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2- β-D Glucopyranosyl-1, 3, 6, 7-Tetrahydroxy-9H-Xanthen-9-One (*Mangiferin*): Isolation, Functional Group Modification and Antimicrobial Activities

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ABSTRACT

This study focused on the functional group modification of *Mangiferin* using hydrazinyl (P2) and phenylhydrazinyl (P3) substituent to enhance its physicochemical and antimicrobial properties. The solubility profile improved from insoluble (P1) to slightly soluble (P2 and P3) in water, suggesting enhanced bioavailability potential. Characterization by Fourier-transform infrared spectroscopy (FTIR) confirmed the successful introduction of amine groups (3358.3, 3330.4, 1205.8 and 3322.9 cm^{-1}), while preserving key structural features such as hydroxyl groups (3542.8, 3505.6 and 3516.7 cm^{-1}) and aromatic moieties (1645.6, 1459.3 and 1420.1 cm^{-1}). Gas chromatography-mass spectrometry (GC-MS) analysis showed new molecular weight for the samples. For sample P1, the observed molecular ionic peak [M+] shows m/z = 410 [M-12H]. P2 on modification, has observed molecular ion peak m/z = 481.8 [M+Na+2H] while sample P3 has the observed molecular ion peak m/z = 576.5 [M+2Na]. Antimicrobial activity assays demonstrated that both modified compounds (P2 and P3) exhibited moderate activity at high concentrations compared to the unmodified compounds (P1) against a panel of pathogenic microorganisms, *including Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus. Bacillus subtilis* and *Candida albican*. The minimum inhibitory concentration (MICs) and minimum bactericidal/fungicidal concentrations (MBCs/MFCs) of P2 and P3 were significantly higher than that of P1.

Keywords: *Mangiferin,* hydrazinyl, phenylhydrazinyl, FTIR, GCMS, Antimicrobial activities

INTRODUCTION

Mangiferin is a natural polyphenolic compound that has gained significant attention in the scientific community due to its pharmacological properties and therapeutic potential. *Mangiferin* is extracted from the leaves, bark, and fruit of the *Mangifera indica* (mango tree).

Mangiferin has been the subject of several research for its antimicrobial, antioxidant, anti-inflammatory, and various other biological activities [1, 2].

The chemical structure of *mangiferin* (xanthone core and a C-glucosyl moiety) (Figure 1) provides opportunities for functional group modifications to enhance its pharmaceutical and therapeutic applications [3]. Modifications of the *mangiferin* structure, such as the introduction of new functional groups or the derivatization of existing ones, can lead to the development of novel *mangiferin*-based compounds with improved pharmacological properties, including enhanced antimicrobial activity.

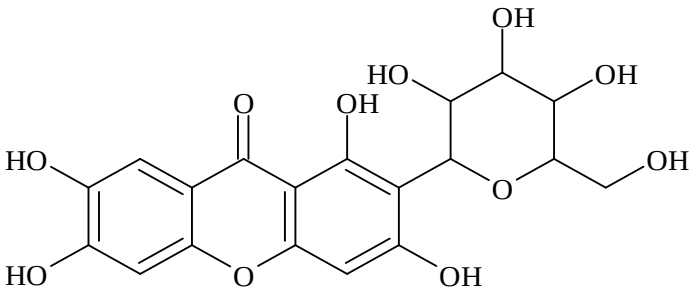


Figure 1: Structure of *Mangiferin*

The leaves, bark, or fruit of the mango tree *(Mangifera indica* L.) serve as the primary sources for the isolation of *mangiferin*. The plant materials are typically collected, washed, and dried before the extraction process [4, 5]. Several extraction methods have been employed for the selective extraction of *mangiferin*, including supercritical fluid extraction (SFE), solvent extraction, and ultrasound-assisted extraction (UAE) [5-7]. The polarity of the target chemical, the existence of interfering compounds, and the extraction efficiency all influence the extraction technique selection. The crude extract containing *mangiferin* is subjected to various purification techniques to isolate the compound in a high-purity form. Common purification methods include column chromatography, preparative high-performance liquid chromatography (prep-HPLC), and crystallization [5, 7]. The antimicrobial potential of *mangiferin* and its derivatives has been extensively investigated, as these compounds have shown promising inhibitory effects against some pathogenic microorganisms such as viruses, bacteria and fungi [2, 3]. This is assessed using in vitro assays, such as the disc diffusion method, broth dilution method, and time-kill kinetics [2, 8]. These methods allow for the determination of the minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC), and the rate of microbial growth inhibition or killing.

In spite of the numerous traditional and antimicrobial properties of *mangiferin*, its practical applications are limited due to issues like low solubility, poor bioavailability and inadequate permeability. *Mangiferin* has low aqueous solubility (0.111 mg/mL) and oral

bioavailability (less than 2%) due to its poor lipophilicity and intestinal permeability, which limits its therapeutic efficacy [2]. The antimicrobial mechanisms of *mangiferin* and its derivatives involve various strategies, such as membrane disruption, inhibition of microbial enzymes, interference with quorum sensing, and disruption of viral replication processes [2, 3]. The specific mechanisms may vary based on the target microorganism and the structural modifications of the *mangiferin* derivatives. Modifications of the functional groups, such as the introduction of benzoyl, acetyl, or methyl substituents, can significantly impact the antimicrobial efficacy of the compounds [9].

