Abstract No: 2025_388

Computational investigation of the endocrine-disrupting potential of Bisphenol F and its sulfate metabolite targeting the RAR-γ receptor

B.P. Welagedara, J.N. Dahanayake*

Department of Chemistry, Faculty of Science, University of Kelaniya, Kelaniya 11600, Sri Lanka.
** jayangikadh@kln.ac.lk*

Endocrine-disrupting compounds (EDCs) have been known to interfere with hormonal signaling pathways by interacting with significant biological receptors, leading to negative impact on human health. This study evaluates the endocrine-disrupting potential of two selected compounds, the Bisphenol A analog Bisphenol F (BPF) & its metabolite Bisphenol F mono-sulfate sodium salt (BPF-S) through their interaction with the human RAR-γ receptor. The Auto Dock Vina was used to perform molecular docking to predict binding affinities, binding orientations and key interaction profile within the receptor binding site. The results indicated that BPF-S exhibited stronger binding affinity (-9.2 kcal/mol) compared to the parent compound, BPF (-8.4 kcal/mol), forming stable hydrogen bonds and hydrophobic interactions with critical amino acid residues that were linked with the receptor activity. To further validate these findings, molecular dynamic simulations were carried out using GROMACS for 25 ns to assess the stability and dynamic behavior of the ligand-receptor complexes under physiological conditions. Structural stability and conformational behavior of the complexes were analyzed using RMSD, RMSF, Hydrogen bonds and radius of gyration (Rg). The BPF-S-RAR-γ complex had lower values of RMSD and lower fluctuations of the residues, indicating enhanced stability and potential to alter the receptor conformation. In contrast, BPF ligand showed comparatively greater fluctuations and lack of interaction stability. These findings suggest that BPF-S possesses a greater potential to disrupt normal functioning of the receptor RAR-γ and may act as a stronger endocrine-disrupting compound. This study highlights the value of computational approaches in elucidating the molecular mechanisms underlying endocrine disruption as well as the assessment of their possible impact on risk assessment of human health.

Keywords:

endocrine disruption, endocrine-disrupting compounds, molecular docking, molecular dynamic simulation

Acknowledgment:

Financial assistance by Department of Chemistry, Faculty of Science, University of Kelaniya.