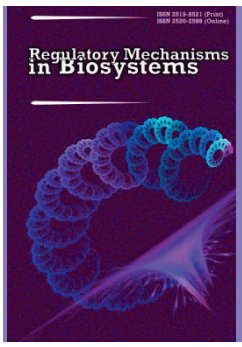

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Potential α-glucosidase inhibitor in nyale worm (*Eunice* sp.) extract for anti-diabetic type 2 target

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Nyale (Annelida, Eunicida, Eunicidae) is a typical sea worm of Kuta-Mandalika beach, Central Lombok, Indonesia. Diabetes mellitus is a chronic disease characterized by high blood sugar levels (glucose). Diabetes occurs because the body cannot produce enough insulin or cannot use insulin effectively. The α-glucosidase enzyme is a potential target in managing diabetes mellitus, particularly type 2 diabetes. This enzyme plays a role in the breakdown of complex carbohydrates into simple sugars in the small intestine. These sugars are then absorbed into the bloodstream and then blood sugar levels are raised. By targeting the α-glucosidase enzyme through the use of α-glucosidase inhibitors, the rate of carbohydrate breakdown and absorption can be slowed down. This mechanism needs to be explored using an *in silico* approach with the molecular docking method to see the potential of compounds contained in Nyale to inhibit the α-glucosidase enzyme. Compounds contained in Nyale were determined using the gas chromatography-mass spectrometry (GC-MS) method. Molecular docking in this study used Pyrx 0.8 software. Three compounds have the potential to be α-glucosidase enzyme inhibitors, namely tricyclo[10.2.1.02,11] pentadic-4,8-diene, myristic acid, tricyclo[8.6.0.02,9] hexadecane-3,15-diene where the binding affinity value of the three compounds is lower than the innate ligand of α-glucosidase enzyme α-D-glucopyranose. Lower binding affinity values indicate relatively greater stability and mechanism of α-glucosidase enzyme inhibition.

Keywords: nyale; seaworm; diabetes mellitus; α-glucosidase; molecular docking, myristic acid.

Introduction

Nyale is a type of seaworm that appears seasonally along the coast, especially around Seger Beach and Kuta Beach, Central Lombok, Indonesia. The tradition of catching Nyale, known as Bau Nyale, is an important part of life for the Sasak people of Lombok. Every year, in February or March, thousands of people gather on the coast to catch Nyale, which are believed to appear in large numbers only at a particular time. Apart from being the moment to catch Nyale, this celebration is a social gathering and religious ritual full of historical and cultural significance. The Bau Nyale tradition shows local wisdom in utilizing natural resources and preserves folklore and myths that bind the community spiritually and socially. In addition, Nyale are also believed to bring good luck and fertility to fields and sea catches. Locals and tourists gather on the beach in the early morning to catch Nyale. These worms can be processed into various traditional dishes. The Nyale sea worm phenomenon not only enriches the local culture but also attracts the attention of domestic and foreign tourists, making it one of the top tourist attractions in Lombok (Fazalani, 2018).

Diabetes mellitus is a chronic disease characterized by high blood sugar (glucose) levels (Mukhtar et al., 2020). The disease occurs because the body is unable to produce enough insulin or cannot use insulin effectively (Banday et al., 2020). Insulin is a hormone produced by the pancreas and has the function of regulating blood sugar levels (Marušić et al., 2021). There are two main types of diabetes mellitus: type 1 diabetes, which occurs when the body's immune system attacks and damages the insulin-producing cells in the pancreas, and type 2 diabetes, which occurs when the body becomes resistant to insulin or the pancreas does not produce enough insulin. Risk factors for type 2 diabetes include obesity, a sedentary lifestyle, an unhealthy diet, and a family history of diabetes. Common symptoms of diabetes mellitus include frequent urination, excessive thirst, unexplained weight loss, fatigue, and blurred vision. If not managed properly, diabetes can lead to severe complications such as heart disease, kidney damage, visual impairment, and hard-to-heal wounds. Diabetes management includes lifestyle changes, such as a healthy diet and regular exercise, as well as treatment with oral medications or insulin injections to control blood sugar levels (Khalid et al., 2021). Early detection and proper management are essential to prevent complications and improve the quality of life of people with diabetes (Riordan et al., 2020).

