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Review Article

Exploring Egyptian Ecosystems for Bioactive Actinomycetes: A Review of Diversity and Therapeutic Potential

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Abstract

The growing threat of antimicrobial resistance (AMR) has intensified the global search for novel bioactive compounds. Actinomycetes, particularly *Streptomyces* species, represent one of the most promising microbial groups due to their ability to produce diverse secondary metabolites with antibacterial, antifungal, and antiviral activities. This review highlights the diversity and therapeutic potential of Actinomycetes isolated from Egypt's distinct ecosystems, including soil, rhizosphere, marine, freshwater, desert, and other extreme habitats. Adaptation to these challenging environments has fostered the evolution of unique strains with remarkable biosynthetic capacities. Egyptian Actinomycetes have shown strong activity against multidrug-resistant pathogens such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Candida albicans*, and members of the Enterobacteriaceae family. Despite this promise, several challenges remain, including the difficulty of culturing rare strains, limited genomic insights, and scalability issues in drug production. Recent advances—such as genome mining, metagenomics, synthetic biology, and nanotechnology-based delivery systems—offer new opportunities for unlocking and harnessing their hidden biosynthetic potential. Beyond antimicrobials, compounds derived from Actinomycetes show applications in oncology, immunotherapy, and agriculture. To fully exploit Egypt's microbial biodiversity, interdisciplinary collaborations and sustainable bioprospecting approaches are essential. Expanding exploration into under-investigated Egyptian ecosystems may open new frontiers for the discovery of clinically relevant therapeutics.

Keywords: Green chemistry, multicomponent reactions, catalysis, nanoparticles, cosmetics, pharmaceutical Manufacturing.

Introduction

The term *actinomycetes* is derived from the Greek words *aktis* (meaning ray) and *mykes* (meaning fungus). This name highlights their filamentous, fungus-like structure, their ray-like appearance and their fungal-like morphology. Although they share structural similarities with fungi—such as forming branching filaments and spores—actinomycetes are distinct prokaryotic organisms and are classified within the kingdom Bacteria (Bhatti et al., 2017). Actinomycetes are a varied group of Gram-positive bacteria classified under the order Actinomycetales within the phylum Actinobacteria. They are distinguished by their filamentous growth and high guanine-cytosine (G+C) content in their DNA. They form complex mycelium-like structures and produce spores, features that contribute to their ecological success and industrial relevance. Despite their morphological resemblance to fungi, actinomycetes differ significantly in genomic organization and taxonomic classification. Advances in molecular and cultivation Advancements in techniques have facilitated the identification of numerous actinomycete genera across diverse environments, including soil, marine and freshwater ecosystems, as well as extreme habitats like deserts and polar regions. (Dede et al., 2020; Ibrahim et al., 2023). These bacteria thrive under diverse physicochemical conditions, varying in temperature, pH, salinity, and moisture—which has driven their remarkable metabolic adaptability. As a result, actinomycetes have attracted significant attention in agriculture, ecology, biotechnology, and especially medicine (Nouioui et al., 2024). Actinomycetes are among the most prolific producers. Actinomycetes are prolific producers of bioactive secondary metabolites, such as antibiotics, anticancer compounds, immunosuppressants, antifungals, and a range of industrial enzymes. Out of approximately 23,000

known secondary metabolites, more than 10,000 have been derived from actinomycetes, highlighting their critical role in pharmaceutical innovation. Remarkably, nearly two-thirds of all clinically important antibiotics originate from this group derived from actinomycetes, primarily from the *Streptomyces* genus. Additionally, "rare actinomycetes," such as those belonging to *Micromonosporaceae*, *Pseudonocardiaceae*, and *Thermomonosporaceae*, account for a growing share of novel bioactive compounds (Takahashi & Nakashima, 2018; Nouioui et al., 2024; Ibrahim et al., 2023).Although actinomycetes have attracted widespread global attention, the microbial diversity within certain geographical regions—especially those with rich and varied ecosystems—remains insufficiently studied. Egypt, in particular, presents a remarkable range of environmental settings, including deserts, oases, coastal areas along the Mediterranean and Red Seas, freshwater bodies like rivers and lakes, and expansive agricultural lands. These diverse ecological zones provide fertile ground for microbial diversity and hold significant potential for the discovery of novel actinomycete strains. As such, Egypt stands out as a valuable source of unexplored bioactive microbial resources (Elsayed et al., 2020; El-Ramady & Abdalla, 2021).

Given their exceptional biosynthetic potential and broad ecological distribution, actinomycetes continue to play a vital role in drug discovery and innovation. This review highlights the recent findings on bioactive metabolites produced by actinomycetes isolated from various Egyptian ecosystems, with a focus on studies published over the past five years.

Actinomycetes Across Ecosystems

Actinomycetes are prevalent in diverse natural ecosystems, including soil, rhizosphere soil, freshwater, marine environments, sponges, animal feces, plants, deserts, and insect intestines (Anavadiya et al., 2024). Although the majority of actinomycetes are saprophytic bacteria inhabiting freely in soil and water, many isolates establish symbiotic relationships with host organisms, including fungi, plants, insects, and animals. These interactions are predominately mutualistic or commensal; however, they may occasionally be parasitic. Symbiotic actinomycetes, including *Micromonospora* and *Frankia*, form endophytic relationships with plants, facilitating nitrogen fixation in return for nutrients supplied by the host (Praptiwi et al., 2023; Anavadiya et al., 2024; Diarra et al., 2024). Members of Actinobacteria inhabit diverse ecological enviroments, that includes terrestrial and aquatic ecosystems (e.g., *Streptomyces*, *Micromonospora, Rhodococcus, Salinispora*), animal and plant pathogens (e.g., *Corynebacterium, Nocardia, Mycobacterium*), along with gastrointestinal commensals (e.g., *Bifidobacterium spp*.) (Barka et al., 2016). Actinomycetes can be categorized as extremophiles, organisms capable of enduring and reproducing in extreme environmental circumstances, such as low or high temperatures, extreme pH levels, high salinity, pressure, and desert environments. Some Actinomycetes have been isolated from distinct extreme environments, such as Antarctic areas and desert soils, exhibiting exceptional adaptation to severe physicochemical conditions. Their adaptability to harsh settings is due to unique survival strategies and physiological characteristics (Silva et al., 2020; Hui et al., 2021). This remarkable ecological and physiological diversity is strongly linked to their metabolic versatility, enabling the production of structurally diverse and biologically potent secondary metabolites. As a result, actinomycetes are of considerable biotechnological and pharmacological significance owing to their capacity to synthesize a variety of bioactive metabolites with antibacterial, antifungal, anticancer, and other therapeutic attributes (Hui et al., 2021; Saez et al., 2025).

