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Assessment of anti-diabetic molecular docking studies of two foraging fruit berries *Morinda citrifolia* L. and *Morinda tinctoria* Roxb. (Rubiaceae)

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Abstract

Plants have served as companions to humanity for millennia, not just as a source of sustenance but also as healers. Rubiaceae members *Morinda citrifolia* and *Morinda tinctoria* fruits were selected for the study. Methanolic extract of both the fruits were prepared and it was screened for phytochemicals using standard procedures. The fruit extract with maximum phyto-constituents was subjected to GC-MS analysis to identify the bioactive compounds. The pharmacological activity of these GCMS compounds were examined using PASSonline and it was further docked against Maltase glucoamylase, a diabetic protein target. The present study reveals that *M. tinctoria* contained higher levels of flavonoids, phenols, tannins and saponins compared to *M. citrifolia*. The GC-MS analysis of *M. tinctoria* fruit extract yielded 30 active components along with the retention duration, area percentage, molecular formula and molecular weight. Myristic acid glycidyl ester; 9- Octadecenoic acid (Z)-,2,3-dihydroxypropyl ester; 9- Octadecenoic acid (Z)-, oxiranylmethyl ester; Cyclopropanoic acid, 2-[[2-[(2-Ethylcyclopropyl) Methyl] Cyclopropyl] Methyl]-, Methyl Ester and 7-Hydroxy-3-methoxy-2-p-methoxyphenyl-4H-chromen-4-one are the molecules with anti-diabetic activity. The Myristic acid glycidyl ester exhibits the highest docking score of -262.47 with a confidence score of 0.9046, alongside a single hydrogen bond interaction (TRP-406). These scores suggest a strong and confident binding affinity towards the target, making it a promising compound. These findings highlight *M. tinctoria* as a promising source of natural anti-diabetic compounds, with Myristic acid glycidyl ester warranting further investigation for its potential therapeutic application.

Keywords: *M. citrifolia*, *M. tinctoria*, fruit, phytochemicals, GC-MS analysis, molecular docking, antidiabetic activity

Introduction

Herbal medications are chosen and used as an alternative to modern drugs in therapies all over the world due to concerns about the toxicity, side effects and adverse reactions of modern drugs. Plants are an excellent source of drugs and a storehouse for numerous active chemicals (Ranvir *et al.*, 2017) ^[1]. According to the most recent and thorough estimates, diabetes is currently among the top 10 major causes of mortality and disability worldwide, with a prevalence rate of 6.1% (Ong *et al.*, 2023) ^[2]. Diabetes affects more than half a billion people globally, impacting men, women and children of all ages and the number is expected to more than double to 1.3 billion people in the next 30 years, with a rise in every country. An estimated 77 million Indians over the age of 18 have type 2 diabetes and another 25 million are prediabetics, meaning they have a higher chance of getting the disease in the near future (Anjana *et al.*, 2023) ^[3].

Phytochemicals, plant-derived compounds, have gained popularity for their diverse applications. Finding novel sources of compounds with therapeutic and industrial significance, such as alkaloids, flavonoids, phenolic compounds, saponins, steroids, tannins, terpenoids, etc., is largely dependent on phytochemical screening (Akhtar and Mirza, 2018) ^[4]. Gas Chromatography Mass Spectroscopy is the most popular method for identification and quantification, which produces a hyphenated system that is highly compatible. It is possible to identify the unknown organic chemicals in a complicated combination by interpreting the data and comparing the spectra to those of reference samples (Rautela *et al.*,

2018) [5]. Molecular docking studies provide an opening into the molecular interactions between two or more molecules, making them a cornerstone in computational biology and drug development (Basu *et al.*, 2020) [6]. This advanced computational method predicts the proper binding orientation and affinity of the drug molecule to its target by simulating the interaction between a tiny molecule, frequently a prospective medicine and a target protein or nucleic acid (Ahmed *et al.*, 2018) [7].

