Nutrigenomics and Computational Screening of Traditional Plant Phyto compounds against Tankyrase in Hepatocellular carcinoma

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Abstract

Hepatocellular carcinoma (HCC), a major global health concern, is frequently driven by deregulation of the WNT/β-catenin signaling pathway. Tankyrase (TNKS1 and TNKS2) play a crucial role in modulating this pathway and have emerged as viable molecular targets for intervention. In this study, a nutrigenomics based *in silico* approach was employed to identify potential dietary phytochemicals capable of inhibiting TNKS1/2, thereby attenuating oncogenic signaling in HCC. Molecular docking, ADME profiling, predictive toxicity, DFT, and MD simulations were used to screen a 170 phytocompounds derived by screening three traditionally hepatoprotective plants, including *Hemidesmus indicus*, *Phytanthus niruri* and *Pithecellobium dulce.* Among them four lead compounds such as, Pitheduloside I, Ellagic acid, Lariciresinol dimethyl ether and Benzyl benzoate, exhibited good binding affinities with TNKS1/2 and good pharmacokinetic and toxicological performances. The high binding energies of TNKS1- pitheduloside I (-7.4 kcal /mol) and TNKS2-Ellagic acid (-7.0 kcal /mol), low predicted toxicity, and electronic properties also suggest that these diets contain compounds that are involved in HCC and can be reported using computational nutrigenomics and traditional medicinal knowledge. The DFT are also balanced by -0.15 to 0.22 eV, which indicates a good degree of electronic stability and reactivity conducive to bioactivity. High-binding energies of both compounds. This study highlights the potential of integrating computational nutrigenomics with traditional medicinal knowledge to identify dietary compounds may involve in HCC. These findings support the development of functional foods or nutraceuticals targeting key oncogenic pathways in HCC, advancing the field of personalized nutrition and disease prevention.

Keywords: Hepatocellular Carcinoma, Nutrigenomics, Tankyrase Inhibitors, Cancer, WNT/β-Catenin Signaling, Computational Approach