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RESEARCH ARTICLE

A scientific pharmacognosy on Gaucher's disease: an in silico analysis

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Abstract

From ancient times, studies on herbal medicine and pharmacognosy have increased gradually worldwide, due to the increased side effects, adverse drug reactions, and charge lines of modern medicines. Plants are well known for their medicinal effects and nutritional values. They contain bioactive compounds which display a wide spectrum of therapeutic effects. Gaucher's disease (GD) is a rare autosomal recessively inherited metabolic disorder caused due to the defect in Glucosylceramidase beta gene coding for the enzyme acid-β-glucosidase in humans. We revealed the profound binding efficiency of five selected bioactive compounds from different plants against the main enzyme acid-β-glucosidase responsible for GD through molecular docking. An in silico approach along with the ADMET profiles of phytocompounds was done using the Schrodinger software. The preventive measure of GD leads to side effects, inaccessible and unaffordable which put forth the emergence of phytocompounds which have fewer toxic effects, and one such compound is β-D-Glucopyranose with the best docking score (–10.28 kcal/mol) and an excellent binding affinity than other ligands, which could be further analyzed for stability using molecular dynamics study and in vitro. Being a dietary supplement, these compounds could be prepared in any form of formulation as a drug.

Keywords Acid-β-glucosidase · Pharmacognosy · In silico analysis · ADMET · Phytocompounds

Abbrevations

GD	Gaucher's disease
GBA	Glucosylceramidase beta gene
ADMET	Absorption, distribution, metabolism, excretion, and toxicity
PDB	Protein Data Bank
CNS	Central nervous system

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Introduction

The majority of the world's population relies mainly on plants and plant extracts for health care. The World Health Organization (WHO) reports have indicated that over 40% of all plant species present in the world can be used for medicinal purposes at one time or another. Identifying and predicting the pharmacological basis of the bioactive compounds of traditional plants are a great achievement for modernizing their use. In silico models are increasingly popular in the drug development process against specific diseases and across clinical research.

Pharmacognosy is the study of the physical, chemical, biochemical, and biological properties of drugs, drug substances of natural origin, as well as the search for new drugs from natural sources. Since ancient times, the use of traditional herbal medicine in India has been documented (Charaka & Dridhbala 1996). Sixty percent of the world's population use alternative medicines which are used by rural masses as well as the developed countries where modern medicines dominate (Ballabh and Chaurasia 2007). In India, the traditional medical practitioner prepares their formulations using their recipes and dispenses them to patients. The interest in traditional medicine has been growing rapidly,

due to the increased side effects, adverse drug reactions, and charge lines of modern synthetic medicines. Thus, it is believed that herbal medicine can be utilized to prevent and control the consequence of disease and illness in a more rational way.

Natural products or secondary metabolites, the organic molecules with low molecular weight which are produced by living organisms like microbes and plants. In India, out of 17,000–18,000 flowering plant species, around 7000 plant species are currently used as medicinal plants (National Medicinal Plants Board 2000). The range of pharmaceutical products that can be derived from plants are antimicrobials, antivirals, antifungals, neuroprotective products, therapeutic proteins, and drugs.

Modern genetic research can determine which gene or gene packet codes the substances that can fight a particular disease through the "in silico pharmacology." One of the most rapidly growing areas that globally covers the development of techniques for using software to capture, analyze and integrate biological and medicinal data from diverse sources, which can be used to make predictions suggest hypotheses, and ultimately provides discoveries or advances in medicine and therapeutics (Ekins et al. 2007). The first and foremost task in drug discovery is the identification of a suitable drug target. The targets could be the biomolecules which could be DNA, RNA, and proteins such as receptors, transporters, enzymes, and ion channels. The compound is believed to be druggable when it meets all the standard requirements of being a drug in terms of efficacy, safety, and displaying a positive gesture in the clinical trials (Mohd Hassan et al. 2014).