Terrestrial Actinomycetes

Soil Actinomycetes

Actinomycetes are among the most widespread microorganisms in soil, forming thread-like filaments that contribute to the characteristic "earthy" aroma of freshly turned, healthy soil. As aerobic organisms, their abundance decreases with increasing soil depth, with the highest concentrations typically found in the topsoil layer (Bhatti et al., 2017; Javed et al., 2020).

Within soil-dwelling actinomycetes, the *Streptomyces* genus is the most prevalent and has been widely utilized for various applications (Nazari et al., 2022). The diversity and bioactivity of soil actinomycetes are shaped by a range of environmental factors, including geographical location and key abiotic elements such as soil temperature, type, depth, pH, organic matter content, farming practices, aeration, and moisture levels. Consequently, it is essential to document both the soil type and atmospheric conditions at the time of sample collection (Qaddoumi et al., 2018).

Rhizosphere soil

Actinobacteria, commonly found in the rhizosphere, are crucial for plant growth, improving nutrient

availability, synthesizing growth regulators, and suppressing phytopathogens. Their interactions with plants positively influence soil fertility, inhibit soil-borne pathogens, and overall plant health. Actinobacteria responsible for plant growth promotion, and the biocontrol of phytopathogens This symbiotic interaction promotes sustainable agriculture and reduces the use of chemical fertilizers and pesticides. Rhizospheric actinomycetes are a good source of lytic enzymes, antibiotics, and bioactive metabolites, producing various bioactive compound (Bhatti et al., 2017; Mitraet al., 2022). In addition to their agricultural benefits, rhizospheric Actinomycete produce several bioactive secondary metabolites with antibacterial, antifungal, and antiviral properties (Elshafie & Camele, 2022).

Aquatic Actinomycetes

Marine

Oceans cover more 70% of the Earth's surface with a great biological of life than in the terrestrial environment. Geographically, the coastal area of the sea represents only 7-8% and the remaining is for the deep sea. The nature of the marine environment particularly, the deep sea extremely differs from the terrestrial environment. The deep sea has high pressure, low temperature, darkness, and inconstant salt and oxygen concentrations. With such extreme conditions, marine Actinobacteria is expected to possess unique features and consequently secrete different and Marine environments, with their diverse and largely unexplored microbial communities, are a rich source of actinomycetes that often produce novel bioactive compounds not typically found in their terrestrial counterparts. These marine actinomycetes have evolved unique secondary metabolites to adapt and survive in their specialized habitats. New and rare species—including previously unidentified genera and families, have been isolated from a wide range of marine settings, such as coastal, tidal, and deep-sea sediments, marine organisms (e.g., sponges, corals, and ascidians), seawater, and mangrove ecosystems. By 2010, around 220 rare actinomycete species had been identified from marine sources (Subramani & Sipkema, 2019). In addition, marine actinobacteria have been recovered from both swimming and sessile marine vertebrates and invertebrates.

Several genera belong to different families such as Micrococceae, Dermatophilaceae and Gordoniaceae, were found to be associated with sponges. The actinobacterium Nocardiopsis dassonvillei was isolated from ovaries of the puffer fish. Although the existence of indigenous actinobacteria in the marine environs still elusive, culture-dependent studies revealed several marine indigenous actinobacterial genera. These include *Dietzia, Rhodococcus, Streptomyces, Salinispora, Marinophilus, Salinibacterium, Aeromicrobium marinum, Verrucosispora, Actinomadura, Actinosynnema, Arthrobacter, Blastococcus, Brachybacterium, Frankia, Geodermatophilus, Gordonia, Kitasatospora, Micromonospora, Micrococcus, Microbacterium*, *Nocardioides, Nocardiopsis, Psuedonocardia, Rhodococcus, Saccharopolyspora, Serinicoccus, Solwaraspora,, Streptosporangium, Tsukamurella, Turicella*.

Marine actinobacteria produce enormous numbers of bioactive compounds with a wide array of applications in agricultural, industrial, biotechnology and medical fields Actinobacteria have long been considered the prolific producers of a wide array of secondary metabolites with potential activities against viruses, fungi, bacteria, malaria, parasites and cancers. Thousands of bioactive compounds were produced by several actinobacterial genera such as *Streptomyces*, *Actinomyces*, *Corynebacterium, Micrococcus, Micromonospora*. Among members of the actinobacteria, more than 500 species of the genus *Streptomyces* responsible for about 80% of the total actinobacterial secondary metabolites with numerous biological activities (Shuikan et al., 2025)

Freshwater

Actinobacteria from freshwater habitats have received comparatively less attention than those from other environments in the search for pharmaceutically valuable compounds. However, studies have shown that freshwater sediments from rivers and lakes harbor abundant actinobacterial populations. These isolates have demonstrated promising potential for producing antimicrobial bioactive compounds. The association of actinobacteria with freshwater sediments highlights their capacity as a valuable source for novel secondary metabolites with potential therapeutic applications (Zothanpuia et al., 2018).

Extremophilic environments

desert

Deserts, though often overlooked, represent a unique and extreme ecosystem that supports a wide range of actinobacteria with promising biotechnological applications. The growing concern over multidrug-resistant pathogens and environmental challenges has intensified interest in discovering

functional actinobacteria from such habitats. Between 2000 and 2021, researchers identified 129 new species from 35 different deserts around the globe. The majority of these belonged to the genera *Streptomyces* and *Geodermatophilus*, alongside other extremophilic strains such as thermophiles, alkaliphiles, halotolerant, and psychrotolerant species. To tap into the full potential of desert actinobacteria, it is essential to enhance isolation techniques that recover both culturable and previously unculturable strains, which also aids in understanding how these microbes adapt to harsh environmental conditions. The primary bioprospecting workflow includes isolating actinobacteria using selective media, incubating them under suitable conditions, and selecting key strains for further study. Many of the compounds derived from desert actinobacteria are currently being investigated for their potential in biotechnology, particularly in the field of medicine. So far, over 50 novel compounds have been discovered, exhibiting a broad spectrum of biological activities, such as antimicrobial effects against MDR pathogens, as well as anti-inflammatory, antiviral, antifungal, antitumor, antibacterial, antiallergic, and cytotoxic properties (Xie & Pathom-Aree, 2021).