The α-glucosidase enzyme is a potential target in managing diabetes mellitus, especially type 2 diabetes. This enzyme plays a role in the breakdown of complex carbohydrates into simple sugars in the small intestine, which are then absorbed into the bloodstream, resulting in increased blood sugar levels (Kashtoh & Baek, 2022). The carbohydrate breakdown and absorption rate can be slowed by targeting the α- glucosidase enzyme by using α- glucosidase inhibitors, such as acarbose and miglitol. This helps to control postprandial (after-meal) blood sugar spikes, which are a significant challenge in the management of type 2 diabetes (Daub et al., 2020). α-glucosidase enzyme inhibitors work by inhibiting the activity of the α-glucosidase enzyme, so the glucose will released more slowly into the bloodstream, allowing the body to manage it more effectively (Bhatnagar & Mishra, 2022). This mechanism not only helps keep blood sugar levels stable but may also reduce the risk of long-term complications associated with diabetes, such as cardiovascular disease and organ damage. In addition, α-glucosidase inhibitors can be used in combination with other anti-diabetic drugs and healthy lifestyle changes, such as a balanced diet and regular exercise, to improve overall glycemic control and enhance the

quality of life of people with diabetes (Dirir et al., 2022; Kashtoh & Baek, 2022).

Natural herbal medicines are often better than synthetic drugs for several reasons (Mosaddad et al., 2021). First, herbal medicines have fewer side effects because they are derived from natural ingredients used for thousands of years in various medicinal traditions (Nugraha et al., 2020). Second, herbal medicines usually contain active compounds that work synergistically, providing a more holistic and balanced therapeutic effect than single compounds in synthesized drugs (Zhang et al., 2021). Third, herbal medicines are often more affordable and more accessible, especially in rural communities or developing countries, where access to synthesized medications may be limited (Tangkiatkumjai et al., 2020). In addition, the use of herbal medicines can support environmental sustainability and conservation, as many synthetic drugs are produced through industrial processes that can damage the environment (Howes et al., 2020). Furthermore, there is a belief that herbal medicines work more in harmony with the human body, strengthening the body's natural healing mechanisms without causing dependency as sometimes happens with synthetic drugs. However, it is essential to note that the effectiveness and safety of herbal medicines must be backed by rigorous scientific research to confirm their benefits. Therefore, combining traditional knowledge and modern research can optimize the use of herbal medicine in medicine (Silveira et al., 2020).

Based on research conducted by Khalil et al. (2021), myristic acid compounds are useful for reducing hyperglycemia in type 2 diabetes model mice. Myristic acid compounds have the potential to be antidiabetic drugs, but their effects vary and depend on the conditions of use. The study showed myristic acid can lower fasting blood glucose levels and improve glucose tolerance in a mouse model of type 2 diabetes, which shows increased insulin sensitivity (Khalil et al., 2021).

The molecular docking method is critical in drug discovery, as it allows researchers to screen thousands of candidate ligands virtually before conducting laboratory experiments, saving time and money (Stanzione et al., 2021). In addition, molecular docking techniques can help understand the molecular mechanism of ligand-protein interactions and design new ligands with higher affinity and better selectivity. Molecular docking can also be used in the study of protein-protein interactions and the design of enzyme inhibitors (Yang et al., 2022).

The antihyperglycemic properties of Nyale have not been widely studied. Therefore, this research needs to analyze the potential of α-glucosidase inhibitor compounds for diabetic conditions using molecular docking methods with an *in silico* approach. Compounds from Nyale will be compared with standard drugs for the target mechanism of inhibition of the α-glucosidase enzyme.

Materials and methods

Sample collection and extraction. Nyale worms were collected from the coastal waters of Kuta Mandalika, Central Lombok, and dried. 24 grams of dry samples were ground using a mortar and macerated in 250 mL of 96% ethanol for 24 hours and n-hexane (99%) for 8 hours. Nyale residue was extracted three times with ethanol until it was colorless for ethanol extraction. The liquid extract was evaporated at 68 °C to remove the solvent (n-hexane).

Chemistry. To identify bioactive compounds in the Nyale worm extract, quantitative analysis by gas chromatography-mass spectrometry (GC-MS) using Shimadzu 2010 was performed.

Protein/macromolecule. The enzyme α-glucosidase (PDB: 3A4A) was obtained from rscb.org (www.rcsb.org) in Protein Data Bank (PDB) format. The structure of α-glucosidase consists of one chain, the A chain. The chain contains the inhibitor ligand α-D-glucopyranose. The PDB structure of α-glucosidase was prepared using PyMOL 2.5.2.