Gaucher's disease (GD) is a rare, autosomal recessively inherited metabolic disorder, caused due to the defect in the Glucosylceramidase beta gene (GBA1; OMIM Id: 606,463) coding for the enzyme acid-β-glucosidase (PDB Id: 2NT1) in humans. Its prevalence is 1:50,000 to 100,000 in the general population. The inactivating mutations in the GBA1 gene restrict the acid-β-glucosidase enzyme from cleaving the β-glucosyl linkage of Glucocerebroside, which is required to break down the glycolipid glucocerebroside into glucose and ceramide (Stone et al. 2000). The human GBA1 gene has 12 exons and 11 introns which are located on chromosome 1q22 which has a homologous pseudogene sequence located 16 kb downstream (Horowitz et al. 1989). The gene mutations lead to the amino acid replacement in glucocerebrosidase which can reduce the protein stability reducing the essential catalytic activity. GD is displayed clinically as a heterogeneous disorder that is divided into three phenotypes: Type 1 is non-neuronopathic GD, which is the most common form of the condition. Most individuals experience thrombocytopenia, hepatosplenomegaly, infarction, bone crises, avascular necrosis, and osteoporosis. Type 2 is acute neuronopathic GD that occurs in newborns and infants which is characterized by neurological complications due to the abnormal accumulation of enzymes in the brain. They experience splenomegaly, hepatomegaly, hypotonia, spasticity, strabismus, dysphagia, retroflexion, failure to thrive, stridor due to laryngeal spasm, anemia, and thrombocytopenia. Type 3 is chronic neuronopathic GD, which occurs during the first decade of life. In addition to blood and bone abnormalities, other neurological complications like mental deterioration, ataxia, myoclonic seizures, horizontal and vertical gaze palsy, and interstitial lung diseases may be experienced.

Acid-β-glucosidases hydrolyze the glycosyl residues, oligosaccharides, flavonoids, and isoflavonoid glucosides. These molecules are present in bacteria, archaea, eukaryotes, fruits, red wines, soybeans, tea, plants, and vegetables. The innovative treatment measures for GD are enzyme replacement therapy (ERT), substrate reduction therapy (SRT), and certain synthetic drugs, which are inaccessible and unaffordable but merely help to control the symptoms, prevent irreversible damage, and improve the quality of life.

In our study, we construct the network of relationships among the medicinal plants, natural compounds, and biological targets of diseases. We hereby performed a deep virtual screening through molecular docking studies to test the binding efficiency of selected bioactive compounds from plants as a drug candidate against the acid-β-glucoside enzyme. We thereby elucidate the basics of the effects of the natural compounds in medicinal plants and predict their potential pharmacological activities, thus attempting to find an alternative solution for GD.

The systematic literature review of the in silico analysis of the GD is elucidated in Fig. 1. About 46% of articles are referred regarding the selection of the phytocompounds followed by 31% regarding the Gaucher disease, its causes, symptoms, and works underwent. Last but not the least, articles on the computational tools mainly the in silico works are also referred to.

Materials and methods

Structure-based drug designing

In this study, the use of an iterative process called structure-based drug designing, which is the main part of an entire drug lead discovery process, was done. In this process, it directs the discovery of a drug lead, which is not a drug product but, especially, a compound with at least micromolar affinity for a target (J. Antel 1999). The compound information from a plant is the initial raw material for determining the basis of the herb's pharmacological properties. Compound information is mainly collected from literature reports and small molecule compound databases.

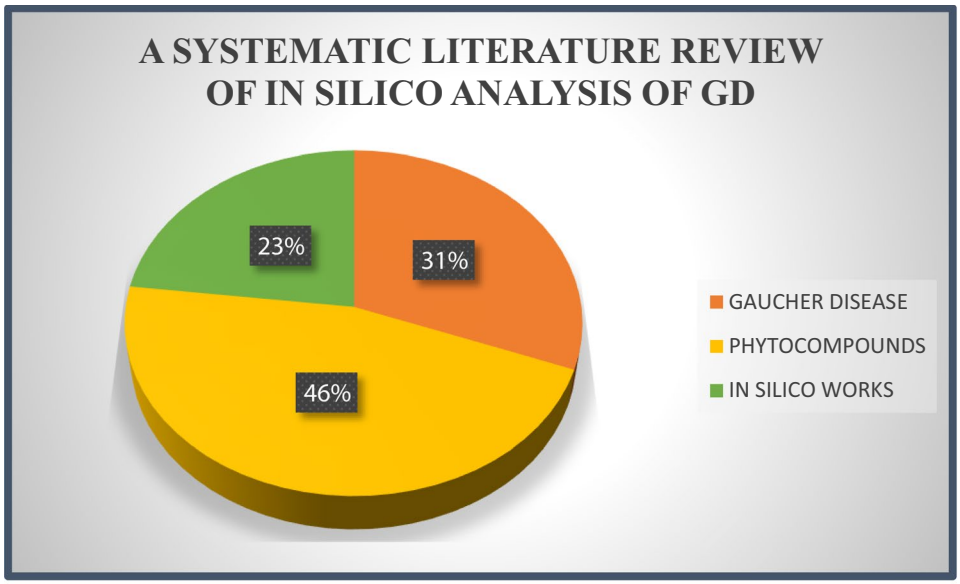

Fig. 1 A systematic literature review conducted throughout the study on various subjects mainly about the phyto-compound selection (46%), Gaucher's disease (31%), and in silico works (23%)

