The influence of ruthenium complex geometry in the interaction with human serum albumin.

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Ruthenium complexes with pyridine ligands have been proven promising in treatment of various cancer types..[1] One important parameter to determine the way of interaction between a molecule and human serum albumin (HSA - the main carrier of substances by the human body) is it geometry.[2] With this in mid the interaction between HSA and the complexes [Ru^{II}(bapydip)Cl_2] (bapydip = N,N-bis(7-methyl-2-pyridylmethylene)-1,3-diiminopropane) (figure 1A) and [Ru^{II}(Dimebipy)DMSO Cl] (Dimebipy = 4,4'-dimethyl-2,2'-bipyridyl) (figure 1B), two literature already known molecules, was investigated.

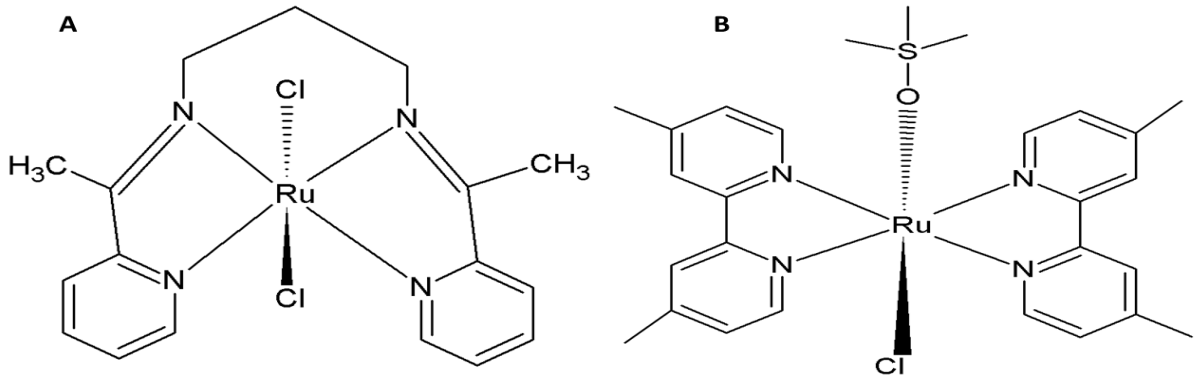

Figure 1: Representations of the structures of A) [Ru^{II}(bapydip)Cl_2] and B) [Ru^{II}(Dimebipy)DMSO Cl].

The experimental results showed that both complexes interact effectively and by different forms with protein. While the complex A quenching the intrinsic fluorescence of HSA by static mechanism, complex B quenching by a dynamic mechanism and with a higher value of Stern-Volmer constant of suppression (K_{Sv} order of 10^3 L mol^{-1} with complex A and 10^4 L mol^{-1} with complex B, with ascetation at 280 and 295 nm).[3] The less rigid structure of complex B makes easy his dispersion between the protein framework, allowing more collisions between the molecule and the fluorophore groups HSA and promoting the dynamic mechanism. The binding constants of $1{,}27x10^3$ L mol^{-1} to complex A and $2{,}55x10^5$ L mol^{-1} to complex B (both at 298 K) suggest that the interaction between HSA and this complex is really the most effective.

Studies with probes allowed the localization of complexes at the protein framework. This experiment suggest that complex A bind to protein by subdomain IIA and complex B by subdomain IIIA or a region near of this. This differences reveals that molecule geometry really affect the way similar ruthenium complexes brings to HSA.

References:

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