Ligand and drug screening. GC-MS identified nineteen compounds in Nyale worm extract. The identity of the compounds was confirmed through a chemical search using the PubChem database (https://pubchem.ncbi.nlm.nih.gov). The bioavailability of the compounds was assessed according to Lipinski's Rule of Five using Swiss ADME (www.swissadme.ch). Human intestinal uptake assessment (HIA) was performed using the PreADMET predictor (https://preadmet.webservice.bmdrc.org). Ligands were prepared using Avogadro 1.2 (Snyder & Kucukkal, 2021).

Molecular docking software. Molecular docking of nineteen compounds in Nyale worm extract to α-glucosidase protein was performed with PyRx v.0.8 software (Trott & Olson, 2010). The target areas of molecular binding were X: 21.4318, Y: -8.6043, Z: 23.8624, and Dimension (A) X: 10.0408, Y: 10.3607, Z: 10.1888, which is the binding site of α-D-glucopyranose, which is an α-glucosidase inhibitor. The active binding site on α-glucosidase was observed in the Computed Atlas of Surface Topography of Proteins (CASTp) (sts.bioe.uic.edu/castp/index.html?3A4A) (Tian et al., 2018). Protein interaction results and the identification of ligand binding residues was visualized with PyMOL 2.5.2 and Discovery Studio R17.

Molecular docking is a theoretical simulation method used to study the interactions between molecules, such as ligands and receptors, with the aim of predicting their binding modes and affinities. To better understand the binding mechanism between the compounds contained in Nyale and the α-glucosidase enzyme, a molecular docking analysis was carried out in this study. Based on the data, α-glucosidase from baker's yeast has a sequence similarity of 73% and an 85% similarity with isomaltase (PDB ID: 3A4A) from *Saccharomyces cerevisiae*. This high sequence similarity indicates that the resulting 3D model of α-glucosidase structure is of good quality, so it is valid for use in molecular docking simulations.

Results

Figure 1 shows the results of the visualization of tricyclo[8.6.0.02,9]-hexadeca-3,15-diene, myristic acid, pentadecylic acid, tricyclo[10.2.1.02,11]pentadeca-4,8-diene, methyl myristate, and linoleic acid. The compounds identified in the worms were screened by Lipinski's rule of five with the parameters of molecular weight (Da), H donor, H-acceptor, and Log P, and then the analysis was carried out by identifying Human Intestinal Absorption (HIA). After the initial identification, the binding affinity value of the compound interaction with the α-Glucosidase protein was identified, which can be seen in Table 1 and the results of the visualization of the compound interaction can be seen in Table 2.

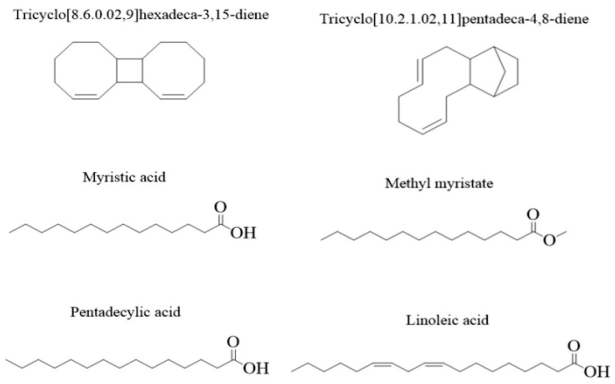
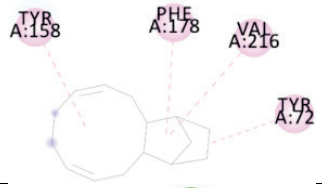
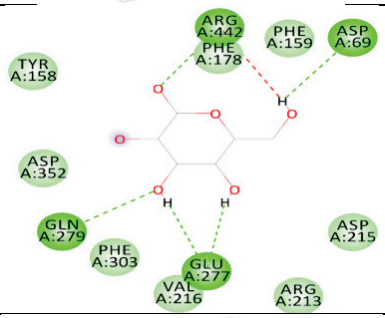
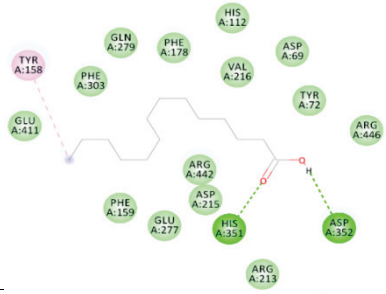
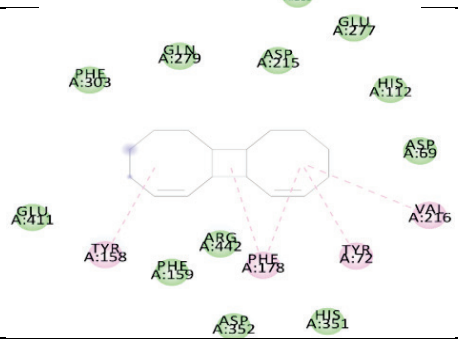


