TARGET IDENTIFICATION OF HIV RELATED GANODERIC ACIDS USING MOLECULAR DOCKING

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ABSTRACT

Four Ganoderic acids (α, B, C1 H) were studied using molecular docking approach. Both reverse molecular docking and molecular docking were combined to elucidate suitable target(s) for these Ganoderic acids. Outcomes from molecular docking were compared and correlated to experimental data. Compound with the best performance in both molecular docking and correlation analysis were further studied by looking at its molecular interaction with potential target. 1HVR (a type of HIV-1 protease) and Ganoderic acid B performed better in cluster analysis of molecular docking compared to other compounds. Similar ΔG trend to experimental data obtained from el-Mekkawy and co-workers (el-Mekkawy et al. 1998) were also observed. Molecular interaction study revealed Ganoderic acid B interactions with ILE50 and ILE50' residues. These two residues has been identified as important residues and plays important roles in ligand-protein interaction in HIV-1protease (Lebon and Ledecq 2000). These interactions not only suggested HIV-1 protease in general is a suitable target for ganodericacid B, they also indicated a huge potential for HIV drug discovery based on this compound.

ABSTRAK

Empat jenis asid Ganoderik (α, B, H C1) telah dipelajari dengan menggunakan pendekatan doking molekul. Kedua-dua jenis doking molekul iaitu doking molekul berbalik dan docking molekul digabungkan untuk mengenal pasti target yang sesuai untuk asid-asid Ganoderik ini. Hasil dari doking molekul dibandingkan dan dikorelasikan dengan data yang didapati menerusi eksperimen. Sebatian dengan prestasi terbaik di kedua-dua doking molekul dan analisis korelasi dikaji lebih terperinci dengan melihat interaksi diperingkat molekul. 1HVR (sejenis HIV-1 protease) dan asid Ganoderik B didapati memiliki keputusan analisis kelompok doking molekul yang lebih baik dibandingkan dengan sebatian yang lain. Trend ΔG juga didapati sesuai dengan data eksperimen yang diperolehi dari el-Mekkawy dan rakan kerja (el-Mekkawy et al. 1998). Kajian interaksi molekul mendedahkan asid Ganoderik B berinteraksi dengan residu ILE50 dan ILE50 '. Kedua-dua residu ini telah dikenal pasti sebagai residu penting dan memainkan peranan besar dalam interaksi ligan-protein HIV-1 protease (LebondanLedecq 2000). Interaksi ini tidak hanya mengesahkan HIV-1 protease pada umumnya merupakan target yang sesuai untuk asid Ganoderik B, ia juga menunjukkan potensi yang sangat besar bagi penemuan ubat HIV berdasarkan sebatian ini.

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ΔG : free binding energy

A^{o} : Angstrom

RMSD : root mean square deviation

IC_{50} : Half inhibitory concentration

1HVR : A type of HIV-1 Protease

1DIF : A type of HIV-1 Protease