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Research Article

In silico Docking Studies of Some Isolated Compounds of *Clausena Lansium* (*Lou.*) Against Diabetic Activity

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Abstract

The aim of this study is to perform molecular docking studies to identify potential binding affinities of the phyto-compounds from compounds claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol for searching of lead molecule for anti-diabetic activity.

Computer assisted drug design approach has contributed to successfully disclosure of against diabetic agent. Molecular docking keeps on being a great promise in the field of computer based drug design.

The procedure of molecular docking includes investigation of various holding methods of one ligand with targeted receptors protein. We have found that numerous values of Molecular docking score by Schrodinger. Compounds claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol respectively. Among all the compounds Clausenaline E showed the best docking score. So from this investigation we can say that this compound Clausenaline E can be suggested for further experiment for the grater pharmacological effect in diabetic patient.

INTRODUCTION

In South Asian countries diabetes has become the seventh leading attributable risk factor [1,2]. By 2035 the number of affected people is expected to increase to 592 million globally [3]. About 80% of adults suffer in diabetes in low- and middle-income countries [4]. Diabetes is a serious complex condition which can affect the entire body. Blood glucose is the main source of energy and comes from the food we eat. Diabetes is a disease that occurs when blood glucose is too high. Insulin, a hormone is prroduced by the pancreas which enables glucose from food to get into our cells to be used for energy. Therefore, there has been a developing interest to analyze the antidiabetic properties of plants. A large number of plants and plant-parts have been investigated for their beneficial role and anti-diabetic properties [5,6].

Clausena lansium (Lou.) has a place with the family Rutaceae and is started from Southern China and discovered likewise in Bangladesh, India and so forth. The mash can be utilized to plan organic product mugs, sweets, stick, or jam. What's more, the matured natural product can be utilized to plan carbonated refreshments like champagne, albeit dried *Clausena lansium* is a more attractive product. Previous investigations of bioactivities, especially the concentrates of its leaf and seed, for the most part centered around the hepatoprotective, antiplatelet, hypoglycemic, antifungal and antiviral activities. In any case, no methodical investigation has been directed on the Clausena lansium peel despite the fact that it is utilized as a people medication in China for the treatment of stomachic, and bronchitis and additionally it goes about as a vermifuge. Out of the blue, this examination researched the cancer prevention agent and anticancer exercises of the Clausena lansium peel removes and showed the strong bioactivities of the concentrates appropriate to be utilized as characteristic cell reinforcement mixes or pharmaceutical supplements [7-11].

Molecular docking is a key apparatus in computer-assisted drug design and development. Docking has been used to perform virtual screening on extensive libraries of compounds and propose basic theories of how the ligands bind with the target

with lead optimization. Another potential use of docking is optimization stages of the drug-discovery cycle.

MATERIALS AND METHODS

Protein preparation

3D crystal structure of Pancreatic Alpha-Amylase With A Carbohydrate Inhibitor is downloaded from Protein Data Bank [12]. By using the Protein Preparation Wizard of Schrödinger-Maestro v 10.1 the structure was prepared and refined. Charges and bond orders were assigned, hydrogens are added to the heavy atoms, were converted to methionines, and all waters were deleted. By Using force field OPLS_2005 minimization was carried out setting maximum heavy atom RMSD to 0.30 Å.

Preparation of ligand

Compounds were retrieved from Pubchem databases, i.e claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol. The 2D structures for these were built by using Schrödinger-Maestro v 10.1.

Receptor grid generation

Receptor grids were calculated for prepared proteins such that various ligand poses bind within the predicted active site during docking.Grids were generated keeping the default parameters of van der Waals scaling factor 1.00 and charge cutoff 0.25 subjected to OPLS 2005 force field in glide. A cubic box of specific dimensions centred around the centroid of the active site residues (Reference ligand active site) was generated for receptor. For docking experiments, The bounding box was set to 14 × 14 × 14.

Glide standard precision (SP) ligand docking

SP flexible ligand docking was carried out in Glide of Schrödinger-Maestro v10.1 [13,14], within which penalties were applied to non-cis/trans amide bonds. Van der Waals scaling factor and partial charge cutoff was selected to be 0.80 and 0.15, respectively for ligand atoms. Final scoring was performed on energy-minimized poses and displayed as Glide score. The lowest Glide score value was recorded for each ligand as the best docked pose.