Fig. 1. The structural form of compounds in Nyale

Table 1
Identification of the potential α-glucosidase inhibitor compounds contained in Nyale worm extract based on their bioavailability and HIA

No.	Compound Name	Molecular formula	Da	H-donor	H-acceptor	LogP	HIA, %	Binding affinity, kcal/mol
1	Tricyclo[8.6.0.02,9]hexadeca-3,15-diene	$C_{16}H_{24}$	202.34	0	0	4.02	100	–5.7
2	alpha-D glucopyranose (native ligand)	$C_6H_{12}O_6$	180.16	5	6	0.24	22.35	–5.6
3	Margaric acid	$C_{17}H_{34}O_2$	270.45	1	2	5.57	98.40	–4,2
4	9-Octadecenal	$C_{18}H_{34}O$	266.46	0	1	5.94	100	–3.5
5	Myristic acid	$C_{14}H_{28}O_2$	228.37	2	1	4.45	97.84	–5,9
6	Pentadecylic acid	$C_{15}H_{30}O_2$	242.40	1	2	4.84	98.11	–5.0
7	Stearic acid	$C_{18}H_{36}O_2$	284.48	1	2	5.93	98.44	–3.7
8	Linoleic acid	$C_{18}H_{32}O_2$	280.45	1	2	5.45	98.37	–4.4
9	Palmitic acid	$C_{16}H_{32}O_2$	256.42	1	2	5.20	98.29	–4.2
10	Methyl myristate	$C_{15}H_{30}O_2$	242.40	2	0	4.81	100	–5.3
11	Ethyl arachidonate	$C_{22}H_{36}O_2$	332.52	0	2	6.42	100	–1.7
12	Octadec-9-enoic acid	$C_{18}H_{34}O_2$	282.46	1	2	5.71	98.43	–3.8
13	Benzene, 1,2-dimethyl-	$C_6H_4(CH_3)_2$	106.17	0	0	2.83	100	–4.8
14	Hexadecanoic acid	$C_{18}H_{36}O_2$	284.48	0	2	5.79	100	–3.6
15	Tricyclo[10.2.1.02,11]pentadeca-4,8-diene	$C_{15}H_{22}$	202.34	0	0	4.02	100	–7.0
16	Methyl palmitate	$C_{17}H_{34}O_2$	270.45	0	2	5.54	100	–4.5
17	Ethyl myristate	$C_{16}H_{32}O_2$	256.42	0	2	5.17	100	–4.0
18	Ethyl palmitate	$C_{18}H_{36}O_2$	284.48	2	0	5.90	100	–3.8
19	Methyl stearate	$C_{19}H_{38}O_2$	298.50	0	2	6.24	100	–2.9
20	Ethyl stearate	$C_{20}H_{40}O_2$	312.53	0	2	6.71	100	–3.7

Table 2
Compound interaction

No.	Compound Name	Molecular Visualization	Interaction
1.	Tricyclo[10.2.1.02,11]pentadeca-4,8-diene		TYR158, PHE178, VAL216, TYR72
2.	alpha-D glucopyranose (native ligand)		ARG442, PHE178, PHE159, ASP69, ASP215, ARG213, GLU277, VAL216, PHE303, GLN279, ASP352, TYR158
3.	Myristic acid		TYR158, ASP352,HIS351, PHE303, GLN279, PHE178, HIS112, VAL216, ASP69, TYR72, ARG446, ARG213, ASP215, ARG442, GLU277, PHE159, GLU411
4.	Tricyclo[8.6.0.02,9]hexadeca-3,15-diene		PHE303, GLN279, ASP215, GLU277, HIS112, ASP69, VAL216, TYR72, HIS351, PHE178, ASP352, ARG442, PHE159, TYR158, GLU411

A visualization of each molecule with the protein α-Glucosidase binding to the active side of the protein can be seen in Figure 2. Tricyclo [8.6.0.02,9]hexadeca-3,15-diene molecules, myristic acid, tricyclo [10.2.1.02,11]pentadeca-4,8-diene, and alpha-D-glucopyranose are compounds that have the highest binding affinity value that can bind to α-Glucosidase.

