

Recent advances on natural depsidones: sources, biosynthesis, structure-activity relationship, and bioactivities

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ABSTRACT

Depsidones are a class of polyphenolic polyketides that have been proposed to be biosynthesized from oxidative coupling of esters of two polyketidic benzoic acid derivatives. They are principally encountered in fungi and lichens. In addition to their diversified structural features, they revealed varied bioactivities such as antimicrobial, antimalarial, cytotoxic, anti-inflammatory, anti-*Helicobacter pylori*, antimycobacterial, antihypertensive, anti-diarrheal, antidiabetic, phytotoxic, anti-HIV, anti-osteoclastogenic, and butyrylcholinesterase, tyrosinase, hyaluronidase, and acetylcholinesterase inhibition. The current work was targeted to provide an overview on the naturally reported depsidones from various sources in the period from 2018 to the end of 2022 including their structures, biosynthesis, sources, and bioactivities, as well as the reported structure-activity relationship and semisynthetic derivatives. A total of 172 metabolites with 87 references were reviewed. The reported findings unambiguously demonstrated that these derivatives could be promising leads for therapeutic agents. However, further *in-vivo* evaluation of their potential biological properties and mechanistic investigations are needed.

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Additional Information and
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INTRODUCTION

Nature affords unlimited riches of novel biomolecules that are derived from living organisms, including animals, plants, and microorganisms (*Abdel-Razek et al., 2020*). These metabolites have played a fundamental role for thousands of years as remediation for various human illnesses because of their availability and low cost, particularly in developing countries. Also, their chemical diversity with broad bioactivities makes them

invaluable sources of drug development and discovery (*Abdel-Razek et al., 2020; Shen, 2015*).

Depsidones are polyphenolic polyketides featuring a tricyclic framework that have a central seven-membered lactone ring; 11H-dibenzo[b,e][1,4]dioxepin-11-one (*Nguyen et al., 2020; Sedrpoushan, Haghi & Sohrabi, 2022*). This ring is resulted from ester and ether linkages joining the two β -orcinol or orcinol-derived rings (*Bay et al., 2020; Bai, Yang & Bai, 2021*). Biosynthetically, three to seven carbon chains may be connected at C-1 and C-5 of the rings relying on the starting precursor utilized by PKSs (polyketide synthases) to assemble their backbones (*Singh et al., 2021*). Also, they are proposed to be originated from depsides, which are formed by ester-linking among two orsellinic acid derivatives followed by ether formation (*Ibrahim et al., 2018, 2021; Burt, Harper & Cool, 2022*). Their biosynthesis had been previously discussed in some reports (*Ibrahim et al., 2018, 2021; Singh et al., 2021*). Additionally, ring modifications and side chains constitute the characteristic features of different depsidones (*Jin et al., 2018; Mathioudaki et al., 2018*). Some of the reported derivatives possess halogen atoms, like chloride as a substituent on their skeletons (*Duong et al., 2015*). Other reported halogenated derivatives were biosynthesized as a result of modification of the culture media using KBr, NaBr, or porcine NaBr (*Guo et al., 2022; Morshed et al., 2018; Sureram et al., 2013*). These metabolites were principally encountered in fungi, lichens, and plants and were rarely reported from marine sources (*Hartati, Megawati & Antika, 2022; Sepúlveda et al., 2022; Ismed et al., 2021*). Naturally occurring depsidones have been reported to display a span of bioactivities including antimicrobial, antimalarial, cytotoxic, anti-*Trypanosoma*, anti-inflammatory, anti-*Helicobacter pylori*, antimycobacterial, antihypertensive, anti-diarrheal, larvicidal, antidiabetic, herbicidal, antileishmanial, phytotoxic, anti-HIV, anti-osteoclastogenic, and butyrylcholinesterase, aromatase, tyrosinase, hyaluronidase, and acetylcholinesterase inhibition (*Addo et al., 2021; Ibrahim et al., 2018*). These compounds have attracted considerable research interest because of their structural diversity and varied bioactivities. This class of metabolites had been reviewed in some previous works. For example, a review by *Ibrahim et al. (2018)* discussed the isolation, structural characterization, biosynthesis, and bioactivities of 84 depsidones reported from fungal sources. Additionally, two published reviews by *Ureña-Vacas et al. (2022)* and *Stojanovic, Stojanovic & Smelcerovic (2012)* focused on lichen depsidones, including their structures and biological activities. Due to the rapid research growing on these metabolites, the current review is an update to the formerly published review in 2018 (*Ibrahim et al., 2018*). In addition, the current work focused on the reported depsidones from various sources in the period from 2018 to the end of 2022 as shown in [Fig. 1](#) and [Table S1](#).

It described a comprehensive summary of the published information on depsidones regarding their sources (fungi, lichens, and plants) ([Fig. 2](#)), separation, structural characterization, biosynthesis, semi-synthesis, bioactivities, and structure-activity relation.

This work aimed to provide natural product researchers with comprehensive references that can help them in the identification of separated depsidones from various sources. Additionally, highlighting the reported bioactivities and structure-activity relationship of

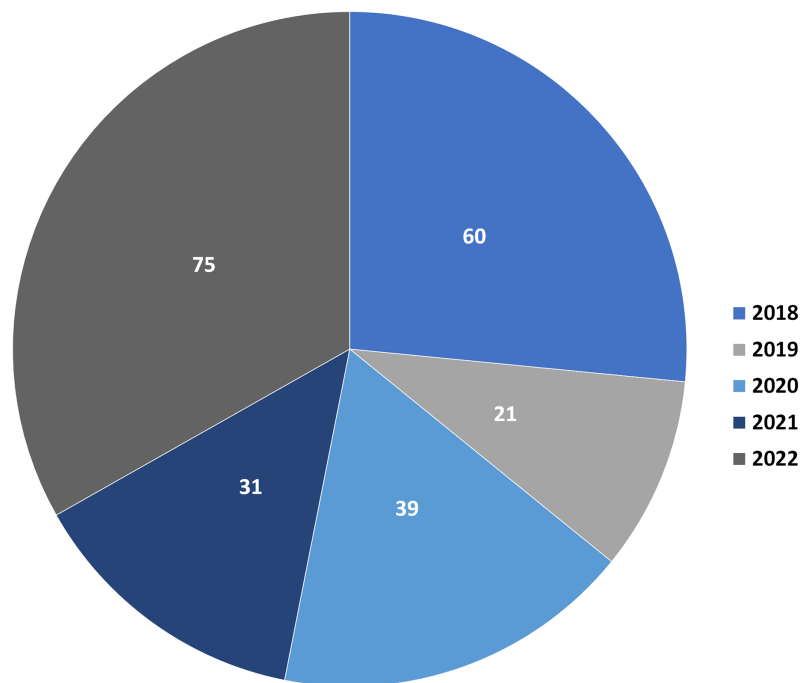


Figure 1 Number of reported depsidones per year in the period from 2018 to 2022.

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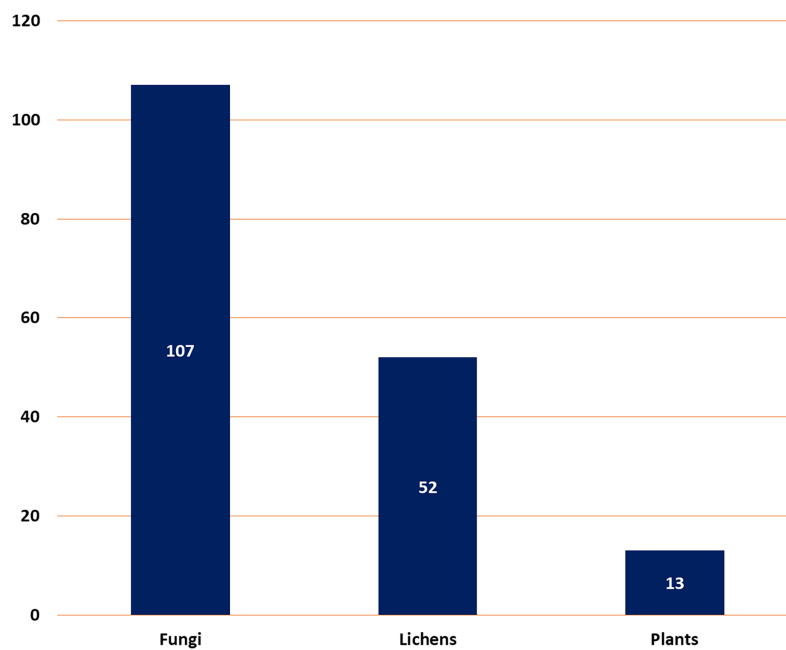


Figure 2 Number of reported depsidones from different sources.

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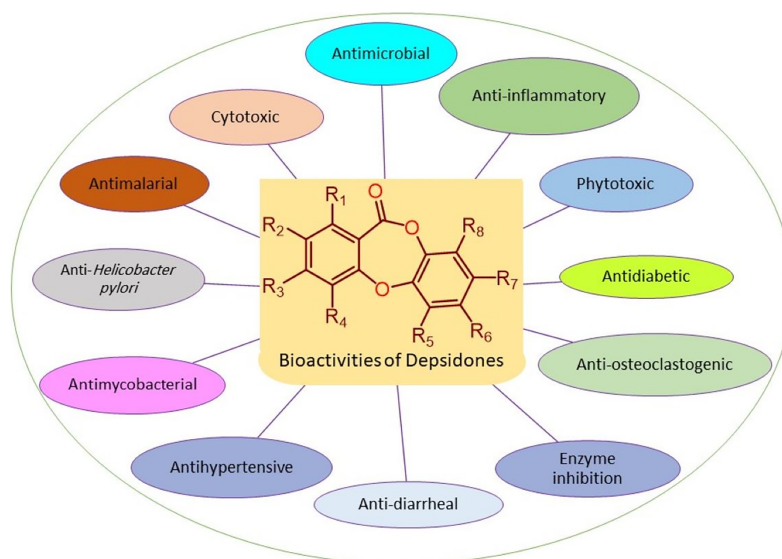


Figure 3 Reported bioactivities of depsidones.

Full-size DOI: 10.7717/peerj.15394/fig-3

these compounds may draw the interest of medicinal and synthetic chemists for the synthesis and discovery of new agents utilizing known depsidones as start materials.

METHODOLOGY

The published data on depsidones was obtained by searching articles on various databases and Publishers such as Google-Scholar, PubMed, Science Direct, Bentham, Thieme, Springer, Scopus, Taylor/Francis, and Wiley. The search was done utilizing the keywords: “Depsidone + Lichens”, OR “Depsidone + Fungi”, OR “Depsidone + Plant” OR “Depsidone + Biological activity” OR “Depsidone + Biosynthesis” OR “Depsidone + Semi-synthesis” OR “salazinic acid”, “protocetraric acid”, “lobaric acid”. This work included the English language published articles in peer-reviewed journals in the period from 2018 to the end of 2022. The published articles reported new biological evaluation of metabolites reported before 2018 had been included. A total of 83 articles had been reviewed. The no full access (*e.g.*, conference proceedings), irrelevant, and non-reviewed journals published articles had been excluded. For the non-English articles, the data are extracted from the English abstracts.

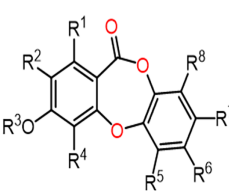
BIOACTIVITIES OF DEPSIDONES

The reported depsidones were assessed for various bioactivities (Figs. 3–13, Tables S2–S6).

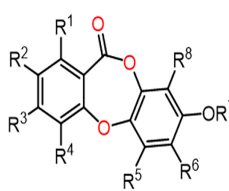
It is noteworthy that some of the reported metabolites had more powerful efficacy than the positive controls. The results of the reported bioactivities were listed and discussed below.

Antimicrobial activity

Currently, antibiotic resistance of microbes has become one of the utmost serious menaces to human health (Fjell *et al.*, 2012). The global amplification and rapid growth of multi-resistant microbes that are untreatable with the current antimicrobial therapy have



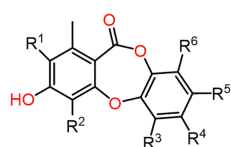
Compound	R1	R2	R3	R4	R5	R6	R7	R8
Polyanthradepsidone A (1)	OH	CH ₃	CH ₃	OH	CH ₃	OH	CH ₃	CH ₃
Cetraric acid (2)	CH ₃	H	H	CHO	CH ₃	COOH	OCH ₃	CH ₂ OCH ₂ CH ₃
Psoromic acid (3)	CH ₃	H	H	CHO	COOH	H	OCH ₃	CH ₃
Methyl psoromate (4)	CH ₃	H	H	CHO	COOCH ₃	H	OCH ₃	CH ₃
Virensic acid (5)	CH ₃	H	H	CHO	CH ₃	H	OH	CH ₃



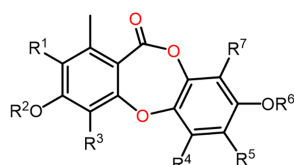
Compound	R1	R2	R3	R4	R5	R6	R7	R8
Cordidepsine (6)	CH ₃	H	OH	CHO	OH	CH ₃	CH ₃	H
Corynesidone A (7)	H	OH	H	CH ₃	H	OH	H	CH ₃
Corynesidone D (8)	CH ₃	H	OH	H	CH ₃	COOH	H	H
Hypoprotocetraric acid (9)	CH ₃	H	OH	CH ₃	CH ₃	COOH	H	CH ₃
Conhypoprotocetraric acid (10)	CH ₃	H	OH	CH ₃	CH ₃	COOH	H	CH ₂ OH
Gangaleoidin (11)	CH ₃	Cl	OH	Cl	CH ₃	COOCH ₃	CH ₃	H
Dioxepin-11-one (12)	CH ₃	H	OH	CH ₃	CH ₃	H	H	CH ₃

Figure 4 Chemical structures of depsidone (1–12).

