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Isolation and Screening of Antibacterial-Producing Endophytic *Actinomycetes* from Hollyhock (*Alcea rosea*)

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Abstract

Actinomycete bacteria are widely recognized for their ability to produce diverse bioactive compounds, particularly antibiotics, and contribute significantly to the discovery of naturally derived antimicrobial agents. This study focused on isolating and characterizing actinomycete strains from hollyhock (*Alcea rosea*) plant tissues to assess their antibacterial potential against clinically relevant pathogens. The target pathogens included *Bacillus cereus*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli*. 110 bacterial isolates were obtained, with 62 isolates confirmed as *Actinomycetes* through PCR amplification of the 16S rRNA gene. Approximately 46.5% of these isolates exhibited antibacterial activity, with pronounced effects against *B. cereus* and *S. aureus*, suggesting their potential role in combating antibiotic-resistant bacteria. Genetic analysis revealed the presence of non-ribosomal peptide synthetase (*NRPS*) genes, indicating that the produced antimicrobial compounds may originate from NRPS pathways. However, no polyketide synthase (*PKS*) genes were detected, which may limit the diversity of bioactive metabolites. These findings highlight the pharmaceutical potential of hollyhock-associated *Actinomycetes* as promising sources of novel antimicrobial agents.

1. Introduction

Actinomycetes, a prominent group within the bacterial domain classified under the phylum *Actinomycetota*, are notable for their filamentous structure and significant genomic capacity to produce a wide array of secondary metabolites, including natural antibiotics. These Gram-positive bacteria are primarily found in diverse environments such as soil, marine sediments, and extreme habitats, which enhances their ability to synthesize unique bioactive compounds (Jagannathan et al., 2021; Khan et al., 2023).

Research indicates that the 10,000 identified *Actinomycetes* compounds are responsible for over 45% of all bioactive microbial metabolites, many of which serve as antibiotics in clinical settings (Izhar et al., 2023). Notably, over 70% of all naturally derived antibiotics in clinical use originate from this group (Genilloud, 2017). Their extensive genomic capacity allows for the biosynthesis of various compounds, including antibacterial, antifungal, and anticancer agents. Members of the genus *Streptomyces* are especially prolific in antibiotic production, contributing

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significantly to the antibiotic arsenal used to combat multidrug-resistant pathogens (Kim et al., 2021).

Actinomycetes thrive in diverse environments, playing essential roles across ecosystems. In soil, they contribute to nutrient cycling and the synthesis of bioactive compounds, supporting ecological balance (Jose & Jebakumar, 2014). Within the rhizosphere, the region surrounding plant roots, they foster plant growth and act as natural defenders against infections (Van der Meij et al., 2017). Freshwater systems benefit from their ability to enhance microbial diversity and ecological functions (Bredholt et al., 2008). In marine environments, *Actinomycetes* inhabit sediments and hypersaline habitats and produce unique secondary metabolites with distinct biochemical properties (Jensen et al., 1991; José & Jebakumar, 2014). On plants, particularly leaf surfaces known as the phyllosphere, they form symbiotic relationships that help prevent plant diseases and promote overall plant health (Wati et al., 2023).

Most *Actinomycetes* are aerobic and prefer neutral to alkaline soils, although some species can thrive in more acidic environments (Javad et al., 2021). Their adaptability to different soil conditions contributes to their ecological significance and potential for biotechnological applications, particularly in antibiotic production (Setiawati & Yusan, 2022).

In addition to their ecological roles, *Actinomycetes* have significant applications in medicine, agriculture, and environmental remediation, highlighting their importance in biotechnology and drug discovery (Meenakshi et al., 2024). *Alcea rosea*, commonly known as hollyhock, has been utilized for medicinal purposes since ancient times, with applications including anti-inflammatory, analgesic, and antioxidant effects (Dar et al., 2017; Ahmadi et al., 2012; Azadeh et al., 2023). The plant contains various bioactive compounds, such as flavonoids and mucilaginous polysaccharides, which contribute to its therapeutic properties (Zareii et al., 2014; Hanif et al., 2019). Many medicinal compounds found in plants are synthesized by endophytes, microorganisms residing within plant tissues. These endophytes can produce bioactive compounds similar to those of their host plants, enhancing the plant's medicinal properties (Zhao et al., 2011; Khan et al., 2023). Endophytes are microorganisms capable of synthesizing various secondary metabolites with pharmaceutical potential, including compounds with antibacterial, antiviral, and anticancer properties (Aharwal et al., 2016; Choudhury et al., 2023; Staniek et al., 2008). This symbiotic relationship offers a rich source of novel natural products for pharmaceutical applications (Li et al., 2014). Recent advances in genome mining and coculture techniques have further enhanced the discovery of novel secondary metabolites from *Actinomycetes*, underscoring their potential as sources of new therapeutic agents (Jagannathan et al., 2021).