Two varieties of *Morinda* species were selected for the present study to determine its active chemical constituent and anti-diabetic activity. Among the ethnic plants of tropical nations, the genus *Morinda* has long been utilized in traditional medicine. It has been discovered that a large number of these species are rich in secondary metabolites with potential medicinal uses. *Morinda citrifolia* L (Rubiaceae), also known by the common name "Noni," is an evergreen tree or shrub that grows to a height of 3 to 6 meters. Leaves are oval, bright green and deeply veined, measuring 10 to 30 cm. The flowers are tubular and white. The fruit has a bumpy surface covered in portions that are polygonal in shape and it can develop to a maximum size of 12 cm or more (Fidrianny *et al.*, 2018) [8]. The young fruit is vivid green in colour and firm. The fruits turn translucent yellow or white and get extremely soft as they ripen. The ripe fruit tastes like soap and has an unpleasant butyric and cheesy smell. An air sac linked to one end of the seeds makes them buoyant (Vuanghao and Laghari, 2017) [9].



M. citrifolia fruit

Morinda tinctoria (Roxb.), often known as Nunaa, is grown in many places of Southeast Asia, particularly in agricultural and undeveloped areas. The plant of significant therapeutic value that is employed in several traditional medical systems, including Unani, Siddha and Ayurveda (Rex *et al.*, 2018). It is merely a small tree or evergreen shrub that reaches a height of 5 to 10 meters. The leaves are lanceolate to oblong and 15-25 cm long. The flowers are about 2 cm long, white, fragrant, and tubular. The fruit is a 2-2.5 cm-diameter green syncarp. Its leaves, stems and fruits are used to treat a variety of conditions including fever, inflammation, gout, dyspepsia, diarrhoea and stomach ulcers (Chandra and Meel, 2020) [11]. The present study, investigates the presence and pharmacological activity of phyto-constituents present in the fruits. Thereby to suggest the best varieties of the fruit for diabetic people for consumption in order to improve their quality of life.

Materials and Methods

Plant Collection

Matured fruits of *Morinda citrifolia* L. and *Morinda tinctoria* Roxb. were collected from the Nirmala College Campus, Coimbatore. The collected fruits were washed, cleaned from dirt and it was allowed to ripe. Then, the ripen fruits were cut into small pieces and shade dried for 2 weeks. The dried pieces were powdered and stored in an air-tight container.



M. tinctoria fruit

Extraction

10 g of fruit powders were mixed with 100 ml of ethanol. The solution was kept in the shaker for 72 hours. Then it was strained and the extract was collected and stored.

Preliminary Phytochemical Screening: The ethanolic extracts of the two *Morinda* species was screened for different phytoconstituents using standard procedures (Harbone, 1998).

Test for Alkaloids (Mayer's test): Few drops of Mayer's reagent were added to the extract. Cream colour precipitate indicates the presence of alkaloids.

Test for Flavonoids (Alkaline Test): Extract was treated with few drops of aqueous NaOH solution and noted for the yellow colour which becomes colourless on the addition of dilute acids. Then it was treated with conc. H₂SO₄ A

yellowish to orange colour indicates the presence of flavonoids.

Test for Phenols (Ferric Chloride Test): To 2ml of extract, 2ml of 1% ferric chloride solution was added in a test tube. Bluish green colour indicates the presence of phenolic compound.

Test for Terpenoids (Salkowski's Test): 5ml of chloroform and 2ml conc. H₂SO₄ was added to 2ml of extract. Reddish brown colouration of interface indicates the presence of terpenoids.

Test for Tannins (Ferric Chloride Test): To the extract 1ml of 5% ferric chloride solution was added, formation of bluish black or greenish black precipitate indicates the presence of tannins.

Test for Steroids (Liebermann Test): 2 ml of chloroform and conc. H_2SO_4 were added with the 5 ml aqueous plant crude extract. In the lower chloroform layer red colour appeared that indicated the presence of steroids.

Test for Glycosides (Keller-Kiliani Test): 2 ml of glacial acetic acid, few drops of 5% ferric chloride and Conc. H_2SO_4 were added to the extract. Reddish brown colour at the junction of two liquid layers and upper layer appears bluish green indicates the presence of glycosides.