Caves

Caves are distinctive geological structures marked by hollow rock chambers, complete darkness, consistently low temperatures, limited nutrient availability, and high humidity. These factors contribute to the formation of an oligotrophic ecosystem, often containing less than 2 mg/L of total organic carbon. The harsh and competitive nature of such environments drives microbial inhabitants to enhance their metabolic capabilities, particularly in the production of diverse bioactive secondary metabolites (Girma et al., 2025).

Among the microbial communities inhabiting caves, actinomycetes are one of the most prevalent and functionally significant groups. In recent years, these microorganisms have drawn increasing attention due to their ability to generate novel compounds with antimicrobial, antioxidant, and anticancer effects. Extensive efforts have been made to isolate actinomycetes from culturable cave samples, resulting in the identification of new species with notable biological potential. Genera such as *Streptomyces*, *Micromonospora*, and *Nocardiopsis* are frequently reported, with *Streptomyces* being the most studied due to its widespread presence, resilience, and versatile metabolism.

Despite their evident importance, knowledge about the distribution, ecological function, and metabolic pathways of cave actinomycetes remains limited. Deeper investigations are needed to uncover their roles in cave ecosystems and their broader biotechnological applications. Depending on the environmental conditions and type of cave, actinomycetes may comprise between 2% and 93% of the total microbial community. While *Streptomyces* generally dominates, other genera such as *Microbacterium*, *Micrococcus*, *Nocardioides*, *Agromyces*, *Rhodococcus*, and *Saccharothrix* are also present, with their abundance influenced by cave-specific stressors and ecological factors (Farda et al., 2022).

Endophytic actinomycetes

Endophytic actinomycetes are a group of microorganisms that inhabit the internal tissues of healthy plants without causing them harm. These microbes have been identified in various plant types, including agricultural crops, medicinal herbs, halophytes, and certain tree species. Notably, the diversity of actinomycetes found in medicinal plants and their potential for biotechnological use has become a key area of interest in recent research. Growing studies suggest that these endophytic actinomycetes, particularly those associated with medicinal plants, are a valuable source of new bioactive compounds with antimicrobial, antiviral, anticancer, and anti-inflammatory potential (Shan et al., 2018).

Microbial Metabolite Potential of Actinomycetes

Actinomycetes are widely recognized as one of the most important microbial producers of antibiotics and other bioactive secondary metabolites. They are estimated to contribute around 55% of all known antibiotics, with the majority, approximately 75% originating from the genus *Streptomyces*. The remaining 25% are produced by non-*Streptomyces* actinomycetes. In addition to antibiotics, these organisms are credited with producing about 70% of all microbial secondary metabolites, including compounds with antimicrobial, antifungal, anticancer, and immunomodulatory properties. For comparison, fungi account for roughly 20% of such metabolites, *Bacillus* species about 7%, and other bacterial genera contribute just 1–2% (Ngamcharungchit et al., 2023).

Beyond their antimicrobial significance, actinomycetes are particularly valued for their contributions to cancer research. They synthesize a wide variety of structurally diverse antitumor compounds—such as polyketides, non-ribosomal peptides, alkaloids, and terpenoids—that act through mechanisms

like triggering apoptosis, halting cell proliferation, disrupting the tumor microenvironment, and targeting oncogenic signaling pathways. These metabolites have positioned actinomycetes as a vital resource in the search for new anticancer drugs, offering promising avenues for the development of natural product-based therapies and supporting innovation in cancer treatment (Rui et al., 2025).

Biological Activity of Secondary Metabolites from Actinomycetes and Their Applications

Unique Egyptian contributions to Biological Activity of Secondary Metabolites from Actinomycetes

In one of the few in-depth metabolomic studies from Egypt, *Amycolatopsis keratiniphila* DPA04 was isolated from agricultural soil using selective media and contaminant suppression. The strain's cultivation under different conditions (ISP-2, M1) led to the detection of 45 distinct metabolites (across multiple chemical classes), including the bioactive compound ECO-0501, with minimum inhibitory concentrations against Gram-positive bacteria in the range of ~19.5–39 μg/mL (Hamed et al., 2023). This case highlights how Egyptian actinomycetes, when carefully cultivated and screened, can yield a rich chemical repertoire.

When compared with reports from other regions, *A. keratiniphila* DPA04 stands out in its breadth of metabolite yield. For instance, in India, soil-derived actinobacteria often yield fewer metabolites per strain, and many studies focus on more common *Streptomyces* isolates with more limited chemical diversity (Sharma & Thakur, 2020). In China and Saudi Arabia, actinomycete surveys frequently report novel strains from extreme or marine settings, but often describe two or a few bioactive metabolites rather than dozens per isolate; under harsh or oligotrophic environments, limited metabolite yields may reflect regulatory or cultivation constraints (Helmi, 2025). Thus, the Egyptian isolate's high metabolite count underscores the potential of Egypt's ecosystems and suggests that underexplored soils may harbor strains with unusually rich biosynthetic capabilities (Osama et al., 2022).

Antibacterial Agents

Antibiotic resistance has become a critical threat to global health, as reported by the World Health Organization (WHO), with an estimated 700,000 deaths each year attributed to drug-resistant infections. Among these, multidrug-resistant tuberculosis is responsible for around 230,000 deaths. Infections affecting the respiratory and urinary tracts, as well as sexually transmitted infections, are increasingly difficult to treat. Alarmingly, lower respiratory tract infections remain the leading cause of death among communicable diseases, particularly in low-income regions.