The present study aimed to investigate the antibacterial properties of endophytic *Actinomycetes* associated with *Alcea rosea*. By isolating and characterizing these microorganisms, we sought to assess their potential antibacterial activity against pathogenic microorganisms. This study provides a basis for further exploration of endophytic *Actinomycetes* as potential sources of novel antimicrobial agents.

2. Materials and Methods

2.1 Sample Collection and Isolation of Endophytic *Actinomycete*

Hollyhock plant samples were collected in the spring of 2020 from various regions in Ilam Province, Iran. These samples were stored in sterile plastic bags and transported to the laboratory on ice to preserve microbial integrity.

In the laboratory, the plant samples underwent a modified six-step surface sterilization process within 24 hours, as described by Quin et al. (2011). The sterilized plant parts were processed according to the method described in Hajizadeh et al. (2023).

2.2 Morphological Characterization

The preliminary identification of isolates was conducted based on morphological characteristics, including colony morphology (size, shape, color, margin, and elevation), microscopic features (Gram stain reaction, aerial and substrate mycelium formation, and spore morphology), and pigmentation (production of diffusible or non-diffusible pigments) following methods described by Cook (2003).

Table 1: List of Oligonucleotide Primers used in the Study

Primer name	*Sequence (5'-3')*	*Gene*	*Product size (bp)*	*Reference*
ACT235f	*CGCGGCCTATCAGCTTGTTG*	*16S rRNA*	*640*	***Stach et al., 2003***
ACT878r	*CCGTACTCCCCAGGCGGGG*			
A3F	*GCSTACSYSATSTACACSTCSGG*	*NRPS*	*700-800*	***Ayuso-Sacido & Genilloud, 2005***
A7R	*SASGTCVCCSGTSCGGTAS*			
KIF	*TSAAGTCSAACATCGGBCA*	*PKS-I*	*1200-1400*	***Metsä-Ketelä, 1999***
M6R	*CGCAGGTTSCSGTACCAGTA*			
PKS-II-A	*TSGCSTGCTTCGAYGCSATC*	*PKS-II*	*600*	***Ayuso-Sacido & Genilloud, 2005***
PKS-II-B	*TGGAANCCGCCGAABCCGCT*			

2.3 DNA Extraction and Molecular Characterization of *Actinomycetes*

Genomic DNA was extracted from endophytic isolates using a boiling method (Tavarideh et al., 2022) and identified with *Actinomycetes*-specific primers listed in Table 1 via PCR (Stach et al., 2003).

2.4 Evaluation of Antibacterial Activity of *Actinomycete*

All actinomycetal isolates were fermented, and their resulting extracts were screened according to previous research without modifications (Hajizadeh et al., 2023). The antibacterial activity of the actinomycetal strains was evaluated using two Gram-negative reference strains (*Escherichia coli* PTCC 1330, *Pseudomonas aeruginosa* PTCC 1430), and two Gram-positive pathogens (*Bacillus cereus* PTCC 1015, *Staphylococcus aureus* ATCC 33591). The bacteria were cultured overnight at 37ºC in Mueller-Hinton (MH) broth, and each culture was then adjusted to a turbidity level of 0.5 McFarland standard. A ciprofloxacin disk was used as the positive control and ethyl acetate as the negative control. Following the procedure described by Hajizadeh et al. (2023), bacterial lawns were first created on MH agar in 6 mm wells, into which 100 µL of crude extracts were added. The plates were left at room temperature for one hour before being incubated at 37ºC. After 24 hours, the inhibition zones were assessed in millimeters (mm), utilizing 100 µL of ethyl acetate as the control.

2.5 Detection of *PKS-I, PKS-II*, and *NRPS* genes

Genes encoding non-ribosomal peptide synthetases (*NRPS*) and polyketide synthases I and II (*PKS-I* and *PKS-II*) were detected via PCR using specific primers (Table 1). Amplifications were performed with 30 cycles of denaturation (95°C, 1 minute), annealing (58°C or 60°C, 1 minute), and extension (72°C, 1 minute). PCR products were analyzed on 1.5% agarose gels.

2.6 Statistical Analysis

All experiments were performed in triplicate. The results were presented as mean ± standard deviation, and statistical significance was determined using two-way ANOVA in GraphPad Prism version 9.0. A p-value <0.05 was considered statistically significant.

