RESEARCH PAPER

Molecular Docking Study Of Glibenclamide, Curcumin And Glibenclamide-Curcumin Conjugate Against Dpp-4 Protein

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ABSTRACT
Type 2 diabetes mellitus (T2DM) remains a major global health burden, and despite the availability of several oral hypoglycaemic agents, issues such as adverse effects, loss of efficacy and drug resistance persist. Dipeptidyl peptidase-4 (DPP4) is a validated therapeutic target in glucose homeostasis, and both synthetic inhibitors and natural compounds such as curcumin have shown DPP4-modulating potential. Glibenclamide, a second-generation sulfonylurea, is widely used but associated with hypoglycaemia and weight gain. Rationally designing a glibenclamide–curcumin conjugate may enhance efficacy and safety by combining complementary mechanisms. The crystal structure of human DPP4 (PDB ID: 5Y7H) was retrieved from the Protein Data Bank and prepared using AutoDock Tools by removing water molecules and co-crystallized ligands, adding non-polar hydrogens and Kollman charges, and saving structures in pdbqt format. Curcumin, glibenclamide and their conjugate were sketched in ChemDraw, energy-minimized in Chem3D (MM2), converted to 3D, and prepared with Gasteiger charges and defined rotatable bonds. Molecular docking was performed using AutoDock Vina in PyRx. Binding energies and interaction profiles were analysed using PyMOL and Biovia Discovery Studio. Docking scores against DPP4 were −7.2 kJ/mol for curcumin, −7.8 kJ/mol for glibenclamide and −8.5 kJ/mol for the glibenclamide–curcumin conjugate, indicating superior affinity of the conjugate. Key interactions included multiple conventional hydrogen bonds, π–π stacking, π–anion and hydrophobic contacts with critical residues such as Glu205, Tyr662, Phe357, Arg125, Arg356 and Arg669, supporting enhanced complex stability. The glibenclamide–curcumin conjugate demonstrated stronger predicted binding to DPP4 than either parent molecule alone, suggesting a promising dual-acting scaffold for anti-diabetic drug development. These in silico findings warrant further in vitro and in vivo validation..

Keywords: Curcumin, Glibenclamide, DPP4 inhibitor, Molecular docking, Diabetes mellitus
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INTRODUCTION

Diabetes is one of the leading health concerns worldwide affecting millions of peoples with wider secondary complications **[1]**. Because of its rising incidence, insulin resistance, and long-term consequences linked to hyperglycemia, type 2 diabetes mellitus (T2DM) treatment continues to rank among the most important worldwide health concerns **[2]**. Wide number of oral hypoglycemic agents are available including sulfonylureas, biguanides, thiazolidinediones, and DPP4 inhibitors**,** still there is tremendous need for safe and most effective therapeutic interventions continued due to the various challenges of drug resistance, adverse effects, and loss of efficacy over time **[3]**.

Among these therapeutic targets, dipeptidyl peptidase-4 (DPP4) has gained considerable attention for its role in glucose homeostasis **[4]**. Incretin hormones that are necessary for insulin production and glucagon release inhibition, including glucose-dependent insulinotropic peptide (GIP) and glucagon-like peptide-1 (GLP-1), are broken down by DPP4 **[5]**. Therefore, DPP4 inhibition increases insulin secretion, lowers blood glucose levels in a glucose-dependent way, and prolongs incretin activity **[6]**. There are already a number of synthetic DPP4 inhibitors (gliptins) on the market; however, prolonged use of these medications is frequently linked to issues including hepatotoxicity, pancreatitis, and cardiovascular hazards **[7]**. Finding new, natural, and biocompatible DPP4 inhibitors that can supplement or replace traditional treatment in a safer manner is therefore of increasing interest.

A bioactive polyphenolic chemical obtained from Curcuma longa **(Figure 1)**, or turmeric, curcumin has been the

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subject of much research due to its many pharmacological characteristics, which include antidiabetic, anti-inflammatory, and antioxidant effects **[8]**.