Full-size [DOI: 10.7717/peerj.15394/fig-4](https://doi.org/10.7717/peerj.15394/fig-4)



Compound	R1	R2	R3	R4	R5	R6
Parmosidone A (13)	H	CHO	CH ₂ OH	OH	COOH	CH ₃
Parmosidone B (14)	H	OH	CH ₂ OH	OH	COOH	CH ₃
Parmosidone E (15)	H	CHO	CH ₃	OH	COOH	CH ₃
Vicanicin (16)	Cl	CH ₃	CH ₃	Cl	OCH ₃	CH ₃
Protocetraric acid (17)	H	CHO	CH ₃	COOH	OH	CH ₂ OH



Compound	R1	R2	R3	R4	R5	R6	R7
1H-Dibenzo[b,e][1,4]dioxepin-11-one,3,8-dihydroxy-4-(methoxymethyl)-1,6-dimethyl (18)	H	H	CH ₂ OH	CH ₃	H	H	H
Flavicansone (19)	Cl	CH ₃	H	CH ₃	Cl	CH ₃	CH ₃
Baillonc acid (20)	H	CH ₃	H	COOH	COOH	CH ₃	H
Botryorhodine A (21)	H	H	CHO	CH ₃	H	H	H
Botryorhodine B (22)	H	H	CH ₃	CH ₃	H	H	CH ₃
Botryorhodine C (23)	H	H	CH ₂ OH	CH ₃	H	H	CH ₃
Botryorhodine D (24)	H	H	CH ₂ OH	CH ₃	H	H	H
Botryorhodine G (25)	H	H	CH ₂ OCH ₃	CH ₃	H	H	H
Botryorhodine I (26)	H	H	CH ₂ OH	CH ₃	H	H	OH
Simplicidone A (27)	H	H	CH ₂ OCH ₃	CH ₃	H	H	CH ₃
Simplicidone B (28)	H	H	CH ₂ OCH ₂ CH ₃	CH ₃	H	H	CH ₃

Figure 5 Chemical structures of depsidone (13–28).

Full-size [DOI: 10.7717/peerj.15394/fig-5](https://doi.org/10.7717/peerj.15394/fig-5)

been associated with growing morbidity and mortality rates (*Dhingra et al., 2020*). Despite, immense knowledge of this universal health dilemma, developing new-generation antibiotics that combat these microbes has been proven to represent a significant defy (*Bahar & Ren, 2013*). In this regard, many natural metabolites have gained much attention from scientific and pharmaceutical communities because of their antibiotic potential (*Khameneh et al., 2019*). The majority of reported depsidones were assessed for their capacities on various pathogens including antitubercular, anti-phytopathogenic,

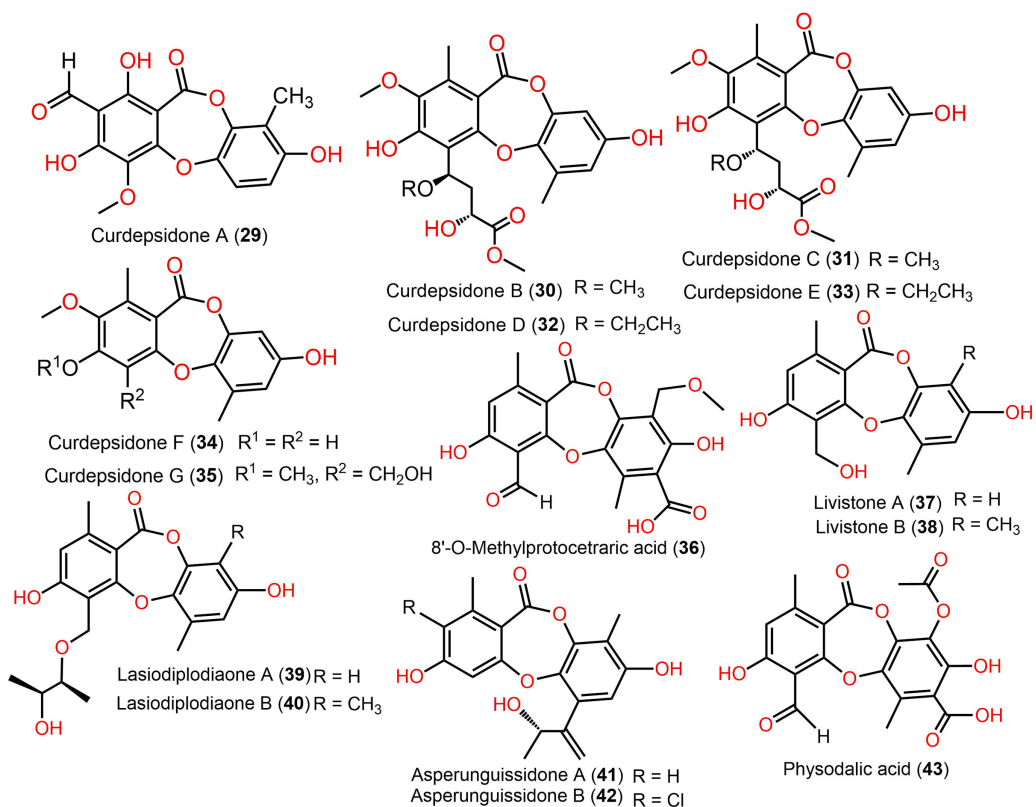


Figure 6 Chemical structures of depsidone (29–43).

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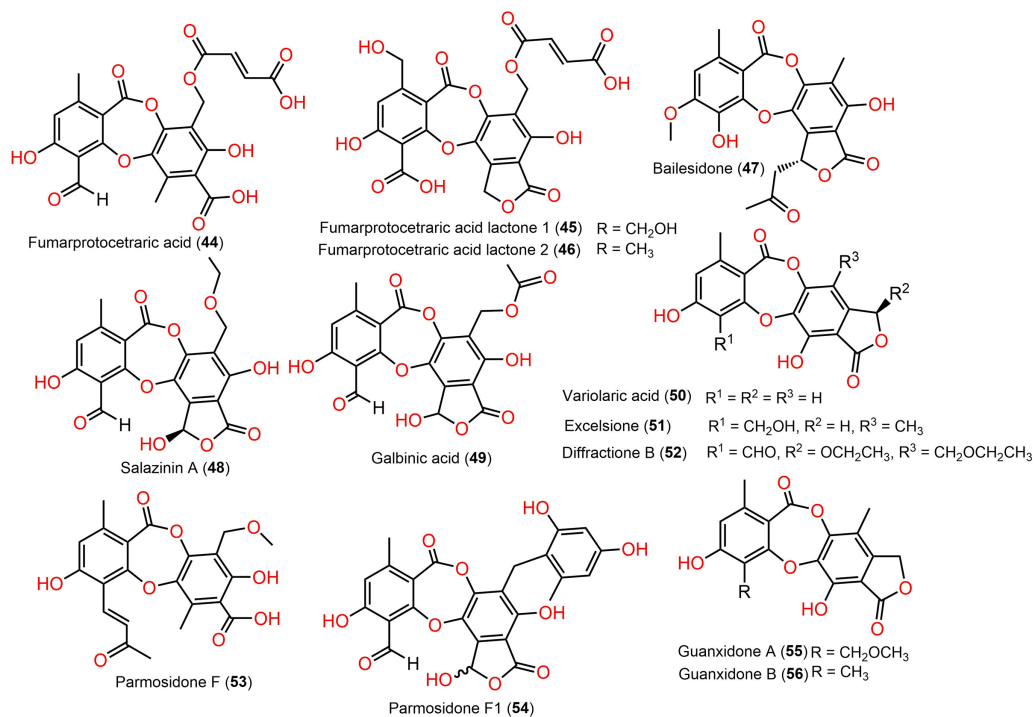
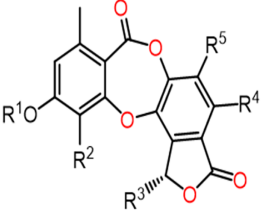


Figure 7 Chemical structures of depsidone (44–56).

Full-size DOI: 10.7717/peerj.15394/fig-7



Compound	R1	R2	R3	R4	R5
Connorstictic acid (57)	H	CH ₂ OH	CH ₃	H	CH ₃
Ceratalone (58)	CH ₃	OH	OCH ₂ CH ₃	OH	CH ₃
Stictic acid (59)	CH ₃	CHO	OH	OH	CH ₃
Norstictic acid (60)	H	CHO	OH	OH	CH ₃
8'-O-Methylstictic acid (61)	CH ₃	CHO	OCH ₃	OH	CH ₃
8'-O-Ethylstictic acid (62)	CH ₃	CHO	OCH ₂ CH ₃	OH	CH ₃
Neotricone (63)	H	COOH	H	OH	CH ₃
Conneotricone (64)	H	COOH	H	OH	CH ₂ OH
Salazinic acid (65)	H	CHO	OH	OH	CH ₂ OH
Perisalazinic acid (66)	H	COOH	OH	OH	CH ₂ OH
8'-O-Methylsalazinic acid (67)	H	CHO	OH	OH	CH ₂ OCH ₃
Norperistictic acid (68)	H	COOH	OH	OH	CH ₃
Menegazziac acid (69)	H	CH ₂ OH	OH	OH	CH ₃
1-Hydroxy-11-(hydroxymethyl)-4,10-dimethoxy-5,8-dimethyl-7H-benzo[6,7][1,4]dioxepino[2,3-e]isobenzofuran-3,7(1H)-dione (70)	CH ₃	CH ₂ OH	OH	OCH ₃	CH ₃
3'-O-Demethylcryptostictinolide (71)	CH ₃	CH ₂ OH	H	OH	H
Cryptostictic acid (72)	CH ₃	CH ₂ OH	OH	OH	CH ₃
Peristictic acid (73)	CH ₃	COOH	OH	OH	CH ₃

Figure 8 Chemical structures of depsidone (57–73).

Full-size  DOI: 10.7717/peerj.15394/fig-8

antimalarial, and antibacterial activities. In many studies, they possessed a broad range of activity.

Two new derivatives, simplicildones J (**89**) and K (**90**) and related known compounds **21**, **22**, **27**, and **28** were obtained and characterized from *Simplicillium lanosoniveum* PSUH168 and PSUH261 associated with *Hevea brasiliensis* leaves. Compounds **22** and **27** demonstrated notable antibacterial effectiveness against *Staphylococcus aureus* and MRSA (Methicillin-resistant *S. aureus*, MICs 32.0 µg/mL), while **90** was 4-fold less active compared to vancomycin (MIC 0.5 µg/mL), whilst **90** had (MIC 32 µg/mL) antifungal influence against *Cryptococcus neoformans* ATCC90113 in comparison to amphotericin B (MIC 0.5 µg/mL) (Rukachaisirikul et al., 2019).

From *Eucalyptus exserta*-associated *Chaetomium* sp. Eef-10 cultures, new depsidones, mollicellins O–R (**101–104**), in addition to known mollicellins **96–98** were purified using SiO₂, Sephadex LH-20, and HPLC and elucidated by spectral analyses. Among these metabolites, **97** (IC₅₀s 5.14 and 6.21 µg/mL, respectively) had notable antibacterial capacity against *S. aureus* (ATCC-29213) and *S. aureus* (N50, MRSA) compared to streptomycin sulfate (IC₅₀ 1.05 µg/mL for *S. aureus* ATCC-29213) in the broth dilution assay (Ouyang et al., 2018).

New members of mollicellin family; mollicellins **108–111**, together with **92**, **94**, **95**, **97**, **99**, **100**, and **104** were separated utilizing SiO₂ CC/preparative TLC from Thai rice-accompanied *C. Brasiliense* (Promgool et al., 2022). Compounds **92–95**, **108**, and **109** had powerful antibacterial potential against *Bacillus subtilis* and *Bacillus cereus* (MICs 2.0–8.0 µg/mL) which was close to kanamycin (MICs 2.0 µg/mL), however, they displayed moderate efficacy on *S. aureus* ATCC25923 (MICs 16.0–64.0 µg/mL). Besides, **91**, **92**, **97**,