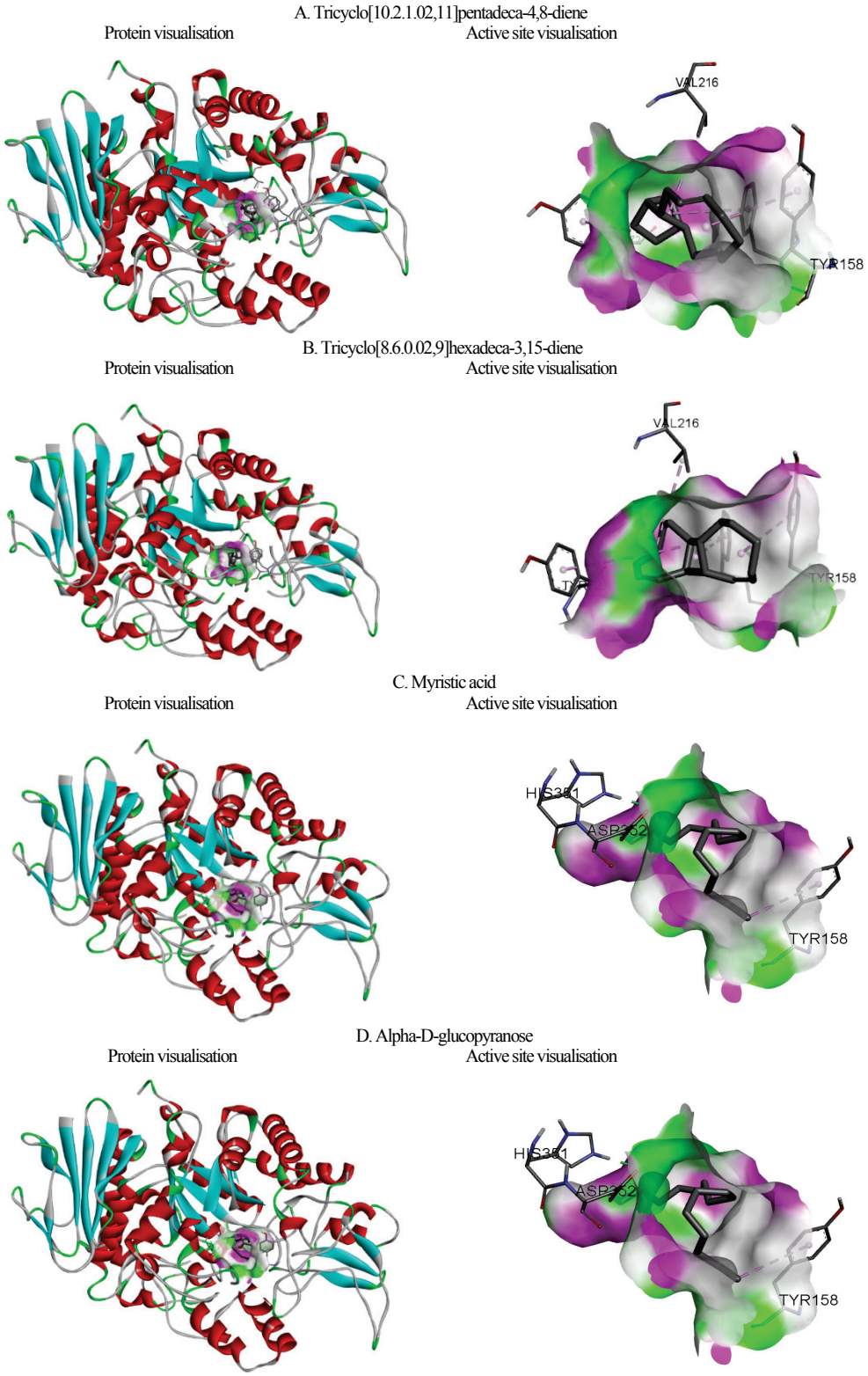


Fig. 2. Molecular visualization

Discussion

Mechanism of α-glucosidase enzyme inhibition. Attenuating the glucose uptake process to maintain blood glucose levels within the normal range has become a promising strategy for managing T2DM. Delaying carbohydrate digestion can reduce the portion of glucose entering the blood vessels, thereby reducing postprandial glucose levels. Based on the established mode of action, in 1995, the first α-glucosidase inhibitor (AGI), named acarbose, was developed and approved by the FDA. The α-glucosidase enzyme is a hydrolytic enzyme that breaks complex carbohydrates down into simpler monosaccharides, especially glucose. The pathway mechanism of this enzyme begins when α-glucosidase recognizes and binds to its substrate, which is an oligosaccharide or polysaccharide with an α-1,4-glycosidic bond. Once the substrate is bound to the enzyme's active site, the enzyme facilitates hydrolysis of the glycosidic bond through a series of catalytic steps involving amino acid residues on the active site. This process includes the protonation of the glycosidic oxygen by acidic residues on the enzyme, resulting in the cleavage of the glycosidic bond and forming a carboxylation intermediate. This will result in the formation of the end product, a monosaccharide, such as glucose. Glucose