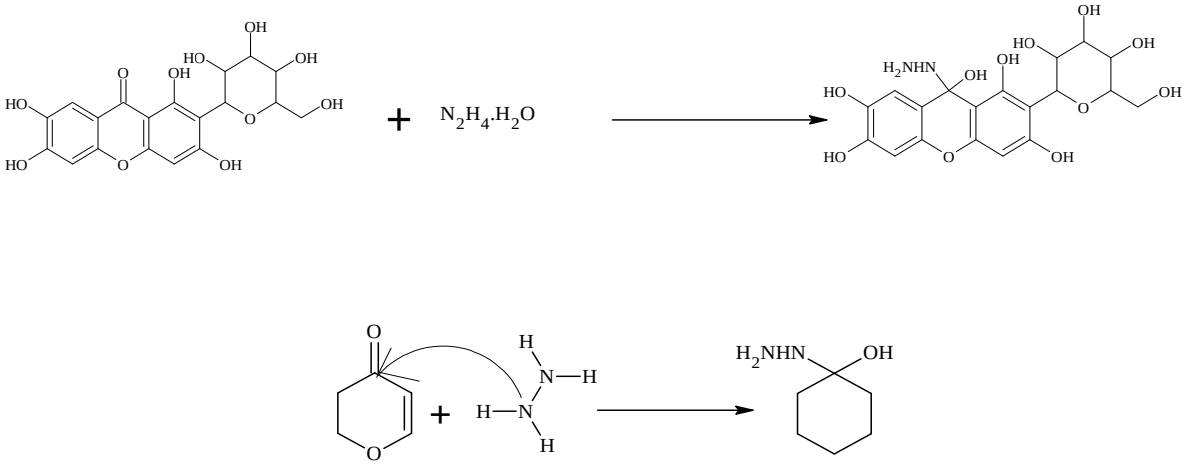
The aim of this research is to isolate *mangiferin*, perform functional group modification, and evaluate the antimicrobial activities of the modified and unmodified *mangiferin* through the following sets of objectives: to isolate and purify *mangiferin* from *Mangifera indica* bark; to carryout functional group modification of the *mangiferin*; to characterize the modified and unmodified compounds using GC-MS and FTIR and to evaluate and compare antimicrobial activities of the modified and unmodified *mangiferin*.

MATERIALS AND METHODS

Material/Reagents: Mango bark, Phenyl hydrazine (C_6H_5-NH-NH_2) (spectrum chemical MFG corp), Hydrazine hydrate (NH_2-NH_2.H_2O) (Alfa India), Dimethyl sulfoxide (DMSO) (Aquarius pro life), Ethanol (C_2H_5OH) (walgreens).

Procedure for functional group modification using hydrazine hydrate

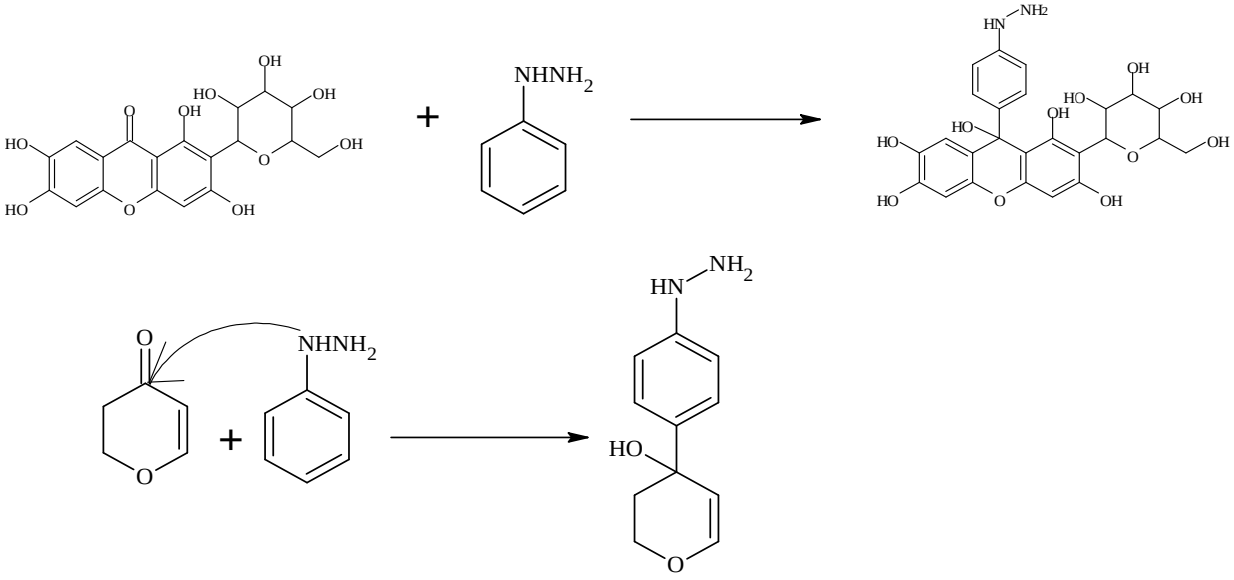
The method used was the Schiff Hoff condensation reaction [10, 11]. A mass of 4.35 g (10.3 mmol) of *mangiferin* was weighed into a round bottom flask and 35 ml of solvent (DMSO) was added to it, heated at 20 ^oC for 5 min to dissolve the *mangiferin*. Then 1 ml (20.6 mmol) of hydrazine hydrate was added to the mixture and reflux at 10 ^oC for about 10 h. The reaction mixture was cooled and filtered, washed with water and dried. The reaction progress was monitored using TLC (n-hexane:ethylacetate - 4:1).



