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Screening of secondary metabolites produced by *Fusarium globosum* isolated from infected *Coccinia grandis* of Malabar region of Kerala, India

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Fusarium, one of the most common fungal genera, has received considerable attention because of its biosynthetic properties and production of varieties of secondary metabolites. An attempt was made to study the active secondary metabolites produced by *Fusarium globosum* isolated from infected fruit of *Coccinia grandis*. Based on the PCR amplification and genomic sequencing of internal transcribed spacer region (ITS), the isolated fungus was characterized and confirmed as *Fusarium globosum* CBS430.97. Methanol and ethyl acetate extracts of *Fusarium globosum* were used for qualitative and quantitative analysis. In qualitative analysis, phytochemicals were present in both methanol and ethyl acetate extracts while alkaloids and saponins were absent in methanolic extract.Total phenolic content was found to be higher in methanolic extract (145.48 mg/g) and lower (90.92 mg/g) in ethyl acetate extract.Tannin content was found high (153.36 mg/g) in methanolic extract and low (32.11 mg/g) in ethyl acetate extract. High amount of flavonoid (33.17 mg/g) was found in methanol extract and low (27.55 mg/g) in ethyl acetate extract. GC-MS analysis of methanolic extract showed high peaks in ergosterol, n-hexadecanoic acid and oleic acid among the thirty compounds. This investigation revealed that the secondary metabolites produced by *Fusarium globosum* can be a potential source of novel natural bioactive metabolites compounds.

Key words: FT-IR,GC-MS, phylogenetic tree, phytochemicals

INTRODUCTION

A fungus is one of the most diverse microorganisms that inhabit different environmental sources such as soil, plant parts (leaves, root and fruits), water and food sources (Sartori *et al*. 2013).Plant diseases caused by a variety of fungi may cause significant losses on vegetable crops. Plant pathogenic fungi that are basically classified as necrotrophs, hemibiotrophs and biotrophs. It is one of the most infectious agents in plants, causing alterations during developmental stages including post-harvest, gaining nutrients from the plants they invade and, therefore, resulting in huge economic damage (Agrios, 2005).

Fungi contain rich sources of secondary metabolites and it act as analgesic, antipyretic, anti-inflammatory activities, eczema, hepato protective, hypoglycemic and tuberculosis (Perez-Nadales *et al*.,2014). The vegetable contains different nutrients, these nutrients support the growth of fungi which produce enzymes that degrade the nutrients (Wogu and Ofuase,2014). *Fusarium globosum* was first isolated from maize *Zea mays* L. harvested in the former Transkei region of South Africa and subsequently from wheat (*Triticum aestivum* L.) culms in subtropical Japan. *Fusarium* is one of the most common fungal genera and has received considerable attention because of its biosynthetic properties and production of many varieties of secondary metabolites. Different species have also been shown to produce structurally diverse secondary metabolites of potential pharmacological relevance (alkaloids, peptides, amides, terpenoids, quinones, and pyranones) (Li and Wang, 2009). Some compounds present in *Fusarium,* can cause plant, human and animal diseases (bakanae, foot rot, scab, and head blight).

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Coccinia grandis is one of the important perennials and herbaceous climber. It belongs to family Cucurbitaceae, commonly known as Ivy gourd or little gourd. It is a tropical plant and is occasionally cultivated as a garden vegetable. It is a dioecious, and trailing vine with glabrous stems and tuberous roots (Manju and Betsy, 2019). The plant is native to Bengal and other parts of India, grows abundantly all over India, tropical Africa, Australia, and throughout other oriental countries (Kumar *et al*. 2018). Ivy gourd is one of the edible and common vegetable in Malabar region.Therefore, the present investigation was made to isolation, identification and molecular characterization of fungi from *Coccinia grandis* and analysis of their active secondary metabolites were characterized.

MATERIALS AND METHODS

Sample collection

Infected and healthy *Coccinia grandis* were collected from the Malabar region of Kerala during October 2020. Samples were collected in polythene bags and brought to the laboratory for further analysis.