Databases

In this study, 5 naturally occurring bioactive compounds from 3 different plant species were selected for this docking analysis. All these phyto-ligands were retrieved from a chemical database, i.e., PubChem (https://pubchem.ncbi.nlm.nih.gov/), a database specifically for small molecules. The PubChem compounds were retrieved in.sdf file format. The target protein was retrieved from (PDB) Protein Data Bank (https://www.rcsb.org/).

Ligand preparation

The ligands of phytocompounds were converted into the 3D structure using the Ligprep tool in Maestro Schrodinger version 10.2. The ligands were geometrically optimized, and then, the 2D sdf files were converted into 3D structures using the Ligprep tool.

ADMET selection

When the drug-likeness is established from the analysis of physiochemical properties and structural features of bioactive compounds of plants, the ADMET (absorption, distribution, metabolism, excretion, toxicity) properties play a crucial role in drug filtering. Due to the inaccessibility and unaffordability of the available drugs for Gaucher's disease, there is a need to discover a lead from bioactive molecules. Therefore, predicting the ADMET properties of drug molecules before drug designing and performing this screening can reduce the cost of drug development as well as improve the success rate of the whole procedure. Five compounds were successfully scored well in all the ADMET properties analyzed using the QikProp version 4.4 in the Schrodinger suite (QikProp, molecule 4.4, 2012). Some of the major parameters like CNS, molecular weight, donor hydrogen bonds, acceptor hydrogen bonds, human oral absorption, percent human oral absorption, Lipinski's rule of five, and Jorgensen's rule of three were also analyzed along with other QikProp properties. The bioactive phytocompounds which displayed pragmatic result were chosen for the ADME, and preferable docking poses has been tabbed for the rationale of docking (Vijayakumar et al. 2017).

Protein preparation

The proteins were prepared by removing the native auto and all water molecules. Hydrogen was added using the templates for the protein residues using Maestro 10.2 version. The goal of protein preparation is to generate one or more protein models that represent the bioactive conformation(s) of the protein when ligands are bound, thus becoming an essential process by rectifying the confrontations in protein structure. The water molecules were removed from the structure and thereby increasing the entropy of the target molecule.

Molecular docking

Molecular docking is used to positioning the computer-generated 3D structure of small ligands into a receptor structure in a variety of orientations, conformations, and positions,

thus making it helpful in drug discovery and medicinal chemistry providing insights into molecular recognition. In this study, Maestro v10.2 was used to perform the extra precision (XP) docking for speculating the binding affinity and analyzing the efficacy of the ligand and inhibitory constant of the ligand against the target. In this study, the entire ligand was docked with the target molecule flexibly using the Glide Xtra precision (XP) tool. As a result of successful docking, we have obtained better docking scores and poses with accurate hydrophobic contacts between target residues to ligand (Prabhu et al. 2017).

From the methodology, we elucidate that we can treat a single medicinal plant with the same complexity as a synthetic drug, utilizing the technical means from the bioinformatics and molecular docking analysis to explore the bioactive compounds and the potential pharmacological foundation of plant effects. This in silico trial reduces the need for animal models and human cohorts, reducing the time and cost of studies, and offers one type of solution to current problems in drug development. Similarly, the modelling of diseases at computational network levels enables a high demand for personalized treatment measures, providing the potential to enable precision medicine for complex diseases with variable treatment responses across the patient population.

Results

ADMET analysis

ADME describes the absorption, distribution, metabolism, and excretion of phytocompounds which are analyzed for its drug-like properties. In addition, 26 parameters were analyzed including central nervous system (CNS); molecular weight; total solvent accessible surface area (SASA) and their hydrophilic (FOSA), hydrophobic (FISA), π (PISA), and weakly polar (WPSA) components; volume; donor and acceptor hydrogen bonds; human oral absorption; percent human oral absorption; Lipinski's rule of five and Jorgensen's rule of three; metabolic reactions; stars; amide; rotor; number of reactive functional groups (rtvFG); QPlogPoct; QPlogPw; QPlogPo/w; QPPCaco; QPlogBB; QPlogKp; and QPlogKhsa. Statistics estimate that almost half of the candidate drugs do not undergo clinical trials because they fail to meet suitable levels of efficacy and around 40% fail because they have a toxic effect on the body, making them unsafe for use in humans (Pellegatti 2012). According to literature study, about 50 compounds were selected for ADME analysis; from them, only 5 compounds from 3 different plants *Iris hollandica*, *Ginkgo biloba*, and *Waltheria indica* were obeying the suitable levels of efficacy, helping to accelerate the drug discovery pipeline (Table 1).