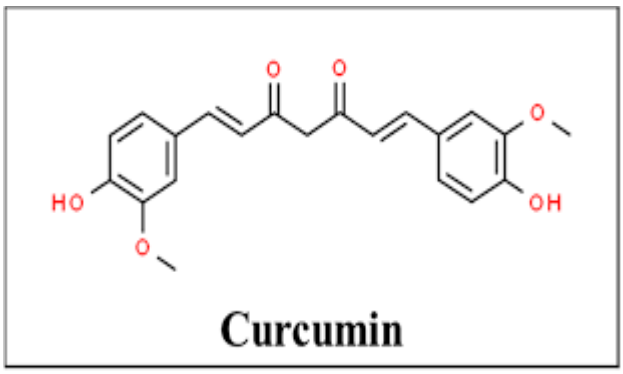

Fig 1: Chemical structure of Curcumin

It is well known that curcumin alters a number of biological targets related to inflammation, insulin signaling, and glucose metabolism **[9]**. Its therapeutic profile gains a hopeful feature from its capacity to inhibit DPP4 activity. Nevertheless, curcumin's quick metabolism, restricted bioavailability, and poor water solubility severely limit its therapeutic application despite these positive benefits **[10]**. However, the well-known antidiabetic medication Glibenclamide **(Fig 2)**, By blocking ATP-sensitive potassium channels in pancreatic β-cells, a second-generation sulfonylurea boosts the synthesis of insulin **[11]**. Although glibenclamide is helpful in regulating blood sugar levels, it is often linked to adverse effects such weight gain, hypoglycemia, and diminished efficacy over time **[12]**. Thus, it makes sense to combine a natural substance like Curcumin with a traditional antidiabetic drug like Glibenclamide in order to maximize therapeutic benefits and reduce adverse effects.

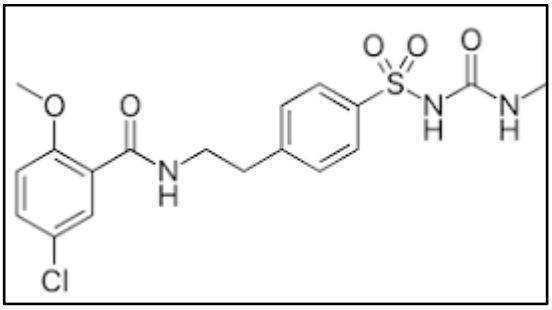

Fig 2: Chemical structure of Glibenclamide

The present research aims to explore the molecular docking interactions of Glibenclamide, Curcumin, and their conjugate with the DPP4 receptor, providing a structural basis for understanding their binding affinities and potential inhibitory effects. Molecular docking is a computational method that predicts the chemical interactions of small molecules with target proteins, making it easier to find viable lead compounds for medication development **[13]**. This study aims to determine whether conjugating glibenclamide with curcumin can improve the complex's overall stability and binding affinity for DPP4, suggesting possible synergistic or additive effects. The conjugate approach may combine the potent insulinotropic action of glibenclamide with the multifunctional antioxidant and anti-inflammatory benefits of curcumin, leading to a dual-action molecule capable of modulating glucose levels more efficiently while providing additional protective effects against oxidative stress and inflammation—two major contributors to diabetic complications.

The rationale behind designing the glibenclamide–curcumin conjugate lies in the hypothesis that chemical conjugation may improve pharmacokinetic and pharmacodynamic properties, such as solubility, stability, and bioavailability, while maintaining or enhancing biological activity **[14]**. Curcumin's ability to interact with key residues in DPP4's active site, combined with glibenclamide's established affinity for diabetic targets, may result in stronger binding interactions and improved inhibition of DPP4 activity, as supported by docking studies. Moreover, such a conjugate could potentially reduce the effective dose required for Glibenclamide, thereby minimizing associated adverse effects like hypoglycemia. Additionally, curcumin's inherent antioxidant and anti-inflammatory actions could provide further protection to pancreatic β-cells, improving insulin sensitivity and delaying the progression of diabetic complications. Thus, this study not only investigates the molecular interactions and binding energies of these compounds but also proposes a novel therapeutic strategy that integrates natural and synthetic pharmacophores to enhance efficacy and safety in diabetes management. Overall, the molecular docking analysis provides a theoretical framework to justify future experimental validation of glibenclamide–curcumin conjugates as promising DPP4 inhibitors with improved pharmacological potential.