This crisis has been driven by several factors, including the overuse and misuse of antibiotics in both medical and agricultural settings. In response, global health organizations such as the WHO and the Centers for Disease Control and Prevention (CDC) have introduced strategic initiatives aimed at enhancing diagnostic methods, refining therapeutic practices, and enforcing preventive policies to slow the spread of resistance. A growing concern is the over-prescription of antibiotics in clinical environments, which not only accelerates resistance in harmful bacteria but can also lead to resistance in benign, commensal microbes. Once these resistant strains enter the broader environment, They pose a heightened risk to vulnerable populations and act as reservoirs for transferring resistance genes to pathogenic bacteria.

Given this context, the diverse range of antibiotic compounds produced by actinomycetes represents a valuable resource in the fight against antibiotic resistance. These bacteria are capable of synthesizing numerous classes of antibiotics, including aminoglycosides, peptides, ansamycins, β-lactams, tetracyclines, macrolides, lincosamides, epoxides, and aminocoumarins. Their biosynthetic versatility makes them key contributors to the discovery of novel antimicrobial agents (De Simeis & Serra, 2021).

On a global scale, actinomycetes have demonstrated promising antibacterial activity. For instance, biosurfactants produced by actinomycetes isolated from the rhizosphere of the Sidoarjo mud region in Indonesia showed inhibitory effects against *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 6538P (Arifiyanto et al., 2020). Similarly, in India, five *Streptomyces* isolates (IMA13, IMA25, IMA43, IMA46, and IMA47) exhibited antibacterial activity against *E. coli*, *S. aureus*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* (Dar & Ahmad, 2024).

As summarized in **Table 1**, the majority of antibacterial compounds were derived from crude extracts and identified metabolites of *Streptomyces* species. However, some of effective compounds were also isolated from rare actinomycetes, including *Amycolatopsis* and *Micromonospora*, recovered from various Egyptian ecosystems—further highlighting the potential of underexplored environments in

antimicrobial discovery.

Specimen type	Isolation site/ Study area	Isolated strains	Actinomycetes Isolation (*Serial dilution on selective media)*	Bioactive/chemical compound(s)	Tested microorganism	Reference
			Soil			
Agricultural soil	Giza (Agricultural Experiment and Research Station of Cairo University)	Amycolatopsis keratiniphila	starch-nitrate agar	ECO-0501, AK_1 and N-demethyl ECO-0501	Escherichia coli O157:H7, Methicillin-resistant Staphylococcus aureus strain ATCC 43300, Staphylococcus aureus strain ATCC 6538P, Salmonella Typhimurium strain ATCC 14028, Listeria monocytogenes strain ATCC 19115, Bacillus cereus strain ATCC 33018 and Pseudomonas aeruginosa strain ATCC 9027	(Hamed et al., 2023)
Agricultural soil	Beni-Suef (Sherif-Pasha village)	*Streptomyces* sp. SH4, SH8, SH10 and SH13	starch casein agar	Tetracycline, Oxytetracycline and A macrolide antibiotic (novamethymycin).	Staphylococcus aureus (ATCC 43300), Listeria monocytogenes (ATCC 7644), Bacillus subtilis (environmental sample), Escherichia coli (clinical isolate) and Salmonella enterica (ATCC 14028)	(Osama et al., 2022)
Agricultural soil	El-Menoufia	*Streptomyces* enissocaesilis BS1	starch nitrate agar	silver-nanoparticles (Ag-NPs) of cell-filtrate	Staphylococcus aureus ATCC 6598, Pseudomonas aeruginosa ATCC 9027, Salmonella Typhi ATCC 12023 and Escherichia coli ATCC 8739	(Shaaban et al., 2024)
Agricultural soil	Suez	*Streptomyces* SUN1	starch casein broth	tributyl acetyl citrate, 1,4-benzenedicarboxylic acid, bis(2-ethylhexyl) ester, bis(2-ethylhexyl) phthalate and butyl citrate	Methicillin-resistant Staphylococcus aureus, Staphylococcus aureus and Pseudomonas aeruginosa	(Awad et al., 2023)
soil	Aswan (Wadi Allaqui Biosphere Reserve, eastern side of Lake Nasser)	*Streptomyces* djakartensis NSS-3	starch casein agar	pyomelanin	Pseudomonas aeruginosa (PA-09), Escherichia coli (EC-03), Klebsiella pneumoniae (KP-01) and Staphylococcus aureus (SA-04)	(El-Zawawy et al., 2024)
soil	Minufyia(Menuf)	*Streptomyces* roseolus	Glucose Yeast Malt Agar	silver-nanoparticles (Ag-NPs) of cell-filtrate	Bacillus cereus (ATCC 14579), Bacillus subtilis (ATCC 6633), Listeria monocytogenes (ATCC 19116), Staphylococcus aureus (ATCC 6538), Escherichia coli O157:H7, Klebsiella pneumoniae and Aeromonas hydrophila	(Elnady et al., 2022)

soil	Mansoura	*Streptomyces* sp. ASM19	starch nitrate agar	gold nanoparticles (Ac-AuNPs) of cell-filtrate	Staphylococcus aureus ATCC 25923, Escherichia coli ATCC 8739 and Bacillus cereus ATCC 10876	(Aati et al., 2025)
superficial soil layer	Beni-Suef (Ihnasia City)	*Streptomyces* sp. MS. 10	International Streptomyces Project (ISP) 4 agar	crude extract	Sarcina lutea (environmental sample), Bacillus subtilis (environmental sample), Enterococcus faecalis (food sample), Salmonella enterica ATCC 35664, Pseudomonas aeruginosa ATCC 9027, Proteus sp. (clinical sample), Escherichia coli (clinical sample) and Methicillin-resistant Staphylococcus aureus (MRSA) (clinical sample)	(Sebak et al., 2021)
			Rhizosphere Soil			
Wild desert valley soil (olive and Banat vineyard)	Marsa Matrouh (Al Najila, Matrouh and Ras El-Hikma)	*Streptomyces* sp. AMM1	starch nitrate agar	crude extract	Staphylococcus aureus ATCC 6538, Bacillus subtilis ATCC 6633, Pseudomonas aeruginosa ATCC 9027 and Escherichia coli ATCC 7839	(Bast et al., 2024)
Agricultural soil (Trifolium, Solanum lycopersicum, and Pelargonium graveolens)	Eastern Province and Nile Delta	Actinomycetes-6,7 and 8	starch-nitrate agar	2,4-Di-tert-butylphenol, 3-Chloropropionic acid, heptadecyl ester, 1,2-Benzenedicarboxylic acid, 3-nitro, Benzenepropanoic acid, 3,5-bis(1,1-dimethylethyl)-4-hydroxy-, octadecyl ester, 1-Monopalmitin, 2TMS derivative, 1-Docosene, 1-Nonadecene and 1-Nonacosene	Escherichia coli O157 (ATCC 9311) and Bacillus cereus (ATCC 33018)	(Elsayed et al., 2020)
rhizosphere clay soil	Sharkia	*Streptomyces misakiensis* and *Streptomyces coeruleorubidus*	starch-nitrate agar	ursolic acid methyl ester	Staphylococcus aureus, Listeria monocytogenes, Bacillus cereus ATCC 36621, Streptococcus equi, Streptococcus pyogenes, Streptococcus agalactiae, Escherichia coli, Pseudomonas aeruginosa, Salmonella enterica, Klebsiella pneumoniae, Aeromonas hydrophila and Flavobacterium columnare	(Abdelaziz et al., 2023)
rhizosphere soil(rice, wheat, and flowers)	Not specified	Phage-resistant Streptomyces abietis	starch casein nitrate agar	telomycin	Listeria monocytogenes ATCC 35152, Escherichia coli O157 ATCC 43895,	(Abdelaziz et al., 2024)

