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MEETING ABSTRACTS

MOLECULAR MODELING STUDIES ON THE INTERACTIONS OF AFLATOXIN B1 AND ITS METABOLITES WITH PHERIPHERAL AND CATALYTIC ANIONIC SITES OF HUMAN ACETYLCHOLINESTERASE

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Aflatoxins are secondary metabolites of the fungi *Aspergillus flavus* and *A. parasiticus*. Among them Aflatoxin B1 (AFB1) is the most frequent type in nature and the most carcinogenic and hepatotoxic for mammals. AFB1 is also inhibitor of the enzyme acetylcholinesterase (AChE) and, therefore, a potential chemical and biological warfare agent, as well as its metabolites. In order to investigate this, we performed inedited theoretical studies on the interactions of AFB1 and its metabolites inside the catalytic and the peripheral anionic sites (CAS and PAS) of human acetylcholinesterase (*Hss*AChE), to verify their stability, suggest the preferential ways of inhibition, and compare their behavior to each other. Molecular docking, molecular dynamics and MM-PBSA calculations for the systems *Hss*AChE/AFB1-metabolites, on both sites were performed. All the metabolites presented negative values of interaction energies in comparison to AFB1. This suggests that they can be better inhibitors of *Hss*AChE. Also, the energy values obtained for the CAS were lower than for the PAS for all metabolites, suggesting that they may preferentially bind in the CAS and come closer to the active site. This behavior is different from the experimentally observed for AFB1, pointing to a different way of inhibition for its metabolites.

Keywords: aflatoxin B1; metabolites; acetylcholinesterase; pheripheral anionic site; catalytic anionic site

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