Table 1 Analysis of ADME properties for the plant compounds using QikProp

Molecule/ PubChem ID	#Rotor	Mol_ MW	Dipole	SASA	Donor HB	Acce ptor HB	#Metab	Human oral absor ption	Percent human oral absor ption	Rule of five	Rule of three	CNS	Volume	QPlog Poct	QPlog Pw	QPlog Po/w	QPlog BB	PISA	QPlogKp	Stars	Amide	#rtvFG	FOSA	FISA	Q PP Caco	Q Plog Khsa
β-D-glucopyranose (64,689)	6	180.157	2.953	356.652	5	10.2	4	2	46.68	0	0	−2	563.938	16.751	18.175	−2.234	−1.573	0	−5.146	4	0	1	128.619	228.034	68.148	−0.878
Isorhamnetin (5,281,654)	5	316.267	5.409	540.609	3	5.25	5	3	65.627	0	0	−2	919.031	17.574	12.529	1.204	−1.929	212.907	−4.62	0	0	0	92.713	234.989	58.546	−0.156
2,3-Dihydro-3,5-dihydroxy-6-methyl-4 h-pyran-4-one (15,114,468)	2	158.154	3.72	339.284	1	5.2	3	3	82.08	0	0	0	537.926	8.461	7.389	0.019	−0.286	6.917	−3.094	0	0	0	235.182	97.185	1186.583	−0.816
Kaempferol (5,280,863)	4	286.24	5.622	501.402	3	4.5	4	3	64.746	0	0	−2	840.36	16.695	12.28	1.06	−1.803	266.185	−4.533	0	0	0	0	235.218	58.255	−0.196
Ginkgetin (5,271,805)	7	566.52	11.634	849.057	2	7.5	6	1	66.315	1	1	−2	1600.865	28.124	15.074	4.618	−2.847	394.857	−4.477	2	0	0	181.815	272.385	25.875	1.134

Molecular docking

The molecular docking study was conducted to analyze the optimized conformation of ligand-receptor complex indicated by least binding energy. This scaffold approach is used to understand drug-biomolecular interactions for the purpose of rational drug design. Molecular docking generates different possible adduct structures that are ranked and grouped together based on the scoring function (Dar & Mir 2017). In this study, the protein acid-β-glucosidase (PDB ID: 2NT1) was considered as target, and interactions with phytocompounds from the plants *Iris hollandica*, *Ginkgo biloba*, and *Waltheria indica* were carried out. The docking results were observed with Glide score (G. score), interacting residues, and bond length (Table 2).

β-D-glucopyranose

Among the 5 ligands, the compound β-D-glucopyranose from *Iris hollandica* had the least Glide score of –10.28 kcal/mol (Table 1). The compound interacted with residues of ASN 377, ASN 262, SER 447, and GLU 446. The protein had formed 6 hydrogen bonds with the residues of ASN 377 of length 1.8 and 2.1 Å, ASN 262 of 2.9 and 2.5 Å, and SER 447 and GLU 446 each with one bond of length 2.1 and 1.7 Å respectively (Fig. 2).

Isorhamnetin

Isorhamnetin from *Ginkgo biloba* has the second G. score of –9.68 kcal/mol and interacted with 3 hydrogen bonds with the residues of GLU 446, GLY 379, and ASN 377. The bond lengths were observed as 2.3, 2.1, and 1.7 Å, respectively (Fig. 3).

3-Dihydro-3,5-dihydroxy-6-methyl-4 h-pyran-4-one (DDMP)

The third docking scores were received by the ligand 2,3-dihydro-3,5-dihydroxy-6-methyl-4 h-pyran-4-one (DDMP) from the plant *Waltheria indica* with –9.38 kcal/mol of G. score. This compound formed only one hydrogen bond with the interacting residue TRP 69 with a bond length of 1.9 Å (Fig. 4). Even though the interactions were less, the interacted residue had an appreciable glide score.