is then released from the enzyme's active site, allowing the enzyme to interact with a new substrate molecule. In a physiological context, α-glucosidase activity mainly occurs in the small intestine, where this enzyme plays an important role in the digestion process of dietary carbohydrates, thus ensuring that the glucose produced can be absorbed into the bloodstream to be used as the main energy source by the body's cells. α-glucosidase inhibitors are used in treating type 2 diabetes mellitus to reduce the speed of carbohydrate digestion and control postprandial blood sugar spikes (Zheng et al., 2020; Liu et al., 2021; Lam et al., 2024).

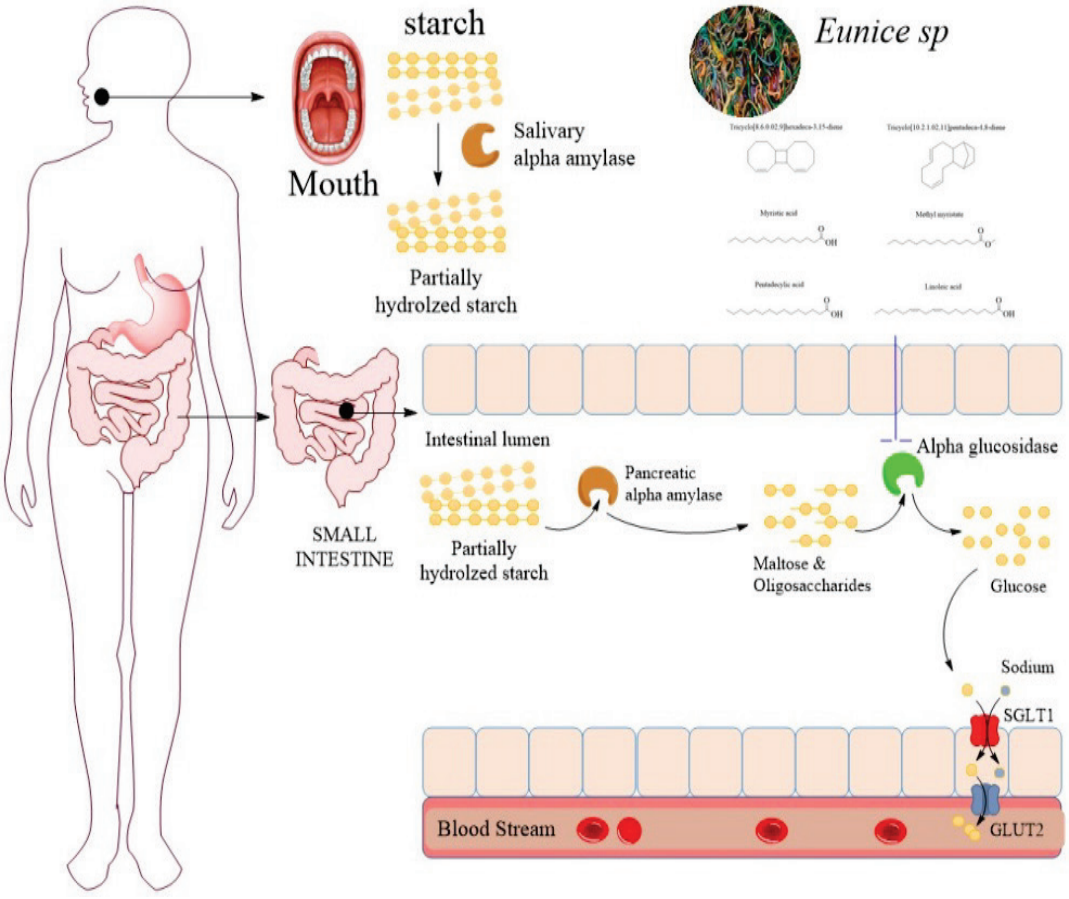


Fig. 3. α-Glucosidase inhibitor working mechanism

Human intestinal absorption (HIA). Percentage HIA (% HIA) is the ability of a compound to be absorbed into the small intestine. Table 1 shows that the compounds in Nyale worm extract have a high absorption rate (HIA > 90%). Human Intestinal Absorption (HIA) is the process by which nutrients and drugs are absorbed from the lumen of the small intestine into the blood circulation. This process is crucial for fulfilling the body's nutritional needs and the therapeutic effectiveness of drugs. HIA begins when ingested substances reach the small intestine, where they interact with the intestinal mucosa, which is extensive and has fold structures and microvilli that enlarge the surface area for absorption. Factors influencing HIA include the physicochemical properties of the absorbed substances, such as water and lipid solubility, molecular size, and ionization. In the context of pharmacology, HIA is a critical aspect in determining a drug's bioavailability, i.e. the fraction of the drug that reaches the systemic circulation in the active form. Drugs designed for oral administration must be formulated in such a way that they can cross the intestinal barrier and reach the desired therapeutic target. Thus, an in-depth understanding of the mechanisms of HIA is essential in developing effective nutrients and drugs and managing clinical conditions associated with malabsorption (Chivere et al., 2020).

Lipinski's rule of five. The Lipinski's Rule of Five result data can be seen in Table 1. This assay is a guideline for designing drugs with good oral bioavailability potential. The rule consists of five physicochemical parameters that small molecules must fulfill to be more likely to be absorbed efficiently in the human body. These parameters are: (1) the molecule should not have more than 5 hydrogen bond donors (NH or OH groups), (2) the molecule should not have more than 10 hydrogen bond acceptors (nitrogen or oxygen atoms), (3) the molecular weight should be less than 500 Daltons, (4) the log p-value (octanol-water partition coefficient) should be less than 5, indicating appropriate lipophilicity, and (5) the molecule should not have more than 10 free spins, although this is often not considered part of the original rule (Pandi et al., 2022).

