ANTIDIABETICACTIVITY OF NIGELLA SATIVA (BLACK SEED) — BY MOLECULAR MODELING ELUCIDATION, MOLECULAR DYNAMICAND CONCEPTUAL DFT INVESTIGATION

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Abstract -
Background and Purpose: Molecular Docking, Molecular Dynamics simulations, quantum chemical calculations, QM/MM calculations and 2D-, 3D- and 4D-QSAR, ADMET prediction have been widely used to drug discovery. This theoretical approach enables to predict the mode of interaction of a ligand with its receptor. However, synthetic inhibitors were identified as the most efficient ones, indeed, the most commercialized treatment of disease type 2 diabetes (T2DM)is Gliptine. On the other hand, natural inhibitors have also provided good activities via the Dipeptidyl peptidase-4 (DPP-4)enzyme (p-Cymene ,Thymoquinone , Carvacrol , α-Pinene , β-Pinene , Limonene).
Method: In this work we present a theoretical study of Dipeptidyl peptidase-4 enzyme inhibitors by natural inhibitors including solvatation parameter. Tocarry out this work, we used different molecularmodeling approach esasmolecularm echanics.
Results: The moleculardynamicsstudy was done for the best natural inhibitors (deducted from the docking best scores for Lig5andLig3,andlowestscorefor Lig ref). Theinteractionsbetweenthestudiedinhibitorsandourtargetwasfurtherexploredthrough molecularzocking and molecular dynamics simulations. A few key residues(GLU205, GLU206 (H-donneur, ionic) atthebinding siteofDDP-4wasidentified.

Conclusion:Obtained Docking moleculardynamicsresult, both lead to the same conclusion and predict that Dithymoquinone (essential oil Nigella Sativa)present better interaction ofDipeptidyl Peptidase-4 Enzymeinpresenceofwatermoleculeswhilemoleculardynamicsandconsequentlycanbethebestinhibitorcandidatetobe in vitroand in vivoinvestigated.

Keywords - Molecular modeling – Diabetes (T2DM) - Nigella - MOE (Molecular Operating Environment).