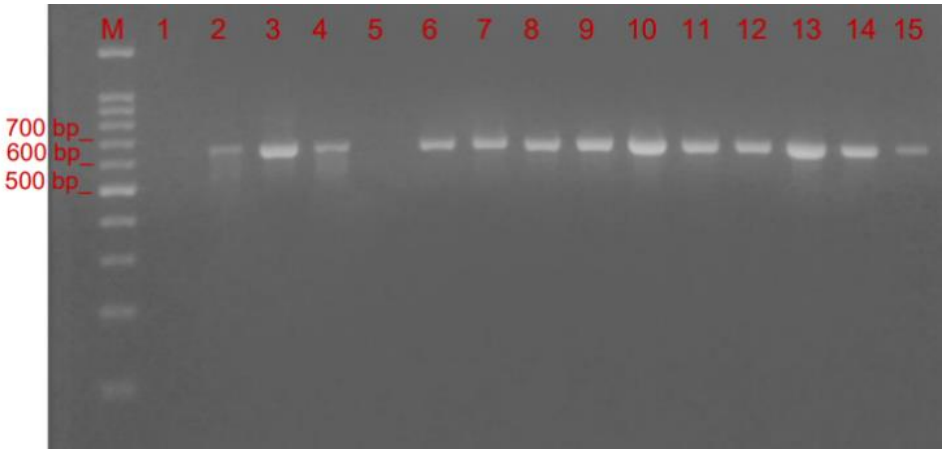
3. Results and Discussion

3.1. Isolation and Identification of *Actinomycetes*

One hundred and ten bacterial isolates were obtained from surface-sterilized tissues of the hollyhock. The morphological characterization revealed that 70 isolates were Gram-positive, predominantly exhibiting a filamentous structure characteristic of *Actinomycetes*. This morphological trait aligns with the well-established features of this bacterial group, known for their filamentous growth and ability to produce a variety of bioactive compounds.

To further confirm the identity of the isolates, PCR amplification of the 16S rRNA gene was performed on 62 isolates, producing a product of approximately 640 base pairs (Fig 1). The high success rate of PCR amplification suggests a high level of genetic diversity among the isolates, indicating that *Alcea rosea* harbors a rich community of *Actinomycetes*.

Figure 1: Agarose Gel Electrophoresis of 16S rRNA PCR Products from Bacterial Isolates



Note. Lane M: DNA size marker; Lane 1: Negative control; Lanes 2–15: PCR products from bacterial isolates showing a 640 bp band representing the amplified 16S rRNA gene.

3.2. Antibacterial Activity

The antibacterial activity of the 62 PCR-positive actinomycete isolates was evaluated against four pathogenic bacterial strains: *Bacillus cereus*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli* (Table 2). Of these 30 isolates, 14 (46.5%) exhibited antibacterial activity against *Bacillus cereus*, 7 (23.5%) against *Staphylococcus aureus*, 6 (20%) against *Pseudomonas aeruginosa*, and 3 (10%) against *Escherichia coli*. These findings suggest that *Actinomycetes* associated with plants like *Alcea rosea* produce bioactive compounds that are effective against Gram-positive and Gram-negative bacteria. This broad spectrum of activity aligns with previous research indicating that *Actinomycetes* are key producers of antibiotics, including streptomycin, erythromycin, and tetracycline (Roy & Banerjee, 2015).

3.3. Specific Pathogen Responses

- *Bacillus cereus*: Fourteen isolates exhibited notable antibacterial activity against *B. cereus*, with inhibition zones ranging from 12 mm to 25 mm. These findings suggest that certain *Actinomycetes* isolated from *Alcea rosea* may produce compounds effective against foodborne pathogens, which is highly relevant in the context of food safety concerns.