MATERIAL & METHODS

Preparing proteins and identifying active sites

A vital resource for structural biology, the X-ray crystal structures of proteins DPP-4 (PDB ID: 5Y7H) were carefully selected and obtained in PDB format from the well-known Protein Data Bank database. These carefully chosen protein structures were then put into the AutoDock Tools program for additional processing and analysis after this retrieval procedure. The co-crystallized ligand was first separated from the complex to guarantee the maximum integrity of the protein structures during this phase, enabling a more thorough analysis of the protein's properties. To prevent any potential influence in the next analyses, any superfluous water molecules, as well as irrelevant chains or heteroatoms, were methodically eliminated prior to the protein production process. Non-polar hydrogen atoms were added where needed to improve the accuracy of the docking simulations, and Kollman charges were added to the structures to precisely reflect the proteins' electrostatic characteristics. Lastly, all revised protein structures were exported as pdbqt files, which are compatible with different docking programs. Using

sophisticated visualization tools like PyMOL and Biovia Discovery Studio, which enable a thorough comprehension of the protein-ligand interactions at a molecular level, a thorough investigation of the binding pockets on the proteins was carried out for visualization purposes **[15-17]**.

Ligand preparations

ChemDraw Ultra v10.0 from Cambridge Software was used to meticulously design the ligand structures. Energy minimization (MM2) in Chem3D Ultra v10.0 was then used to convert the ligands' two-dimensional representations into three-dimensional structures. Until the root mean square deviation (RMSD) fell below 0.001 kcal/mol, this reduction procedure was carried out. The integrated features of Chem3D Extreme v10.0 were then used to export the energy-minimized structures in PDB format. The ligand molecules had to be imported into AutoDock Tools in order to give Gasteiger charges. Combining non-polar hydrogens and identifying and modifying rotatable bonds were also steps in this procedure. The change in free energy related to the loss of a torsional degree of freedom following binding was assessed using the torsional degree of freedom (TORSDOF). Ultimately, the finished ligand structure was stored in the pdbqt AutoDock file format [18-20].

Molecular docking analysis

Accurately predicting the complex interactions between our carefully chosen ligand molecules and the particular protein receptors that we were closely examining was the main objective of our molecular docking research. To carry out this important investigation, we utilized the highly regarded Pyrx software, specifically the AutoDock Vina module, which is widely recognized in the scientific community for its effectiveness in molecular docking analyses. The purpose of the docking analysis was to systematically link the chosen protein receptors with three different inhibitors that we had discovered during initial research. The binding energy was used as a symbolic representation of this important interaction, and the overall results of the docking process were expressed in terms of binding affinities. It is crucial to remember that the binding affinity precisely illustrates the degree of binding and the favorable interactions between the ligand and the target receptor. It also indicates the strength and stability of the chemical binding that takes place between the ligand and the receptor [21, 22].

RESULTS AND DISCUSSION

Molecular docking study of curcumin, glibenclamide, and conjugate

The binding interactions of curcumin, glibenclamide, and a new glibenclamide-curcumin compound with the receptor Dipeptidyl Peptidase-4 (DPP4), a well-known therapeutic target in the treatment of diabetic mellitus, were examined using molecular docking. The docking scores, which indicate binding affinities, were found to be -8.5 kJ/mol for the conjugate, -7.2 kJ/mol for curcumin, and -7.8 kJ/mol for glibenclamide. The glibenclamide-curcumin conjugate exhibited the most favorable docking score of -8.5 kJ/mol, highlighting its potential as a robust DPP4 inhibitor. These results demonstrate the superior binding potential of the glibenclamide-curcumin conjugate compared to the individual compounds, suggesting enhanced receptor affinity and interaction stability.