					Acinetobacter baumannii ATCC 17978, Micrococcus luteus ATCC 9341 and Methicillin-resistant vancomycin-intermediate Staphylococcus aureus (MRSA-VISA) strain No. P59	
			Marine			
Marine sponges (Coscinoderma mathewsi)	The Red Sea (North of Hurghada)	Micromonospora sp. UA17, Gordonia sp. UA19 and Nocardia sp. UA 23	M1, ISP2, and Marine Agar	crude extract of co-cultivation	Staphylococcus aureus NCTC 8325, Enterococcus faecalis, Escherichia coli and Pseudomonas aeruginosa	(Shamikh et al., 2020)
Marine sponges (Sarcophyton convolutum)	The Red Sea (Makadi bay, Saphaga)	*Streptomyces* sp.MORSY 17 and MORSY 22	ISP2 medium	crude extract	Escherichia coli (ATCC 9637), Pseudomonas aeruginosa (ATCC 15442), Klebsiella pneumoniae (ATCC 13883), Proteus vulgaris (ATCC 8427), Staphylococcus aureus (ATCC 43300), Bacillus cereus (ATCC 12826) and Streptococcus pyogenes (ATCC 19615)	(El-Gendy et al., 2021)
marine sediment	The Red Sea	Actinomyces sp. AW6	starch nitrate agar with 50% salt water	C1: umbelliferone, and C2: 1-methoxy-3-methyl-8-hydroxy-anthraquinone.	Bacillus subtilis (ATCC66), Staphylococcus aureus (ATCC6538-P), Methicillin-resistant Staphylococcus aureus (MRSA) (ATCC25923), Escherichia coli (ATCC14169), Pseudomonas aeruginosa (ATCC 27853), Klebsiella pneumoniae, Salmonella typhi and Salmonella enterica	(Agour et al., 2022)
marine sediment	The Red Sea (Hurghada)	*Streptomyces parvulus* MAR4	starch nitrate agar medium with 50% salt water	selenium/chitosan-Nanoconjugate of cell-filtrate	Salmonella typhi ATCC-9992, Proteus vulgaris ATTC7829, Escherichia coli ATCC25955 and Staphylococcus aureus NRRL B-767	(Hassan et al., 2024)
marine water	The Red Sea (Hurghada)	*Streptomyces sp*. SMGL39	starch-casein agar	iron oxide nanoparticles (FeNPs) of cell-filtrate	Escherichia coli (ATCC 8739), Pseudomonas aeruginosa (ATCC 90902), Methicillin-resistant Staphylococcus aureus and Listeria monocytogenes (ATCC 7644)	(Attea et al., 2024)
Marine soft coral (Dendronephthya hemprichi)	The Red Sea (Hurghada)	*Streptomyces sp*. ALAA-R20	starch casein agar	undecylprodigiosin	methicillin-resistant Staphylococcus aureus and multidrug-resistant Pseudomonas sp.	(Alzahrani et al., 2021)
marine sediments	The Mediterranean Sea,	*Streptomyces tunisiensis* W4	starch casein agar with sea water	MT573222 pigment	Staphylococcus aureus (ATCC 25923), Escherichia coli (ATCC	(Ibrahim et al., 2023)