Table 2: Antibacterial Activities of *Actinomycetes* Isolated from *Alcea rosea*

No	Strain code	*B. cereus*	*E. coli*	*P. aeruginosa*	*S. aureus*	Mean and Standard Deviation of Inhibition Zone (mm)[a]
1	Lk				> 25 mm	28.5±2.3
2	Pc		≥10<15 mm			12.0±1.5
3	Ll			≥10<15 mm		14.2±1.8
4	Lg				> 25 mm	27.8±2.1
5	Ph				> 25 mm	26.5±2.4
6	Ri			10-15 mm		18.7±1.9
7	Ln				> 25 mm	29.0±2.5
8	Po				10-15 mm	16.3±1.7
9	Pp				10-15 mm	17.0±1.6
10	Sj		≥10<15 mm			11.5±1.4
11	Ps			10-15 mm		19.2±1.8
12	Pq			10-15 mm		20.0±1.9
13	Lr	10-15 mm				22.5±2.0
14	PL_2	10-15 mm				21.8±2.1
15	Pz_1	10-15 mm				23.0±2.2
16	Sa_2	10-15 mm				22.7±2.0
17	Rb_2	> 25 mm				30.5±2.6
18	Pc_2	10-15 mm				21.5±1.9
19	Sd_2				10-15 mm	16.8±1.7
20	Re_2				≥10<15 mm	13.5±1.6
21	Pt			≥10<15 mm		14.0±1.7
22	Pg_2	10-15 mm				20.5±1.8
23	Su	> 25 mm				31.0±2.7
24	Lv	> 25 mm				29.5±2.4
25	Pw	≥10<15 mm				12.8±1.5
26	Sj_2			10-15 mm		18.5±1.8
27	Lx	≥10<15 mm				13.0±1.6
28	Py	≥10<15 mm				12.5±1.5
29	Sf_2	10-15 mm				19.8±1.9
30	Lv_2	10-15 mm				20.2±1.8

Note. [a] significant difference ($p < .05$) was seen between inhibition zones of *Actinomycetes* and the control.

- *Staphylococcus aureus*: Seven isolates demonstrated activity against this clinically important pathogen, with inhibition zones between 10 mm and 20 mm. Given the increasing antibiotic resistance in *S. aureus*, these results are promising for the development of alternative treatments for infections caused by this pathogen.

- *Pseudomonas aeruginosa*: Six isolates exhibited activity against this opportunistic pathogen, with inhibition zones ranging from 8 mm to 18 mm. The ability to inhibit *P. aeruginosa*, known for its resistance to many antibiotics, further emphasizes the significance of these *Actinomycetes* in combating multi-drug-resistant bacteria.

- *Escherichia coli*: Three isolates showed moderate antibacterial activity against *E. coli*, with inhibition zones ranging from 9 mm to 15 mm. While the inhibition was less pronounced than for other pathogens, the findings suggest that these isolates could still have the potential to address *E. coli*-related infections.

Overall, the data indicate that *Actinomycetes* associated with *Alcea rosea* possess a diverse array of bioactive compounds with significant antibacterial activity. The antibacterial potential observed against foodborne and clinically relevant pathogens suggests the importance of these isolates in future antimicrobial drug discovery.

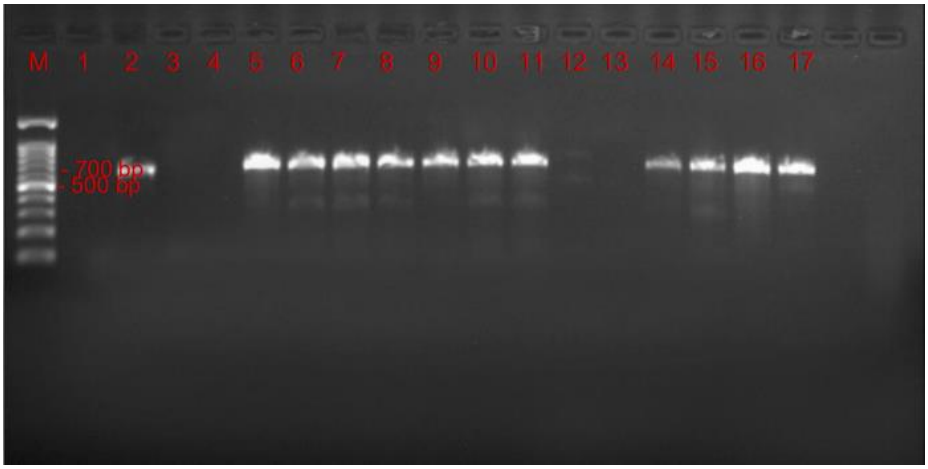
3.4. Genetic Screening for Biosynthetic Pathways

To further investigate the biosynthetic potential of the isolated *Actinomycetes*, PCR was conducted to detect genes associated with secondary metabolite production, particularly those related to non-*NRPS* and *PKS*. These pathways are crucial for the production of bioactive compounds, including antimicrobial agents.

3.5. Findings on *NRPS* and *PKS* Genes

Among the 62 PCR-positive isolates, 38 were found to possess *NRPS* genes, which are associated with the production of non-ribosomal peptides (Fig 2). This finding is significant as *NRPS* are known for their broad spectrum of biological activities, including antibacterial properties. The presence of *NRPS* genes in the isolates suggests that many *Actinomycetes* from *Alcea rosea* can synthesize bioactive compounds. This indicates their potential to produce *NRPS*, known for its diverse biological activities, including antibacterial, antifungal, and anticancer effects (Hur et al., 2012; Zobel et al., 2016).