Scheme 1: Functional group modification of *Mangiferin* hydrazinyl (P2)

Procedure for Functional Group Modification Using Phenyl hydrazine

A mass of 2.14 g (5.05 mmol) of *mangiferin* was weighed into a round bottom flask and 30 ml of solvent (DMSO) was added to it, heated at 20 ^{o}C for 5 min to dissolve the *mangiferin*. Then 1 ml (10.1 mmol) of phenylhydrazine was added to the mixture and reflux at 10 ^{o}C for about 10 h. The reaction mixture was cooled and filtered, washed with water and dried. The reaction progress was monitored using TLC (n-hexane:ethylacetate - 4:1).



Scheme 2: Functional group modification of *Mangiferin* phenyl hydrazinyl (P2).

Characterization

The synthesized compounds were subjected to spectroscopic techniques: FTIR spectrometry was carried out on both modified (P2 and P3) and unmodified (P1) compound. Gas Chromatography Mass Spectrometry (GC-MS) of both modified (P2 and P3) and unmodified (P1) compound was also recorded.

Biological Screening

The modified (P2 and P3) and unmodified (P1) compounds were subjected to antibacterial and antifungal evaluation using selected clinical isolates. The methods were adopted by Ghulam *et al.,* [12]. Fungus (*Candida albican*), bacteria (*Escherichia coli, Pseudomonas aeruginosa*), and bacteria (*Stapylococcus aureus, Bacillus subtilis*) that were Gram positive were collected. The concentration of the extract solution was 1000 µg/mL. The paper discs were then filled with extract, put on the nutrient agar medium that had been infected with the test bacteria, and incubated for twenty-four hours at 37 °C. As standard, 10 µg/mL of ciprofloxacin was employed.

RESULTS AND DISCUSSION

Table 1 summarizes the outcome of the product formed including their % yield, calculated molecular weights and solubility profile.

Table 1: Isolation and functional group modification of *mangiferin*

Samples	Functional Group modification	Calculated Molecular weight (g/mol)	% Yield	Solubility in	
				Water	Ethanol
P1	Unmodified	422.34	78	Insoluble	Insoluble
P2	$+NHNH_2$	457.41	59	Slightly soluble	Soluble
P3	$+C_6H_5NHNH_2$	530.48	63	Slightly soluble	Soluble

P1: 1,3,6,7-tetrahydroxy-2-(3,4,5,6-tetrahydroxytetrahydro-2H-pyran-2-yl)-9H-xanthen-9-one;

P2: 9-hydrazinyl-2-(3,4,5,6-tetrahydroxytetrahydro-2H-pyran-2-yl)-9H-xanthene-1,3,6,7,9-pentaol;

P3: 9-(4-hydrazinylphenyl)-2-(3,4,5,6-tetrahydroxytetrahydro-2H-pyran-2-yl)-9H-xanthene-1,3,6,7,9-pentaol

The isolation and functional group modification of *mangiferin* (P1-P3) was successfully achieved with good to appreciable yields (59% to 78%). The unmodified *mangiferin* (P1) showed a high yield of 78% with a calculated molecular weight of 422.34 g/mol. Functional group modifications with hydrazine derivatives resulted in P2 ($+NHNH_2$) and P3 ($+C_6H_5NHNH_2$) with calculated molecular weights of 455.41 g/mol and 530.48 g/mol respectively, and yields of 59% and 63%. The solubility in water and ethanol of P1 is described

as "insoluble," which is a known characteristic of *mangiferin* due to its polyhydroxylated xanthonoid structure [2, 13]. The slightly soluble nature in water and ethanol of P2 and P3 indicates a change in polarity compared to the unmodified *mangiferin*, likely due to the introduction of the more polar hydrazinyl group, which can participate in hydrogen bonding with water molecules [14].

Figures 1-3 show the FTIR spectral of sample P1-P3, while Table 2 – 4 indicates the identified functional group present for sample P1-P3 respectively.

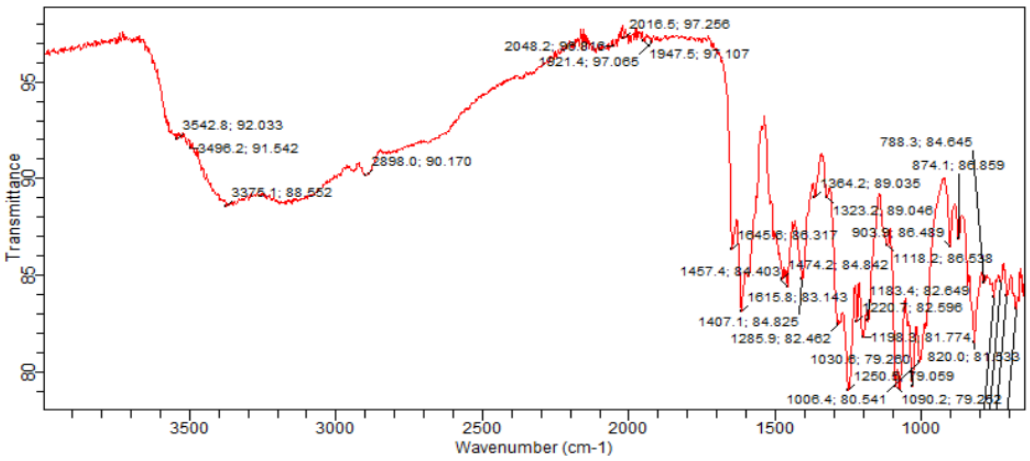


Fig 1: FTIR Spectral representation of P1

Table 2: FTIR Absorption Table for Sample P1

Absorption Peak (cm^{-1})	Reference Absorption Peaks (cm^{-1})	Appearance	Functional Group	Compound Class
3542.8	3650-3400	Medium	O-H stretch	Alcohol
2898.0	2960-2850	Medium	C-H stretch	Alkane
1645.6	1680-1640	Medium	C=O stretch	Carbonyl componds
1457.4	1600-1450	Medium	C=C stretch	Aromatic ring
1474.2	1600-1450	Medium	C=C stretch	Aromatic ring
1118.2	1150-1050	Strong	C-O stretch	Alcohol