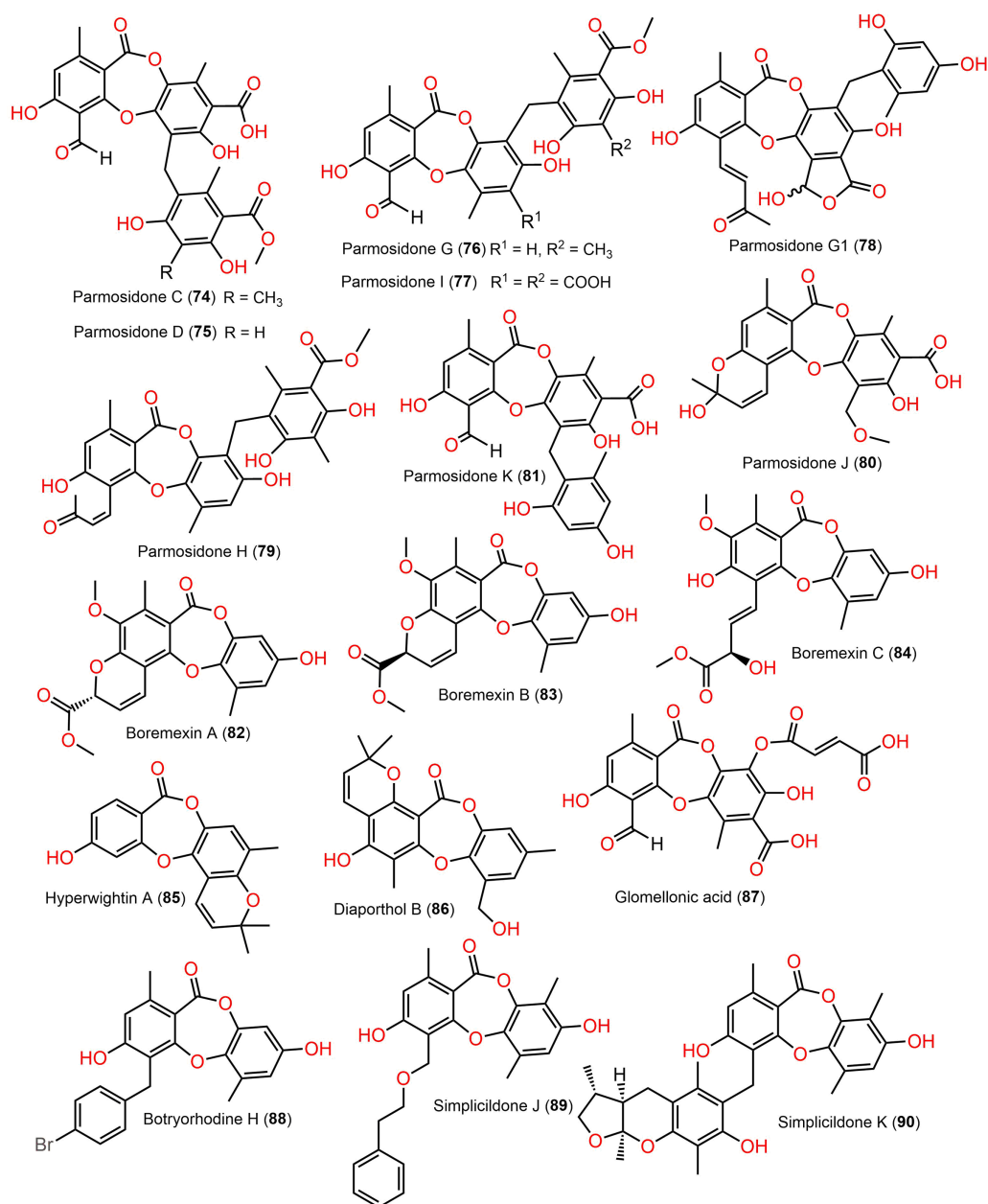


Figure 9 Chemical structures of depsidone (74–90).

Full-size DOI: 10.7717/peerj.15394/fig-9

110, and **111** were moderately active against different MRSA isolates (ATCC33591, ATCC33592, and ATCC43300, MICs 32.0–128.0 µg/mL) with the same MICs as oxacillin (MICs 32.0–128.0 µg/mL), whereas **91** and **92** also had moderate influence (MICs 32.0–128.0 µg/mL) against *S. aureus* SA1-3 clinical isolates (Promgool *et al.*, 2022). It was noted that C-4-CHO and complete lactone ring were significant for antibacterial potential against Gram-positive bacteria (Promgool *et al.*, 2022).

Further, new members of mollicellins: **105–107**, and the known mollicellins **93** and **97** were purified from *C. brasiliense* SD-596 rice media utilizing SiO₂ CC/HPLC and

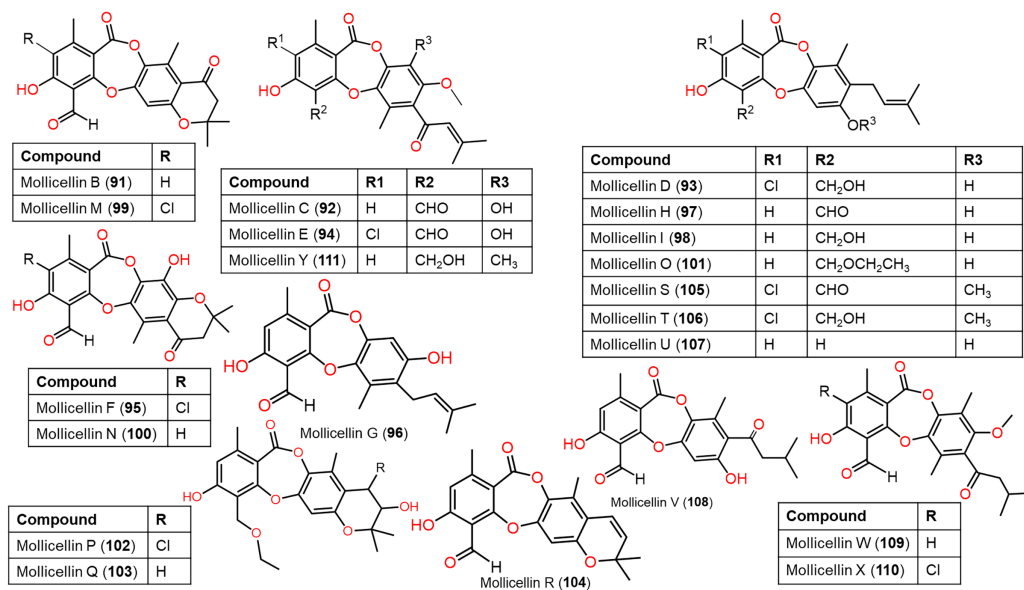


Figure 10 Chemical structures of depsidone (91–111). Full-size [DOI: 10.7717/peerj.15394/fig-10](https://doi.org/10.7717/peerj.15394/fig-10)

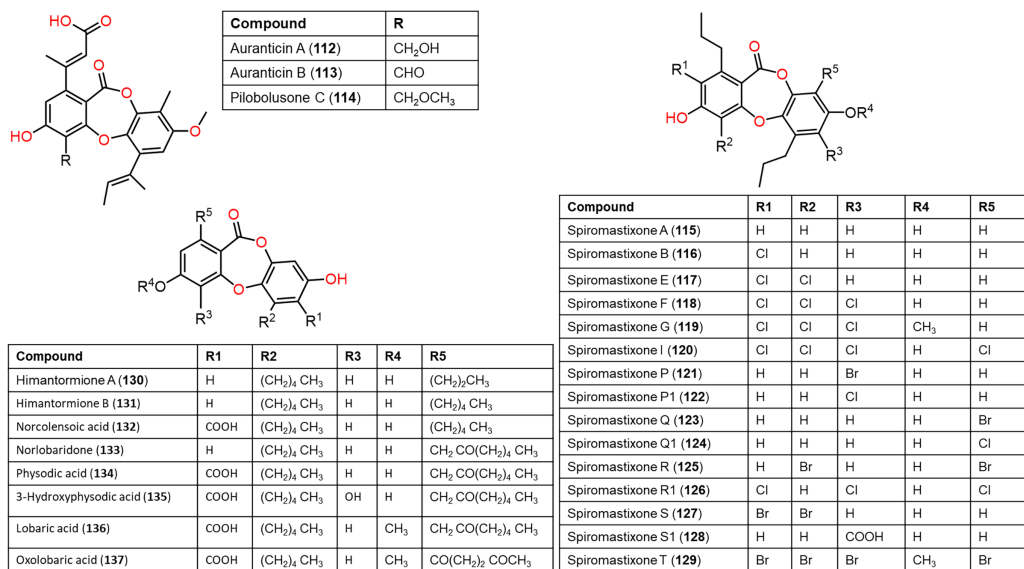
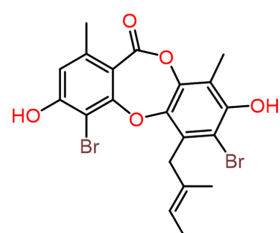


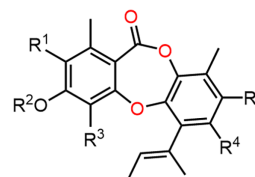
Figure 11 Chemical structures of depsidone (112–137).

Full-size [DOI: 10.7717/peerj.15394/fig-11](https://doi.org/10.7717/peerj.15394/fig-11)

elucidated by spectral analyses (Zhao *et al.*, 2021b). The analogs **97** and **105–107** possessed specific inhibition capacities towards *S. aureus* and MRSA, whereas **105** was the most efficient (MICs 6.25 µg/mL) compared to vancomycin (MICs 1.0 µg/mL); however, they had no efficacy against *Candida albicans* and *Pseudomonas aeruginosa* in the broth microdilution assay. It was noted that substituting 6-OH (in **93**) with OCH₃ (in **106**) and 4-CH₂OH (in **106**) with 4-CHO (in **105**) enhanced the antibacterial capacity. It is worth noting that CHO at C4 and OCH₃ at C7 in **105** could have synergetic efficacy in boosting the antibacterial potential (Zhao *et al.*, 2021b). Zhao *et al.* (2021b) postulated the



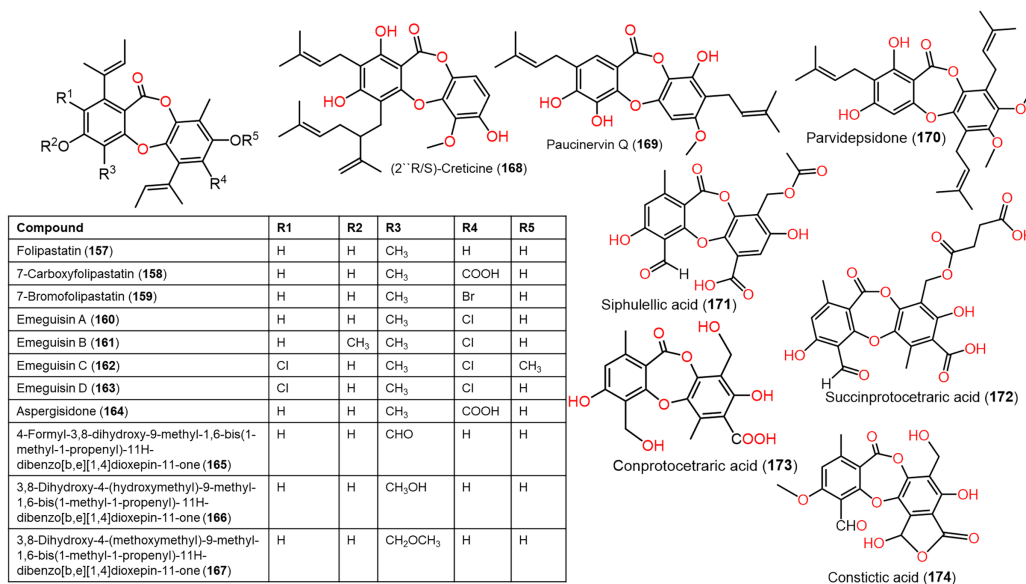
Aspergillusidone F (153)



Compound	R1	R2	R3	R4	R5
Unguinol (138)	H	H	H	H	H
2-Chlorounguinol (139)	Cl	H	H	H	H
2,4-Dichlorounguinol (140)	Cl	H	Cl	H	H
2,7-Dichlorounguinol (141)	Cl	H	CH ₃	Cl	H
4,7-Dichlorounguinol (142)	H	H	Cl	Cl	H
3,1'-Dichlorounguinol (143)	Cl	H	H	Cl	H
2-Chloro-7-bromounguinol (144)	Cl	H	H	Br	H
7-Bromounguinol (145)	H	H	H	Br	H
Nidulin (146)	Cl	H	Cl	Cl	CH ₃
Normidulin (147)	Cl	H	Cl	Cl	H
Aspergillusidone A (148)	H	H	H	COOH	OH
Aspergillusidone B (149)	H	CH ₃	Cl	Cl	OH
Aspergillusidone C (150)	Cl	H	H	Cl	OH
Aspergillusidone D (151)	Br	H	H	Br	OH
Aspergillusidone E (152)	Br	H	H	H	OH
Aspergillusidone H (154)	H	CH ₃	CH ₃	Cl	OH
Aspersidone (155)	Cl	H	H	Cl	OCH ₃
Aspersidone B (156)	Cl	H	H	H	OCH ₃

Figure 12 Chemical structures of depsidone (138–156).