Isolation and Identification of fungi

Surface of the infected *Coccinia grandis* was washed thoroughly with distilled water to remove the dirt particles. A small portion of the spotted area was cut in and out using a sterile scalpel and inoculated onto a freshly prepared Potato Dextrose Agar (PDA) plate. Then the inoculated plates were incubated for 5-10 days at 30 °C and observed for fungal growth. Resulting colonies were then sub-cultured onto a PDA plate to obtain the pure cultures (Udoh *et. al*. 2015).

Pathogenicity test

A healthy *Coccinia grandis* samples were surface sterilized with alcohol and rinsed with distilled water. A sterile metal rod was used to punch out single fruit column from each of the healthy fruits, another sterilized metal rod was used to punch the portion of the mycelium of pure fungal isolates and a glass rod was then used to remove the punched mycelium from the metal rod to replace the punched portion of the fruits. The inoculated portion was then sealed with petroleum jelly to prevent contamination. The inoculated fruits were left at room temperature for 8 days. The spoilage pathogens were isolated from fruits and inoculated onto the potato dextrose agar plate/petri dish and incubated at room temperature for 5-7 days. The resulting colonies were sub-cultured to obtain the pure fungal isolates. The pure fungal isolates were compared with the original colonies from which they were isolated (Ayoola, 2007: Chukwuka *et.al*. 2010).

Morphological characteristics of the isolated fungus

Isolated fungus was identified based on the colony morphology, conidiospore and conidiophore characteristics. Lacto phenol staining technique was used for microscopic identification of the isolate (Nagamani *et al.* 2006).

Molecular characterization of the isolated fungus

DNA was extracted from the isolated fungal pathogen using DNeasy Plant Mini Kit (Qiagen, USA). To amplify the complete sequence of 5.8S ribosomal RNA gene and I and II spacer regions completely and partial sequence of 18S ribosomal RNA gene and 28S ribosomal RNA gene regions of the pathogen, the primer pairs of ITS6 (5'-GAAGGTGAAGTCGTAACAAGG- 3') and ITS4 (5'-TCCTCCGCTTATTGATATGC- 3') were used. A phylogenetic tree was constructed based on ITS sequence of*Fusariumglobosum* isolate with other *Fusarium* species, sourced from GenBank, with the software MEGA - X version 10.2.0 (Kumar *et al.* 2018) using the neighbour- joining (NJ) method under 1,000 bootstrap replicates.

Extraction of metabolites

Extraction of secondary metabolites from the isolated fungus was done by the following method with slight modification (Swathi *et al.* 2013). Isolated fungus producing metabolite was inoculated into 500 ml Erlenmeyer flask containing 200 ml of potato Dextrose Broth medium and then the flask was incubated for 14 days in room temperature under stationary conditions with intermittent shaking. The mycelia and filtrate were separated from the culture broth and equal volume of ethyl acetate/methanol was added to the filtrate. The filtrate was mixed thoroughly for 10 min and kept for 5 min till the formation of two clear immiscible layers. Using the

separating funnel, the upper layer (ethyl acetate/ methanol) containing the extracted compounds was separated. The extract was concentrated by removing the solvents under reduced pressure at 35-40°C with a rotary evaporation and the extract was dissolved in DMSO and stored at 4° C.

Preliminary qualitative analysis of fungal metabolite

Qualitative analysis of methanolic and ethyl acetate extracts of fungal metabolite produced by *Fusarium globosum* was carried out by following the method of Devi *et al*. (2012).

Alkaloids

1 ml crude fungal extract was dissolved in 2N HCl solution and filtered. It was treated with saturated picric acid. The yellow colour precipitate indicated the presence of alkaloids.

Flavonoids

To1 ml crude fungal extract, 0.5 ml of ammonia solution and few drops of concentrated sulfuric acid were added. A change to yellow colour was indicated the presence of flavonoids.

Phenols

To 1 ml of crude fungal extract, few drops of neutral 5% ferric chloride solution were added. A bluish black colour indicated the presence of phenolic compounds.

Saponins

1 ml of crude fungal extract was vigorously shaken with distilled water and allowed to stand for 10 min. Formation of a fairly stable emulsion indicated the presence of saponins.

Steroids

To 1 ml of crude fungal extract, 1 ml of chloroform and few drops of conc. H_2SO_4 were added. A blue green ring indicated the presence of steroids.

