ABSTRACT

Chronic kidney disease is the 9th leading cause of death according to WHO. Most patients undergo hemodialysis as a medical therapy for kidney replacement. An important aspect in the effectiveness of hemodialysis is the biocompatibility of the dialysis membrane in terms of its interaction with blood plasma proteins. Most blood plasma proteins are HSA which have the ability to adsorb onto synthetic surfaces, including dialysis membranes. This can change the conformational structure and function of HSA in the blood. PES polymers are commonly used as dialysis membrane materials because they have high mechanical strength but are hydrophobic and therefore very susceptible to protein adsorption. PVP polymers are rarely used but are hydrophilic which is predicted to be able to prevent HSA protein adsorption. This study aims to determine the effect of interaction distance and interaction energy on the HSA…PES and HSA…PVP complexes, determining the stability of the complex for 50 ns.

HSA protein was used as a receptor, and PES polymers (10 and 15 monomers) served as ligands. The interactions of the HSA...PES and HSA...PVP complexes were calculated in silico using molecular mechanics methods and through two stages: molecular docking and MD using YASARA software for 50 ns. The resulting calculation data included interaction energy, interaction distance, total potential energy, RMSD, Rg, binding free energy (ΔG_{bind}), and changes in receptor-ligand interactions during the simulation.

The interaction energy of the HSA...PES complex was -39.02 kJ/mol, forming 12 hydrogen bonds (2.10–4.07 Å) and 17 hydrophobic interactions (4.25–5.55 Å), while the interaction energy of the HSA...PVP complex was -38.97 kJ/mol, forming 6 hydrogen bonds (2.19–3.98 Å) and 7 hydrophobic interactions (4.15–5.09 Å). The HSA...PES complex forms more interactions than the HSA...PVP complex, allowing for changes in the conformational structure of the HSA protein that cause disruption to the function of HSA. The HSA...PES complex has a total potential energy of -298.64×10^4 kJ/mol, an RMSD value of 5.66 Å and an Rg of 3.56 Å. The HSA...PVP complex has a total potential energy of -299.43×10^4 kJ/mol, an RMSD value of 3.95 Å and an Rg of 3.55 Å. The HSA...PVP complex is more stable overall because it has lower total potential energy, RMSD and Rg values than the HSA...PES complex. Data on dihedral angle changes in the secondary structure of each complex shows that PVP is more capable of maintaining the stability of the secondary structure of the HSA protein.

Keyword: Hemodialysis, HSA, PES, PVP, MD, *molecular docking*