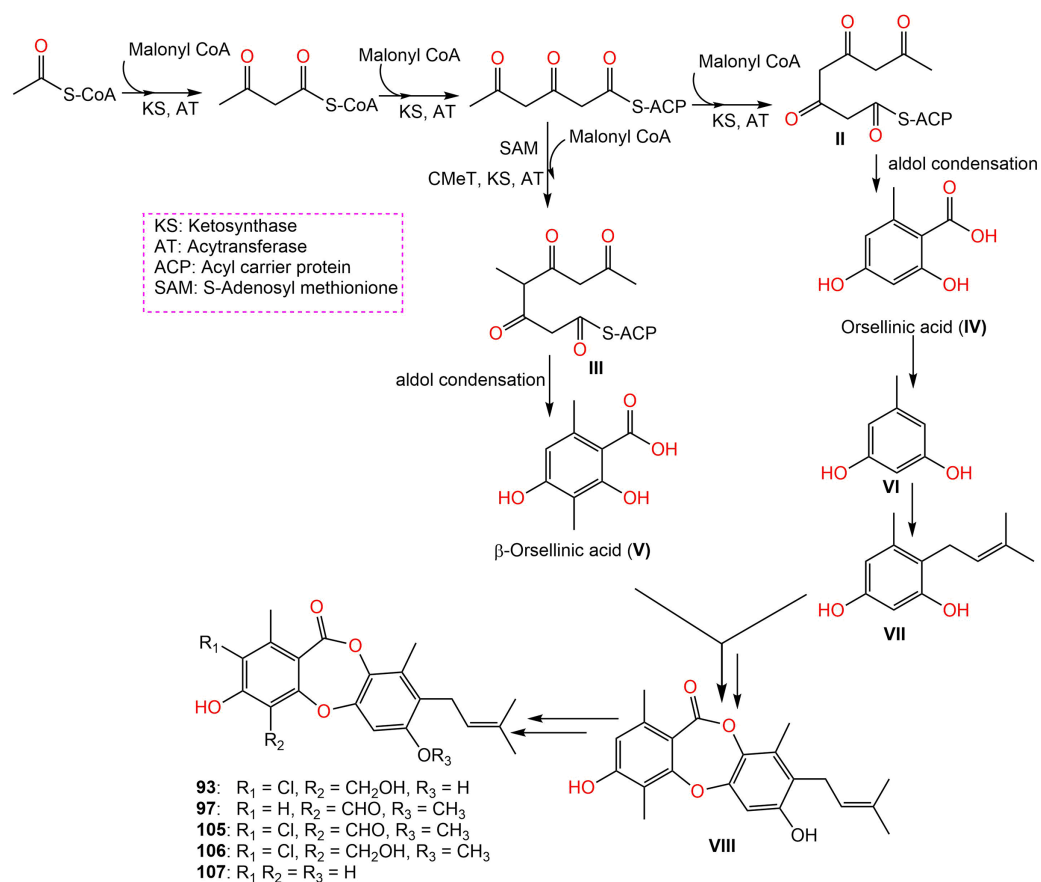
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Compound	R1	R2	R3	R4	R5
Folipastatin (157)	H	H	CH ₃	H	H
7-Carboxyfolipastatin (158)	H	H	CH ₃	COOH	H
7-Bromofolipastatin (159)	H	H	CH ₃	Br	H
Emeguisin A (160)	H	H	CH ₃	Cl	H
Emeguisin B (161)	H	CH ₃	CH ₃	Cl	H
Emeguisin C (162)	Cl	H	CH ₃	Cl	CH ₃
Emeguisin D (163)	Cl	H	CH ₃	Cl	H
Aspergillusidone (164)	H	H	CH ₃	COOH	H
4-Formyl-3,8-dihydroxy-9-methyl-1,6-bis(1-methyl-1-propenyl)-11H-dibenzo[b,e][1,4]dioxepin-11-one (165)	H	H	CHO	H	H
3,8-Dihydroxy-4-(hydroxymethyl)-9-methyl-1,6-bis(1-methyl-1-propenyl)-11H-dibenzo[b,e][1,4]dioxepin-11-one (166)	H	H	CH ₂ OH	H	H
3,8-Dihydroxy-4-(methoxymethyl)-9-methyl-1,6-bis(1-methyl-1-propenyl)-11H-dibenzo[b,e][1,4]dioxepin-11-one (167)	H	H	CH ₂ OCH ₃	H	H

Figure 13 Chemical structures of depsidone (157–174).

Full-size DOI: 10.7717/peerj.15394/fig-13



Scheme 1 Biosynthetic pathway of 93, 97, and 105–107 (Zhao *et al.*, 2021a, 2021b).

Full-size DOI: 10.7717/peerj.15394/fig-15

biosynthetic pathway of these mollicellins as shown in Scheme 1. First, the precursors II and III were biosynthesized by KS (β -ketoacyl synthase) domain, AT (acyltransferase) domain, ACP (acyl-carrier-protein) domain, and Claisen-type/cyclase-thioesterase domain, in addition to CMeT (C-methyltransferase) domain and SAM (S-adenosyl-methionine) only for III. The non-enzymatic aldol condensation of II and III results in orsellinic acid (IV) and β -orsellinic acid (V). Decarboxylation of IV followed by isoprenylation that are catalyzed by decarboxylase and aromatic prenyl transferase, respectively form VII. By oxidase and/or esterase V and VII are connected to produce VIII. Enzymatic oxidation, methylation, or halogenation of VIII yield compounds 93, 97, and 105–107 (Zhao *et al.*, 2021a) (Scheme 1).

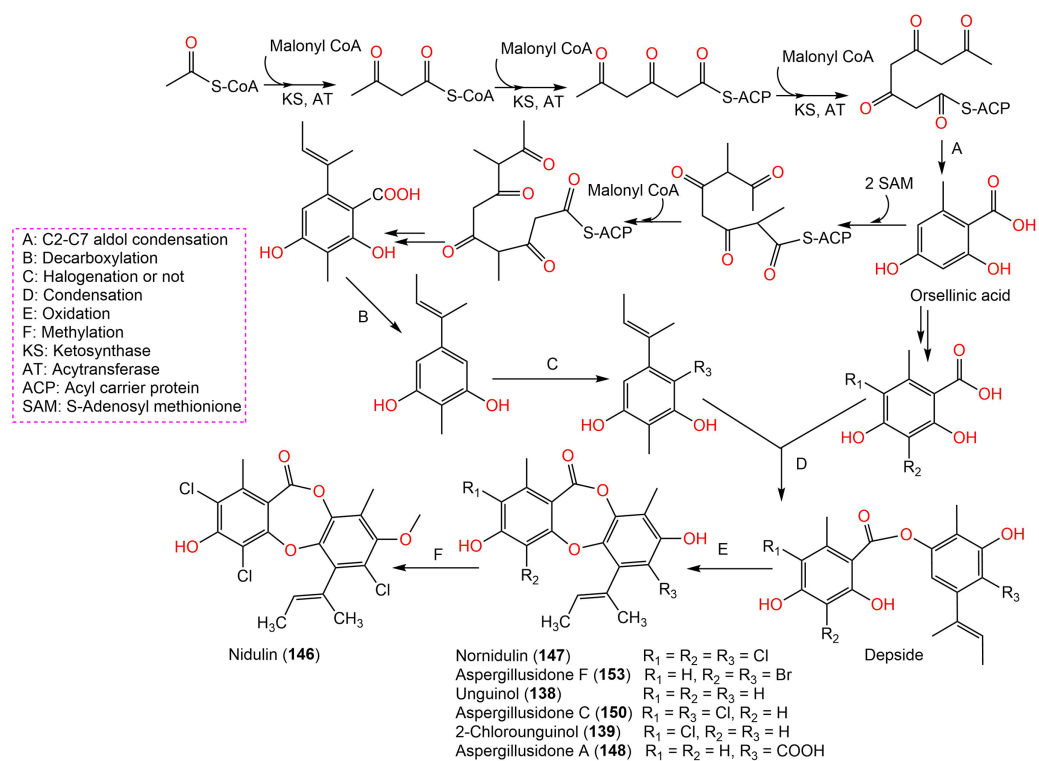
From the deep sea-derived *Spiromastix* MCCC3A00308, 122, 124, 126, and 128 were separated and characterized using Sephadex LH-20/HPLC and spectroscopic data, respectively (Niu *et al.*, 2021a). Compounds 122, 124, 126, and 128 revealed promising antibacterial influence on *S. aureus* ATCC25923, *Bacillus thuringiensis* ATCC10792, and *B. subtilis* CMCC63501 (MIC ranging from 0.5–32 $\mu\text{g/mL}$) compared to chloramphenicol (MIC 1.0 $\mu\text{g/mL}$), while they were weakly active against *E. coli* in the broth microdilution assay. It was found that the tri-chlorinated derivative, 126 (MICs ranged from 0.5 to 1.0

µg/mL) was more powerful than di-chlorinated analog **124**, whereas the latter had more potential than **122** (Niu et al., 2021a). Guo et al. separated from ant (*Monomorium chinensis*)-associated *Spiromastix* sp. MY-1 cultivated on KBr-supplemented medium, new brominated derivatives; **121**, **123**, **125**, **127**, and **129** and the known depsidones **115–120** by SiO₂ CC/HPLC. These metabolites except **116** and **123** displayed potent growth inhibitory effectiveness (MICs ranged from 5.2–27.6 µM) against plant pathogens; *Xanthomonas oryzae* pv. *oryzae* (Xoo, B1 and B2 strains), *Erwinia amylovora* (B3), *Pseudomonas syringae* pv. *lachrymans* (B4), and *Clavibacter michiganense* subsp. *sepedonicus* (B5), whereas **127** had the strongest potential against *X. oryzae* pv. *oryzae* (MIC 5.2 µM) compared to kanamycin (MICs ranged from 0.54–4.3 µM). *X. oryzae* pv. *oryzae* causes bacterial blight, which is a worldwide devastating rice disease, leading to up to 60% annual yield loss in Asia, it represents one of the utmost fatal rice diseases (Guo et al., 2022; Xu et al., 2015). Mutualistic microbes with ants were reported as effective protection against plant pathogens and herbivores (González-Teuber, Kaltenpoth & Boland, 2014; Guo et al., 2022). These findings revealed that **127** could be a potential lead for bactericides to control rice bacterial-blight disease and the ant-accompanied fungi might be a prominent source of bactericide against rice pathogens in the rice system (Guo et al., 2022). It is noteworthy that compounds **123**, **125**, **127**, and **129** reported by Guo et al. have the same nomenclatures as **122**, **124**, **126**, and **128** isolated by Niu et al. (2021a) however, they have different structures.

From Antarctic lichen *Himantormia lugubris*, two new analogs, himantormiones A (**130**) and B (**131**) were separated and identified by Koo et al. (2022) Compound **130** featured propyl and pentyl units at C-1 and C-8, respectively, while **131** has two pentyl moieties. These compounds exhibited inhibitory capacity on *S. aureus* (IC₅₀s 35.09 and 7.01 µM) in the broth microdilution assay. Nugraha et al. (2022) stated that **136** reported from Indonesian lichen *Candelaria fibrosa*, had antibacterial efficacy against *B. cereus* and *S. aureus* (MICs 88.0 and 39.6 µM, respectively) in the microdilution method.

Furthermore, **139**, **142**, **144**, **145**, **150–153**, and **160** reported from *Aspergillus unguis* demonstrated potent antifungal potential against *S. cerevisiae* (ATCC 9763) (MICs 2.3–25.0 µg/mL), compared to clotrimazole (MIC 0.4 µg/mL). Besides, **142**, **144**, **145**, **158**, and **159**, along with earlier reported **138**, **139**, **146**, **147**, **150–153**, **157**, and **160** were found to have antibacterial effectiveness against *B. subtilis* and *S. aureus* (MICs 0.8–41.1 µg/mL) in comparison with ampicillin (MIC 0.2 and 3.1 µg/mL, respectively). Whilst **146**, **147**, **157**, **159**, and **160** (MICs 0.8, 1.6, 0.8, 1.6, and 0.8 µg/mL, respectively) revealed the powerful efficacy against *B. subtilis*, also **144**, **151**, **157**, **159**, and **160** with MICs 2.6, 1.6, 1.6, 3.1, and 2.9 µg/mL, respectively were the most active against *S. aureus*. Structure-activity relationship revealed the role of bromo- and/or chloro-substitution in enhancing the potency and maintaining selectivity against bacteria and yeast (Morshed et al., 2018).

Aspergisidone (**164**), a new metabolite, along with **138–140**, **146–150**, **155**, **157**, and **160** were obtained from soil-associated *A. unguis* PSU-RSPG204 mycelia and broth EtOAc extract using Sephadex LH-20/SiO₂ CC/preparative TLC and assigned by spectral analyses (Phainuphong et al., 2018). Compounds **155** and **160** had powerful antibacterial influence



Scheme 2 Biosynthetic pathway of 138, 139, 146–148, 150, and 153 (Yang et al., 2018; Sureeram et al., 2013). Full-size DOI: 10.7717/peerj.15394/fig-16

against MRSA and *S. aureus* (MICs 0.5 $\mu\text{g}/\text{mL}$) as vancomycin (MICs 0.5 and 0.25 $\mu\text{g}/\text{mL}$, respectively), whereas 139, 146, 150, and 157 were weakly active (MIC ranged from 1–8 $\mu\text{g}/\text{mL}$). In the antifungal assay, 139 exhibited potent effectiveness on *C. albicans* (MIC 8 $\mu\text{g}/\text{mL}$), whereas 160 (MICs 0.5 $\mu\text{g}/\text{mL}$) was two-fold more effective than 157 (MIC 1 $\mu\text{g}/\text{mL}$) on flucytosine-resistant *C. neoformans* and 150 had the strongest effect on *Microsporium gypseum* (MIC 2 $\mu\text{g}/\text{mL}$) in the broth dilution method (Phainuphong et al., 2018). Norcolensoic acid (132) was purified for the first time from *Lachnum virgineum* using SiO_2 CC that showed intense blue color with 10% vanillin/ H_2SO_4 on TLC plates. This compound displayed antimicrobial effectiveness against *Aspergillus clavatus* F318a, *S. aureus* NBRC13276, and *P. aeruginosa* ATCC-15442 (MICs 50, 25, and 25 $\mu\text{g}/\text{mL}$, respectively), however, it was inactive against *C. albicans* (Shiono, Koseki & Koyama, 2018). In Yang et al. (2019) purified depsidone analogs: 138, 139 146–148, 150, and 153 from plasma-mutant *Aspergillus unguis* or by *A. unguis* in a medium supplemented with epigenetic modifiers (procaine, NaBr, or procaine/NaBr) that were characterized by optical rotation, spectral, and CD analyses. These metabolites had antimicrobial efficacy against *P. aeruginosa*, MRSA, *Vibrio parahaemolyticus*, and *C. albicans* (IZDs ranged 6.0 to 17.7 mm, Conc. 10 $\mu\text{g}/\text{disc}$) compared to ampicillin (IZDs 9–14 mm) and ketoconazole (IZD 22 mm for *C. albicans*), whereas 148 demonstrated potent influence on *P. aeruginosa*, MRSA, and *C. albicans*. Structure-activity relationship revealed that the ring C carboxyl group was crucial for antifungal potential (Yang et al., 2018). Also, 138, 139, 146–148, 150,

and **153** were assumed to be generated through depside production from orcinol derivatives and orsellinic acid that were derived from the PKS pathway and post-PKS modification (Scheme 2) (Yang *et al.*, 2018). In previous work by Sureram *et al.* (2013), unguinol (**138**) and aspergillusidones D–F (**151–153**) were proposed to be biosynthesized through an oxidative coupling of depsides that are produced from the condensation of orcinol derivatives (aspergillusphenols A and B) and orsellinic acid. It is noteworthy these biosynthetic intermediates were co-isolated along with these depsidones (Sureram *et al.*, 2013).