Tannins

One ml of crude fungal extract was treated with alcoholic $FeCl_3$ reagent. A bluish black colour indicated the presence of tannins.

Terpenoids

To 1 ml of crude fungal extract, 2 ml of chloroform and 3 ml of conc. H_2SO_4were added to form a layer. Formation of reddish-brown precipitate at the interface indicated the presence of terpenoids.

Quantitative analysis of fungal metabolite

Total Phenols

The total phenolic content was determined by using Folin-Ciocalteu (FC) method (Kumar 2018). 0.1 ml of fungal extract was made up to 0.25 ml with distilled water and mixed with 0.25 ml of FC phenol reagent. After 3 min, 0.5 ml of 20% sodium carbonate solution was added to the mixture and made up to 5 ml by adding distilled water. The resultant mixture was kept in the dark for 30 min, and absorbance was read at 760 nm. The result was expressed as μg of gallic acid equivalents/ mg of the sample extract.

Flavonoid

An aliquot of 0.5 ml of fungal extract was mixed with 1.5 ml of methanol, 0.1 ml of 10% $AlCl_3$, 0.1 ml of 1M potassium acetate and 2.8 ml of distilled water. After incubation at room temperature for 30 min, the absorbance of the reaction mixture was measured at 415 nm. The amount of flavonoid content was expressed as μg of quercetin/mg of extract (Singleton and Rossi, 1965).

Tannin content

Estimation of tannin was done by the following method (Price and Butler, 1977). 20 μl of the sample was aliquoted into a test tube containing 980 μl of distilled water. To this, 500 μl of 1% $K_3Fe(CN)_6$ and 100 μl of 1% ferric chloride ($FeCl_3$) were added and made up to 3 ml with distilled water. After 10 min, the reaction mixture was measured using a UV spectrophotometer at 720 nm. The tannin content was expressed as μg of tannic acid equivalents/ mg of the sample extract (Chang *et al*. 2002).

GC - MS Analysis

Crude methanol extract of funguswas used to evaluate the chemical composition by GC–MS analysis. Analysis was done using Thermo

Scientific GC Trace 1310 equipped with MS 8000 by using column, Agilent DB 5MS (30-meter x 0.25 mm). Helium was used as carrier gas. EI ionization mode was used to obtain mass spectrum analysis. Ion source temperature was maintained at 220 °C and MS transfer line temperature was 260 °C. Interpretation on mass spectrum of GC-MS was made using the database of National Institute of Standards and Technology (NIST) having not less than 62, 000 patterns. The mass spectrum of the unknown component was compared with the spectrum of known components stored in the NIST library.

FT- IR Analysis

Methanol extract of isolated fungal metabolite was used to test the ATR- FTIR analysis (Alpha e-Bruker spectrometer -Japan) using existing database at a frequency in the range of 400-4000 wave numbers $cm^{-1}$with a resolution of $4cm^{-1}$ and baseline of the smoothened spectra was corrected. By comparing with the standard peaks available in the literature, ATR-ETIR spectra was carried out.

RESULTS

Morphological and molecular characterization of fungi

Based on morphological characteristics the isolated fungus was identified as *Fusarium globosum* which belongs to *Ascomycota* (Fig.1).The DNA from the isolate was collected and subjected to molecular identification. Fungal ITS gene sequencing results confirms that the fungal isolate was *Fusarium globosum* CBS490.97. Following BLASTN analysis, similar sequences were retrieved from Genbank, and a phylogenetic tree was generated using the neighbor-joining method **(**Fig**.** 2**).**

In pathogenicity test, isolated fungus exhibited the similar symptoms in the healthy fruit also. Therefore, reisolating and inoculating steps were repeated to confirm the pathogen. *Fusarium globosum* showed the lowest decay diameter and cause soft rot in the affected area.

Qualitative and quantitative analysis of metabolites

Qualitative analysis of ethyl acetate extract of fungal metabolite showed the presence of alkaloids, phenols, flavonoids, steroids and tannins but terpenoid content was absent. Saponins and alkaloids were absent in methanolic extract (Table 1). In quantitative assay, total phenol content was high (145.48 ± 0.01 mg/g) in ethyl acetate extract and low (90.92 ± 0.030 mg/g) in methanolic extract.The flavonoid content was found to be higher in methanolic extract (33.17 ± 0.030 mg/g) and lower(27.55 ± 90.92 ± 0.02 mg/g) in ethyl acetate extract. Methanolic extract showed high (153.36 ± 2.32 mg/g) amount of tannin compared to ethyl acetate extract (32.11±0.01 mg/g)(Fig**.** 3).

