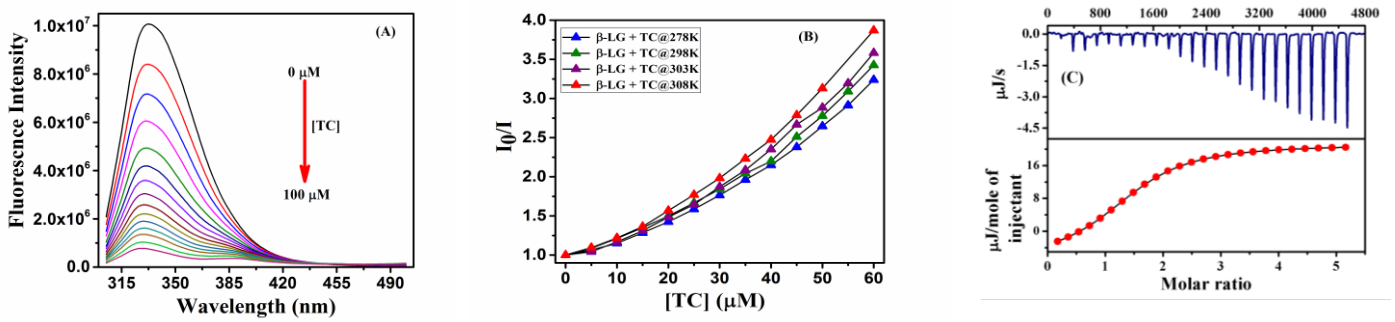

Figure: (A) Emission spectra of *β*LG upon addition of [TC]. (B) Stern-Volmer plot at different temperatures. (C) Isothermal Titration Calorimetry profile: Integrated heat change (above) and enthalpogram (below).

References and Notes:

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