The docking scores of the molecules are presented in **Table 1.**

Table 1: Docking scores of Glibenclamide, Curcumin and Curcumin + Glibenclamide

Compound	Protein	Dock score
Glibenclamide	DPP4	-7.8
Curcumin	DPP4	-7.2
Curcumin + Glibenclamide	DPP4	-8.5

Interaction analysis:

Curcumin:

The molecular docking study revealed that curcumin exhibited a binding score of –7.2 kJ/mol, indicating a moderate affinity toward the DPP4 receptor. The docking analysis identified several key amino acid residues—Tyr662, Glu205, Ser630, Tyr666, Glu206, Phe357, and Arg358—as crucial contributors to the ligand–receptor interaction. Three traditional hydrogen bonds that curcumin formed with Tyr662 (2.22 Å), Glu205 (1.74 Å), and Glu206 (2.00 Å) are crucial for the complex's stability. In addition to hydrogen bonding, various non-covalent interactions were observed, including π–π stacking interactions with Phe357 and Tyr666, carbon–hydrogen interactions with Ser630 and Arg356, and hydrophobic contacts involving Ser630, Tyr662, and Arg358. All of these interactions work together to make the curcumin–DPP4 complex more stable. The predominance of hydrophobic and hydrogen bonding interactions suggests that curcumin effectively occupies the active site of DPP4, thereby highlighting its potential as a natural modulator of DPP4 activity with possible therapeutic implications in metabolic disorders such as diabetes.

The interaction between Curcumin and DPP4 protein is presented in **Fig 3.**

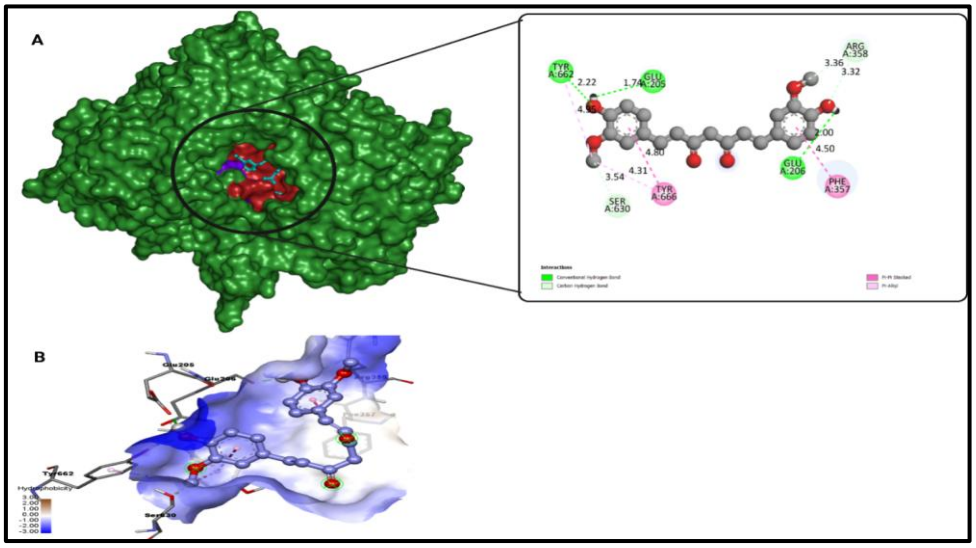

Fig 3: (A) shows a surface picture of curcumin interacting with DPP4 protein in two dimensions. Red represents non-polar areas, while blue indicates polar areas. (B) Show curcumin's hydrophobic interactions with the DPP4 protein.

Glibenclamide

Glibenclamide exhibited a higher binding score of -7.8 kJ/mol compared to curcumin, showcasing its effectiveness as a standalone DPP4 inhibitor. Various amino acid residues were found during docking analysis as binding sites including Trp:629, Ser:630, Asn:710, Arg:125, Glu:206, Tyr:547, and Phe:357.

Glibenclamide showed four conventional hydrogen bonds with Ser:630 (1.99 Å), Asn:710 (2.88 Å), Arg:125 (2.29 Å), and Tyr:547 (4.27 Å) that may be helpful in establishing and stabilising the complex. Apart from hydrogen bonds, non-covalent interactions were also observed including Pi-alkyl interaction with Trp 629, Pi-sigma interaction with Phe 357, Pi-anion interaction with Glu 206 and hydrophobic interactions with Asn 710, Ser 630, Arg 125, and Glu 206. These findings reaffirm Glibenclamide' s strong receptor binding capabilities, driven by a combination of hydrogen bonding and diverse non-covalent interactions.

