Biomolecular interactions of 1,3-bis(2-arylimino)isoindolate-based palladium(II) complexes: Substitution kinetics, DNA/protein-binding, and molecular docking approaches

Abstract

A series of 1,3-bis(2-arylimino)isoindoline Pd(II) complexes core *viz.;* Chlorido(1,3-bis(2-pyridylimino)isoindoline)palladium(II), **Pd1**, Chlorido(1,3-bis(4-methyl-2-pyridylimino)isoindoline)palladium(II), **Pd2**, Chlorido(1,3-bis(2-pyridylimino)benz(*f*)isoindoline)palladium(II), **Pd3** and Chlorido(1,3-Bis(1-isoquinolylimino)isoindoline)palladium(II), **Pd4** were synthesized, appropriately characterized and the crystal structure of **Pd2** elucidated. The kinetics and mechanism of the substitution of the chloride ligand with thiourea ligands, **Tu**, **Dmtu** and **Tmtu**, from the complexes were investigated under *pseudo*-first-order conditions. The analyses were performed using stopped-flow analyzer or UV–visible spectrophotometer. The reactions proceeded through two consecutive steps for most complexes with exception of **Pd4** showing only a single step. The substitution rates followed the order: **Pd1**>**Pd2**>**Pd3**>**Pd4** due to varying degrees of steric influences and σ-/π-donations caused by the methylation and benzannulation on the *cis*-/*trans*-positions of the pyridyl rings of the BPI. The quenching of the fluorescence of CT-DNA/EB by the Pd(II) complexes suggests static quenching mechanism. The simulated docking of the complexes onto CT-DNA suggests they bind mainly in the minor grooves of DNA. The UV–Visible absorption titrations and quenching of tryptophan (Trp) fluorescence of BSA by the complexes depict reasonable interactions which occur mainly in the hydrophobic domains of the former. The order of strength of the interaction of the complexes with DNA or BSA is consistent with the rates of substitution kinetics.

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