	Alexandria(Abu -Qir coast)				19404), Vibrio fluvialis, Vibrio damsela, Enterococcus faecalis (ATCC 29212), Pseudomonas aeruginosa (ATCC 9027), Bacillus cereus, Bacillus subtilis (ATCC 6633) and Escherichia coli (ATCC 8739)	
marine invertebrate (Molgula citrine)	The Red Sea	*Streptomyces albidoflavus* VIP-1	Reasoner's 2A agar (R2A) with 2% NaCl	polyketides, terpenes and non-ribosomal peptides	Escherichia coli ATCC 10536, Pseudomonas aeruginosa ATCC 25619 and Staphylococcus aureus ATCC 9144	(Sedeek et al., 2025)
marine sediment	The Red Sea (Marsa Allam)	*Streptomyces vinaceusdrappus* AMG31	starch nitrate broth	titanium dioxide nanoparticles (TiO_2-NPs) of cell-filtrate	Bacillus subtilis ATCC 6633, Staphylococcus aureus ATCC 6538, Enterococcus faecalis ATCC 29212, Escherichia coli ATCC 8739, Klebsiella pneumoniae ATCC 13883, Pseudomonas aeruginosa ATCC 90274 and Salmonella typhi ATCC 6539	(Ghareeb et al., 2025)
			Marine and Soil			
marine habitats (Ain Sokhna sediment, Ras Sedr sediment, and Hurghada sea water) and soil habitats (Mansoura)	The Red Sea and Dakahlia	*Streptomyces* sp. 22SH	starch nitrate agar	cis-9-Octadecenoic acid	Staphylococcus aureus ATCC 6538-P, Bacillus subtilis ATCC 6633, Pseudomonas aeruginosa ATCC 27853, Escherichia coli ATCC 25955 and Escherichia coli ATCC 14169	(Hassan et al., 2025)
marine water, sediment and plants	The Red Sea (Hurghada), (Sharm El Sheikh) and The Mediterranean Sea (Alexandria), (Marina)	*Streptomyces* sp. and *Brevibacterium* sp.	Starch Casein Agar, Kuster's agar and ISP-2 agar	3-Hydroxy-3-[(4-methoxyphenyl)methyl]-1,4-dimethyl-2,5-piperazine-dione, 3'-N-Formyl Fusarochromanone and Nb-(5-Methylhexanoyl) tryptamine	Listeria monocytogenes ATCC 7644, Methicillin-resistant Staphylococcus aureus (MRSA) ATCC 43300, Salmonella enterica ATCC 14028 and Escherichia coli (E. coli) ATCC 25922	(Abdel-Razik et al., 2025)
			Freshwater			
lake sediment	Alexandria (Lake Mariout "main basin")	*Streptomyces fulvissimus* EM1 and *Streptomyces mediolani* EM2	ISP2 agar	AgNPs Combined with Crude extract	Pseudomonas aeruginosa ATCC 15442, Escherichia coli ATCC 25922, Proteus vulgaris ATCC 8427, Klebsiella pneumoniae ATCC 700603, Salmonella Typhimurium ATCC 14028, Bacillus cereus ATCC 33019, Staphylococcus aureus ATCC 29213 and Enterococcus faecalis ATCC 29212	(Eltarahony et al., 2021)
lake sediment	Wadi El-Natron(El-Hamara Lake)	*Streptomyces thinghirensis* WAE1	starch nitrate agar	crude extract	Listeria monocytogenes (ATCC 19116), Escherichia coli (ATCC 25922), Clostridium	(Osman et al., 2024)

					sporogenes (ATCC 3584), Staphylococcus aureus (ATCC 29213), Salmonella enterica (ATCC 25566), Cronobacter sakazakii (ATCC 29544), Pseudomonas aeruginosa (ATCC 27853), Klebsiella pneumoniae (ATCC 27736) and Streptococcus pneumoniae (ATCC 49619)	
Extremophilic Environment						
Desert soil & Rhizosphere of medicinal plant (Zilla spinosa and Zygophyllum album)	Beni-Suef (Eastern Desert)	Micromonospora sp. ISP-2 27	ISP-2 agar	CuO NPs/Zn–Al LDH nanoparticle of cell filterate	Methicillin-resistant Staphylococcus aureus strain ATCC 43300, Listeria monocytogenes strain ATCC 7644, Salmonella Typhimurium strain ATCC 14028 and Pseudomonas aeruginosa strain ATCC 9027	(Eweis et al., 2024)
groundwater , ancient stones , desert rocks , medicinal plants, and industrial wastewater	Not specified	Micromonospora sp1	Starch Casein broth	crude extract	Escherichia coli NCMB 11943 and Staphylococcus aureus NCMB 6571	(Nafie et al., 2021)
cave soil	Beni-Suef	Actinobacteria Am 43, Am 90, Am 139, Am 152, and Am 183	yeast extract/malt extract (ISP2) and MM media	crude extract	Bacillus subtilis ATCC 6633, Bacillus cereus ATCC 10876, Staphylococcus aureus ATCC 6538, Escherichia coli ATCC 25922, Klebsiella pneumoniae ATCC 10031, Pseudomonas aeruginosa ATCC 25668 and Salmonella typhi ATCC 9992	(Abdel-Fattah et al., 2024)
desert soil	Sinai Desert Saint Catherine City	*Streptomyces* sp. DH7	mineral salt medium, basal medium, and starch casein medium	Actinomycin D analogs (Compounds 1–4)	Staphylococcus aureus ATCC 6538 and Multidrug-resistant S. aureus (clinical isolates)	(Amin et al., 2021)

Table 1. Diversity and different antibacterial activities of actinomycetes isolated from various environments in Egypt

Antifungal Agents

Polyenes represent a group of broad-spectrum antifungal compounds primarily produced by *Streptomyces* species. One of the earliest discoveries in this category was nystatin, isolated in 1950 from the fermentation broth of *Streptomyces noursei*, which remains in clinical use today as a topical treatment for fungal infections. Shortly thereafter, several other polyene antifungals, such as fracidin, rimocidin, endomycin, ascosin, trichomycin, and antimycoin were identified during the early 1950s. In 1955, *Streptomyces nodosus* was reported as the source of amphotericin A and B, with the latter recognized for its significant role in treating systemic mycoses (Denning & Hope, 2010).

More recently, novel antifungal metabolites have been identified through analysis of crude extracts from various *Streptomyces* strains. Additionally, rare actinomycetes—such as those from the genera *Amycolatopsis* and *Micromonospora*—isolated from diverse Egyptian habitats, have yielded

promising antifungal compounds (**Table 2**). Similar findings have been reported globally. For example, the actinomycete strain WA23-4-4, isolated from the gut of Periplaneta americana, exhibited potent antifungal activity against *Candida albicans* ATCC 10231 and *Aspergillus niger* ATCC 16404. (Fang et al., 2018).

Likewise, *Streptomyces felleus*, recovered from coal mine environments in India, has shown inhibitory effects against *Candida albicans* (Sarika et al., 2021), further highlighting the potential of actinomycetes as a rich source of antifungal agents.