Saetang *et al.* (2021) purified the new derivatives; asperunguissidones A (**41**) and B (**42**) in addition to **138**, **139**, **146–148**, **150**, **157**, **160**, **161**, and **164** from *A. unguis* PSUMF16 utilizing SiO₂/RP-10 CC/preparative TLC. All the 1-methyl-6-(2-methylbut-2-enyl) depsidone derivatives (**41**, **138**, **139**, **146–148**, and **150**) possessed remarkable antibacterial effectiveness against *S. aureus* ATCC25923 and MRSA (MICs 1.0–8.0 µg/mL) except for non-chlorinated derivatives; **41**, **138**, and **148** (Phainuphong *et al.*, 2018). Structure-activity relationship revealed that C-4, C-2, and C-7 chlorination dramatically boosted antibacterial capacity. It is noteworthy that the C-4 chlorine atom remarkably elevated antifungal efficacy against *C. neoformans* (e.g., **147** and **146** vs **150**). Moreover, **41** with 3-substituted-2-hydroxy-3-butenyl unit instead of the 2-methylbut-2-enyl unit in **138** was 2-fold more active against MRSA than **138**, however substituting H-7 (e.g., **138**) with C=O group (e.g., **148**) led to the loss of antibacterial potential. In the 4-methyl-1,6-di(2-methylbut-2-enyl)depsidone derivatives (**157**, **160**, **161**, and **164**), the non-chlorinated **157** was more potent than **138** against *S. aureus*, MRSA, and *C. neoformans* (MICs 2.0, 1.0, and 1.0 µg/mL, respectively) (Phainuphong *et al.*, 2018), while **164**, the carboxyl derivative of **157** was 16-, 64-, and 64-fold less active against *S. aureus*, MRSA, and *C. neoformans* than **157**. Also, **160** (7-chloro derivative of **157**) demonstrated better potential against *S. aureus*, MRSA, and *C. neoformans* than **157** (MICs 0.5 µg/mL). Besides, lacking **161** (3-methoxy derivative of **160**) antimicrobial potential, indicating 3-OH's importance for activity (Saetang *et al.*, 2021).

A chemical investigation of marine-derived *A. unguis* EtOAc extracts using RP-18 CC and HPLC resulted in new depsidone, **156** with the known analogs, **138**, **139**, **143**, **146**, **147**, **149**, **155**, **157**, and **160** (Anh *et al.*, 2022). Compounds **156** revealed antimicrobial effectiveness against *B. subtilis*, *Micrococcus luteus*, and *S. aureus* (MICs 10.7, 10.7, and 5.3 µM, respectively), compared to kanamycin (MICs 1.0, 0.5, and 1.0 µM, respectively) in the broth dilution assay (Anh *et al.*, 2022).

From coral-derived *A. unguis* GXIMD-02505, new metabolite; aspergillusidone H (**154**), along with **147**, **149**, and **150** were purified by Zhang *et al.* (2022) using SiO₂/RP-18/HPLC and determined by spectral and physicochemical data. These compounds had inhibitory potential against marine biofilm-producing bacteria; MRSA, *Marinobacterium jannaschii*, *Microbulbifer variabilis*, and *Vibrio Pelagius* in the broth microdilution method. It is noteworthy that **147** possessed significant effectiveness against MRSA (MIC 2.0 µg/mL) compared to ampicillin (MIC 1.0 µg/mL). Besides, **147** and **150** exhibited moderate efficacies against *M. variabilis* and *M. jannaschii* (MICs ranged from 8.0–32.0 µg/mL) (Zhang *et al.*, 2022).

Sadorn et al. (2022) reported a new metabolite; **163**, in addition to **8**, **138**, **139**, **141**, **142**, **146–150**, **157**, and **160–164** from *Coriandrum sativum*-associated *A. unguis* BCC-54176 using Sephadex LH-20 CC/HPLC that were assigned by spectral analyses and chemical transformation, as well as X-ray data for **163**. Compounds **8**, **139**, **141**, **146**, **147**, **149**, **150**, and **160–164** displayed broad antibacterial effectiveness against *B. cereus* (MICs 1.56–25.00 µg/mL), while **163** had the potent efficacy (MIC 1.56 µg/mL) compared to rifampicin and vancomycin (MICs 0.31 and 0.08 µg/mL, respectively) (*Sadorn et al., 2022*). Assessing the anti-phytopathogens activity of these metabolites revealed that **139**, **147**, **150**, and **164** were active (MICs 6.25–50 µg/mL) on *Alternaria brassicicola* and **139**, **141**, **146–148**, **150**, **160**, and **164** demonstrated anti-*Colletotrichum acutatum* (MICs 3.13–50.00 µg/mL) using CFDA (5(6)-carboxyfluorescein diacetate) fluorometric assay compared to amphotericin B (MIC 1.56 µg/mL). Whilst all of them did not possess any effect on *A. baumannii* (Conc. 50 µg/mL) (*Sadorn et al., 2022*). Structure-activity relation showed that metabolites with two (E)-1-methylprop-1-enyl units at C-6 and C-1 (e.g., **157** and **160–164**) and the ones with C-7 Cl-atom (e.g., **160**) had more potential against *B. cereus* than the non-chlorinated analog (e.g., **157**). On the other hand, compounds with C-2 and C-7 two Cl-atoms had better activity (**163** and **162**) than the compound with one Cl-atom (as in **160**). In addition, the C-3 methoxy group led to the loss of activity (**160** vs **161**), while the C-7 carboxy boosted the efficacy (**157** vs **164**). Further, more (E)-1-methylprop-1-enyl moiety and Cl-atoms in the compounds led to more activity (*Sadorn et al., 2022*).

Antimalarial and antimycobacterial activities

Compound **44** purified from *Cladonia pyxidata* was found to have marked growth inhibitory potential against *Mycobacterium tuberculosis* H37Ra and six MDR (multidrug-resistant) *M. tuberculosis* clinical isolates with MICs 7.81–31.25 µg/mL, compared to rifampicin (MICs 0.2–100 µg/mL) using the XRMA method (*Thuan et al., 2022*). Further, **65** and **136** reported from *Usnea laevis* possessed potent antimycobacterial capacity against MDR strains of *Mycobacterium smegmatis* (MDR-40 and MDR-R) (MICs 50 µg/mL) than rifampicin (MICs 100 and >200 µg/mL, respectively), also **136** had potent (MICs 50 µg/mL) efficacy towards *M. tuberculosis* (MDR-A8 and MDR-V791) compared to rifampicin (MICs 100 and >200 µg/mL, respectively) (*Tatipamula & Annam, 2022*).

Among the reported derivatives; **8**, **138**, **139**, **141**, **142**, **146–150**, **157**, and **160–164** from *C. sativum*-associated *A. unguis* BCC-54176, **149**, **157**, and **160–163** revealed anti-*Plasmodium falciparum* (K1, MDR-strain, IC₅₀s 7.69–9.02 µM) in the micro-culture radioisotope assay compared to dihydroartemisinin (IC₅₀ 2.60 nM) and chloroquine (IC₅₀ 0.51 µM) (*Sadorn et al., 2022*) (Table S3), whilst **138**, **139**, **150**, **160**, **162**, and **163** exhibited anti-*Mycobacterium tuberculosis* (MICs 15.0–50 µg/mL) relative to ofloxacin, rifampicin, streptomycin, ethambutol, and isoniazid (MICs 0.39, 0.01, 0.31, 0.94, and 0.05 µg/mL, respectively) in the GFPMA (green fluorescent protein microplate assay) (*Sadorn et al., 2022*).

Cytotoxic activity

Some of the reported depsidones were assessed for their cytotoxic capacities against different cancer cell lines that were highlighted below, and the results of the potential metabolites were listed in [Table S4](#).

Flavicansone (**19**) a 2,7-dichloro-3,8-dimethoxy-1,6,9-trimethyl-11H-dibenzo[b,e][1,4]dioxepin-11-one was separated as a new metabolite, along with **16** from *Teloschistes flavicans* lichen utilizing SiO₂ CC and Sephadex LH-20 that were specified by different spectral tools. Compound **19** is structural like **16** with differences in substitution at C-3 and C-4, having 3-OCH₃ instead of 3-OH in **16** and lacking 4-CH₃ in **16**. Compound **19** possessed moderate cytotoxic effectiveness against HL-60 cells in the CCK-8 assay (IC₅₀ 58.18 μM) compared to quercetin (IC₅₀ 61.1 μM) and 5-fluorouracil (IC₅₀ 9.5 μM) ([Sanjaya et al., 2020](#)). Botryorhodine I (**26**) was reported as a new derivative, along with **18**, **21**, **22**, **24**, and **27** from sediment-obtained *Lasiodiplodia theobromae* M4.2-2 rice cultures using Sephadex LH-20 CC and HPLC. Only **18** possessed noticeable cytotoxic potential (IC₅₀ 7.3 μM) on L5178Y compared to kahalalide F (IC₅₀ 4.30 μM) in the MTT assay, while other metabolites were inactive ([Umeokoli et al., 2019](#)). The cytotoxic effectiveness of **23–25** and **88** against MMQ and GH3 cells showed that **88** had potent cytotoxic potential against GH3 and MMQ cell lines (IC₅₀ 3.64 and 3.09 μM, respectively), while **23** (IC₅₀ 31.62 and 19.72 μM, respectively) displayed moderate effectiveness and **24** and **25** were inactive in the MTT assay ([Zhang et al., 2018](#)).

A new depsidone, curdepsidone A (**29**) purified from white croaker-associated *curvularia* sp. IFB-Z10 EtOAc extract by macro-porous resin CC and HPLC and assigned by spectral analyses. It displayed marked cytotoxic efficacy against BEL7402 and BEL7402/5-Fu (IC₅₀s 9.85 and 2.46 μM, respectively), compared to 5-fluorouracil (IC₅₀s 14.0 and 1,630.0 μM, respectively) in the MTT assay ([An et al., 2018](#)). A novel depsidone, bailesidone (**47**), which is an 8`S-configured analog of **69** with unparalleled B-ring substituents was biosynthesized by *Usnea baileyi*. This metabolite had moderate potential against the A549 cell line (IC₅₀ 92.94 μM) and no influence against the HT-29 cell line ([Van Nguyen et al., 2018](#)). [Bui et al. \(2022\)](#) purified and characterized a new derivative; ceratinalone (**58**) along with **47**, **59**, **61**, and **62** using SiO₂ CC and spectral data. Compounds **58** and **61** were moderately cytotoxic against MCF-7, HeLa, HepG2, and NCI-H460 in the SRB assay. Besides, **61** revealed a notable influence against HeLa cells (IC₅₀ 15.61 μg/mL) ([Ouyang et al., 2018](#)). Compounds **65** and **134** demonstrated high cytotoxic efficacy against DLD-1 and HCT116 cells through modulation of NF-κB, Nrf2, and STAT3 pathways. It was found that **65** was the most potent modulator of these pathways ([Papierska et al., 2021](#)).

The new depsidones: boremexins A–C (**82–84**), in addition to **7**, **30**, **31**, and **34** were biosynthesized by *Boeremia exigua* harboring potato that were separated and specified utilizing SiO₂/RP-18 CC/HPLC and spectral/ECD analyses, respectively. Compounds **82** and **83** were obtained as a racemic mixture having 10R ([α]_D + 199.2) and 10S ([α]_D – 206.5) configurations, respectively that were further separated into enantiomers on chiral

HPLC column. In the MTT assay, **83** (IC₅₀ 33.1 μM) possessed cytotoxic capacity against MCF-7 compared to taxol (IC₅₀ 0.008 μM) (Chen et al., 2020).

Nakashima et al. (2018) purified **86** from *Phellodendron amurense*-associated *Diaporthe* sp. ECN.137 culture by SiO₂ CC, which was assigned by spectral and X-ray analyses. Its effect against TGFβ1, which boosts the tumor cell invasion was examined. It was found (Conc. 20 μM) to repress TGFβ1-caused wound closing of MDA-MB-231 cells, indicating its possible potential as a tumor metastasis inhibitor (Fig. 9). On the other hand, **96** revealed prominent cytotoxic efficacy against HepG2 and HeLa cells (IC₅₀s 19.64 and 13.97 μg/mL, respectively), whereas **97** had better cytotoxic potential on HepG2 (IC₅₀ 6.83 μg/mL) in comparison to camptothecin (IC₅₀s 3.6 and 6.3 μg/mL, respectively) in the MTT assay (Ouyang et al., 2018).

A study by Promgool et al. (2022) showed that mollicellins **91**, **92**, **94**, **95**, **97**, **99**, **100**, **104**, and **108-110** exhibited cytotoxic efficacy against HeLa, KB, HepG2, MCF-7, and HT-29 cell lines (IC₅₀s 4.79–92.11 μM), where **95**, **97**, and **110** (IC₅₀s 4.79, 10.64, and 9.83 μM, respectively) and **91**, **95**, and **110** (IC₅₀s 10.66, 7.10, and 11.69 μM, respectively) were potent against KB and HepG2 cell lines, respectively. These metabolites were cytotoxic on Vero cells (IC₅₀s 5.65–54.06 μM) except **111**. The findings indicated that the complete lactone ring and C-4-CHO group were substantial for activity, whereas the replacement of C-4-CHO with CH₂OH resulted in the loss of activity (e.g., **111**) (Promgool et al., 2022).

