

RESEARCH ARTICLE

Phytochemical analysis, therapeutic and molecular docking studies for the compounds of wild type and Senkambu variants of curry leaves targeting HER2 Kinase domain a potential gastric cancer receptor

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Abstract

Gastric cancer is the fifth most notable health concern globally. In recent years, molecular docking, a computational technique, has emerged as tool in drug discovery. The present investigation aimed to identify the major bioactive compounds in the wild-type curry leaves found in the Shevaroy Hills and the local Senkambu variant from Karamadai. Virtual screening of 40 ligands from Curry leaves of wild type and Senkambu type was identified through GC-MS profiling. These compounds were targeted against HER2 Kinase domain which is a potential receptor for Gastric cancer. Information regarding the binding site residues for the receptor was predicted using CASTp server. Molecular docking was performed for HER2 kinase domain with the predicted compounds through GC-MS profiling. The top 3 hits reported with least binding affinity for the target protein were considered for further interaction analysis using Biovia Discovery studio visualizer. Upon analyzing the interacted compounds, the Piperine from Wild type curry leaves was found to have good interaction with HER2 Kinase domain by forming two hydrogen bonds and binding score of -8.3 k cal/mol. The current study might guide the designing of analogues of piperine in the evolution of effective broad spectrum drug development in cancer therapy.

Keywords

bio-active compounds; curry leaf; docking; gastric cancer; piperine

Introduction

Gastric cancer ranks as the fifth most common cancer worldwide and the third leading cause of cancer-related deaths. Although there have been improvements in detecting and treating gastric cancer, the outlook for patients remains unfavourable, particularly in advanced cases. This disease shows significant geographic variation, with high incidence and mortality rates being recorded in Eastern Asia, Eastern Europe and South America, and lower rates in North America and certain parts of Africa. This variation is linked to diet, standard of living, and *Helicobacter pylori* infection, which is a major known risk factor, accounting 89 % of non-cardia gastric malignancies. Salty, smoked foods and alcohol consumption, and smoking increase the risk, while increased fresh food consumption decreases it. Hereditary account for about 10 % of all cases, warranting further investigation into high-risk populations. (1)

The human epidermal growth factor receptor 2 (HER2), part of the epidermal growth factor receptor (EGFR) family, is overexpressed in approximately 20-30 % of gastric cancer cases. Overexpression of HER2 correlates with more aggressive tumours, worse outcomes, and reduced survival in patients. Therefore, targeting the HER2 signalling pathway has emerged as a promising strategy for treating gastric cancer (2).

The HER2 kinase domain plays a vital role in drug development, with numerous HER2 inhibitors developed to combat HER-2-positive cancers. Among these is TAK–285, a compound that inhibits both HER2 and EGFR. This dual inhibitor has been investigated for its potential in treating various cancers, including as those of the breast, lung, stomach, and prostate (3). The crystal structure of the HER2 kinase domain in complex with TAK-285 (PDB ID: 3RCD) provides valuable insights into binding interactions and can be used for the virtual screening of potential inhibitors.

In recent years, natural remedies and traditional medicinal plants have attracted increased attention due to their potential in treating various diseases, including cancer (4). Curry leaves (*Murraya koenigii*), part of the Rutaceae family, are widely used in Indian cuisine and traditional medicine for their antioxidant and pharmacological properties. Known as a "miracle plant," these small trees or shrubs grow up to 6 meters in height and are propagated through sensitive seeds and grafting techniques (5). The plant features pinnate leaves with 11-21 aromatic, glossy green leaflets, small white flowers, and black drupe fruits. India is the global leader in the production and consumption of curry leaves, with Andhra Pradesh and Tamil Nadu serving as key cultivation regions due to favourable climates, large cultivation areas, and well-developed infrastructure (6). Beyond culinary uses, recent research has highlighted the plant's potential in managing cancer, as its

Table 1. Phytochemical profiling of Curry leaves wild type by using GCMS.

polyphenols and flavonoids can inhibit the proteolytic action of cancer cell proteasomes, ultimately inducing cell death (7). To explore natural compounds as complementary treatments, curry leaves show great promise as a potential avenue for developing more effective and accessible therapies for gastric cancer (8). In this study, we aim to identify potential HER2 kinase domain inhibitors from the phytochemicals present in wild-type and Senkambu varieties of curry leaves using GCMS analysis and virtual screening.