Specimen type	Isolation site/ Study area	Isolated strains	Actinomycetes Isolation (Serial dilution on selective media)	Bioactive/chemical compound(s)	Tested microorganisms	Reference
Soil						
Agricultural soil	Beni-Suef (Sherif-Pasha village)	*Streptomyces* sp. SH4, SH10, SH13 and SH8	starch casein agar	Tetracycline, Oxytetracycline and A macrolide antibiotic (novamethymycin).	Candida albicans (ATCC 60193)	(Osama et al., 2022)
Agricultural soil	Suez	*Streptomyces* SUN1	starch casein broth	tributyl acetyl citrate, 1,4-benzenedicarboxylic acid, bis(2-ethylhexyl) ester, bis(2-ethylhexyl) phthalate and butyl citrate	Fusarium solani, Aspergillus fumigatus and Penicillium chrysogenum	(Awad et al., 2023)
Rhizosphere soil						
Wild desert valley soil (olive and Banat vineyard)	Marsa Matrouh (Al Najila, Matrouh and Ras El-Hikma)	*Streptomyces* sp. AMM1	starch nitrate agar	crude extract	Candida albicans ATCC 10231	(Bast et al., 2024)
rhizosphere clay soil	Sharkia	*Streptomyces misakiensis* and *Streptomyces coeruleorubidus*	starch-nitrate agar	tetradecamethyl cycloheptasiloxane	Candida albicans, Cryptococcus neoformans, Cryptococcus gattii, Aspergillus flavus, Aspergillus niger and Aspergillus fumigatus	(Abdelaziz et al., 2023)
Marine						
Marine sponges (Coscinoderma mathewsi)	The Red Sea(North of Hurghada)	*Micromonospora sp*. UA17, *Gordonia sp*. UA19 and Nocardia sp. UA 23	M1, ISP2, and Marine Agar	crude extract of co-cultivation	Candida albicans 5314 (ATCC 90028)	(Shamikh et al., 2020)
Marine sponges (Sarcophyton convolutum)	The Red Sea (Makadi bay, Saphaga)	*Streptomyces sp.* MORSY 17 and MORSY 22	ISP2 medium	crude extract	Aspergillus flavus (ATCC 9643), Candida albicans (ATCC 60193), Candida tropicalis (ATCC 1369), Microsporum canis (ATCC 36299), Trichophyton mentagrophytes (ATCC 9533), Trichophyton	(El-Gendy et al., 2021)

					rubrum (ATCC 28188) and Geotrichum candidum (ATCC 7115)	
marine sediment	The Red Sea	*Actinomyces sp.* AW6	starch nitrate agar with 50% salt water	C1: umbelliferone, and C2: 1-methoxy-3-methyl-8-hydroxy-anthraquinone.	Candida albicans (ATCC10231), Candida albicans (ATCC9080) and Aspergillus niger (NRRL A-326)	(Agour et al., 2022)
marine sediment	The Red Sea (Hurghada)	Streptomyces parvulus MAR4	starch nitrate agar medium with 50% salt water	selenium/chitosan-Nanoconjugate of cell-filtrate	Aspergillus flavus NRRLA326, Aspergillus niger AN512, Rhizoctonia sp. Cy064 and Candida albicans ATCC10231	(Hassan et al., 2024)
marine water	The Red Sea(Hurghada)	*Streptomyces* sp. SMGL39	starch-casein agar	iron oxide nanoparticles (FeNPs) of cell-filtrate	Fusarium oxysporium and Aspergillus niger	(Attea et al., 2024)
Marine soft coral (Dendronephthya hemprichi)	The Red Sea (Hurghada)	Streptomyces sp. ALAA-R20	starch casein agar	undecylprodigiosin	Trichophyton mentagrophytes, Trichophyton rubrum, Trichophyton vaoundei, Microsporum gypseum, Microsporum canis, Microsporum cookei and Epidermophyton floccosum	(Alzahrani et al., 2021)
marine sediments	The Mediterranean Sea, Alexandria (Abu-Qir coast)	*Streptomyces tunisiensis W*4	starch casein agar with sea water	MT573222 pigment	Rhizoctonia solani (ATCC 6599), Fusarium solani (ATCC 10557) and Candida albicans	(Ibrahim et al., 2023)
marine invertebrate (Molgula citrine)	The Red Sea	*Streptomyces albidoflavus VIP-1*	Reasoner's 2A agar (R2A) with 2% NaCl	polyketides, terpenes and non-ribosomal peptides	Candida albicans ATCC 90028	(Sedeek et al., 2025)
soft coral (Sarcophyton glaucum)	The Red Sea (Hurghada)	*Streptomyces sp. HC14*	ISP2 medium	pyrrolo[1,2-a] pyrazine-1,4-dione, hexahydro-3-(phenylmethyl) and di-n-octyl phthalate.	Candida albicans	(Abdella et al., 2023)
marine sediment	The Red Sea (Marsa Allam)	*Streptomyces vinaceusdrappus* AMG31	starch nitrate broth	titanium dioxide nanoparticles (TiO_2-NPs) of cell-filtrate	Aspergillus niger (AUMC 14260), Mucor circinelloides (AUMMC 11656), Trichoderma harzianum (AUMC 5408), Penicillium glabrum	(Ghareeb et al., 2025)

					(OP694171) (AUMC 15597) and Candida albicans (ATCC 10221)	
Freshwater						
lake sediment	Alexandria (Lake Mariout "main basin")	*Streptomyces fulvissimus EM1* and *Streptomyces mediolani EM2*	ISP2 agar	AgNPs Combined with Crude extract	Candida albicans ATCC 10231, Aspergillus brasiliensis ATCC 16404 and Alternaria species	(Eltarahony et al., 2021)
lake sediment	Wadi El-Natron (El-Hamara Lake)	Streptomyces thinghirensis WAE1	starch nitrate agar	crude extract	Candida albicans (ATCC 10231)	(Osman et al., 2024)
Extremophilic Environments						
Desert soil & Rhizosphere of medicinal plant (Zilla spinosa and Zygophyllum album)	Beni-Suef (Eastern Desert)	*Micromonospora sp*. ISP-2 27	ISP-2 agar	CuO NPs/Zn–Al LDH nanoparticle of cell filterate	Candida albicans strain ATCC 60913	(Eweis et al., 2024)
groundwater, ancient stones, desert rocks, medicinal plants, and industrial wastewater	Not specified	Micromonospora sp1	Starch Casein broth	crude extract	Candida albicans	(Nafie et al., 2021)
cave soil	Beni-Suef	Actinobacteria Am 43, Am 90, Am 139, Am 152, and Am 183	extract (ISP2), and MM media	crude extract	Candida albicans ATCC 90028 and Aspergillus niger ATCC 16404	(Abdel-Fattah et al., 2024)

Table 2. Diversity and different antifungal activities of actinomycetes isolated from various environments in Egypt

Antitumor Activity

Actinomycetes are gaining attention in cancer therapy because of their capacity to generate bioactive compounds that offer therapeutic benefits with fewer side effects than traditional chemotherapy. A notable example is salinosporamide A, which has shown considerable anticancer potential. One of the earliest and most significant contributions from this group is adriamycin (doxorubicin), originally derived from *Streptomyces peucetius*, which acts by disrupting DNA replication and is widely used as a chemotherapeutic agent.