Test for Saponins (Foam Test): A small amount of extract was taken in a test tube with little quantity of water and shake it vigorously for at least one a minute. Appearance of foam persisting for 10 minutes indicates the presence of saponins.

Cardiac glycosides (Keller-Kiliani Test): A solution of glacial acetic acid (4.0 ml) with 1 drop of 2.0% FeCl_3 mixture was mixed with the 10 ml aqueous plant extract and 1 ml H_2SO_4 concentrated. A brown ring formed between the layers which showed the entity of cardiac steroidal glycosides.

Gas Chromatography - Mass Spectroscopy (GC-MS): The GC-MS analysis of ethanolic fruit extract of *M. tinctoria* was performed using GCMS QP2010 SE Single Quadrupole (Ukwubile *et al.*, 2019). The QP-2010 Ultra quadrupole mass spectrometer and the GC-2010 Plus gas chromatograph with dual inlet differential vacuum system (179L/sec + 185L/sec for He) are included in this package. Important characteristics include a mass range of 1.5-1090, a maximum scan speed of 20,000 μsec (achieved with proprietary technology), and a recently invented "Ecology mode" that drastically lowers power and carrier gas consumption. In scan mode, this device can detect 1 pg of OFN (octafluoronaphthalene) at more than 500/1 RMS. All Shimadzu GCMS Systems come with front ion source access and are designed to be easily maintained. One Split / Splitless injection port with AFC is included with this GC. The septum purge flow and split ratio are just two of the injection port parameters that can be controlled by the AFC (Advanced Flow Control). The oven can be programmed in 20 temperature increments and cools down quickly—it takes only 2.7 minutes to go from 350°C to 50°C. The identification of components was based on Willey and NIST libraries as well as comparison of their retention indices. Willey and NIST libraries were used for component identification, and their retention indices were compared. The components of the GC-MS instrument were identified by comparison with those found in the computer library (Willey and NIST), and the outcomes were tabulated.

Molecular Docking Study

Preparation of Receptor

The chosen targeting protein for diabetes activity is maltase glucoamylase. The target protein's 3D structure was extracted from the Protein Databank in.pdb format file.

Preparation of Ligand

The 3D structure of ligand was retrieved from Pubchem in.sdf format. This.sdf format was converted into.pdb format using Openbabel software (<http://openbabel.org>).

Molecular Docking

The Docking analysis was performed using Hdock software which is a freely accessible online computational tool (Sampangi-Ramaiah *et al.*, 2020). This performs molecular docking between the ligand and the targeted protein. This shows the Docking score, Confident score, Ligand rmsdo, and 3D image of the ligand-protein interaction. PyMOL 2.5.7 was used to visualize the 3D structure of the protease-ligand interaction, whereas Biovia Discovery Studio 21.1.0.20298 was used to display the 2D structure of the molecular interaction. The data tabulated are docking score, confident score, number of Hydrogen bonds and H-bond to which the ligand is attached.

Results and Discussion

Qualitative Phytochemical Analysis: Preliminary phytochemical screening of ethanolic extracts of *Morinda citrifolia* and *Morinda tinctoria* fruits revealed interesting differences. *M. tinctoria* contained higher levels of flavonoids, phenols, tannins and saponins compared to *M. citrifolia*. Conversely, both extracts lacked alkaloids, steroids, glycosides and cardiac glycosides (Table 1 & Plate I). The present result helps to know the pharmaceutical significance and role of possible medicinal values of these plants. Generally, these phytoconstituents are responsible for the all-biological activity. Flavonoids, for instance are a well-studied group with antioxidant and anti-inflammatory properties, potentially contributing to *M. tinctoria* bioactivity. Similarly, the presence of phenols and tannins suggests potential antioxidant and astringent properties. Likewise, saponins, found in higher quantities in *M. tinctoria*, might contribute anti-inflammatory and cholesterol-lowering effects.