Also, Koo et al. (2022) reported that in the MTS assay of **130** and **131** against HCT-116 cells, **131** showed potent cytotoxic potential (EC₅₀ 1.11 μM) than 5-fluorouracil (EC₅₀ 9.4 μM), suggesting its potential as an anticancer lead against colon cancer. Additionally, physodic acid (**134**) identified from *Hypogymnia physodes* European lichen (Fig. 11) was found to exhibit cytotoxic potential against A-172, T98G, and U-138 MG cell lines (IC₅₀s 42.41, 50.57, and 45.72 μM, respectively) in the MTT assay (Studzińska-Sroka et al., 2021). Additionally, Cardile et al. investigated **134**'s potential on DU-145 and LNCaP cell growth and its apoptotic capacity on TRAIL-resistant LNCaP cells in combination with TRAIL (tumor-necrosis factor-related apoptosis-inducing ligand) using MTT assay. Lactate dehydrogenase (LDH) release is a marker of membrane breakdown. It prohibited both cell viability (Conc. 12.5–50 μM) without affecting normal cells and no observed increase in LDH (lactate dehydrogenase) level, which is a marker for membrane integrity. In addition, it activated apoptosis and raised ROS formation. Interestingly, it sensitized LNCaP cells to TRAIL-produced apoptosis. Thus, combining **134** with other anti-prostatic cancer drugs could be a prominent treatment strategy that required further studies (Cardile et al., 2022).

Anh et al. (2022) stated that **138**, **139**, **143**, **146**, **147**, **155–157**, and **160** were found to have cytotoxic potential against PC-3, NCI-H23, HCT-15, NUGC-3, ACHN, and MDA-MB-231 with IC₅₀s ranging from 3.4 to 27.7 μM, whereas **138**, **139**, and **143** were the most potential metabolites (IC₅₀s 3.4–6.2 μM). It was observed that the number of chlorine and substitution had no significant effect on activity, while free C-4-OH (**157**) was substantial for activity.

Zwartsen et al. (2019) reported that **138** and **151** reduced MDA-MB-231 cell viability (Conc. M50 μM), while they did not affect cell proliferation (Fig. 12). Additionally, they caused MDA-MB-231 cell cycle arrest (Conc. 100 μM). It is noteworthy that **138** potency

was less than **151**, this variation may be due to two bromine atoms in **151** compared to **138** that enabled the halogen bonds formation (Fig. 12).

New depsidones: **142**, **144**, **145**, **158**, and **159**, along with earlier reported **138**, **139**, **146**, **147**, **150-153**, **157**, and **160** were biosynthesized by *A. unguis* using yeast extract sucrose culture media supplemented with KBr or NaCl (Morshed et al., 2018). In the MTT assay, they demonstrated cytotoxic potential against NS-1 cell line (MICs 6.3 to 50 µg/mL) compared to 5-fluorouracil (MIC 0.1 µg/mL), whereas **138**, **157**, **159**, and **160** (MICs 12.5, 6.3, 12.5, and 12.5 µg/mL, respectively) were the most active (Morshed et al., 2018).

Phainuphong et al. (2018) reported that **160** revealed the potent inhibition activity on HCT-116 cell (IC₅₀ 23.5 µM, inhibition 87.06%), while **138-140**, **146-150**, **155**, **157**, and **164** had weak to moderate efficacy (3.98–59.63%). Compound **160** also dose-dependently decreased (IC₅₀s 34.8–84.7 µM) live cells/dead cells numbers in a 3D-culture model relying on the incubation durations, indicating its potential in spheroidal cancer model (Phainuphong et al., 2018). Further, compounds **146**, **147**, and **153** demonstrated notable larvicidal potential on *Artemia salina* (LC₅₀s 4.5–12.8 µM) compared to Hg(NO₃)₂ (LC₅₀ 77.0 µM) (Yang et al., 2018).

Compounds **112-114** and **165-167** separated from the culture of wetland-soil-associated *Pycnidophora dispersa*, utilizing SiO₂/RP-18 CC/HPLC had cytotoxic capacity against HeLa, PC-3, A549, HepG-2, and HL-60 (IC₅₀s ranged from 11.4 to 86.8 µM) compared to cisplatin (IC₅₀s ranging from 5.6 to 15.7 µM) in the CCK-8 assay. Compounds **112** and **165** had marked efficacy on A549 cells (IC₅₀s 13.0 and 11.4 µM, respectively) compared to cisplatin (IC₅₀ 11.8 µM) (Zhao et al., 2020).

From *Garcinia paucinervis* stems, a new depsidone, paucinervin Q (**169**) was separated by SiO₂ and RP-18 CC and assigned by spectral analyses. This compound revealed marked inhibition capacity against PC-3, HL-60, and CaCo-2 (IC₅₀s 18.57, 3.11, and 6.78 µM, respectively) in the MTT assay compared to 5-fluorouracil (IC₅₀s 30.59, 2.39, and 38.77 µM, respectively) (Jia et al., 2019) (Fig. 13).

Anti-inflammatory activity

Inflammation is a complicated defense process, which is induced by pro-inflammatory cytokines secretion by macrophages as a result of stimuli (e.g., infectious agent, tissue ischemia, injury, etc.) (Zhao et al., 2021a; Liang et al., 2022). Impairment of the pro-inflammation mediator secretion can lead to diverse disorders such as asthma, atherosclerosis, psoriasis, periodontal diseases, carcinogenesis, and rheumatoid arthritis (Chen et al., 2018a; Niu et al., 2021b).

Also, polyanthadepsidone A (**1**), a new highly methylated depsidone from the *Garcinia polyantha* leaves dichloromethane extract exhibited *in vitro* suppressive influence on the oxidative burst by serum opsonized zymosan in the whole blood (Lannang et al., 2018).

Chemical investigation guided by HPLC/DAD of the EtOAc extract of the marine-derived *Curvularia* sp. IFBZ10 resulted in new depsidones; **30-35** that were separated by SiO₂ CC/HPLC and their structures and absolute configuration were determined by spectral analyses as well as TDDFT/ECD (time-dependent density functional theory/electronic circular dichroism) and DFT/NMR (density functional

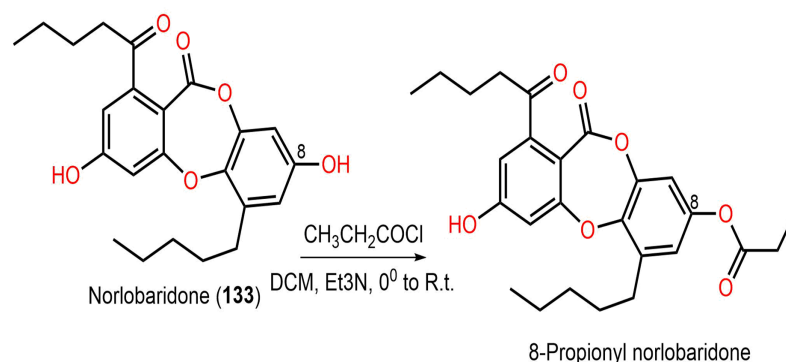
theory/nuclear magnetic resonance) calculations (Duong, 2019). The anti-inflammation potential of **30**, **31**, **34**, and **35** was assessed by measuring IL-1 β production inhibition in *Propionibacterium acnes*-induced THP-1 cells. Compound **31** exhibited noticeable IL-1 β production inhibition (IC₅₀ 7.47 μ M) compared to retinoic acid (IC₅₀ 3.38 μ M), while **30** and **35** (IC₅₀ 18.83 μ M) had no and moderate efficacy, respectively revealing that stereo-configuration had a substantial role in the activity. Further, **31** prohibited the IL-1 β production by selectively minimizing the JNK and ERK phosphorylation. The molecular docking implied that **31** suppressed IL-1 β production *via* binding to the TLR2/1 protein active site (Ding *et al.*, 2019). Compounds **7**, **34**, and **82–84** revealed anti-inflammation potential (IC₅₀s 19.4–34.4 μ M) on NO formation induced by LPS in RAW264.7 macrophages, where **7** and **83** had potent potential (IC₅₀s 22.6 and 19.9 μ M, respectively) relative to PDTTC (IC₅₀ 23.1 μ M, ammonium pyrrolidine dithiocarbamate) (Chen *et al.*, 2020) (Table S5).

Hao *et al.* (2022) purified compound **55**, a new tetracyclic derivative from mangrove-associated *Aspergillus* sp. GXNU-A9 EtOAc extract utilizing SiO₂ CC and HPLC. This metabolite (IC₅₀ 8.22 μ M) displayed a noticeable NO production inhibition capacity in RAW 264.7 cells boosted by LPS compared to dexamethasone (IC₅₀ 5.62 μ M). In another study, He *et al.* (2022) investigated *Melastoma malabathricum subsp. normale* roots utilizing SiO₂/RP-18/Sephadex LH-20 CC/HPLC, resulting in a new derivative, guanxidone B (**56**) together with **12**, **51**, and **55**. Their structures were elucidated by spectral and CD analyses. Compounds **55** and **56** possessed marked anti-inflammation efficacy (IC₅₀s 6.46 to 9.82 μ M, respectively) *via* suppressing NO production utilizing Griess Reagent System compared to dexamethasone (IC₅₀ 2.52 μ M). Compound **56** was structurally similar to **51** having C-4 CH₂OH instead of C-4 CH₃ in **51**. It is noteworthy that **56** had better activity than **55**, indicating that CH₃O at C-4 affected the activity (He *et al.*, 2022).

Lobaric acid (**136**) separated from *Stereocaulon paschale* nordic lichen was found to prohibit TNF- α and IL-1 β secretion and NF- κ B activation boosted by LPS in macrophages. Docking results revealed its binding to PPAR- γ between beta-sheet and helix H3 as a partial PPAR- γ agonist, suggesting its efficacy because of NF- κ B pathway blockage *via* PPAR- γ activation (Carpentier *et al.*, 2018). These findings supported the development of **136** as PPAR- γ agonists for chronic inflammation disorders. From *Usnea subfloridana*, salazinic acid (**65**), galbinic acid (**49**), lobaric acid (**136**), conprotocetraric acid (**173**), and constictic acid (**174**) exerted antigout and antiinflammation capacities through inhibition of 5-LOX, COX1, XO, and COX2 in enzyme inhibition assays. It is noteworthy that **136** and **173** had effective COX2 inhibition capacity (IC₅₀s 7.01 and 7.17 μ M, respectively), compared to indomethacin (7.3 μ M), whereas all of them exhibited potent XO inhibition activity (Nguyen *et al.*, 2021).

Anti-*Helicobacter pylori* activity

The inhibition of *Helicobacter pylori* urease activity is an effective strategy for treating this infectious disease. From *Cladonia rappii* acetone extract, **44** was separated by crystallization ((CH₃)₂CO:CHCl₃ 20:1) and identified by spectral data. This compound



Scheme 3 Semi-synthesis of norlobaridone (133) derivative (Pavan Kumar et al., 2020).

Full-size  DOI: 10.7717/peerj.15394/fig-17

was a marked competitive inhibitor of jack bean urease uricolytic activity. Also, it had a potent (MICs 0.034 to 0.068 μM) growth inhibition effectiveness against six clinical isolates of *H. pylori* than omeprazole (MICs 0.046–0.093 μM) in the broth microdilution assay. Therefore, **44** could be further developed for treating *H. pylori*-linked infections (Lage et al., 2018).

Antioxidant activity

Methylstictic acid (**61**) having β -orcinol core with γ -lactone connected to B ring and aldehyde group at C-3 was separated using SiO_2 CC and HPLC for the first time from *Hypotrachyna caraccensis*. It had reactivity and potency as DPPH $^\bullet$ scavenger as indicated by a kinetic study (EC_{50} 2.66 μM) compared to BHT (EC_{50} 0.11 μM) and ascorbic acid (EC_{50} 0.24 μM). It had optimal lipophilicity and permeability for penetrating the skin that could be utilized as a topical component for preventing oxidative injuries (Leal et al., 2018). The finding of antioxidant testing in the DPPH assay of mollicellins **96–98** and **101–104** showed that only **101** exhibited weak activity (IC_{50} 71.92 $\mu\text{g}/\text{mL}$) compared to BHT (IC_{50} 0.15 $\mu\text{g}/\text{mL}$) (Ouyang et al., 2018). Also, **134** possessed (IC_{50} 160 $\mu\text{g}/\text{mL}$) 5-times less antioxidant potential than resveratrol (IC_{50} 31.0 $\mu\text{g}/\text{mL}$) in the CUPRAC (CUPric-reducing-antioxidant capacity) assay (Studzinska-Sroka et al., 2021).

Ramalina lichenized fungi depsidones; **9–11**, **17**, **50**, **57**, **59**, **60**, **65**, **72**, **73**, and **134** were examined for antioxidant properties utilizing kinetic and thermodynamic calculations in the gaseous phase and aqueous solution. It was found that their BDE (bond-dissociation-energy) values were 74.4–87.7 kcal/mol, whereas **65**, **72**, and **73** had the lowest BDE(C-H)s (76.9, 74.4, and 75.2 kcal/mol $^{-1}$, respectively). These metabolites were significant $\text{O}_2^{\bullet-}$ and HO $^\bullet$ radical scavengers in aqueous media. Thus, depsidones exhibited potential $\text{O}_2^{\bullet-}$ and HO $^\bullet$ radical scavenging capacity (Bay et al., 2020). In a study by Pavan Kumar et al. (2020), **133** isolated from *Parmotrema tinctorum* by SiO_2 CC, along with its semi-synthesized derivative that was prepared using propionyl chloride were assessed for antioxidant potential in ABTS assay (Scheme 3). It was observed that **133** demonstrated potent effectiveness (%ABTS inhibition 98.90%, SC_{50} 20 $\mu\text{g}/\text{mL}$) compared to trolox (%ABTS inhibition 99.78%), while its derivative was inactive (%ABTS inhibition 4.7%, SC_{50} 20 $\mu\text{g}/\text{mL}$).

mL), revealing the importance of the free 8-OH group for the activity ([Pavan Kumar et al., 2020](#)).