RESULT

In order to study the interaction of the compounds claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol with 1PPI, we performed Glide docking analysis by Schrodinger suite v 10.1, where among of these compounds Clausenaline E shows highest docking score -5.467 shown in Table 1. The negative and low value of Piperine glide energy of binding demonstrates a strongly favorable bond between 1PPI and in most favorable conformations. The results of docking analysis was described in Table 1 and Figure 1

Table 1: Docking analysis of claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol with 1PPI.

Compounds	Compound Code	Docking Score	Glide e model	Glide energy
claulamines E	101879361	-5.276	-46.706	-33.319
clausemarin B	101879359	-4.86	-44.094	-34.267
Clausenaline C	101879360	-5.296	-46.246	-35.176
Clausenaline E	86106588	-5.467	-40.039	-28.389
Murrayanine	96942	-5.155	-34.288	-23.629
vanillic acid	8468	-4.634	-33.626	-27.639
Xanthotoxol	65090	-5.21	-37.863	-28.166

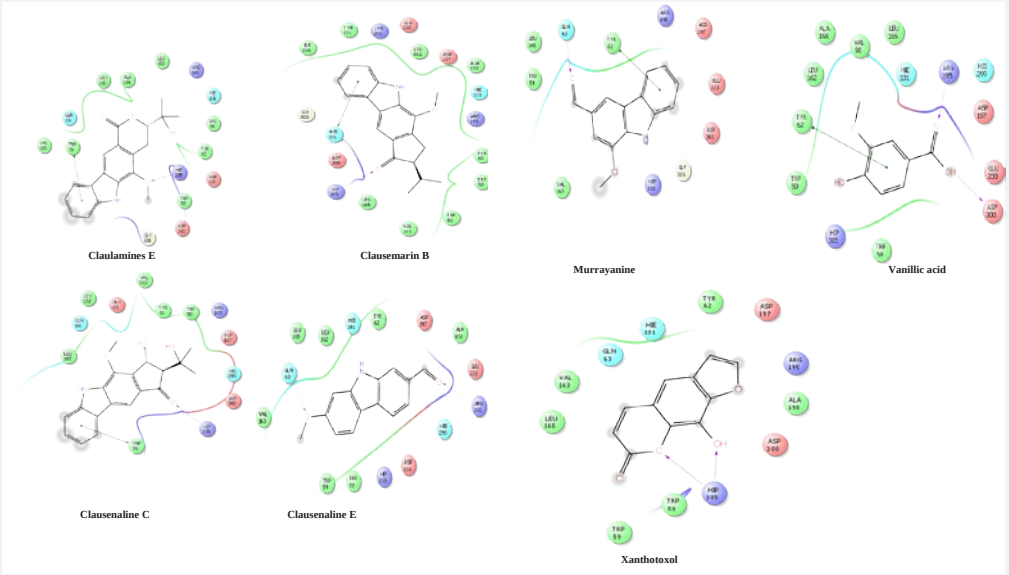

Figure 1 Docking analysis of claulamines E, clausemarin B, Clausenaline C, Clausenaline E, Murrayanine, vanillic acid, Xanthotoxol with 1PPI.

DISCUSSION

Since there is no cure for diabetes yet there are approaches to bring down the dangers. Despite the fact that diabetes is confusion, it can likewise prompt different factors, for example, heart assault, kidney disappointment, or passing. A man with diabetes needs to keep up a sound way of life including eating the correct nourishment, working out, controlling their glucose level, and be hopeful [15-19].

Diabetes happens in a few structures however the real ones are Type I and I. Our computer aided drug-design has successfully discovered the source of several anti-diabetic agents. We tried to find out the maximum effect of compound which may give better therapeutic effect for diabetes with fewer side effects. From the above table we can determine the compound ***Clausenaline E*** shows the greatest binding affinity for the targeted receptor. And the docking score Clausenaline E glide emodel and glide energy shows that the particular compound Clausenaline E can give the better therapeutic effect than others.

CONCLUSION

From overall study we can estimate that the compound can be suggested for further *in vivo* experiments. If we go through all data and studies it shows how it clearly indicated that Clausenaline E can be utilized to care for diabetes. Our investigations may lay the base of further investigation of the - for its ant diabetic potential. The above discoveries additionally approve the ethno pharmacological information on this plant. Thus, it can be inferred that has high potential as ant diabetic particularly against pathway in diabetes.

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