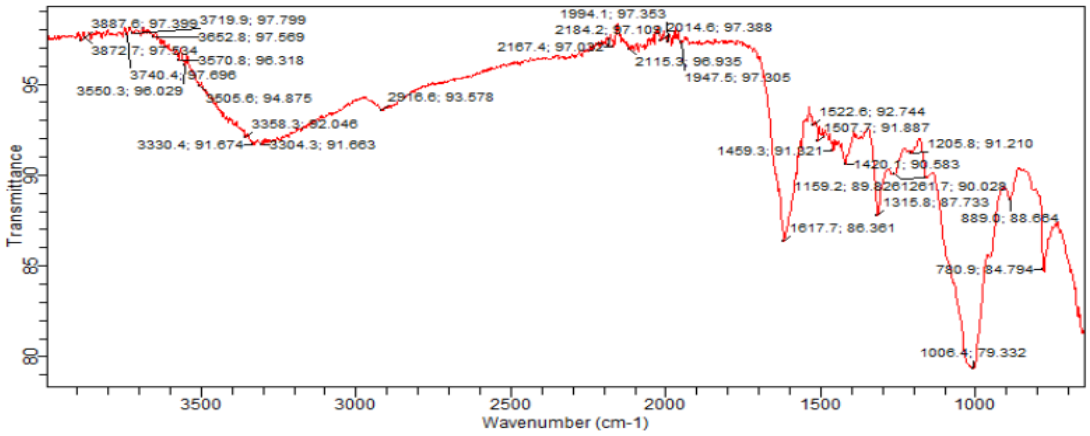


Fig 2: FTIR Spectral representation of P2.

Table 3: FTIR Absorption Table for Sample P2

Absorption Peak (cm^{-1})	Reference Absorption Peaks (cm^{-1})	Appearance	Functional Group	Compound Class
3358.3	3500-3300	Medium, broad	N-H stretch	Amine
3330.4	3500-3300	Medium, broad	N-H stretch	Amine
3304.3	3500-3300	Medium, broad	N-H stretch	Amine
3505.6	3650-3400	Medium	O-H stretch	Alcohol
3570.8	3650-3400	Medium	O-H stretch	Alcohol
3550.3	3650-3400	Medium	O-H stretch	Alcohol
1459.3	1600-1450	Medium	C=C stretch	Aromatic ring
1522.6	1600-1450	Medium	C=C stretch	Aromatic ring
1507.7	1600-1450	Medium	C=C stretch	Aromatic ring
1617.7	1680-1640	Weak	C=C stretch	Alkene
1205.8	1230-1030	Medium	C-N stretch	Amine
1159.2	1230-1030	Medium	C-N stretch	Amine

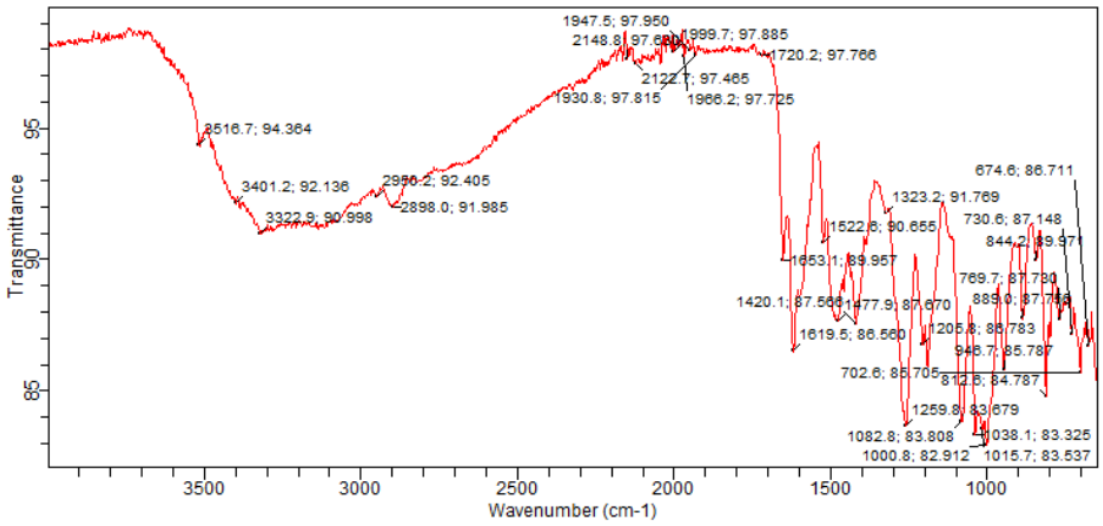


Fig 3: Spectral representation of P3

Table 4: FTIR Absorption Table for Sample P3

Absorption Peak (cm^{-1})	Reference Absorption Peaks (cm^{-1})	Appearance	Functional Group	Compound Class
3322.9	3500-3300	Medium	N-H stretch	Amine
3516.7	3650-3400	Weak	O-H stretch	Alcohol
3401.2	3650-3400	Medium	O-H stretch	Alcohol
1420.1	1600-1450	Medium	C=C stretch	Aromatic ring
1522.6	1600-1450	Medium	C=C stretch	Aromatic ring
1082.8	1150-1450	Strong	C-O stretch	Alcohol
1205.8	1230-1030	Medium	C-N stretch	Amine
2950.2	2960-2850	Medium	C-H stretch	Alkane
2898.0	2960-2850	Medium	C-H stretch	Alkane
1653.1	1680-1640	Medium	C=C stretch	Alkene

Characterization of the compounds

Fourier transform infra-red spectrometry analysis

A useful method for determining the functional groups that are present in a molecule is FTIR spectroscopy [14]. The Tables (Table 2 –Table 4) compare the absorption peaks of the samples with reference absorption peaks for various functional groups.