A phytochemical study by Sajani and Maya, 2020 explored the phytoconstituents present in aqueous extract of *M. citrifolia*. Large amount of steroids, cardiac glycosides, tannins, terpenoids, carbohydrates, flavonoids and proteins were present and resins, anthraquinones and phyloabtanins were absent. Phytochemical profiling of seven *Morinda* spp was done by Singh *et al.*, 2022 [16]. The total amounts of iridoids, flavonoids, triterpenoids, anthraquinone glycosides, lignans and coumarins were found to vary depending on the methanol extract obtained from the leaves of *M. umbellata*, *M. jasminoides*, *M. parvifolia* and *M. persicaefolia*. Leaves, bark and roots of *M. lucida* contains steroids, alkaloids, terpenoids, tannins, saponins, flavonoids, phenols and glycosides (Adeleye *et al.*, 2018) [17]. From this studies *M. tinctoria* has greater phytochemical values than *M. citrifolia*. Therefore *M. tinctoria* was selected for the further studies.

Table 1: Qualitative Phytochemical screening of Ethanolic fruit extracts of *M.citrifolia* and *M. tinctoria*

S. No	Phytochemicals	<i>M. citrifolia</i>	<i>M. tinctoria</i>
1	Alkaloids	-	-
2	Flavonoids	++	+++
3	Phenols	+	++
4	Terpenoids	-	+
5	Tannin	+	++
6	Steroids	-	-
7	Glycosides	-	-
8	Saponins	+	++
9	Cardiac glycosides	-	-
(+++ High) (++ Medium) (+ Low) (- Absent)			

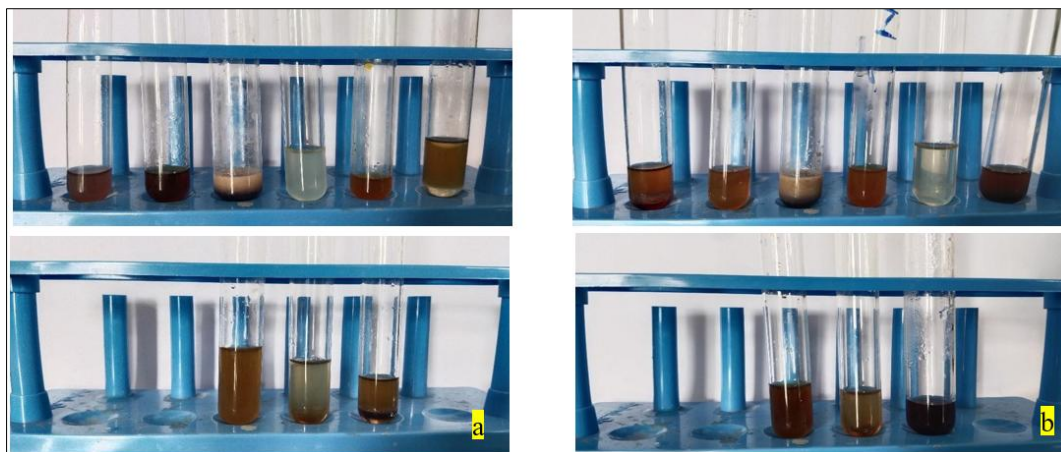


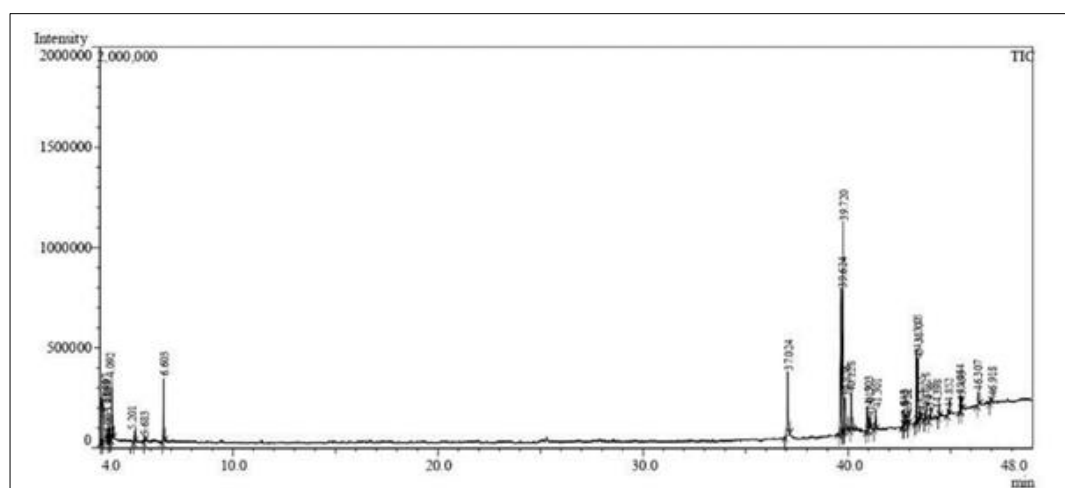
Plate 1: Phytochemical Analysis of a) *M. citrifolia* b) *M. tinctoria*