Table 2 Molecular docking analysis of plant compounds with acid-β-glucosidase (2NT1)

Medicinal plant	Name of ligand/PubChem ID	Glide score (Kcal/mol)	Residues interacted	Bond length (Å)	No. of bonds
Iris hollandica	β-D-glucopyranose (64,689)	–10.28	ASN 377 (H–O)	1.8	6
			ASN 377 (H–O)	2.1	
			ASN 262 (H–O)	2.9	
			ASN 262 (O–H)	2.5	
			SER 447(O–H)	2.1	
			GLU 446 (H–O)	1.7	
Ginkgo biloba	Isorhamnetin (5,281,654)	–9.68	GLU 446 (H–O)	2.3	3
			GLY 377 (O–H)	2.1	
			ASN 377 (H–O)	1.7	
Waltheria indica	2,3-Dihydro-3,5-dihydroxy-6-methyl-4 h-pyran-4-one (15,114,468)	–9.38	TRP 69 (O–H)	1.9	1
Ginkgo biloba	Kaempferol (5,280,863)	–9.13	ARG 252 (O–H)	2.2	6
			ASN 262 (O–H)	2.1	
			ASN 377 (H–O)	1.8	
			GLU 446 (H–O)	2.9	
			GLU 446 (O–H)	2.6	
			GLU 446 (H–O)	2.5	
Ginkgo biloba	Ginkgetin (5,271,805)	–6.13	ASN 377 (H–O)	2.4	4
			ARG 252 (O–H)	2.3	
			GLU 446 (H–O)	2.1	
			ARG 444 (O–O)	3.1	

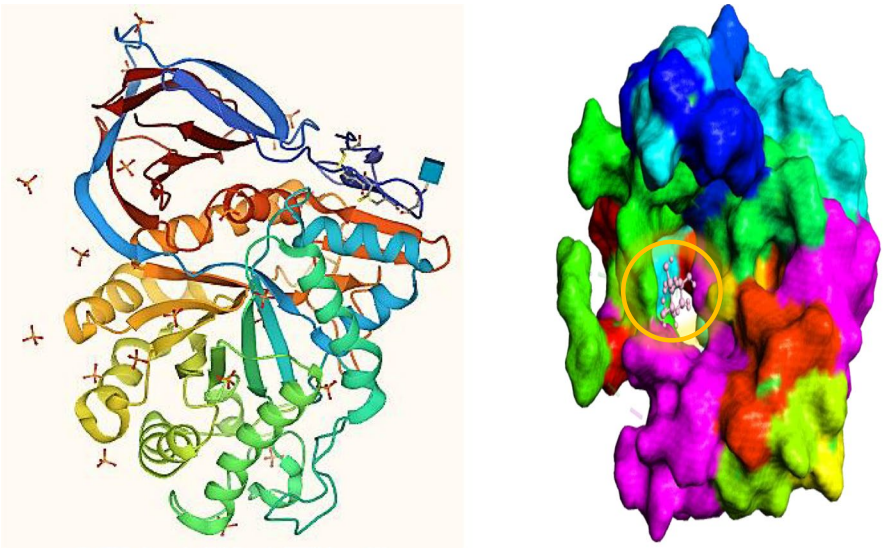

Fig. 2 Interaction of phyto-ligand β-D-glucopyranose with the target enzyme acid-β-glucosidase (2NT1) having a least Glide score of –10.28 kcal/mol extracted from the plant *Iris hollandica* indicating a suitable drug candidate molecule with enlarged image of target protein on the right

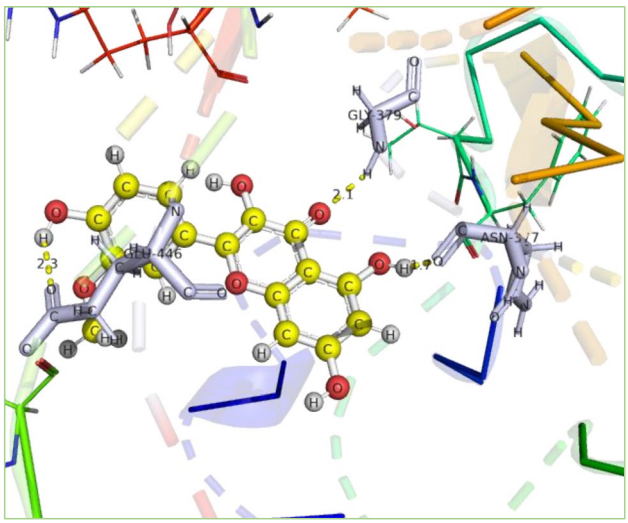

Fig. 3 Interaction of isorhamnetin with the target enzyme acid-β-glucosidase (2NT1) having the least Glide score of –9.68 kcal/mol extracted from the plant *Ginkgo biloba*