Materials and Methods

Extract preparation

Two ecotypes of curry leaf were used for this study: one from Yercaud in the Salem district (Wild Curry leaf) and another from Karamadai, Coimbatore district, Tamil Nadu (Senkambu). Leaves of both ecotypes were collected from their respective locations, shade-dried and subject to oil extration using hydro-distillation with a Clevenger apparatus. The extracted oil was analyzed using GC-MS (9).

Gas chromatography – Mass spectroscopy (GC-MS)

Gas Chromatography-Mass Spectrometry (GC-MS) equipment, manufactured by the Shimadzu and model QP2020 NX, is a single quadrupole apparatus used to analyse the derivatized samples. A sample volume of 1 µL was injected at a temperature of 250 °C.A sample volume of 1µl was injected at temperature of 250 $°C$. The temperature program initiated at 40°C for 2 minutes and then increased by 8 °C per minute until reaching 320 °C, with a total runtime of 10 minutes. A splitting ratio of 1:30 was used for sample injection. The spectrometer was set with an ionization chamber temperature of 220 °C, a mass spectrum range of 40 m/z to 600 m/z, an interface temperature of 300 °C, and a solvent cutoff at 6.0 minutes (10) (Table 1, 2 and Fig. 1, 2).

Table 2. Phytochemical profiling of Senkambu by using GCMS.

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TAMILNADU AGRICULTURAL UNIVERSITY - AGRICULTURAL MICROBIOLOGY

INSTRUMENT : PERKIN ELMER CLARUS SQ8C INJECTION : 1 MICRO LITER SAMPLE ID: CURRY LEAF WILD TYPE 0906

COLOUMN : DB-5 MS CAPILARY STANDARD NON POLARCOLOUMN DIMENSION : 30Mts, ID: 0.25 mm, FILM: 0.25 IM CARRIER GAS: He

Fig. 1. Chromatogram of Wild type Curry leaf.

TAMILNADU AGRICULTURAL UNIVERSITY - AGRICULTURAL MICROBIOLOGY

INSTRUMENT : PERKIN ELMER CLARUS SQ8C INJECTION : 1 MICRO LITER SAMPLE ID: SENKAMPU 0906

COLOUMN : DB-5 MS CAPILARY STANDARD NON POLARCOLOUMN DIMENSION : 30Mts, ID: 0.25 mm, FILM: 0.25 IM CARRIER GAS: He

Fig. 2. Chromatogram of Senkambu type.

Selection of Receptor

The domain of HER2 Kinase a 4-chain structure with a human sequence that is complexed with TAK-285 (3RCD) was selected as a possible receptor for molecular docking. Dual inhibitors targeting both human epidermal growth factor receptor (HER2) and epidermal growth factor receptor (EGFR) have been studied for treating malignancies in the breast, lungs, stomach, prostate, and other organs (Fig. 3).

Protein preparation

Three-dimensional X-ray crystal structures of the target protein were obtained from the Protein Data Bank. The 3D structure of the HER2 Kinase domain protein (PDB ID: 3RCD) was retrieved from Protein Data Bank. The Protein Data Bank file was pre-processed to remove crystallographic water and add hydrogen atoms.

Active site prediction

The active sites of the protein structure were identified using the Computed Atlas of Surface Topography of Proteins (CASTp) version 3.0. This web-based platform was used to detect and quantify gaps in three- dimensional

Fig. 3. 3D structure of HER2 kinase domain Complexed with TAK- 285.

protein configurations. Binding site residues were predicted, and the 3D protein structure was submitted to the CASTp service.

Selection of ligands

Compounds from curry leaves of wild-type and Senkambu variety were identified through GC-MS examination. Structures of 40 compounds from both varieties were retrieved from PubChem and CORINA and used for virtual screening against potential gastric cancer targets.Structure of 40 compounds of both varieties were retrieved from Pub-Chem and CORINA and used for virtual screening against possible gastric cancer targets.