Gas Chromatography - Mass Spectroscopy Analysis:

Morinda tinctoria was investigated further for GC-MS analysis based on the phytochemical screening results. The GC-MS analysis of *M. tinctoria* fruit extract yielded 30 active components. The name of the molecule, retention duration, area percentage, molecular formula and molecular weight are listed in Table 2 and Graph 1. The structures of the bioactive molecules were extracted from Pubchem source are given in Table 3. The most abundant compound recorded was Oleic acid, trimethylsilylester with retention time 39.72 and area 20.86% followed by 9,12-Octadecadienoic acid (Z,Z)-, TMS derivative with retention time 39.624 and area 13.53%, Acetonitrile, trifluoro- with retention time 3.640 and area 7.04%, Cis-3-Hexenyllactate with retention time 4.092 and area 6.48%, Palmitic Acid, TMS derivative with retention time 37.024 and area 6.39% and Benzenepropanoic acid, trimethylsilylester with

retention time 3.597 and area 6.23%. The remaining compounds are less than 5% area.

Oleic acid and its derivatives are known for their beneficial effects on health, including anti-inflammatory and cholesterol-lowering properties (Nair *et al.*, 2018) [18]. 9,12-Octadecadienoic acid (Linoleic acid) is an essential fatty acid important for various bodily functions (Adekunle *et al.*, 2023) [19]. Palmitic Acid is a common saturated fatty acid found in plants and animals (Adewole *et al.*, 2021) [20]. Acetonitrile, trifluoro-, and Benzenepropanoic acid, trimethylsilylester might have specific industrial or pharmaceutical applications, depending on their structure and reactivity (Casuga *et al.*, 2016) [21]. Cis-3-Hexenyllactate is likely involved in the plant's fragrance or flavour profile, given its structure related to esters found in fragrances and flavours (Olivia *et al.*, 2021) [22].