Kaempferol

Kaempferol from *Ginkgo biloba* had the next leading docking score of –9.13 kcal/mol of G. score. Their interacting residues were ARG 252, ASN 262, ASN 377, and GLU 446. The protein had formed 6 hydrogen bonds with these residues of ARG 252, ASN 262, ASN 377 had one hydrogen bonds each with 2.2, 2.1, and 1.8 Å of bond lengths respectively (Fig. 5). The remaining residue GLU 446 had interacted with the protein and formed three hydrogen bonds with 2.9, 2.6, and 2.5 Å of bond length.

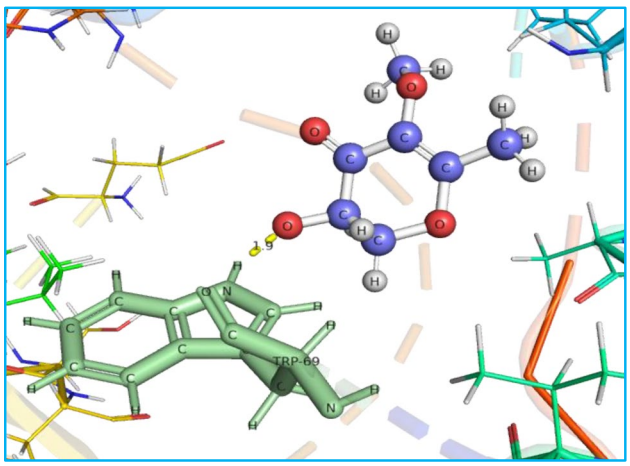

Fig. 4 Interaction of phyto-ligand 2,3-dihydro-3,5-dihydroxy-6-methyl-4H-pyran-4-one with the target protein acid-β-glucosidase (2NT1) having a Glide score of –9.38 kcal/mol extracted from the plant *Waltheria indica*

Ginkgetin

The compound Ginkgetin from the plant *Ginkgo biloba* had the lowest docking score among the phyto-ligands. The docking score for this compound is –6.13 kcal/mol of G. score. The protein has formed four hydrogen bonds with the following residues: ASN 377, ARG 252, GLU 446, and ARG 444. These residues had formed 4 hydrogen bonds altogether with bond lengths of 2.4, 2.3, 2.1, and 3.1 Å with their respective residues ASN 377, ARG 252, GLU 446, and ARG 444 (Fig. 6).

Among the random protein-residue interaction, the following are the residues that had interaction with the plant compounds: ASN 377, ASN 262, SER 447, GLU 446,

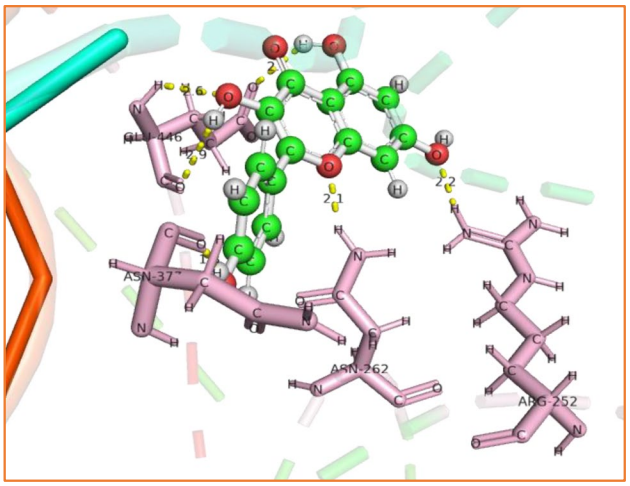

Fig. 5 Interaction of phyto-ligand kaempferol with the target protein acid-β-glucosidase with the Glide score of –9.13 kcal/mol extracted from the plant *Ginkgo biloba*

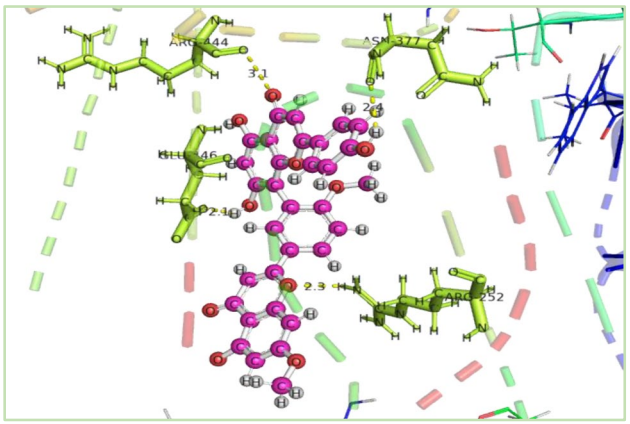

Fig. 6 Interaction of phyto-ligand ginkgetin with the target protein acid-β-glucosidase with a Glide score of –6.13 kcal/mol extracted from the plant *Ginkgo biloba*