Lipinski's rule of five was devised based on the observation that most successful oral drugs adhere to such criteria, which is empirically linked to the ability to pass through cell membranes and reach therapeutic targets in the body. Although not all molecules that adhere to this rule will be effective drugs, and there are exceptions, especially for drugs targeted at specific active transporters or receptors, this rule is very useful in the early phases of drug discovery and development. By screening molecules based on these rules, researchers can estimate the tested compounds' basic pharmacokinetics, such as absorption, distribution, metabolism, and excretion (ADME) (Sisakht et al., 2021). Lipinski's Rule of Five is not meant to be a rigid criterion but rather a guide to optimizing the pharmacokinetic properties of a drug candidate molecule. The rule also highlights the importance of the balance between aqueous solubility and lipophilicity in drug design (Narkhede et al., 2020).

Molecular docking. Based on the results (Table 1), three compounds have the potential to be candidates for α-glucosidase enzyme inhibitors: tricyclo[10.2.1.02,11] pentadeca-4,8-diene, myristic acid, and tricyclo [8.6.0.02,9]hexadeca-3,15-diene. Molecular docking is a computational technique to predict the interaction between two molecules, usually between a small ligand and a target protein (Li et al., 2019). The aim is to identify a ligand's optimal orientation and conformation when bound to a protein's active site, which then allows assessment of binding affinity and potential biological activity. This process involves using algorithms to simulate various possible positions and orientations of the ligand within the binding site, as well as assessing binding energies to find the most stable conformation (Pagadala et al., 2017). Scoring functions are used to calculate the binding energy and determine the effectiveness of the ligand in interacting with the target (Fan et al., 2019; Li et al., 2019). Based on the

results of the energy formed, three compounds were obtained whose binding affinity values were lower than α-D-glucopyranose, the default ligand of the α-glucosidase enzyme.

The interaction of α-glucosidase enzyme with α-D-glucopyranose, which is a built-in ligand, can be seen in Table 2, where the GLU277 residue chain interacts with two hydrogen molecules to form a hydrogen bond, the GLU277 residue is a catalytic residue found on the active side of the enzyme (Yamamoto et al., 2010). Hydrogen bonding is an electrostatic interaction between a hydrogen atom bound to an electronegative atom (such as oxygen, nitrogen, or fluorine) and another electronegative atom from a different molecule or part of the same molecule. In addition, the compound α-D-glucopyranose binding residue GLN279 binds to molecular oxygen to form hydrogen bonds, where hydrogen atoms bound to oxygen form hydrogen bonds with oxygen from other water molecules, creating a complex network of bonds. Hydrogen bonds play an important role in determining the physical properties of water, the stability of DNA and protein structures, and various other biological and chemical interactions (Jena et al., 2022). Residues ARG442 and ASP69 bind hydrogen molecules that form hydrogen bonds to the built-in ligand compound. Residues TYR158, PHE178, PHE159, ASP215, ARG213, VAL216, PHE303, and ASP352 form van der Waals bonds. Van der Waals bonds are weak interactions that occur between molecules or parts of molecules that do not involve covalent or ionic bonds. Although weak, van der Waals bonds play an important role in determining the physical properties of substances, such as boiling point and solubility, as well as the stability of molecular structures (Iyakutti et al., 2023).