10	39.624	9,12-Octadecadienoic acid (Z,Z)-, TMS derivative	13.53	C ₂₁ H ₄₀ O ₂ Si	352
11	39.72	Oleic acid, trimethylsilyl ester	20.86	C ₂₁ H ₄₂ O ₂ Si	354
12	39.826	Oleic acid, trimethylsilyl ester	4.24	C ₂₁ H ₄₂ O ₂ Si	354
13	40.128	Stearic acid, TMS derivative	3.09	C ₂₁ H ₄₄ O ₂ Si	356
14	40.903	Myristic acid glycidyl ester	2.32	C ₁₇ H ₃₂ O ₃	284
15	41.017	9(E),11(E)-Conjugated linoleic acid, trimethylsilyl ester	1.11	C ₂₁ H ₄₀ O ₂ Si	352
16	41.301	10-Nonadecenoic acid, (Z)-, TMS derivative	1.48	C ₂₂ H ₄₄ O ₂ Si	368
17	42.642	9,12-Octadecadienoic acid (Z,Z)-, 2,3- dihydroxypropyl ester	0.4	C ₂₁ H ₃₈ O ₄	354
18	42.725	9-Octadecenoic acid (Z)-, 2,3- dihydroxypropyl ester	0.31	C ₂₁ H ₄₀ O ₄	356
19	42.922	Arachidic acid, TMS derivative	0.3	C ₂₃ H ₄₈ O ₂ Si	384
20	43.305	Linoleyl acetate	5.86	C ₂₀ H ₃₆ O ₂	308
21	43.38	9-Octadecenoic acid (Z)-, oxiranylmethyl ester	5.88	C ₂₁ H ₃₈ O ₃	338
22	43.475	Cyclopropaneoctanoic acid, 2-[[2-(2-ethylcyclopropyl)methyl]cyclopropyl] methyl]-, methyl ester	0.61	C ₂₂ H ₃₈ O ₂ CAS	334
23	43.729	Myristic acid glycidyl ester	0.79	C ₁₇ H ₃₂ O ₃	284
24	43.956	1-{2,4,6-Tris[(trimethylsilyl)oxy] phenyl} propan-1-one	0.45	C ₁₈ H ₃₄ O ₄ Si ₃	398
25	44.398	5-tert-Butyl-2,4-dihydroxybenzophenone, bis(trimethylsilyl) ether	0.56	C ₂₃ H ₃₄ O ₃ Si ₂	414
26	44.852	E, E, Z-1,3,12-Nonadecatriene-5,14- diol	0.41	C ₁₉ H ₃₄ O ₂	294
27	45.444	7-Hydroxy-3-methoxy-2-p-methoxyphenyl-4H-chromen-4-one	1.36	C ₁₇ H ₁₄ O ₅	298
28	45.495	Docosanoic acid, trimethylsilyl ester	0.44	C ₂₅ H ₅₂ O ₂ Si	412
29	46.307	Tetrapentacontane	1.14	C ₅₄ H ₁₁₀	758
30	46.918	Tetracosanol, O-TMS	0.46	C ₂₇ H ₅₈ O ₂ Si	426

Table 3: 2D structures of bioactive chemicals from *M. tinctoria* using GCMS analysis

1	2	3	4	5	6
7	8	9	10	11, 12	13
14, 23	15	16	17	18	19
20	21	22	24	25	26
27	28	29	30		

Docking Studies on Antidiabetic Molecular Target:

The inhibitors α -amylase and α -glucosidase slow down the breakdown of carbohydrates, reduce postprandial hyperglycemia and treat prediabetes and T2DM (Berraquero-García *et al.*, 2023). Maltase glucoamylase was selected as the drug target and the structure was obtained from PDB using PDB Id 2QLY. Using the Marvin feature in the PASSonline software, the pharmacological activity of

these thirty compounds from GC-MS analysis was studied. The compounds possessing anti-diabetic activity were consequently selected for docking experiments. Myristic acid glycidyl ester (RT - 40.903, Area% - 2.32); 9-Octadecenoic acid (Z)-,2,3-dihydroxypropyl ester (RT - 42.725, Area% - 0.31); 9-Octadecenoic acid (Z)-, oxiranylmethyl ester (RT - 43.38, Area% - 5.88); Cyclopropaneoctanoic acid, 2-[[2-(2-

Ethylcyclopropyl]Methyl]Cyclopropyl]Methyl]-,Methyl Ester (RT - 43.475, Area% - 0.61) and 7-Hydroxy-3-methoxy-2-p-methoxyphenyl-4H-chromen-4-one (RT - 45.444, Area% - 1.36) are the molecules with anti-diabetic activity. These selected compounds were verified for drug-likeness and docked against maltase glucoamylase and the results are tabulated in Table - 4. The 2D and 3D docking images are given in Plate II, respectively.

Myristic acid glycidyl ester exhibits the highest docking score of -262.47 with a confidence score of 0.9046, alongside a single hydrogen bond interaction (TRP-406). These scores suggest a strong and confident binding affinity towards the target, making it a promising candidate. The high docking score indicates that the compound might fit well into the binding site and the high confidence score reinforces the reliability of this prediction. 9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl ester comes next with a docking score of -198.19 and a confidence score of 0.7239. It forms three hydrogen bonds (ARG-526, HIS-600 and ASP-542), which may contribute to a more stable binding