Figure 2: Agarose Gel Electrophoresis of NRPS gene PCR Products from *Actinomycete* Isolates



Note. Lane M: DNA size marker; Lane 1: Negative control; Lanes 2–17: PCR products from *Actinomycetes* isolates, displaying bands between 700–800 bp, indicative of the amplified *NRPS* gene.

*NRPS*s are complex multimodular enzymes that synthesize these peptides through a series of catalytic domains, each responsible for incorporating specific monomeric units into the peptide chain (Butz et al., 2008). The ability of these *Actinomycetes* to produce *NRPS*-derived compounds highlights their potential in pharmaceutical applications, particularly in developing new therapeutic agents targeting various diseases (Li et al., 2014).

The presence of *NRPS* genes in *Actinomycetes* derived from *Alcea rosea* is consistent with findings from various studies on endophytic *Actinomycetes*, which collectively highlight their significant biosynthetic potential. A study conducted on endophytic *Actinomycetes* sourced

from tropical plants revealed that 100% of the tested strains possessed *NRPS* genes. This finding underscores a robust potential for secondary metabolite production, even though some strains did not yield detectable metabolites (Janso et al., 2010). Research focusing on endophytic *Actinomycetes* associated with medicinal plants indicated that 28.9% of the isolates contained *NRPS* genes, which were correlated with broad-spectrum antimicrobial activity (Hanh et al., 2020). Similarly, a study on endophytic *Actinomycetes* from tea plants demonstrated a high prevalence of *NRPS* genes, directly linked to their antimicrobial capabilities (Shan et al., 2018).

However, none of the isolates contained *PKS-I* or *PKS-II* genes, which are involved in the biosynthesis of polyketides (data not shown). While the absence of these genes may limit the potential for producing certain polyketide antibiotics, it does not diminish the overall relevance of these strains in the search for new antimicrobial agents. The identification of *NRPS* genes corresponds closely with the antibacterial activity observed, indicating that the bioactive compounds synthesized by these strains are likely to be *NRPS*. The lack of polyketide synthase (*PKS-I* and *PKS-II*) genes in the isolates tested implies that the bioactive compounds produced are predominantly sourced from *NRPS* pathways or other metabolites not investigated in this study. *PKS* genes are generally linked to the biosynthesis of polyketides, which represent another important category of secondary metabolites recognized for their varied biological activities, including antibiotic effects (Ayuso-Sacido et al., 2004; Zhao et al., 2010).

The lack of *PKS* gene detection indicates that these isolates may not produce polyketide-derived compounds, which could limit the range of bioactive metabolites available from these *Actinomycetes*. Instead, the focus on *NRPS*-derived compounds may highlight a different metabolic pathway that could be explored for novel therapeutic agents (Gohain et al., 2015). This finding emphasizes the need for further investigation into other biosynthetic pathways that may contribute to the bioactivity of these isolates (Mzumdar et al., 2023).

3.6. Implications for Drug Discovery

This study highlights the significant potential of *Alcea rosea*-associated *Actinomycetes* as sources of novel antimicrobial agents. The high incidence of antibacterial activity among the isolates indicates their potential to address the critical issue of antibiotic resistance, particularly in pathogens such as *S. aureus*, *P. aeruginosa*, and *B. cereus*. The presence of *NRPS* genes further supports the idea that these strains may produce non-ribosomal peptides, which could be developed into effective new drugs.

4. Conclusion

In conclusion, this study successfully isolated and characterized *Actinomycetes* from *Alcea rosea*, revealing their significant antibacterial properties and genetic potential for producing bioactive secondary metabolites. These findings not only contribute valuable knowledge to the field of natural product chemistry but also underscore the importance of these microorganisms in the ongoing search for novel antimicrobial agents. The promising antibacterial activity observed in this study highlights the need for continued exploration of *Alcea rosea*-associated *Actinomycetes* as potential sources for combating resistant bacterial strains and advancing drug discovery. Future studies should focus on the isolation and structural characterization of active compounds, elucidation of their mechanisms of action, and in vivo evaluation of their therapeutic efficacy in treating bacterial infections

Conflict of interest

The authors declare that they have no competing interests.

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Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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Conflict of Interest

The authors declare no conflict of interest.

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Authors' Contributions

S.K. and F.P. proposed and designed the research, S.K. collected samples.

S.K., F.P., and M.N. analyzed and interpreted data, S.K., F.P., and M.N. drafted the manuscript, F.P. and M.N. performed statistical analyses, F.P. and M.N. proved the final version of the manuscript.