A strong and broad absorption around 3542.8, 3505.6 and 3401.2 cm^{-1} (Table 2 –Table 4) in both P1, P2 and P3, confirms the presence of multiple hydroxyl (-OH) groups, which is characteristic of *mangiferin*. This is crucial as *mangiferin* is a polyhydroxylated xanthonoid. Aromatic C=C stretch (1457.4 cm^{-1}, 1474.2 cm^{-1}, 1459.3 cm^{-1}, 1420.1 cm^{-1} and 1522.6 cm^{-1}) (Figures 1-3) as seen in all samples (P1, P2 and P3) are consistent with the aromatic rings present in the *mangiferin* structure. The peaks at 2898.0 cm^{-1} (Figure 1) as observed in P1

indicate the presence of C-H bonds in the sugar moiety (pyranosyl ring). The C=O stretch (1645.2 cm^{-1}) (Figure 1) observed in P1, confirms the presence of the carbonyl group (C=O) within the xanthone core of *mangiferin*. N-H stretch (3358.3 cm^{-1}, 3330.4 cm^{-1}, 3304.3 cm^{-1}, and 3322.9 cm^{-1}) (Figures 2 and 3) as seen in P2 and P3 is a key indicator of the successful introduction of the hydrazinyl group (N−H stretch from $-NHNH_2$) and phenylhydrazinyl moiety ($C_6H_5NHNH_2$). This directly supports the proposed modification. C-N stretch (1205.8 cm^{-1} and 1159.2 cm^{-1}) (Table 3 and Table 4) observed in P2 and P3 indicate a C-N stretch confirming the integration of a nitrogen-containing functional group as well as nitrogen-containing phenylhydrazine group. The results reported in this study correspond with Taniya *et al.* [15].

Figures 4-6 show the GC-MS Spectra of sample P1-P3 respectively.

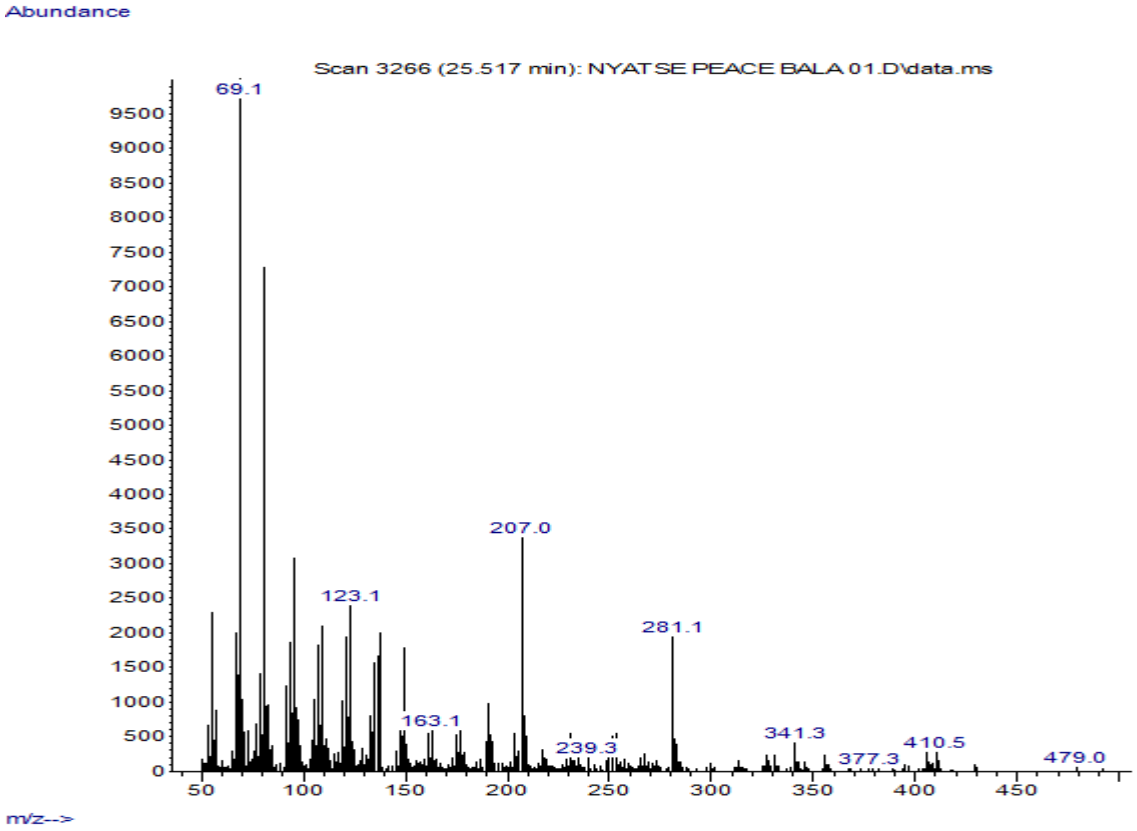


Figure 4: GC-MS Spectrum for Sample P1.