GC- MS analysis

Methanolic extract of metabolite of *F. globosum* was analysed by GC-MS and presented in Fig.4. List of thirty bioactive compounds (Table 2) isolated from metabolite of *F. globosum* with corresponding peaks and their biological activity have been illustrated in Table 3. Ergosterol (14.25), n-Hexadecanoic acid (13.32) and oleic Acid (11.30) were found to be higher in methanolic extract of *F. globosum* and 2-(Dimethylamino) ethyl vaccenoate (0.30) were present low amount in methanolic extract of *F. globosum*.

FTIR analysis

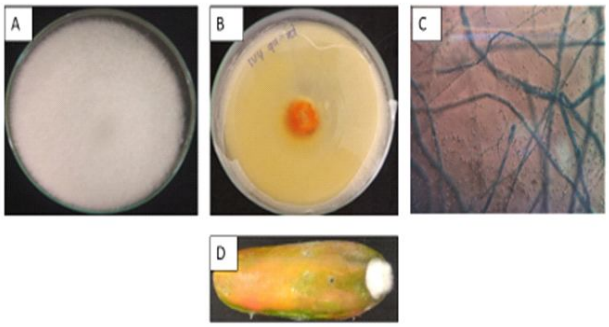

Fig. 1 : A: Morphological view of *Fusarium globosum* (Pure culture), B: *Fusarium globosum* (with metabolite) C: Microscopical view of *Fusarium globosum,* D: Pathogenicity test showing symptoms of *Fusarium globosum* after 7 days of incubation.

Methanolic metabolite extract of *F. globosum* was used for the analysis of functional group FTIR. The FTIR analysis (Fig 5) showed the presence of 19 different functional groups (Table 4).

DISCUSSION

Table 1: Qualitative analysis of fungal metabolites of *Fusarium globosum* isolated from *Cocciniagrandis.*

Phytochemical test	Methanol	Ethyl acetate
Alkaloids	-	+
Flavonoids	+	+
Phenols	+	+
Saponins	-	+
Steroids	+	+
Tannins	+	+
Terpenoids	+	-

+ :Present - : Absent

Fig. 2: Phylogenetic dendrogram constructed based on ITS Sequencing. *Fusarium globosum* genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain CBS430.97.

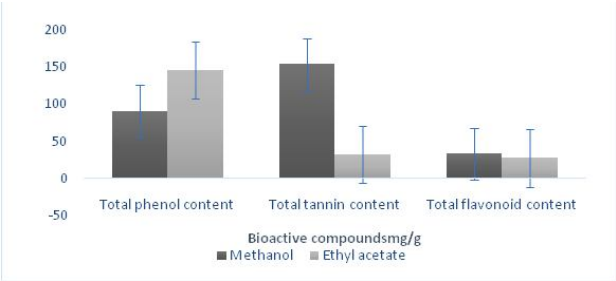

Fig. 3 : Quantitative analysis of fungal metabolites of *Fusarium globosum* isolated from infected *Coccinia grandis*

Fusarium was isolated from eggplant, lemon, onion and tomatoes, four strains of *Fusarium chlamydosporum* were isolated from eggplant, lemon and onion. *Fusarium equiseti, F. oxysporum,* and *F. solani* were isolated from tomato samples. The food associated fungi viz., *Rhizopus stolonifer, Aspergillus niger, Fusarium oxysporum, Saccharomyces* sp., *Aspergillus flavus* have been isolated from various spoiled vegetables. The dominant members of the fungi isolated from spoiled vegetables belong to the genera *Aspergillus* (Al-Najada and Gherbawy, 2015). *Alternaria alternata, Aspergillus flavus, Aspergillus ochraceus, Aspergillus parasiticus, Fusarium proliferatum* and *Penicillium citrinum* were isolated from spoiled beans and peas (Chaudhary and Yadav, 2019). *Aspergillus niger, Rhizopusstolonifer, Fusarium oxysporum, Saccharomyces cerevisiae, Alternaria alternata, Penicillium digitatum*and *Geotrichum candidum* were isolated from spoiled tomatoes (Dijksterhuis, 2013). Fungi affecting tomatoes viz., *Aspergillus phoenicis, Absidia* sp., *Trichoderma* sp., *Alternaria alternata, Fusarium oxysporum, Fusarium moniliformis, Aspergillius niger, Mucor* sp., *Rhizopus stolonifer, Penicillium* sp., *Geotrichum* sp .and *Phytophthora* sp. were isolated (Samuel and Orji, 2015). *Aspegillius* sp., *Penicillum* sp., *Fusarium* sp. and *Saccharomyces* sp.were isolated from spoiled tomato fruits (Etebu *et al.* 2013).