References

[1] Aharwal, R. P., Kumar, S., & Sandhu, S. S. (2016). Endophytic microflora as a source of biotherapeutic compounds for disease treatment. *Journal of Applied Pharmaceutical Science*, *6*(1), 242-249. https://doi:10.7324/JAPS.2016.601034

[2] Ahmadi, M., Rad, A. K., Rajaei, Z., Mohammadian, N., & Tabasi, N. S. (2012). Alcea rosea root extract as a preventive and curative agent in ethylene glycol-induced urolithiasis in rats. *Indian Journal of Pharmacology*, *44*(3), 304-309. https://doi:10.4103/0253-7613.96298

[3] Ayuso, A., Clark, D., González, I., Salazar, O., Anderson, A., Genilloud, O. (2005). A novel actinomycete strain de-replication approach based on the diversity of polyketide synthase and nonribosomal peptide synthetase biosynthetic pathways. *Applied Microbiology and Biotechnology*, *67*(6), 795-804. https://doi.org/10.1007/s00253-004-1828-7

[4] Ayuso-Sacido, A., & Genilloud, O. (2005). New PCR primers for the screening of NRPS and PKS-I systems in *Actinomycetes*: Detection and distribution of these biosynthetic gene sequences in major taxonomic groups. Microbial Ecology, 49(1), 10. https://doi.org/10.1007/s00248-004-0249-6

[5] Azadeh, Z., Asgharian, S., Habtemariam, S., Lorigooini, Z., & Taheri, A. A. (2023). Review of botanical, phytochemical, and pharmacological properties of *Alcea rosea* L. *Future Natural Products*, *9*, 88-101. https://doi:10.34172/fnp.2210-1232

[6] Bredholt, H., Fjærvik, E., Johnsen, G., & Zotchev, S. B. (2008). *Actinomycetes* from sediments in the Trondheim fjord, Norway: Diversity and biological activity. *Marine Drugs*, *6*(1), 12-22. https://doi:10.3390/MD6010012

[7] Butz, D., Schmiederer, T., Hadatsch, B., Wohlleben, W., Weber, T., & Süssmuth, R. D. (2008). Mode extension of a non-ribosomal peptide synthetase of the glycopeptide antibiotic balhimycin produced by *Amycolatopsis balhimycina*. *ChemBioChem*, *9*(8), 1195-1200. https://doi:10.1002/cbic.200800068

[8] Choudhury, S., Baksi, S., Bandyopadhyay, B., & Roy, D. (2023). Assessment of phytochemicals, antioxidant activity, and enzyme production of endophytic fungi isolated from medicinal plant sources. *Journal of Advanced Zoology*, *44*(1), 1-12. https://doi:10.17762/jaz.v44is6.2580

[9] Cook, A. E. (2003). Rapid identification of filamentous *Actinomycetes* to the genus level using genus-specific 16S rRNA gene restriction fragment patterns. *International Journal of Systematic and Evolutionary Microbiology*, *53*(6), 1907–1915. https://doi.org/10.1099/ijs.0.02680-0

[10] Dar, P. A., Ali, F., Sheikh, I. A., Ganie, S. A., & Dar, T. A. (2017). Amelioration of hyperglycaemia and modulation of antioxidant status by *Alcea rosea* seeds in alloxan-induced diabetic rats. *Pharmaceutical Biology*, *55*(10), 1849-1856. https://doi:10.1080/13880209.2017.1333127

[11] Genilloud, O. (2017). *Actinomycetes*: Still a source of novel antibiotics. *Natural Product Reports*, *34*(11), 1203-1215. https://doi.org/10.1039/C7NP00026J

[12] Gohain, A., Gogoi, A., Debnath, R., Yadav, A., Singh, B. P., Gupta, V. K., & Saikia, R. (2015). Antimicrobial biosynthetic potential and genetic diversity of endophytic *Actinomycetes* associated with medicinal plants. FEMS Microbiology Letters, 362(19), fnv158. https://doi.org/10.1093/femsle/fnv158

[13] Hajizadeh, M., Pourahmad, F., & Nemati, M. (2023). Isolation and Screening of Antibacterial Activity of Actinomycetota from the medicinal plant, *Anthemis pseudocotula* Boiss. Archives of Razi Institute, 78(5), 1638. https://doi.org/10.22092/ARI.2023.78.5.1638

[14] Hanh, T., Quang Huy Nguyen, My, T., Ngoc Tung Quach, Thi Nhan Khieu, Hoang, H., & Phi, Q.-T. (2020). Endophytic *Actinomycetes* associated with *Cinnamomum cassia* Presl in Hoa Binh province, Vietnam: Distribution, antimicrobial activity and, genetic features. *Journal of General and Applied Microbiology*, *66*(1), 24–31. https://doi.org/10.2323/jgam.2019.04.004