Antidiabetic activity

Diabetes mellitus is a worldwide rapidly disseminated metabolic disorder that is distinguished by persistent hyperglycemia because of the flaw in insulin action, insulin secretion, or both ([Devi et al., 2020](#)). Unrestrained hyperglycemia promotes protein glycation product formation (advanced-glycation-end products, AGEs). AGEs immoderate accumulation in diabetics enhances diabetic complication pathogenesis, including nephropathy, retinopathy, cardiomyopathy, and neuropathy. It was estimated that the number of diabetic patients has been rose from 108 million in 1980 to 422 million in 2014 ([Zheng, Ley & Hu, 2018](#)). In 2015, five million deaths were reported due to diabetes and its related complications, making it 9th causal factor of diminished life expectancy ([Abubakar, Tillmann & Banerjee, 2015](#)). In 2019, two million deaths were recorded caused by diabetes, and kidney diseases resulted from diabetes ([World Health Organization, 2021](#)). The available oral synthetic antidiabetics *e.g.*, thiazolidinediones, biguanides, meglitinides, and sulfonylureas were reported to produce unwanted effects ([Lorenzati et al., 2010](#)). Thus, searching for new targets and approaches for treating diabetes is extremely recommended. α -Glucosidase (AG) is one of the fundamental enzymes implicated in carbohydrate digestion. It has been proven as an efficient target for diabetes management. However, the usage of the available alpha-glucosidase inhibitors (AGIs) such as miglitol, voglibose, 1-deoxynojirimycin, and acarbose has frequently been accompanied by side effects, in addition to the high costs. Many studies were carried out for identifying and validating the potential of natural products as AGIs for the prevention or curing of diabetes ([Assefa et al., 2019](#)).

The new derivatives, **54**, **67**, and **78**, along with **49** and **65** purified from *Parmotrema dilatatum* whole thalli acetone extract using SiO₂ CC were assayed for their AG inhibition activities. Compounds **54**, **65**, and **78** revealed a notable AG inhibition (IC₅₀s 2.2, 34.8, and 4.3 μ M, respectively) while **49** and **67** were inactive compared with acarbose (IC₅₀ 449 μ M) ([Devi et al., 2020](#)). Structure-activity relation demonstrated the 3'-benzyl and C-3 aldehyde moieties enhanced the activity, while methylation of 8'-OH resulted in losing activity and γ -butyrolactone moiety did not influence the efficacy ([Devi et al., 2020](#)). Additionally, **53**, **76**, **77**, **79**, and **80** new members of the depsidone family were separated from *Parmotrema tsavoense* utilizing SiO₂ CC/TLC and assigned by spectral methods. Compound **80** is a 2H-chromene containing depsidone. Investigating AGI potential of **53**, **76**, and **77** revealed their marked inhibitory effectiveness (IC₅₀s 11.4, 17.6, and 10.7 μ M, respectively) than acarbose (IC₅₀ 449 μ M) in the colorimetric assay ([Duong et al., 2020](#)). Further investigation of *P. tsavoense* by [Nguyen et al. \(2022a\)](#) led to the separation of a new metabolite, **81** that demonstrated a powerful (IC₅₀ 3.12 μ M) AGI capacity than acarbose (IC₅₀ 162.54 μ M). Co-culturing of *Trichoderma* sp. 307 derived from *Clerodendrum inerme* with *Acinetobacter johnsonii* B2A (pathogenic aquatic bacteria) produced a new depsidone, botryorhodine H (**88**) and known analogs, **23–25** that were separated and characterized using Sephadex LH-20 and SiO₂ CC and spectral analyses, respectively.

These metabolites possessed powerful AG inhibition capacity (IC_{50} s 8.1, 11.2, and 10.3 μ M, respectively) than acarbose (IC_{50} 703.8 μ M), whereas **25** displayed 13-fold more inhibition capacity (IC_{50} 54.1 μ M) than acarbose (Table S6). It was indicated that C-3 functional groups influenced AGI activity (**88** vs **24** vs **25**), while the C-3' CH_3 group did not affect the activity (**23** vs **24**) (Zhang et al., 2018).

Antihypertensive activity

RhoA (Ras homolog-gene family-member-A) is a member of the Rho—GTPase superfamily that was originally found to promote migration and cell cycle progress in cancer cells and control actin dynamics that are substantial for preserving the cell's cytoarchitecture. It had been reported to have a marked role in cardiomyopathies and cardiac remodeling (Kilian et al., 2021). Also, the inhibition of RhoA activation reduced the angiotensin II-dependent hypertension development (Olivon et al., 2018). Olivon et al. identified the new metabolite, baillononic acid (**20**) along with **59** from New Caledonian *Meiogyne baillonii* bark EtOAc extract. Only **59** exhibited a significant RhoA-p115 complex GDP/GTP exchange inhibition potential (IC_{50} 187 μ M, 50.5% inhibition) in the Biacore assay, thus it could have a potential for treating high blood pressure (Olivon et al., 2018).

Anti-diarrheal activity

CFTR (cystic fibrosis transmembrane conductance regulator) is a cAMP-activated chloride channel that is accountable for the trans-epithelial secretion of chloride, resulting in the promoting force for intestinal fluid secretion (Li & Naren, 2010). The CFTR's excessive function leads to secretory diarrhea, therefore its prohibition minimized intestinal fluid secretion. The CFTR inhibitory potential of **138**, **139**, **141**, **146**, **147**, **150**, **157**, **160**, and **164** in T84 cell monolayers using short-circuit current analysis was estimated. It is noteworthy that **138**, **139**, **141**, **147**, **150**, **157**, and **160** had remarkable (concentration 10 μ M, >50% inhibition) CFTR-mediated chloride secretion inhibition where **160** and **157** were the most powerful. Compounds **157** and **160** dose-dependently prohibited forskolin-boosted chloride secretion in T84 cells (IC_{50} s 0.5 and 2.0 μ M, respectively) with almost complete suppression at concentrations of 20 and 10 μ M, respectively, whereas **157** was more potent than **160**. Further investigation of **157** for their effect on CT (cholera toxin)-boosted chloride secretion across T84 cells. CT is an enterotoxin accountable for massive symptoms of cholera patients' diarrhea. Compound **157** was found to dose-dependently prohibit CT-induced chloride secretion (IC_{50} 5.0 μ M) with complete prohibition at a concentration of 100 μ M. These findings revealed an anti-secretory potential of **157** and **160** that could be beneficial for diarrhea treatment (Phainuphong et al., 2018).

BChE (butyrylcholinesterase) and AChE (acetylcholinesterase), and phosphodiesterase inhibition activities

Neurodegenerative illnesses, such as Alzheimer's (AD) or Parkinson's disease (PD) represent a critical global health concern. They are a series of procedures that result in the

gradual forfeiture of neuronal function and nerve cell death (*Di Paolo et al., 2019*). BChE (butyrylcholinesterase) and AChE (acetylcholinesterase) are substantial for CNS functions that hydrolyze acetylcholine (*Studzińska-Sroka et al., 2021*). Acetylcholine hydrolysis suppression is substantial in neuro-degenerative illnesses. Moreover, BChE and AChE noncholinergic actions like the impact on cellular adhesion and proliferation process regulation are also crucial in brain tumors (*Studzińska-Sroka et al., 2021*).

Rukachaisirikul et al. (2019) stated that **23** and **27** possessed PDE5 (–5) inhibition capacity (% inhibition 84% and 89% and IC_{50} s 5.69 and 9.96 μ M, respectively). Studzińska-Sroka et al. investigated **134** AChE and BChE inhibition potentials using Ellman's colorimetric method. It only prohibited BChE (%inhibition 8.1%) (*Studzińska-Sroka et al., 2021*). Compound **148** reported from *A. unguis* displayed AChE inhibition potential (IC_{50} 102.4 μ M), while **138**, **139**, **146**, **147**, **150**, and **153** had weak or no effectiveness (*Yang et al., 2018*).

Tyrosinase and hyaluronidase inhibitory activities

Hyaluronic acid (HA) is a brain-extracellular matrix prime component that is generated by Hyaluronan synthase (HAS) and broken down into fragments by hyaluronidase (*Misra et al., 2011*). The resulting fragments were reported to be related to enhanced cancer cell invasion capability and proliferation, as well as proangiogenic and proinflammation processes (*Chen et al., 2018b*).

Studzińska-Sroka et al. (2021) stated that **134** had a high hyaluronidase suppression potential with IC_{50} 0.053 mg/mL that was 6–10 times more powerful than tannic acid (IC_{50} 0.554 mg/mL).

Tyrosinase oxidizes surplus dopamine to form dopamine quinones, quite reactive species that promote cell death and neural damage. It is implicated in neurodegeneration-related illnesses like Parkinson's disease (*Chen et al., 2018b*). Thus, its prohibition is targeted to discover new drugs for these disorders, particularly Parkinson's disease. Compound **134** showed 25% inhibition of tyrosinase enzyme (Conc. 1.6 mg/mL), which was 3-times lower than azelaic acid using L-DOPA (substrate) (*Studzińska-Sroka et al., 2021*).

Anti-osteoclastogenic activity

Bone homeostasis is maintained and regulated by two metabolic processes, bone formation by osteoblasts and bone resorption by osteoclasts (*Jacome-Galarza et al., 2019*). Osteoclast differentiation is controlled by two factors, the M-CSF (macrophage colony stimulation factor) and RANKL (receptor activator of the nuclear factor kappa-B ligand). Signaling pathways of RANKL are considered key targets for prohibiting bone resorption and osteoclast differentiation (*Tan et al., 2020*). NF- κ B has a pivotal function in RANKL-caused osteoclast differentiation (*Zhang et al., 2022*).

Zhang et al. (2022) investigated the inhibitory potential of **147**, **149**, **150**, and **154** on RANKL-induced osteoclastogenesis in RAW264.7 macrophages and BMMs (bone marrow macrophage cells) using luciferase reporter gene and TRAP (tartate-resisant acid

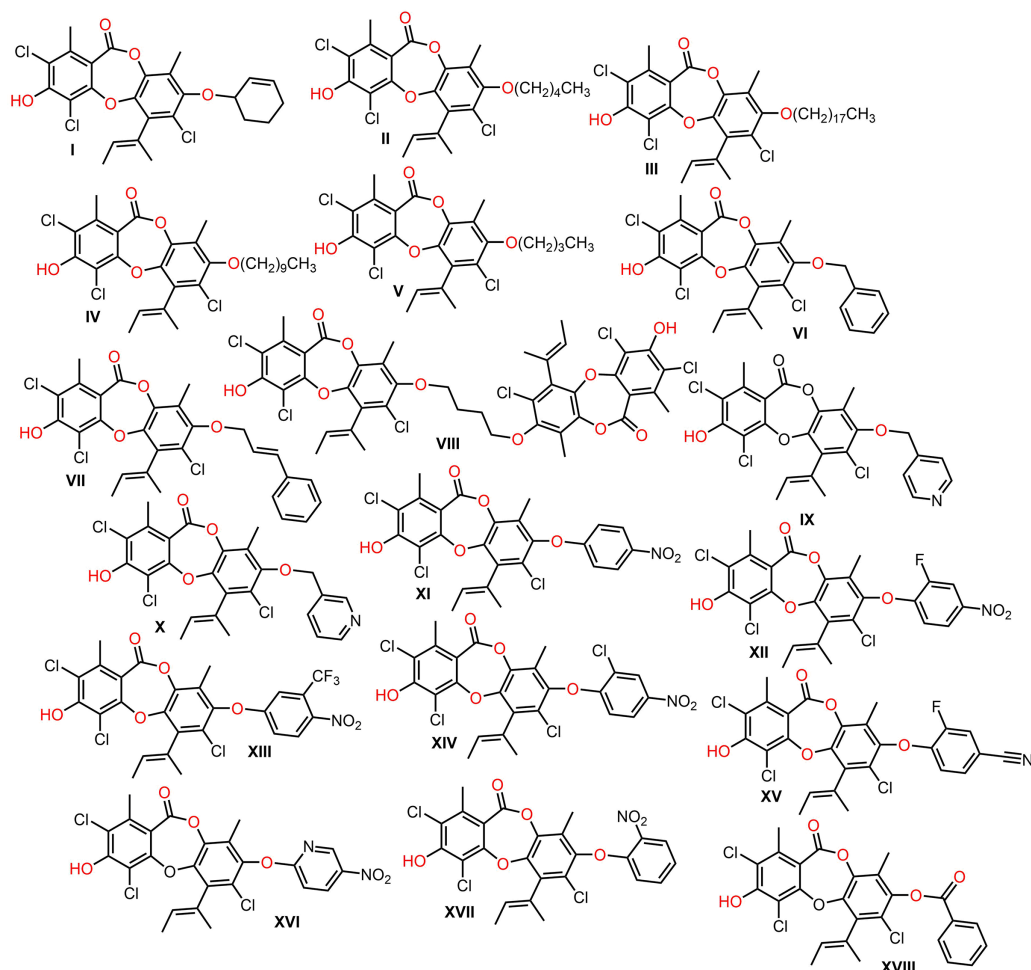


Figure 14 Semisynthetic derivatives of nornidulin (I–XVIII).