Alkaloids, steroids, tannins, flavonoids and phenolic content were present in the fungal metabolite of ethyl acetate extract of *Pinus roxburghii* (Wogu and Ofuase, 2014). *Alternaria alternata* recorded different phytochemicals such as, saponins, steroids, cardiac glycosides and tannins (Bhardwaj *et al.* 2015). The fungus *Geotrichium albida* isolated from *Plumeria acuminata* and *Plumeria obtusifolia* showed the presence of alkaloids, flavonoids, steroids and phenolic compounds (Kamarian and Ghasemlou, 2013).

Endophytes isolated from *Tabebuia argentea* different solvent extracts of showed the presence of tannins, flavonoids, steroids, alkaloids, phenols and proteins (Dhankhar 2012). Chromatogram of GC-MS analysis of the methanol extract of *Fusarium chlamydosporum* recorded a total of thirty one major compounds with corresponding to the peaks viz., DL-Arabinose, D-Glucose, 6-O-áD-galactopyranosyl, á-D-Glucopyranoside, O-á-Dglucopyranosyl,5-Hydroxymethylfurfural, N-(4,6-Dimethyl-2-pyrimidinyl)-4-(4-nitrobenzylidenea,1H-Purin-2-amine,6-methoxy-N-methyl,2-Methyl-9-â-d-ribofuranosyl hypoxanthine, 1-Hexadec-anesulfonic acid, 3,5, -dichloro-2,6-dimeth, Methyl-6,7- benzoisoquinoline, Undeca-2, 4, 6, 8, 10-pentaenal, 11-(2-furyl)-oxime, and 2-Bromotetr-adecanoic acid (Aly, 2008). Twenty one major peakswith bioactive compounds were identified from the methanolic extract of *Fusarium oxysporum.* Most of them are derivatives of volatile compounds like esters, ethers, alkaloids and phenolic compounds and showed resemblance with the natural products and bioactivity was found (Mohammed , 2018).

FT-IR spectroscopy allows to examine the total biochemical profile of intracellular metabolites in fungal cells as well as extracellular metabolites by