[15] Hanif, M., Mehmood, M. H., Ishrat, G., Virji, S. N., Malik, A., Ahmed, M., & Gilani, A. H. (2019). Pharmacological basis for the medicinal use of *Alcea rosea* in airways disorders and chemical characterization of its fixed oils through GC-MS. *Pakistan Journal of*

Pharmaceutical Sciences, *32*(5), 2347-2354. https://doi.org/10.31894065
[16] Hur, G., Jeon, J. H., Lee, J. (2012). Explorations of catalytic domains in non-ribosomal peptide synthetase enzymology. *Natural Product Reports*, *29*(9), 1074-1087. https://doi.org/10.1039/c2np20025b
[17] Izhar, S. K., Rizvi, S. F., Afaq, U., Fatima, F., & Siddiqui, S. (2024). Bioprospecting of metabolites from *Actinomycetes* and their applications. *Recent Patents on Biotechnology*, *18*(4), 273-287. https://doi:10.2174/0118722083269904231114154017
[18] Jagannathan, S. V., Manemann, E. M., Rowe, S. E., Callender, M. C., Soto, W. (2021). Marine *Actinomycetes*, new sources of biotechnological products. *Marine Drugs*, *19*(7), 365. https://doi.org/10.3390/md19070365
[19] Janso, J. E., & Carter, G. T. (2010). Biosynthetic Potential of Phylogenetically Unique Endophytic *Actinomycetes* from Tropical Plants. *Applied and Environmental Microbiology*, *76*(13), 4377–4386. https://doi.org/10.1128/aem.02959-09
[20] Javed, Z., Tripathi, G. D., Mishra, M., & Dashora, K. (2021). *Actinomycetes*—the microbial machinery for the organic-cycling, plant growth, and sustainable soil health. *Biocatalysis and Agricultural Biotechnology*, *31*, 101893. https://doi.org/10.1016/j.bcab.2020.101893
[21] Jensen, P. R., Dwight, R. Y. A. N., Fenical, W. I. L. L. I. A. M. (1991). Distribution of *Actinomycetes* in near-shore tropical marine sediments. *Applied and Environmental Microbiology*, *57*(4), 1102-1108. https://doi.org/10.1128/aem.57.4.1102-1108.1991
[22] José, P. A., & Jebakumar, S. R. D. (2014). Unexplored hypersaline habitats are sources of novel *Actinomycetes*. *Frontiers in Microbiology*, *5*, 242. https://doi:10.3389/fmicb.2014.00242
[23] Khan, S., Gul, A., Jehan, S., Khan, Z., Saeed, J., Shirazi, R. R., & Ullah, H. (2023). Biodiversity of *Actinomycetes* and their secondary metabolites: A comprehensive review. *Journal of Advanced Biomedical and Pharmaceutical Sciences*, *6*, 36-50. https://doi:10.21608/jabps.2022.161607.1165
[24] Khan, M., Shah, S. H., Hayat, F., & Akbar, S. (2023). Endophytic microbial community and its potential applications: A review. *BioScientific Review*, 5, 82. https://doi:10.32350/bsr.53.08https:
[25] Kim, J. H., Lee, N., Hwang, S., Kim, W., Lee, Y., Cho, S., & Cho, B. K. (2021). Discovery of novel secondary metabolites encoded in actinomycete genomes through coculture. *Journal of Industrial Microbiology and Biotechnology*, *48*(1), 1-11. https://doi:10.1093/jimb/kuaa001
[26] Li, G., Kusari, S., Lamshöft, M., Schüffler, A., Laatsch, H., Spiteller, M. (2014). Antibacterial secondary metabolites from an endophytic fungus, *Eupenicillium sp.* LG41. *Journal of Natural Products*, *77*(10), 2335. https://doi.org/10.1021/np500111w
[27] Mazumdar, R., Dutta, P. P., Saikia, J., Borah, J. C., & Thakur, D. (2023). *Streptomyces* sp. strain PBR11, a forest-derived soil Actinomycetia with antimicrobial potential. Microbiology Spectrum, 11, e03489. https://doi.org/10.1128/spectrum.03489-22
[28] Meenakshi, S., Hiremath, J., Meenakshi, M. H., & Shivaveerakumar, S. (2024). *Actinomycetes*: Isolation, cultivation, and its active biomolecules. *Journal of Pure & Applied Microbiology*, *18*(1), 1-8. https://doi:10.22207/jpam.18.1.48
[29] Metsä-Ketelä, M., Salo, V., Halo, L., Hautala, A., Hakala, J., Mäntsälä, P., Ylihonko, K. (1999). An efficient approach for screening minimal PKS genes from *Streptomyces*. *FEMS Microbiology Letters*, *180*(1), 1-6. https://doi.org/10.1111/j.1574-6968.1999.tb08770.x
[30] Qin, S., Xing, K., Jiang, J. H., Xu, L. H., Li, W. J. (2011). Biodiversity, bioactive natural products and biotechnological potential of plant-associated endophytic actinobacteria. *Applied Microbiology and Biotechnology*, *89*(2), 457-472. https://doi.org/10.1007/s00253-010-2923-6
[31] Roy, S., Banerjee, D. (2015). Bioactive endophytic *Actinomycetes* of *Cinnamomum* sp.; isolation, identification, activity-guided purification, and process optimization of active metabolite. *American Journal of Microbiology*, *6*(4), 4-13. https://doi.org/10.3844/ajmsp.2015.4.13
[32] Stach, J. E., Maldonado, L. A., Ward, A. C., Goodfellow, M., Bull, A. T. (2003). New primers for the class Actinobacteria: Application to marine and terrestrial environments. *Environmental Microbiology*, *5*(9), 828-833. https://doi.org/10.1046/j.1462-2920.2003.00483.x
[33] Setiawati, S., & Yusan, R. T. (2022). *Actinomycetes* as a source of potential antimicrobial and antibiofilm agents. *Medical and Health Journal*, *1*(2), 117-125. https://doi:10.20884/1.mhj.2022.1.2.5831
[34] Shan, W., Zhou, Y., Liu, H., & Yu, X. (2018). Endophytic *Actinomycetes* from Tea Plants (*Camellia sinensis*): Isolation, Abundance, Antimicrobial, and Plant-Growth-Promoting Activities. *BioMed Research International*, *2018*, 1–12. https://doi.org/10.1155/2018/1470305
[35] Staniek, A., Woerdenbag, H. J., Kayser, O. (2008). Endophytes: Exploiting biodiversity for the improvement of natural product-based drug discovery. *Journal of Plant Interactions*, *3*, 75. https://doi.org/10.1080/17429140801886293
[36] Tavarideh, F., Pourahmad, F., Nemati, M. (2022). Diversity and antibacterial activity of endophytic bacteria associated with medicinal plant, *Scrophularia striata*. *Veterinary Research Forum*, *13*(4), 409-417. https://doi.org/10.30466/vrf.2021.529714.3174
[37] Van der Meij, A., Worsley, S. F., Hutchings, M. I., & van Wezel, G. P. (2017). Chemical ecology of antibiotic production by *Actinomycetes*. *FEMS Microbiology Reviews*, *41*(3), 392-404. https://doi:10.1093/femsre/fux005
[38] Wati, C., Dewi, R. S., & Subandiyah, S. (2023). Diversity of phyllosphere *Actinomycetes* in Liliaceae plants and their potential as growth inhibitors of *Alternaria porri*. *Biodiversitas*, *24*(1), 1-10. https://doi:10.13057/biodiv/d241003
[39] Zareii, B., Seyfi, T., Movahedi, R., Cheraghi, J., & Ebrahimi, S. (2014). Antibacterial effects of plant extracts of *Alcea digitata* L., *Satureja bachtiarica* L., and *Ferulago*