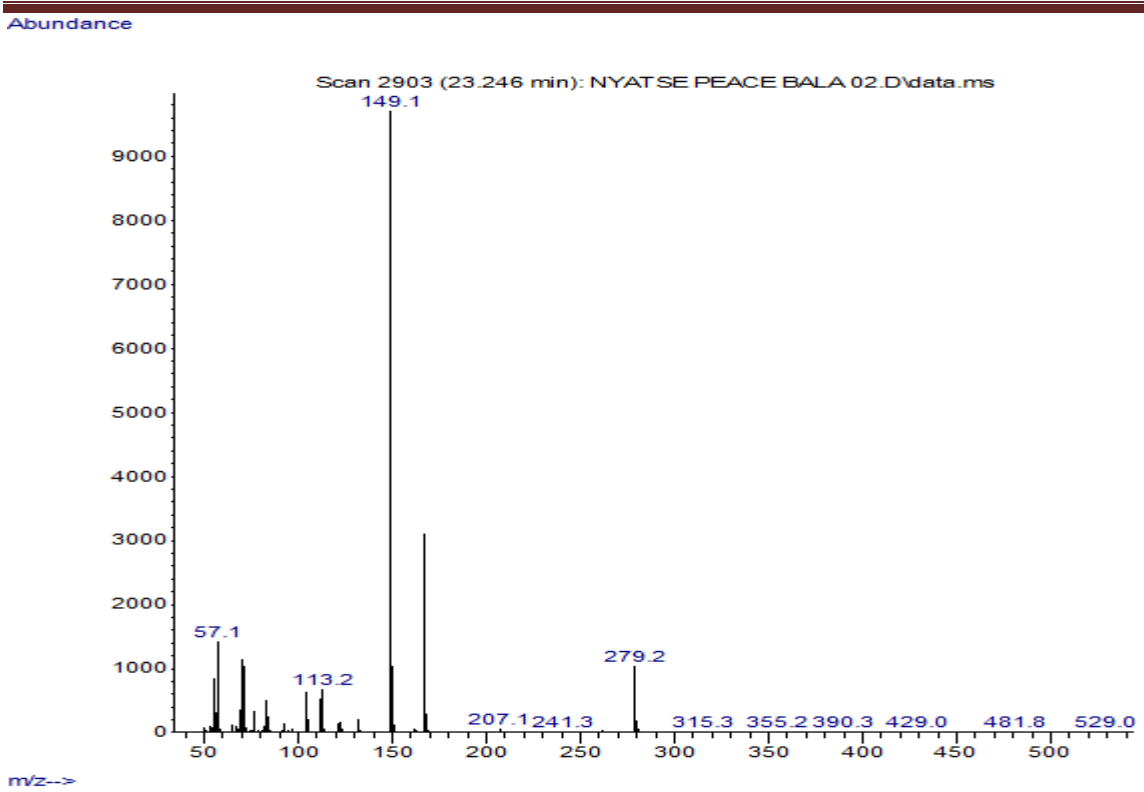


Figure 5: GC-MS Spectrum for Sample P2.

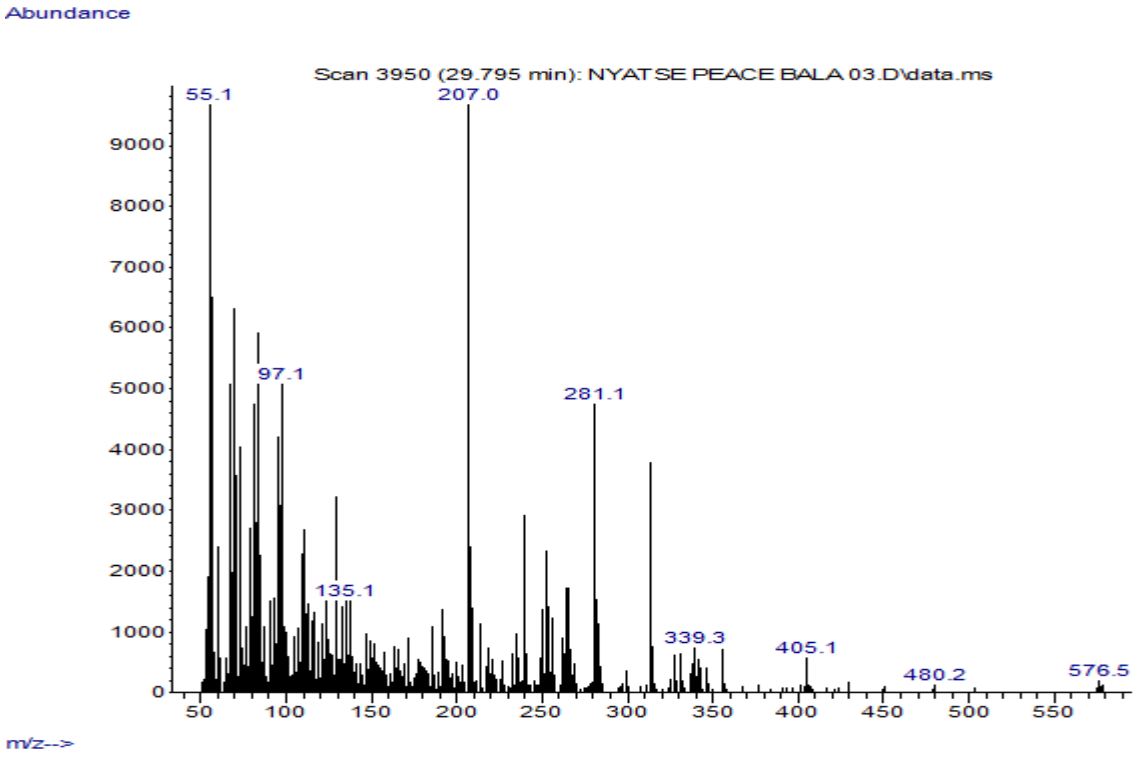


Figure 6: GC-MS Spectra for Sample P3.