Table 2: Identification of metabolites from *Fusarium globosum* by GC-MS method

Peak	Name of the compounds	Retention time	Relative area	Area %
1	2-Pyrrolidinone	6.795	1774663	0.58
2	1-Tetradecanol	11.517	1542370	0.50
3	Tetradecane	11.625	1421212	0.46
4	Hexadecane	14.114	1062222	0.35
5	Tetradecanoic acid	15.898	13318336	4.33
6	Hexadecanoic acid, methyl ester	17.616	10586515	3.44
7	n-Hexadecanoic acid	18.001	40961712	13.32
8	Carbamic acid, N-allyl-N-(3-methylbutyl)-, benzyl	18.060	23187831	7.54
9	Carbamic acid, N-allyl-N-(3-methylbutyl)-, benzyl	18.847	1478748	0.48
10	9,12-Octadecadienoic acid (Z, Z)-, methyl ester	19.242	30012667	9.76
11	9-Octadecenoic acid, methyl ester, (E)-	19.304	15307697	4.98
12	Methyl stearate	19.541	1831819	0.60
13	9,12-Octadecadienoic acid (Z, Z)-	19.613	20787193	6.76
14	Oleic Acid	19.674	34740667	11.30
15	Octadecanoic acid	19.873	11772600	3.83
16	Tetradecanenitrile	21.926	999309	0.33
17	2-(Dimethylamino)ethyl vaccenoate	22.605	936433	0.30
18	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)	23.263	1117005	0.36
19	24-Isopropyl-5,23-cholestadien-3. Beta-ol	24.028	1394987	0.45
20	n-Propyl 9,12-octadecadienoate	24.750	2392214	0.78
21	6,9-Octadecadienoic acid, methyl ester	24.962	4515679	1.47
22	9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl	24.998	4826833	1.57
23	Chloramphenicol	25.057	1530931	0.50
24	6-Octadecenoic acid	25.647	1411642	0.46
25	Squalene	26.086	5832080	1.90
26	Acetamide, N-[2,3-dihydroxy-1-(hydroxymethyl)heptadecyl	26.875	20628499	6.71
27	Acetamide, N-[2,3-dihydroxy-1-(hydroxymethyl)heptadecyl	27.347	20628499	0.87
28	Ergosta-5,7,9(11),22-tetraen-3-ol, (3.beta.,22E)-	27.697	3550673	1.15
29	Acetamide, N-[2,3-dihydroxy-1-(hydroxymethyl)heptadecyl]-, tri	28.047	2064021	0.67
30	Ergosterol	31.290	43823230	14.25