interaction compared to compounds with fewer hydrogen bonds. Despite a lower docking score compared to Myristic acid glycidyl ester, the 9-Octadecenoic acid (Z)-, oxiranylmethyl ester and Cyclopropaneoctanoic acid, 2-[[2-[(2-Ethylcyclopropyl) Methyl] Cyclopropyl] Methyl]-, Methyl Ester show moderate docking and confidence scores, with -189.09 and -160.82 docking scores respectively. Their hydrogen bonding patterns vary, which could influence their binding stability and specificity. 7-Hydroxy-3-methoxy-2-p-methoxyphenyl-4H-chromen-4-one presents a mid-range docking score of -176.15 and a confidence score of 0.6278 but stands out with four hydrogen bonds. This suggests a potentially stable and specific interaction, despite not having the highest docking score. Myristic acid glycidyl ester, despite having only one hydrogen bond, shows the highest docking and confidence scores, suggesting a strong binding affinity and high reliability of this prediction. However, compounds like 7-Hydroxy-3-methoxy-2-p-methoxyphenyl-4H-chromen-4-one, with more hydrogen bonds, might offer more stable but possibly less potent interactions.

Table 4: Molecular docking analysis of selected bioactive compounds of *M. tinctoria* against maltase glucoamylase

S. No	Compound Name	Docking Score	Confident Score	Ligand rmsd (Å)	No. of H-bond	H-Bond
1	Myristic acid glycidyl ester	- 262.47	0.9046	108.49	1	TRP-406
2	9-Octadecenoic acid (Z)-,2,3-dihydroxypropyl ester	- 198.19	0.7239	107.78	3	ARG-526, HIS-600, ASP-542
3	9-Octadecenoic acid (Z)-, oxiranylmethyl ester	- 189.09	0.6861	103.86	1	ARG-526
4	Cyclopropaneoctanoic acid, 2-[[2-[(2-Ethylcyclopropyl)Methyl] Cyclopropyl]Methyl]-,Methyl Ester	- 160.82	0.5539	99.48	2	HIS-600, ASP-327
5	7-Hydroxy-3-methoxy-2- p-methoxyphenyl-4H-chromen-4-one	- 176.15	0.6278	106.2	4	ARG-526, HIS-600, ASP-327, ASP-542