GLY 379, TRP 69, ARG 252, and ARG 444. Most of the phytocompounds like β-D-glucopyranose, isorhamnetin, kaempferol, and ginkgetin interacted with two random residues sites—ASN 317 and GLU 446. Likewise, β-D-glucopyranose and kaempferol interacted with ASN 262. Although the results obtained in this study serve as a base for the future works that need to be carried out on the disease, currently, the medications provided for the disease are scanty, and relying on natural products will be a good alternate source for the better health of human life. Living in compliance with the environment will always be the way forward for the human community, as synthetic drugs do have their own side effects and the harmful toxic substances let out by the medical industry as effluents do impact the environmental stability. Going green and reducing the carbon footprint should be the focus of future works.

Discussion

Chemical impact on health is usually investigated using the concept of ADME. This is how a chemical is adsorbed, distributed, metabolized, or eliminated in living organisms. It is believed that ADME shows the toxicity of small molecules (Mondal et al. 2009). Molecular docking helps in predicting the intermolecular framework formed between a protein and a small molecule or a protein and a small molecule or a protein and protein, suggesting the binding modes responsible for inhibition of the protein. The binding affinity of a molecule to target is reckoned upon the contributions from various factors affecting the receptor molecule to the ligand (Morris and Lim-Wilby 2008). Bioactive molecules are those secondary metabolites exhibiting therapeutic effects, preventing toxicological and immunostimulant activity. These could be plant based or microbe based. The most known plant derived bioactive compounds could be alkaloids, flavonoids, phenolic acids, terpenes, saponins, and tannins (Anulika et al 2016).

β-D-glucopyranose is a synthetic simple monosaccharide, a flavone-derived compound which can be used as an energy source and is present in dietary sources like cereals, carrots, peppers, celery, olive oil, peppermint, thyme, rosemary, and oregano. These molecules contain a wide spectrum of pharmacological activities like anticancer and antioxidant effects (Xiao et al. 2011). A wide range of phytochemical compounds are present in the plant *Iris hollandica*, which could be used for various pharmacological activities like antioxidant, anticancer, antifungal, antibacterial, and anti-inflammatory activities (Kaizal and Hussein 2019).

Isorhamnetin is an O-methylated flavanol from the class of flavonoids. These are present in almonds, chives, dill weed, fennel leaves, red onions, and turnip greens. The main health benefits of this compound are cancer and hypertension prevention, keeping the heart healthy, and also diabetes treatment (J Lee et al. 2009). The neuroprotective effect of isorhamnetin in the brain helps in novel treatment as well as prevention for neurodegenerative diseases (Xu et al. 2012). Among the flavonoids, isorhamnetin had the best effect in inducing the expression of neurofilaments as well as nerve growth factor–induced neurite outgrowth. It has also been proven that isorhamnetin has antitumor and anti-oxidation activities and reduces the superoxide anion in liver cells (Igarashi & Ohmuma 1995).

DDMP is easily available in a wide variety of foodstuff like orange juice, popcorns, onions, soybeans, pears, rambutan fruit, American groundnut, scarlet runner beans, and a variety of leguminous seeds. It is believed to have pharmacological

activities like radical scavenger (Takara et al. 2007), antiproliferative, antioxidant, antimicrobial, autonomic nerve, anti-inflammatory, anti-arthritic, anticancer, antidiabetic, analgesic (Nandagopalan et al. 2015), and pro-apoptotic activities (Ban et al. 2007). Traditionally, the plant *Waltheria indica* has high medicinal values, and they are widely used to treat a variety of diseases like cough, wound healing, sleeping sickness, cancer, malaria, and viral diseases (Banakar and Jayaraj 2018).