The interaction between Curcumin and DPP4 protein is presented in **Fig 4.**

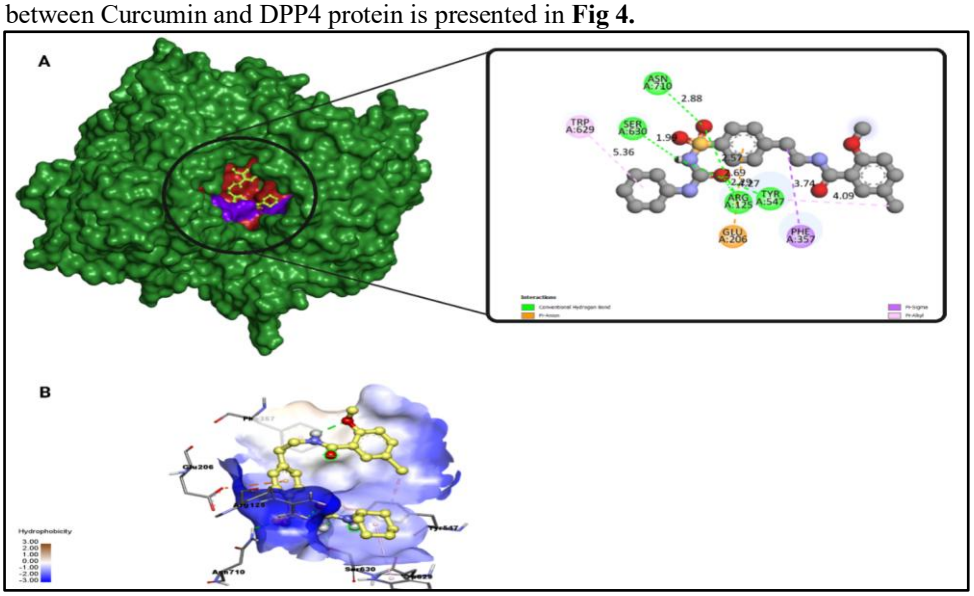

Fig 4: (A) shows a surface picture of glibenclamide interacting with DPP4 protein in two dimensions, with red denoting non-polar areas and blue denoting polar areas. (B) Show glibenclamide's hydrophobic interactions with the DPP4 protein.

Glibenclamide-Curcumin Conjugate:

The molecular docking analysis of the glibenclamide–curcumin conjugate demonstrated a highly favorable

binding value of –8.5 kJ/mol, suggesting a high affinity and potent inhibitory potential against the DPP4 receptor. The conjugate interacted with multiple key residues within the active site, including Lys554, Tyr547, Ser209, Arg669, Glu205, Tyr662, Tyr666, Arg125, Arg356, and Phe357, indicating extensive binding coverage and stability within the catalytic pocket. Three traditional hydrogen bonds were formed with Ser209 (2.08 Å), Arg669 (2.34 Å), and Arg125 (2.70 Å), which greatly aided in the ligand-receptor complex's stability. Furthermore, the presence of π–anion interaction with Glu205, π–π stacking with Phe357, and multiple alkyl and π–alkyl interactions with aromatic and charged residues such as Tyr547, Lys554, Tyr666, Tyr662, and Arg356 reinforced the overall binding strength. Additional hydrophobic contacts involving Ser209, Arg669, Tyr585, Arg125, and Tyr547 further enhanced molecular stability within the binding pocket. These diverse interaction patterns collectively underscore the conjugate's superior binding affinity compared to curcumin alone, suggesting that glibenclamide–curcumin conjugation may synergistically enhance DPP4 inhibition, potentially leading to improved pharmacological efficacy in managing metabolic disorders such as type 2 diabetes.