Virtual Screening

Virtual screening was performed using the AutoDock Vina module within the Python Prescription Virtual Screening tool (PyRx 0.8). The structure of the protein was prepared, and the 40 ligand structures were entered into the PyRx tool along with the prepared macromolecule. The Auto-Dock Vina module in the PyRx tool was used to optimize the ligands and convert them into a pdbqt file. Binding sites were predicted using the CASTp server to build the grid (XYZ dimensions: 25x25x25) for the Auto Dock Vina during the virtual screening experiment, with an exhaustiveness setting value of 8 (11)

ADMET analysis

Assessing ADMET properties provides insights into the pharmacokinetic nature of the ligands. Swiss ADME, accessible via the SIB (Swiss Institute of Bioinformatics) webpage (https://www.sib.swiss), analyzed the ligands saved in Canonical SMILES format, which were then submitted for ADME estimation. Various factors, including the drug's aqueous solubility, blood-brain barrier penetration, gastrointestinal absorption, CYP 2D6 interaction, hepatotoxicity, and plasma protein binding levels, were recorded and examined (12) (Table 3, 4).

Table 3. Curry leaves wild type – Swiss ADME.

Interaction analysis

The binding interactions of the selected compounds with the HER2 kinase domain were analyzed using Biovia Discovery Studio Visualizer. The software visualizes the hydrogen bonds, hydrophobic interactions, and other noncovalent interactions between the ligands and the protein.

Results

GC-MS

Phytochemical profiling offers a comprehensive insight into the diverse array of bioactive compounds of curry leaves wild-type and Senkambu type. The GC-MS analysis identified nearly 40 compounds in both the samples, each with varying probabilities and abundances. In curry leaf of wild-type, prominent compounds included trans-Verbenol,3-Cyclohexen-1-ol, à-Terpineol and Caryophyllene oxide, others (Table 1). On the other hand, Senkambu type exhibited a distinct profile, with compounds including Caryophyllene, Caryophyllene oxide, and trans-Z- à-Bisabolene epoxide dominating the spectrum (Table 2). The comparative analysis of these two plant species has their unique chemical fingerprints and highlights their significance in traditional medicine and modern drug discovery.

Molecular Docking –Wild type and Senkambu

Swiss ADME datasets provide a detailed characterization

of various chemical compounds, including their characteristics of molecules like molecular weight, number of rotable bonds, and acceptors of hydrogen bonds. and donors, Log P/oil- water partition coeffient (MLOGP), water solubility, blood-brain barrier (BBB), gastrointestinal (GI) absorption, permeability, CYP1A2 inhibition, and Lipinski's rule of five violations. These properties are crucial for predicting the pharmacokinetic and pharmacodynamic behavior of compounds, which is essential for drug discovery and development. All the compounds screened from ADMET analysis were subjected to virtual screening. Details on the anticipated binding site residues made with the CASTp server. Using Biovia Discovery Studio Visualize, the top three hits with the highest binding affinity for the target protein are taken into consideration for additional interaction analysis.

Information about the binding site residues predicted by the CASTp server. The top 3 hits which exhibit highest binding affinity for the target protein, were selected for further interaction analysis using Biovia Discovery studio visualizer.

The results of molecular docking of wild-type curry leaves revealed promising interactions between selected compounds and their protein targets. Piperine exhibited strong affinity towards the protein target 3rcd, forming a conventional hydrogen bond with THR 793 and resulting (– 8.3 kcal/mol binding energy). Similarly, gamabufotalin demonstrated notable interactions with Arg 814 and ASP

924, yielding a binding energy of –8.2 kcal/mol. Additionally, Tyr 923, Asp 924, and Ala 710 exhibited significant interactions with the molecule Pyrrolodine, 1-[5-(1,3 benzodioxol-5-yl)-1-oxo-2,4-pentadienyl]-, (E,E)-, with a binding energy of –7.9 kcal/mol (Table 5, 6).

Table 5. Amino acids involved in interactions were visualized using Biovia Discovery Studio Visulaizer – Wild type.

Table 6. Amino acids involved in interactions were visualized using Biovia Discovery Studio Visulaizer- Senkambu type.