The interaction of the α-glucosidase enzyme with the compound tricyclo[10.2.1.02,11]pentadeca-4,8-diene resulted in the lowest binding affinity value (-7.0 Kcal/mol) where a bond was formed with residue TYR158 with the cyclodecane ring forming an alkyl bond. Alkyl bonds in molecules involve alkyl groups. Alkyl groups are formed from alkanes missing one hydrogen atom, allowing them to bond with other atoms or functional groups in the molecule (Kagramanov, 2020). These bonds are covalent, where the carbon atom of the alkyl group shares electrons with another atom, such as carbon, oxygen, or nitrogen. Alkyl groups can affect the chemical and physical properties of compounds, such as solubility, melting point, and reactivity (Costa et al., 2022). In addition, residues TYR178, VAL216, and TYR72 form alkyl bonds with the compound tricyclo[10.2.1.02,11]pentadeca-4,8-diene.

Myristic acid compounds can bind to the α-glucosidase enzyme, producing a binding affinity of -5.9 Kcal/mol. Residue HIS351 binds to molecular oxygen to form hydrogen bonds, while residue ASP352 binds to molecular hydrogen to form hydrogen bonds. Meanwhile, the TYR158 molecule forms a pi-alkyl bond. Residues GLU277 and ASP215 are active side residues of the α-glucosidase enzyme, forming van der Waals bonds with myristic acid compounds (Yamamoto et al., 2010).

Myristic acid is a 14-carbon saturated fatty acid commonly found in various foods like coconut oil and palm oil. Once ingested, MA undergoes typical fat metabolism processes. It is absorbed in the small intestine, transported via chylomicrons through the lymphatic system, and then released into the bloodstream. From there, MA is metabolized primarily in the liver, where it undergoes beta-oxidation to produce energy or is incorporated into triglycerides and phospholipids. The bioavailability of MA is generally high, as with other saturated fatty acids, and it can be stored in adipose tissue or used for energy production (Saraswathi et al., 2022).

The toxicity profile of MA depends on its concentration and duration of exposure. In moderate amounts, MA is generally considered safe for consumption. However, chronic intake of high levels of MA has been associated with adverse health effects, particularly concerning lipid metabolism. Studies indicate that MA can increase levels of low-density lipoprotein (LDL) cholesterol, contributing to cardiovascular risks such as atherosclerosis. Additionally, animal studies suggest that a diet high in myristic acid may exacerbate insulin resistance and inflammatory processes, particularly when consumed in conjunction with a high-fat diet (Saraswathi et al., 2022).

The compound tricyclo[8.6.0.02.9]hexadeca-3,15-diene can bind to the enzyme α-glucosidase, producing a binding affinity value of -5.7 kcal/mol. The residues TYR158, PHE178, TYR72, and VAL216 bind to the cyclooctane ring, forming an alkyl bond. Alkyl bonding of residues to molecules usually involves an alkyl group (such as methyl or ethyl) attached to the main chain of the molecule, often in the context of proteins or organic compounds. These alkyl groups can affect the lipophilicity, stability, and three-dimensional structure of the molecule and play a role in hydrophobic interactions important for protein folding and ligand binding (Cao et al., 2020). This compound also binds to residues GLU277 and ASP215, which are active side residues of the enzyme. The binding mechanism to the enzyme's active site involves a specific interaction between the enzyme and its substrate. The substrate enters the active side, forming an enzyme-substrate complex (Arjita et al., 2022).

Conclusion

This study shows the inhibitory properties of α-glucosidase enzyme using compounds contained in the Nyale worm, using a molecular docking method with an in silico approach. Future studies to develop antidiabetic drugs using Nyale worm extract are highly recommended.

The authors declare no conflict of interest.

The authors hereby declare that the work presented in this article is original and that they will bear any liability for claims relating to the content of this article.

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