angulata L. *Journal of Babol University Of Medical Sciences*, *16*(1), 31-36. http://dx.doi.org/10.18869/acadpub.jbums.16.1.31

[40] Zhao, K., Penttinen, P., Guan, T., Xiao, J., Chen, Q., Xu, J., & Strobel, G. A. (2011). The diversity and antimicrobial activity of endophytic *Actinomycetes* isolated from medicinal plants in Panxi plateau, China. Current Microbiology, 62(2), 182. https://doi.org/10.1007/s00284-010-9685-3

[41] Zhao, J., Shan, T., Mou, Y., Zhou, L., & Zhao, K. (2011). Plant-derived bioactive compounds produced by endophytic fungi. *Mini Reviews in Medicinal Chemistry*, *11*(2), 159-171. https://doi:10.2174/138955711794519492

[42] Zhuang, L., & Zhang, H. (2021). Utilizing cross-species co-cultures for discovery of novel natural products. *Current Opinion in Biotechnology*, *69*, 252-259. https://doi.org/10.1016/j.copbio.2021.01.023

[43] Zobel, S., Boecker, S., Kulke, D., Heimbach, D., Meyer, V., Süssmuth, R. D. (2016). Reprogramming the biosynthesis of cyclodepsipeptide synthetases to obtain new enniatins and beauvericins. *ChemBioChem*, *17*(3), 283-290. https://doi.org/10.1002/cbic.201500649