Full-size  DOI: [10.7717/peerj.15394/fig-14](https://doi.org/10.7717/peerj.15394/fig-14)

phosphatase) assays, respectively. It was found that **147**, **149**, and **154** demonstrated prohibition of LPS-caused NF- κ B activation in RAW264.7 macrophages (Conc. 20 μ M).

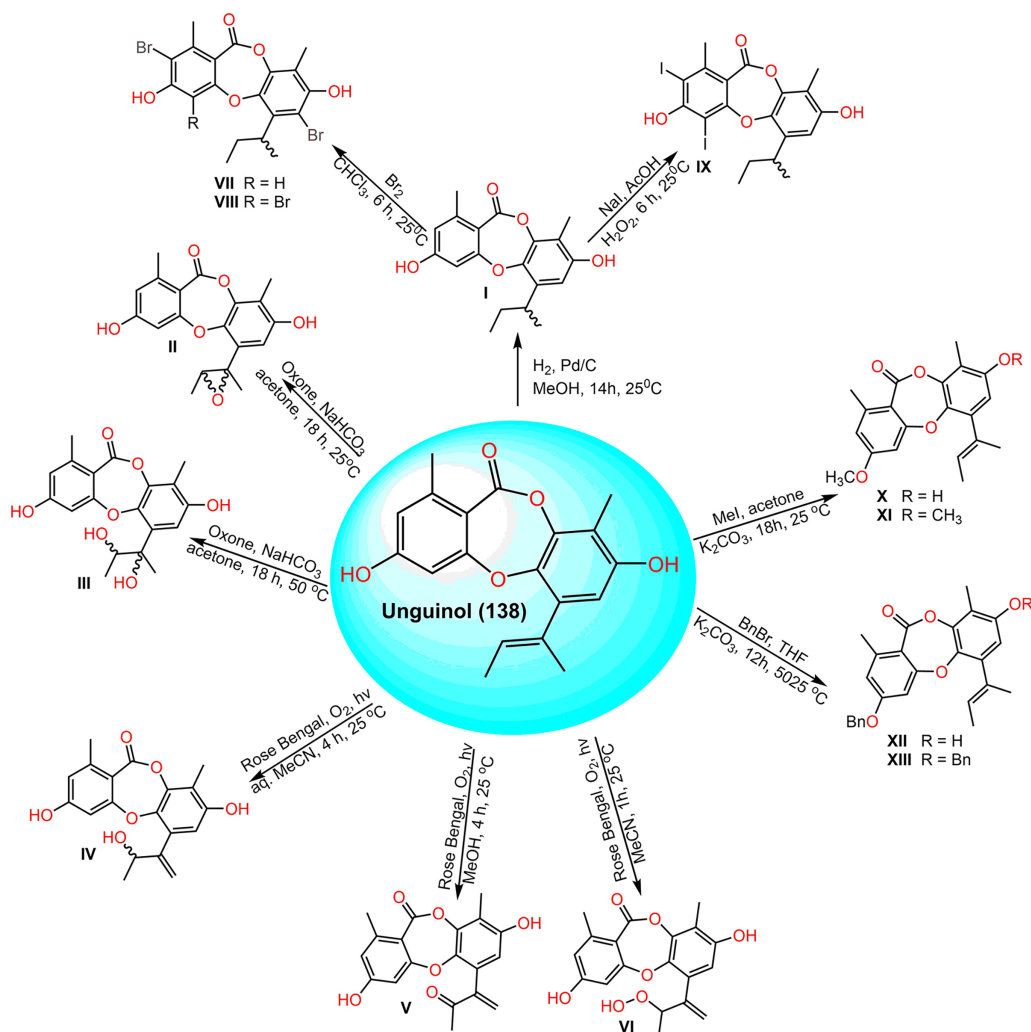
Phytotoxic activity

Norcolensoic acid (**132**) was found to prohibit lettuce seedlings' root growth (% inhibition 92 and 63%, respectively at Conc. 300 and 100 μ g/mL, respectively), whereas it strongly suppressed seed germination at a concentration of 500 μ g/mL (*Shiono, Koseki & Koyama, 2018*).

Antiviral activity

Cordia millenii investigation resulted in a new analog, **6** that was assigned by spectral and X-ray analyses. This compound had promising HIV-1 integrase efficacy (IC_{50} 4.65 μ M) in comparison to chicoric acid (IC_{50} 0.33 μ M) (*Dongmo Zeukang et al., 2019*).

Salazinic (**65**) and protocetraric (**17**) acids were reported as 3CLpro SARS-CoV-2 slow-binding inactivators (K_i of 3.77 and 3.95 μ M, respectively) that could be possible



Scheme 4 Semisynthetic derivatives (I–XIII) of unguinol (138) (Morshed et al., 2021).

Full-size DOI: 10.7717/peerj.15394/fig-18

scaffolds for the development of effective SARS-CoV-2 cysteine enzyme 3CLpro inhibitors (Fagnani et al., 2022).

GnRH (Gonadotropin-releasing hormone) antagonistic activity

Nguyen et al. (2022b) proved that the treatment of female rats with lobaric acid (136) (50 and 100 mg/kg b.w./day) significantly ameliorated tetramethrin (50 mg/kg b.w./day)-induced alteration on estrous cycle. It reversed gonadotropins serum levels through influencing the pituitary/hypothalamic axis and competitively inhibited tetramethrin binding to GnRH receptor in both thermodynamic and kinetic processes.

SEMISYNTHETIC DEPSIDONE DERIVATIVES

Isaka et al. (2019) synthesized derivatives of 146 utilizing regioselective arylation, acylation, and alkylation reactions to give 8-O-substituted analogs that were assessed for their antibacterial potential. Many of the 8-O-alkyl derivatives had more powerful

antibacterial capacities than **146**, whereas 8-O-butyl exhibited the highest potential against *B. cereus* (MIC 0.391 µg/mL), however, the derivatives with long sidechains, as well as acylated derivatives displayed weaker capacity. On the other hand, O-aryl analogs demonstrated powerful antibacterial potential against MRSA (Isaka et al., 2019) (Fig. 14).

Morshed et al. (2021) prepared semisynthetic derivatives of **138** (Scheme 4). Among them, 3-O-(2,4-difluorobenzyl)unguinol and 3-O-(2-fluorobenzyl)unguinol possessed remarkable antibacterial effectiveness against methicillin-susceptible and -resistant *S. aureus* (MIC 0.25–1 µg/mL).

CONCLUSION

Natural metabolites biosynthesized by various living organisms are renowned for their vital contribution to drug design and discovery. In this work, a total of 172 depsidones were reported from various sources from 2018 to 2022 with a greater number separated in 2022. The major depsidone derivatives are reported from fungi (107 compounds, 62.2%), then lichens (52 compounds, 30.3%), and the least number of depsidones were reported from plant sources (13 compounds, 7.5%). These metabolites were commonly separated from the species belonging to the following genera: *Aspergillus*, *Chaetomium*, and *Spiromastix* (fungi); *Usnea*, *Parmotrema*, and *Ramalina* (lichens), and *Melastoma*, *Hypericum*, and *Garcinia* (plants).

It is noteworthy that these metabolites show various structural features according to their sources. It was noted that fungal-derived depsidones possess various substituents such as pyran (e.g., **83**, **86**, **91**, **99**, **100**, and **102–104**), substituted benzyl (e.g., **88–90**), isoprenyl (e.g., **92–94**, **96–98**, and **105–111**), 2-methylbut-2-enyl (e.g., **138–167**), three to five carbon aliphatic chain (e.g., **115–129**), and halogen (bromine (e.g., **121**, **123**, **125**, **127**, **129**, **144**, **145**, **151**, **152**, and **159**) and chlorine (e.g., **116–120**, **139–144**, **154–156**, and **160–163**)) and lichen-derived depsidones feature furan (e.g., **45–52** and **57–73**), substituted benzyl (e.g., **54** and **74–79**), and five to seven aliphatic chains (e.g., **130–137**), while that reported from the plant have isoprenyl substituent (e.g., **168–170**).

These metabolites were evaluated for various bioactivities mainly antimicrobial, cytotoxic, and antidiabetic capacities. Depsidones could have the potential as lead metabolites for neurodegenerative illnesses and diabetes through their inhibition of butyrylcholinesterase, tyrosinase, α-glucosidase, and acetylcholinesterase enzymes. Besides, **127** could be a potential lead for bactericides to control rice bacterial-blight disease. Also, **44** demonstrated powerful anti-*H. pylori* potential that could be further developed for treating *H. pylori*-linked infections. It was found that the ring substitution patterns greatly influenced the activities as highlighted in some reports on structure-activity relation (Shukla et al., 2019; Niu et al., 2021b).

Preparation of semi-synthetic derivatives from these compounds resulted in derivatives with more powerful activity than parent compounds e.g., unguinol and nidulin, which could encourage medicinal chemists to carry out further modification of the structures of other reported metabolites and assess the effect of this modification on the bioactivities. Besides, altering cultural media conditions could be an efficient strategy to get novel biometabolites. Also, the co-culturing of two or more organisms from different species

produced interesting metabolites that have not been produced in the cultivation of the organism alone. Therefore, this approach could be further utilized for discovering more valuable metabolites. Collectively, depsidone derivatives feature diversified chemical entities and numerous bioactivities. These metabolites could be beneficial scaffolds and building blocks for synthesizing various drugs for multiple human health disorders. However, the *in vivo* evaluation of their potential biological properties and mechanistic investigations should indubitably be the focal point of future studies.

LIST OF ABBREVIATIONS

A-172	Glioblastoma cell line
A549	Human lung adenocarcinoma epithelial cell line
ABTS	2,2'-Azinobis-(3-ethylbenzthiazoline-6-sulphonate)
ACHN	Human renal carcinoma cell lines
AChE	Acetylcholinesterase
Bel-7402	Human hepatocellular carcinoma cell line
BHT	Butylated hydroxytoluene
CCK-8	Cell counting kit-8
CD	Circular dichroism
CFTR	Cystic fibrosis transmembrane conductance regulator
CH₂Cl₂	Dichloromethane
COX1	Cyclooxygenase-1
COX2	Cyclooxygenase-2
DPPH	1,1-Diphenyl-2-picrylhydrazyl
EC₅₀	Half maximal effective concentration
ECD	Electronic circular dichroism
EtOH	Ethanol
EtOAc	Ethyl acetate
ESI-MS	Electrospray ionization mass spectrometry
GFPMA	Green fluorescent protein microplate assay
HCT-15	Human colon cancer cell line
HCT-116	Human colon cancer cell line
HeLa	Human cervical epitheloid carcinoma cell line
HepG2	Human hepatocellular liver carcinoma cell line
HPLC	High-performance liquid chromatography
HRESIMS	High resolution electrospray ionization mass spectroscopy
HT-29	Human colon cancer cell line
IC₅₀	Half-maximal inhibitory concentration
IL-1β	Interleukin-1 β
KB	Human oral epidermoid carcinoma cell line
LC₅₀	Lethal concentration that kills 50%
IR	Infrared
LPS	Lipopolysaccharide

5-LOX	5-Lipoxygenase
MCF-7	Human breast adenocarcinoma cell line
MDR	Multidrug-resistant
MDA-MB	
-231	Human breast cancer cell line
Med25	Mediator of RNA polymerase II transcription subunit 25
MeOH	Methanol
MIC	Minimum inhibitory concentration
MRSA	Methicillin-resistant <i>Staphylococcus aureus</i>
MS	Mass spectrometry
MTS	(3-(4,5-Dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium inner salt)
MTT	3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide
TM4 cells	Murine Sertoli cells
NCI-H460	Human non-small cell lung cancer cell line
NCI-H187	Human small-cell lung cancer
NCI-H23	Human lung cancer cell line
NF-κB	Nuclear factor kappa-light-chain-enhancer of activated B cells
NMR	Nuclear magnetic resonance
NUGC-3	Human stomach cancer cell line
NO	Nitric oxide
PC-3	Human prostatic-testosterone-independent cell line
PDE5	Phosphodiesterase
ROS	Reactive oxygen species
PPAR-γ	Peroxisome proliferator—activated receptor gamma
RP-18	Reversed phase-18
SC₅₀	Scavenging concentration 50%
SiO₂ CC	Silica gel column chromatography
PPIs	Protein-protein interactions
T98G	Glioblastoma cell line
TLC	Thin layer chromatography
TNF-α	Tumor necrosis factor alpha
TRAIL	Tumor necrosis factor-related apoptosis-inducing ligand
U-138MG	Glioblastoma cell line
U937	Pro-monocytic, human myeloid leukemia cell line
Vero cell	Normal African green monkey kidney fibroblasts
XO	xanthine oxidase
XRMA	2,3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide (XTT) reduction menadione assay.

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Competing Interests

The authors declare that they have no competing interests.

Author Contributions

- Maan T. Khayat performed the experiments, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.
- Kholoud F. Ghazawi performed the experiments, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.
- Waad A. Samman performed the experiments, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.
- Aisha A. Alhaddad performed the experiments, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.
- Gamal A. Mohamed conceived and designed the experiments, performed the experiments, analyzed the data, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.
- Sabrin R. M. Ibrahim conceived and designed the experiments, performed the experiments, analyzed the data, prepared figures and/or tables, authored or reviewed drafts of the article, and approved the final draft.

Data Availability

The following information was supplied regarding data availability:

This is a literature review.

Supplemental Information

Supplemental information for this article can be found online at <http://dx.doi.org/10.7717/peerj.15394#supplemental-information>.

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