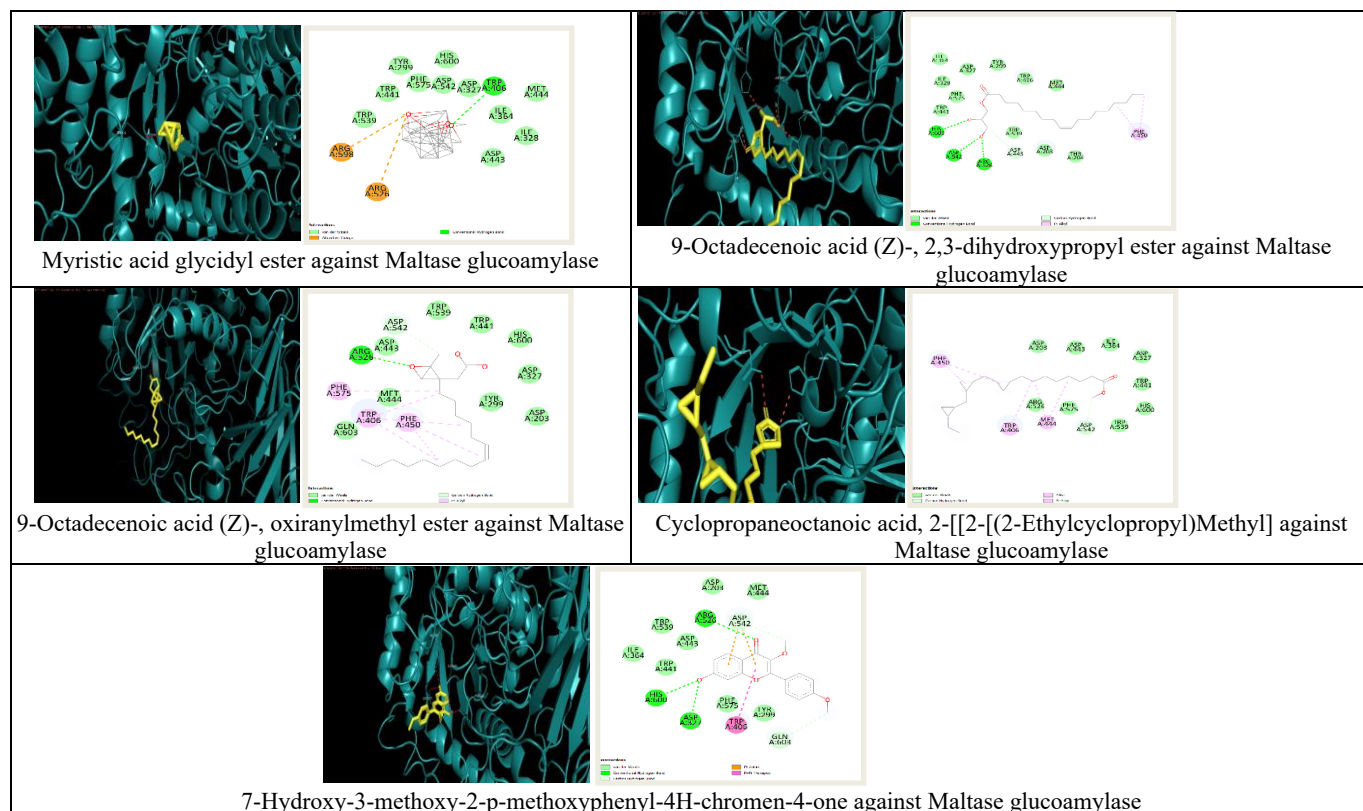


Plate II: 2D and 3D images of Molecular Docking Study of selected bioactive compounds of *M. tinctoria* against Diabetic protein (Maltase glucoamylase)

Qais and Ahmad, 2022 examined the anti-quorum sensing and biofilm inhibitory impact of several medicinal plants against gram-negative bacterial pathogens using *in vitro* and *in silico* experiments. Pyrogallol demonstrated a robust binding affinity in lasI, lasR, RhlR, and CviR, exhibiting binding affinities of 7.6, 6.9, 6.7 and 7.8 kcal mol⁻¹ in each case. Dehydroabietic acid had a strong binding affinity with LasI possessing all hydrophobic residue interactions, just like pyrogallol did. The surrounding amino acids that were supported by hydrophobic interactions were Thr145, Val148, Phe105, Trp33, Val143, Thr144, Phe27, Arg30 and Val26. The iDPPIV-SCM is a sequence-based predictor that can be used to discover and analyze inhibitory peptides of dipeptidyl peptidase IV (DPP-IV) using a scoring card technique was examined by Charoenkwan *et al.*, 2020 [24]. The entire set of 230 discovered DPPIV inhibitory sequences was subjected to an *In-silico* analysis. For the 40 DPP-IV peptides chosen in accordance with the criterion (i.e., IC₅₀ up to 20 times greater than the reference value for the tripeptide IPI). The iDPPIV-SCM program uses a score value to represent its prediction; values more than 294 suggest potential DPP-IV inhibitory peptides.

Conclusion

M. tinctoria, with its richer phytochemical profile, underwent further scrutiny through GC-MS and *In silico* docking studies, uncovering a complex chemical composition that includes 30 active ingredients. Notably, oleic acid, trimethylsilylester emerged as the most abundant compound, suggesting a potential role in modulating lipid metabolism, a crucial aspect in managing diabetes. The GC-MS analysis illustrated the diverse functional capabilities of these compounds, hinting at their synergistic potential in combating diabetic conditions. The *In silico* docking studies, highlighting myristic acid glycidyl ester for its significant binding affinity, suggest a promising avenue for the development of anti-diabetic agents. These findings not only emphasize the potential of *M. tinctoria* as a source of novel anti-diabetic compounds but also underscore the importance of further biochemical and pharmacological studies to elucidate the exact mechanisms of action and to validate the therapeutic efficacy of these bioactive compounds in diabetes management. Therefore, *M. tinctoria* stands out as a significant plant for the development of new, natural anti-diabetic therapies, leveraging its complex and bioactive phytochemical profile.

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