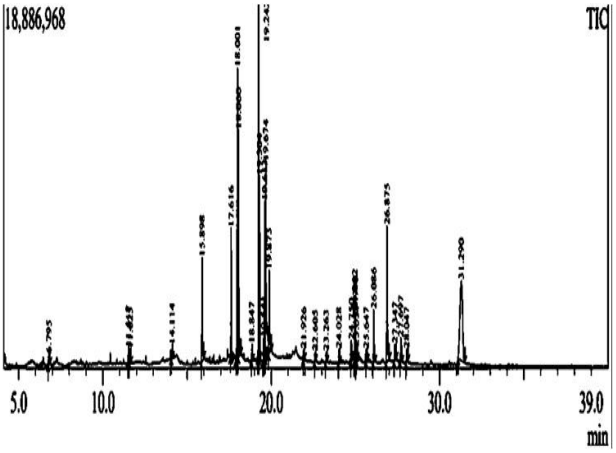

Fig. 4 : GC-MS Chromatogram of methanolic extract of*Fusarium globosum*

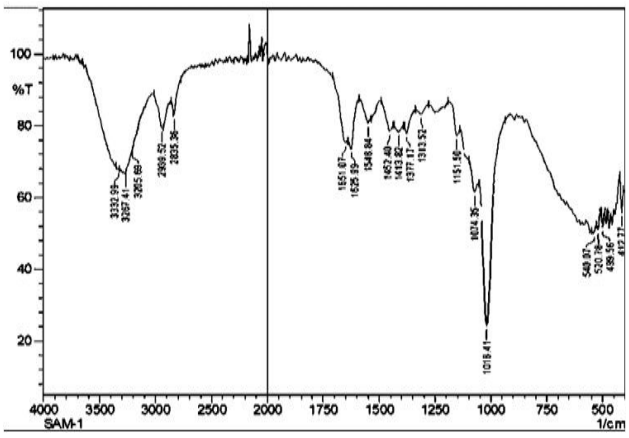

Fig. 5 : FT-IR spectrum of methanolic extract of *Fusarium globosum*

Table 3: Biological activity of isolated compounds from *Fusarium globosum*

Compound name	Biological activity	References
2-Pyrrolidinone	Antibacterial, antifungal, anticancer and anticonvulsant	Hosseinzadeh *et al*. , 2018
1-Tetradecanol	antibacterial and anti-inflammatory (periodontitis) activity	Lopes *et al.,* 2019
Tetradecane	Antimicrobial diuretic, anti-tuberculosis	Singh *et al*. 2015
Hexadecane	Antimicrobial and antioxidant activity	Khan and Javaid, 2019
Tetradecanoic acid	Larvicidal and repellent activity	Sivakumar *et al*., 2011
Hexadecanoic acid, methyl ester	Anti-oxidant, decrease blood cholesterol, anti-inflammatory	Alkhalaf *et al.* ,2019
n-Hexadecanoic acid	Antibacterial and antifungal	Ravi and Krishnan, 2017
9,12-Octadecadienoic acid (Z,Z)-, methyl ester	Anti-cancer	Mahadev, 2012
9-Octadecenoic acid, methyl ester, (E)-	Antioxidant, anti cancer	Asghar and Choudahry, 2011
Methyl stearate	Anti-inflammatory, intestinal Lipid metabolism regulator, Gastrin inhibitor, Antihelmintic (Nematodes), Antinociceptive	Adnan *et al*., 2019
9,12-Octadecadienoic acid (Z,Z)-	Anti-cancer	Bashari *et al.,* 2019
Oleic Acid	Antibacterial	Dilika *et al.* 2000
Octadecanoic acid	Antimicrobial activity	Abubakar and Majinda, 2016
Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)	Antioxidant, hypocholesterolemic, antiandrogenic, flavor, nematicide, hemolytic, 5-alpha reductase inhibitors	Tyagi and Agarwal, 2017
6,9-Octadecadienoic acid, methyl ester	Acidifier, acidulant, anticancer, antitumor, arachidonic acid-inhibitor	Abdel-Rahman *et al.*. 2020
9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl	Acidifier, acidulant, arachidonic acid-inhibitor, increase zinc bioavailability	Adegoke *et al.*2019
Chloramphenicol	Bactericidal activity	Rahal and Simberkoff, 1979
6-Octadecenoic acid	Antioxidant, Antimicrobial	Qureshi, 2019
Squalene	Sugar-phosphatase inhibitor,Gastrin inhibitor, Anti - inflammatory, Antiparasitic, Histamine release inhibitor,Antihelmintic	Adnan 2019
Ergosterol	Immunosuppressive and antitumor activity	Nam, 2001

using high-throughput screening FT-IR measurements and is a non-destructive technique (Gorain, 2018). Considerable variation of *Phoma herbarum* and *T. piluliferum* was observed in amide I and amide II regions. High variation was noticed in *H. lixii* and *M. guilliermondii* in N-H stretching of proteins (Dzurendova, 2020). FTIR spectroscopy delivers a combined advantage for efficient fungal classification as well as simultaneous visualization of chemical composition of the sample (Salman, 2010).

This study detected the profile of pathogenic fungus which cause pathogencity in *Coccinia grandis* of Malabar region of Kerala. High production of secondary metabolites was recorded in *Fusarium globosum*. GC - MS analysis of methanolic extract of *Fusarium globosum* showed the presence of number of bioactive substances and this indicates a potential area for drug development. Metabolites especially, fungal metabolites have been proven to be playing an important role in defense mechanisms and have a significant contribution in pharmaceutical industry as they have shown many biological activities. These compounds have been characterized and applied in pharmaceutical, cosmetics and agricultural industries.This investigation reveals that the metabolites produced by *Fusarium globosum* can be a potential source of novel natural

Table 4: Identification of functional group of *Fusarium globosum* by FT-IR method

Group frequency cm-1 of the samples	Functional group	Origin	Appearance
3332.99	secondary amine	N-H stretching	Medium
3267.41	Alcohol	O-H stretching	weak, broad
3205.69	Alcohol	O-H stretching	weak, broad
2939.52	Alkane	C-H stretching	Medium
2835.36	aldehyde	C-H stretching	Medium
1651.07	cyclic alkene	C=C stretching	Medium
1625.99	α,β-unsaturated ketone	C=C stretching	Strong
1548.84	cyclic alkene	C=C stretching	Medium
1452.40	Alkane	C-H bending	Medium
1413.82	Sulfate	S=O stretching	Strong
1377.17	sulfonate	S=O stretching	Strong
1313.52	sulfone	S=O stretching	Strong
1151.50	aliphatic ether	C-O stretching	Strong
1074.35	primary alcohol	C-O stretching	Strong
1018.41	Alkene	C=C bending	Strong
540.07	monosubstituted	C-H bending	Strong
520.78	monosubstituted	C-H bending	Strong
499.56	monosubstituted	C-H bending	Strong
412.77	monosubstituted	C-H bending	Strong

bioactive and antioxidants compounds. Further studies have to be carried out in the enzyme activity, antifungal activity of the *Fusarium globosum*.

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