International Journal of Basic and Applied Biology
p-ISSN: 2394-5820, e-ISSN: 2349-5839, Volume 3, Issue 3; July-September, 2016, pp. 213-213
© Krishi Sanskriti Publications
http://www.krishisanskriti.org/Publication.html

Binding of Ester and Non Ester Drugs to Human Serum Albumin

Meenu Narwal[1], Rajasri Bhattacharyya[2] and Tapan Mukherjee[3]

[1,2,3]Department of Biotechnology Maharishi Markandeshwar University Mullana, Ambala
E-mail: [1]narwalmeenu11@gmail.com

Abstract—*Binding of certain drugs to Human Serum Albumin (HSA) is a field of profound research. HSA is an abundant plasma protein made up of a single polypeptide chain having 585 amino acids. It also contains three homologous domains. It mainly serves the function of delivery of drugs, fatty acids and hormones by binding to it's specific binding sites. This versatile protein also have enzymatic property which convert prodrugs into active component. This protein is crucial in pharmaceuticals as it can bind to various drugs mainly at two binding sites (site I and II) and overall seven binding sites are spreaded across the protein. The binding of different components to protein modifies their effectivity and delivery which inturn transforms their pharmacokinetic and pharmacodynamic properties. HSA also possess esterase activity which break down drugs with ester moieties. Such phenomenon may be the cause of failure of pharmacological action of certain drugs. This poster aims to show interaction of various ester, prodrugs and non ester drugs with HSA. It has been observed that there was remarkably no difference between binding pattern of drugs from these different categories. Also, none of prodrug belongs to non ester class. Thus, prognosis of HSA binding can contribute drastically to the discovery of new drug candidates. While earlier HSA research shows that HSA interacts with particular type of ligands, this study aims to elaborate potential of HSA to interact with more drugs in order to improve their action. It has also been observed that Warfarin is binding preferably at site 1 and this result is similar to reports by various researchers submitted earlier.*