Gas Chromatography-Mass Spectrometry is a potent analytical method for separating, identifying, and measuring mixture components [16]. Figure 4 shows the GC-MS spectrum of sample P1, which indicates a molecular ion peak at m/z = 410.5 [M - 12H]. The calculated molecular weight of sample P1 (*Mangiferin*) was 422.34 g/mol. The observed molecular ion peak [M+] at m/z = 410.5, suggest the sample lost 12 protons. A study carried out by Mahendran *et al.*, [9] found the molecular ion peak of *mangiferin* to be 444.1 [M+Na -H]. The presence of other peaks observed in the spectrum (e.g., m/z = 479.0, 341.3, 281.1, 207.0) corresponds to the fragments formed from the parent molecules during the mass spectrometry process.

Figure 5 shows the GC-MS spectrum of sample P2. The calculated molecular of sample P2 (hydrazinyl-*mangiferin*) is 457.41 g/mol. The observed molecular ion peak [M+] was found to be m/z = 481.4 [M+Na+2H]. This could be due to sodium adduct formation from the solvent used or from instrumentation. Other observed peaks seen at m/z = 529.0, 279.2, 207.1, 149.1 are fragments formed from the parent molecule.

Figure 6 shows the GC-MS spectrum of sample 3. It indicates a molecular ion peak at m/z = 576.5 [M+2Na]. The calculated molecular weight of sample P3 (Phenylhydrazinyl-*mangiferin*) is 530.48 g/mol. This could be due to sodium adduct formation from the solvent used or from instrumentation. Other fragments formed by the parent molecule are observed at m/z = 480.2, 405, 339.3, 281.

Table 5: Antimicrobial Activity (Zone of Inhibition mm) of *mangiferin* extracts at different concentrations

Extract	Concentration (µg/mL)	Inhibition zone (mm)				
		E. coli	P. aeruginosa	S. aureus	B. subtilis	C. albican
	1000	18	14	20	22	14
	500	15	-	17	18	-
	250	-	-	13	14	-
	125	-	-	-	-	-
	Ciprofloxacin	32	38	32	30	26
	1000	16	12	14	12	14
	500	12	-	-	-	-
	250	-	-	-	-	-
	125	-	-	-	-	-

Ciprofloxacin	32	38	32	30	26
1000	13	12	15	14	13
500	-	-	12	-	-
250	-	-	-	-	-
125	-	-	-	-	-
Ciprofloxacin	32	38	32	30	26

Table 5 shows the Antimicrobial Activity (Zone of inhibition mm) of *mangiferin* extracts at different concentrations. It presents the zone of inhibition (in mm) for P1, P2, and P3 against various bacterial strains at different concentrations (1000 µg/mL, 500 µg/mL, 250 µg/mL). P1 shows dose-dependent antimicrobial activity against all tested bacteria: *E. coli*, *S. aureus*, *P. aeruginosa*, *B. subtilis* and *C. albicans*. At 1000 µg/mL, P1 exhibits moderate to good inhibition zones: 18 mm for E. coli, 14 mm for P. aeruginosa, 20 mm for *S. aureus*, 22 mm for *B. subtilis* and 16 mm for *C. albicans*. The activity generally decreases with lower concentrations (e.g., 13 mm for *S. aureus* and 14 mm for *B. Subtilis* at 250 µg/mL), as expected. The results are higher than those of Ogidi*et al.*, [17], who used the agar well diffusion method to examine the antimicrobial properties of aqueous and methanol extracts of *M. indica* stem bark against a selection of microbes, including *Staphylococcus sp., Shigella sp., Escherichia coli, Penicillium sp., Vibrio sp.*, yeast, and mold isolates. They reported a range of inhibition from 9.3 to 15.4 mm. Its structure of polyhydroxyxanthone and phenolic compounds, which can interfere with DNA synthesis, block enzymes, or damage bacterial cell membranes, is frequently credited with its antibacterial activity [18]. The observed zones of inhibition are consistent with previously reported antimicrobial activities of *mangiferin*.

P2 (Modified *Mangiferin* - Hydrazinyl derivative) generally shows the antimicrobial activity especially at higher concentrations. At 1000 µg/mL, P2 exhibits inhibition zones: 16 mm for *E. coli*, 12 mm for *P. aeruginosa*, 14 mm for *S. aureus*, 12 mm for *B. Subtilis* and 14 mm for *C. albicans. E. coli* exhibited zones at inhibition 12 mm at 500 µg/mL. The introduction of hydrazine moieties into organic compounds is a common strategy in medicinal chemistry to enhance biological activities, including antimicrobial and antifungal properties [19, 20].

P3 (Modified *Mangiferin* - phenylhydrazinylxanthen-ol derivative) demonstrates antimicrobial activity at very high conconcentrations. At 1000 µg/mL, P3 exhibits inhibition zones: 13 mm for *E. coli*, 12 mm for *P. aeruginosa*, 15 mm for *S. aureus*, 14 mm for *B. subtilis*

and 13 mm for C. albicans. These zones are notably larger than those for both P1 and P2. At 250 µg/mL, P3 show activity 12 mm for S. aureus.