Kaempferol is a natural flavonol and present in a wide range of foods and plants such as apples, tomatoes, green tea, onions, broccoli, blackberries, aloe vera, and *Moringa oleifera*. They have a wide range of pharmacological activities including antioxidant, anti-inflammatory, antimicrobial, anticancer, cardioprotective, neuroprotective, antidiabetic, anti-osteoporotic, estrogenic/antiestrogenic, analgesic, and anti-allergic activities (Calderón-Montaño et al. 2011). Kaempferol acts as a scavenger of free radicals and superoxide radicals as well as maintains the activity of various antioxidant enzymes such as catalase, glutathione peroxidase, and glutathione-S-transferase. They exhibit anticancer activity through the activation of caspases and modulation of multiple molecular targets (p53 and STAT3) (Rajendran et al. 2014).

Ginkgetin is a natural nontoxic biflavone that is present in most plants like *Taxus baccata*, *Cephalotaxus harringtonia*, *Elateriospermum tapos*, *Metasequoia glyptostroboides*, *Gaultheria yunnanensis* and *Chamaecyparis obtusa*. They show a wide range of biological activities such as anticancer, anti-inflammatory, antimicrobial, antioxidant, anti-atherosclerosis, hepatoprotective, and neuroprotective activities. Ginkgetin also acts as an inhibitor of thrombin, pancreatic lipase, PLA_2, cAMP-PDE, and cGMP-specific PDE5A1. Similarly, their therapeutic activities are mediated by modulating inducers of autophagy, inflammation mediators, anti-apoptotic proteins, and transcriptional factors (Adnan et al. 2020).

The existence of this mixture of phytomedicines in medicinal plants creates a broad spectrum of drugs against the Gaucher disease targeting one crucial enzyme acid-β-glucoside responsible for the deadly disease. Aside from these phytocompounds, we docked in our study other studies that investigated the binding affinities of other phytocompounds from various geographical origins (Manickam et al. 2014; Subramaniyan et al. 2018). Taken all together, from our study and other studies, we shed the light on the protective and preventive role of traditional medicinal plants against the Gaucher disease.

Managerial implications

The research mainly focussed on the treatment of Gaucher's disease using organic compounds. Synthetic drugs are proved to be efficient but are currently having side effects. For GD, the treatments that are currently available are very few. More therapeutic methods should be developed as a promising treatment for the disease. Our study brings about the use of phytocompounds from various plant sources as an alternate remedy for the existing synthetic drug present for the treatment of the disease. Along with this, environmental sustainability can be also achieved as we aim to reduce the carbon footprint and also rely on green sources for treatment. Traditional medicine is always said to have a positive impact on human life, as we live by the environment. The results provided in this work can be taken further in vivo and provide a promising and cost-efficient remedy for the Gaucher disease.

Conclusion

Medicinal plants are the thriving source of life-saving drugs for most people treating health problems. Many naturally occurring plants and vegetables are available which can be used to cure the deficiency of acid-β-glycosidase. This in silico study on Gaucher's disease can resolve the status of medicinal plants that are difficult to study on a practical level and predict and clarify the mechanisms of the active ingredients in plants. It is found that among the five best phytocompounds, β-D-glucopyranose has the best docking score of –10.28 kcal/mol, which showed the excellent binding affinities with the target protein, and the predicted ADME properties and drug-likeness were also noteworthy, thus suggesting a better drug candidate for Gaucher's disease. These phytocompounds can be used as therapeutic agents against Gaucher's disease but requires further elucidation of the mechanism of actions in in vitro and in vivo biological models.

There were limitations and deficiencies; the proposal of the work included the laboratory needs with instrumental setup and wet labs, but due to the unexpected pandemic, we were forced to narrow down to a facile work. Therefore, the phytocompounds were selected from different plant sources through literature review from the reputed unbiased journals. Although computer-aided drug designing and docking studies have been widely used and developed, they still have some limitations such as the model maturity and computational accuracy and need to be improved further. Due to the structure-based methodology, several compounds are not suitable for the computer-aided designing because of their special structure characteristics.

This in silico methodology can resolve the status of medicinal plants that are difficult to study on a practical level and help to predict and clarify the mechanisms of the active compounds in medicinal plants. Thus, we believe that in the future, this drug candidate will work against the disease efficiently, accurately, and quickly. This drug candidates will be

more widely usable in the future on revealing and predicting its pharmaceutical effects and cost efficiency.

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Author contribution Amritha PS drafted the manuscript and collected the literature, Sreeram S did the PyMOL visualizations, and Sathish-Kumar R did the bioinformatics part of ADME and molecular docking studies and reviewed the manuscript.

Availability of data and materials All data generated or analyzed during this study are included in this published article.

Declarations

Ethics approval and consent to participate No human or animal specimens were used in this work.

Consent for publication Not applicable.

Competing interests The authors declare no competing interests.

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