The interaction between Glibenclamide-Curcumin Conjugate and DPP4 protein is presented in **Fig 5.**

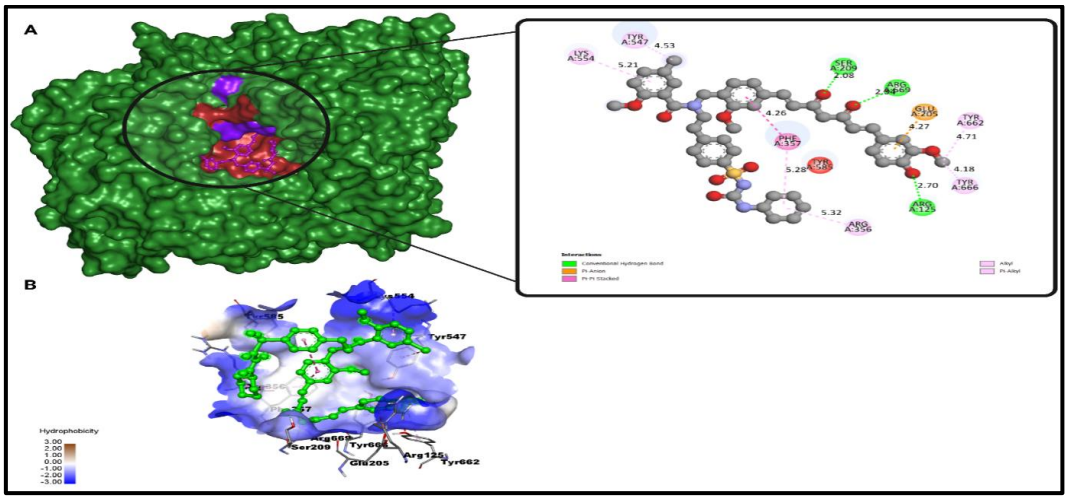

Fig 5: (A) Shows a surface picture of curcumin-glibenclamide conjugate against DPP4 protein, with blue indicating polar areas and red indicating non-polar areas with 2D interactions with curcumin-glibenclamide against DPP4 protein. (B) Show how curcumin-glibenclamide interacts hydrophobically with the DPP4 protein.

The molecular docking outcomes provide compelling evidence that underscores the significant therapeutic potential of the glibenclamide-curcumin conjugate, highlighting its role as a dual-acting compound that presents enhanced binding efficiency to the DPP4 enzyme. This innovative conjugate adeptly combines the natural bioactivity inherent in curcumin with the well-established pharmacological properties of glibenclamide. As a result, it presents a synergistic approach that could greatly aid in the efficient treatment of diabetes mellitus, a condition that affects millions worldwide. The favourable binding energy and comprehensive interaction profile exhibited by the conjugate mark it as a particularly promising candidate for further preclinical and clinical evaluations designed to assess its efficacy in therapeutic settings **[23]**. Furthermore, the research makes it abundantly evident how important certain interactions—like hydrophobic interactions, pi-stacking, and hydrogen bonds—are to the stability of protein-ligand complexes. These insightful discoveries from the docking investigations may provide a framework for the logical design and creation of stronger DPP4 inhibitors. Ultimately, this could significantly enhance the efficacy and effectiveness of current diabetes treatments available in the medical field today.

CONCLUSION:

The Glibenclamide-Curcumin conjugate's substantial therapeutic potential is demonstrated by the molecular docking results, which further emphasize the compound's dual-acting nature and improved binding efficiency to the DPP4 enzyme. This novel compound skilfully blends the proven pharmacological characteristics of Glibenclamide with the intrinsic bioactivity of curcumin. Consequently, it offers a synergistic strategy that may significantly contribute to the efficient treatment of diabetes mellitus, a disease that impacts millions of people globally.

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CONFLICT OF INTEREST: None

AUTHOR CONTRIVUTIONS:

Desai Madhuri Mahesh performed the research work, generated data and drafted the manuscript, Jadhav Sujata Abhay, and Koparde Akshada Amit monitored the project and provided the guidance.

DATA AVAILABILITY STATEMENT:

Data can be made available on reasonable request from corresponding author

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