Table 6: Minimum Inhibitory Concentrations (MIC) of the extracts against the organisms

Extracts	Minimum Inhibitory Concentration (µg/mL)				
	E. coli	P. aeruginosa	S. aureus	B. subtilis	C. albican
P1	125	1000	125	125	1000
P2	1000	1000	1000	1000	1000
P3	1000	1000	1000	1000	1000

Table 7: Minimum Bactericidal Concentrations (MBC) of the extracts against the organisms

Extracts	Minimum Bactericidal/Fungicidal Concentration (µg/mL)				
	E. coli	P. aeruginosa	S. aureus	B. subtilis	C. albican
P1	125	125	1000	1000	1000
P2	1000	1000	1000	1000	1000
P3	1000	1000	1000	1000	1000

Minimum Inhibitory Concentrations of the extracts against the organisms

Table 6 lists the Minimum Inhibitory Concentrations (MICs) in µg/mL, the lowest antibiotic concentration that will stop a microorganism from developing noticeably following an overnight incubation. Greater potency is indicated by a lower MIC. For *E. coli, P. aeruginosa, S. aureus, B. subtilis,* and *C. albicans*, P1 displays MICs of 125 µg/mL, 1000 µg/mL, 125 µg/mL, and 1000 µg/mL, respectively. This correspond to the result of Osei-Djarbeng*et al.*, [21]. These values indicate moderate inhibitory activity, which aligns with previous reports on *mangiferin*'s antimicrobial properties.

P2 (Modified *Mangiferin* - Hydrazinyl derivative) demonstrates higher MICs values than P1: 1000 µg/mL for all organisms, *E. coli, P. aeruginosa, S. aureus,* and *C. albicans*. This indicates that P2 is twice as potent as P1. This quantitatively supports the observed inhibition zones in Table 6.

P3 (Modified *Mangiferin* - phenylhydrazinylxanthen-ol derivative) also exhibits the MICs values as P2. 1000 µg/mL for *E. coli,* 1000 µg/mL for *P. aeruginosa,* 1000 µg/mL for *S. aureus,* 1000 µg/mL for *B. subtilis* and 1000 µg/mL for *C. albicans*. This indicates that P3 is twice as potent as P1.

Minimum Fungicidal Concentrations (MFCs) and Minimum Bactericidal Concentrations of the extracts against the organisms

The Minimum Fungicidal Concentrations (MFCs) and Minimum Bactericidal Concentrations (MBCs) in µg/mL are shown in Table 7. This is the lowest concentration of an antibiotic that, after a certain incubation period, would kill 99.9% of the original inoculum. MBC/MFC values are crucial for determining whether an agent is merely inhibitory or truly cidal. P1 (Unmodified *Mangiferin*) shows MBC/MFC values of 125 µg/mL for *E. coli*, 125 µg/mL for *P. aeruginosa*, 1000 µg/mL for *S. aureus*, 1000 µg/mL for *B. subtilis* and 1000 µg/mL for *C. albicans*. The MBC/MFC values are typically equal to or higher than the MIC values, which was observed in this study. P1 exhibits bactericidal/fungicidal activity, but at higher concentrations.

P2 (Modified *Mangiferin* - Hydrazinyl derivative) shows higher MBC/MFCs than P1: 1000 µg/mL for *E. coli*, 1000 µg/mL for *P. aeruginosa*, 1000 µg/mL for *S. aureus*, 1000 µg/mL for *B. subtilis* and 1000 µg/mL for *C. albicans*. This indicates that P2 is more effective at killing the microorganisms than P1 at high concentrations.

P3 (Modified *Mangiferin* - phenylhydrazinylxanthen-ol derivative) exhibits the lowest MBC/MFCs, confirming its superior cidal activity: 62.5 µg/mL for *E. coli*, 125 µg/mL for *P. aeruginosa*, 62.5 µg/mL for *S. aureus*, and 125 µg/mL for *C. albicans*. P3 demonstrates significantly enhanced killing efficacy compared to both P1 and P2, requiring only a quarter of the concentration of P1 to kill E. coli and S. aureus.

CONCLUSION

This study successfully achieved the isolation and purification of *mangiferin* from *Mangifera indica* bark, yielding a high purity compound (P1) with a molecular weight of 422.34 g/mol. Subsequent functional group modifications through hydrazinyl (P2) and phenylhydrazinyl (P3) attachments were confirmed by FTIR and GC-MS analyses, demonstrating effective chemical transformation with changes in molecular weight, solubility, and spectral characteristics.

The FTIR results verified the introduction of amine functionalities and retention of key structural groups, while GC-MS results supported the FTIR result by showing the presence of new molecular weights, confirming successful modification. Importantly, these modifications enhanced the water solubility of *mangiferin* derivatives, potentially improving their bioavailability.

Biological evaluation revealed that both modified compounds (P2 and P3) exhibited significant antimicrobial activities at higher concentrations compared to the unmodified *mangiferin* (P1). Higher minimum bactericidal/fungicidal concentrations (MBCs/MFCs) and

minimum inhibitory concentrations (MICs) were demonstrated by the modified derivatives against a variety of bacteria, such as *E. coli*, *S. aureus*, *B. subtilis*, *P. aeruginosa*, and *C. albicans.* This enhancement is likely due to the presence of hydrazinyl groups, which may facilitate better interaction with microbial cell targets.

Overall, the study demonstrates that functional group modification of *mangiferin* can effectively enhance its antimicrobial potency and physicochemical properties, supporting its potential as a lead compound for developing novel antimicrobial agents.

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