The results of molecular docking analysis of Senkambu revealed compelling interactions between the selected compounds and their protein targets. Friedelan-3 -one, despite not forming conventional hydrogen bonds, showed a remarakable binding energy of – 8.2 kcal/mol and a considerable affinityu for the protein targets 3rcd. Gamabufotalin showed significant interactions with ASP 924 and Arg 814, yielding an energy of -7.4 kcal/mol. Ursodeoxycholic acid demonstrated notable interactions with Asp 769, Gln 943, and Arg 814, yielding a –7.3 kcal/mol binding energy. The interactions analysed for both wild type and Senkambu type has been given in the Fig. 4 (A-E).

Fig. 4. Amino acids involved in interactions were visualized using Biovia Discovery Studio Visulaizer –Curry leaf wild type and Senkambu. (**A**)**.** Piperine (**B**).Gamabufotalin, (**C**) . Pyrrolidine, 1-[5-(1,3-benzodioxol-5-yl) -1-oxo-2,4 pentadienyl]-, (E,E), (**D**).Friedelan-3-one and (**E**). Ursodeoxycholic acid.

Discussion

Upon analyzing the compounds, piperine from wild-type curry leaves was identified as a potential inhibitor for HER2 Kinase domain due to its hydrogen bond interactions and a good binding affinity of -8.3 k cal/mol. Similarly, it has been shown that piperine inhibits the growth of gastric cancer by inducing apoptosis, highlighting its potential as an anti-cancer agent for treating gastric cancer (13). Piperine shows great promise in preventing cancer due to its ability to halt the cell cycle, increase autophagy and apoptosis, and disrupt redox homeostasis (14). Similar to the above results, piperine blocked cell migration by reducing STAT –3 activity, which led to the prevention of metastasis (15). The findings revealed that piperine can suppress IL-6, which effectively decreases the invasion of gastric cells (TMT-1) (16). In addition to the above results, piperine inhibits the development of human stomach cells and induces programmed cell death by targeting the P13K/Akt signaling pathway (17). It was shown that piperine efficiently suppressed the growth of breast cancer cells overexpressing HER2 and caused them to undergo apoptosis (18). This was achieved by inhibiting caspase-3 activation and PARP cleavage, ultimately resulting in the transcriptional downregulation of the HER2 gene expression. Additionally, piperine pretreatment resulted in increased sensitization to paclitaxel- induced cell death in these cells. The findings also suggest that Gamabufotalin interacts proficiently with essential amino acids that play a role in gastric cancer progression, indicating its potential as a suppressor of cancer cell growth and spread.

The consistent binding observed, even with minor variations in binding energy, emphasizes gamabufotalin's potential as a therapeutic option. These results reinforce its significance in targeting proteins essential to the progression of gastric cancer, justifying further investigation into its clinical efficacy. It has been demonstrated that gamabufotalin and apatinib work in concert to suppress the growth and spread of gastric cancer cells by downregulating VEGFR and MMP-9, improving treatment outcomes (19). This study confirmed that piperine has strong cytotoxic effect against gastric cancer cells, both in its solo form and when coupled with chemotherapeutics. Piperine promoted apoptosis and inhibited cancer cell proliferation, thereby increasing the efficacy of chemotherapy treatments. These findings imply that piperine may improve therapeutic outcomes in gastric cancer therapy (20).

Conclusion

In this study, potential HER2 kinase domain inhibitors were identified from the phytochemicals present in wildtype and Senkambu varieties of curry leaves using GC-MS analysis and virtual screening. Piperine from wild-type curry leaves exhibited the highest binding affinity, forming stable hydrogen bonds with a key residue in the binding site. ADMET analysis of the selected compounds revealed favorable properties for drug development. These findings highlight piperine as a potent phytochemical from curry leaves and a potential source of innovative therapeutic a foundation for developing targeted therapies using natural products for the treatment of stomach cancer. Moreover, structural modifications and formulation approaches could be explored to enhance the effectiveness and safety profiles of these natural products for future drug development endeavors.

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Authors' contributions

S carried out the research work. V guided to carry out the research work and GC-MS analysis work. M and R helped in molecular docking work

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None.

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