Several other effective anticancer drugs have also been obtained from *Streptomyces* species and related actinomycetes, including mitomycin C, actinomycin D, bleomycin, daunorubicin, and members of the mitosane class. These compounds are biosynthesized by strains such as *Streptomyces verticillus*, *S. peucetius*, and *S. caespitosus*, among others.

In addition to terrestrial strains, marine-derived actinomycetes have become a valuable source of novel antitumor compounds. Compounds such as streptochlorin, aureoverticillactam, chalcomycin B, cyanosporasides, komodoquinones, nonactin, resistoflavine, sporolides, tetracenomycin D, thiocoraline, t-muurolol, butenolides, echinosporins, and streptokordin have all shown potential anticancer activity. Among these, secondary metabolites like lynamicins, marizomib, and thiocoraline are of particular interest for their strong cytotoxic effects on tumor cells (Alenaz et al., 2023).

Many of these molecules act through distinct mechanisms to inhibit tumor growth. For instance, actinomycin D—produced by *Streptomyces* species—is one of the earliest approved cancer drugs and works by intercalating into DNA and blocking RNA polymerase activity, thereby halting mRNA synthesis and protein production in rapidly dividing cells. Similarly, mitomycin C, synthesized by

Streptomyces caespitosus, is activated reductively in the cell to form mitosene, a compound that cross-links DNA strands, thereby preventing replication and transcription and ultimately leading to cell death. Other actinomycete-derived agents, such as avermectins, have also demonstrated significant antitumor properties through a variety of mechanisms (Rui et al., 2025b).

Further supporting the antitumor potential of actinomycetes, *Streptomyces* sp. SYP-A7185, isolated from rhizosphere soil, was reported by Xue et al. (2023) to produce angucycline/angucyclinone derivatives, specifically dehydroxyaquayamycin, which demonstrated significant cytotoxic activity against breast cancer cell lines. Similarly, Hu et al. (2020) identified an antitumor metabolite from *Streptomyces* sp. CPCC 204980, which showed promising inhibitory effects on colon cancer cells. These findings reinforce the diverse anticancer potential embedded within actinomycete metabolites, particularly those sourced from unique ecological niches.

Table 3 outlines the key antitumor compounds recently identified from secondary metabolites of actinomycetes, particularly those isolated from Egyptian environments. These discoveries offer promising leads for future drug development and clinical application in oncology.

Specimen type	Isolation site/ Study area	Isolated strains	Actinomycetes Isolation (*Serial dilution on selective media)*	Bioactive/ chemical compound(s)	cell line	Target Cancer	Reference
			Soil				
Agricultural soil	Beni-Suef (Sherif-Pasha village)	*Streptomyces sp*. SH4, SH8, SH10 and SH12	starch casein agar	Tetracycline, Oxytetracycline and A macrolide antibiotic (novamethymycin).	HepG2, MCF-7	liver cancer, breast cancer	(Osama et al., 2022)
Agricultural soil	El-Menoufia	*Streptomyces enissocaesilis BS1*	starch nitrate agar	silver-nanoparticles (Ag-NPs) of cell-filtrate	MCF-7, Caco-2	breast cancer, colon cancer	(Shaaban et al., 2024)
Soil	Aswan (Wadi Allaqui Biosphere Reserve, eastern side of Lake Nasser)	*Streptomyces djakartensis NSS-3*	starch casein agar	pyomelanin	HCT116, HEPG, MCF7	colorectal cancer, liver cancer and breast cancer	(El-Zawawy et al., 2024)
Soil	Mansoura	*Streptomyces sp. ASM19*	starch nitrate agar	gold nanoparticles (Ac-AuNPs) of cell-filtrate	SCC9, SCC25	squamous cell carcinoma	(Aati et al., 2025)
Soil	Not specified	*Streptomyces griseus KJ623766*	16S ribosomal RNA gene sequences	β- and γ Rhodomycinone	HeLa, Caco2	cervix cancer and colon cancer	(Zaid et al., 2021)
			Marine				
Marine sponges (Sarcophyton convolutum)	The Red Sea (Makadi bay, Saphaga)	*Streptomyces sp. MORSY 17* and *MORSY 22*	ISP2 medium	crude extract	HepG2, Caco-2	liver cancer, colon cancer	(El-Gendy et al., 2021)
marine sediment	The Red Sea (Hurghada)	*Streptomyces parvulus MAR4*	starch nitrate agar medium with 50% salt water	selenium/chitosan-Nanoconjugate of cell-filtrate	HepG2, Caki-1 (HTB-46)	liver cancer, renal cell carcinoma	(Hassan et al., 2024)
Marine soft coral (Dendronephthya hemprichi)	The Red Sea(Hurghada)	*Streptomyces sp. ALAA-R20*	starch casein agar	undecylprodigiosin	HCT-116, HepG2, A-549, MCF-7	colon cancer, liver cancer, lung cancer, breast cancer	(Alzahrani et al., 2021)
marine sediments	The Mediterranean Sea, Alexandria (Abu-Qir coast)	*Streptomyces tunisiensis W4*	starch casein agar with sea water	MT573222 pigment	HepG2, A549, PAN1	liver cancer, lung cancer, pancreas cancer	(Ibrahim et al., 2023)

marine water	The Mediterean Sea, (Western Harbour of Alexandria)	*Streptomyces albidoflavus strain EgyAB2*	Not specified	2-D N-methyl imidazole, 2-nonadecene, 1-D-2-methyl imidazole and propane dinitrile	MCF7	breast cancer	(Shata et al., 2025)
marine invertebrate (Molgula citrine)	The Red Sea	*Streptomyces albidoflavus VIP-1*	Reasoner's 2A agar (R2A) with 2% NaCl	polyketides, terpenes and non-ribosomal peptides	HepG2, A549	liver cancer, lung cancer	(Sedeek et al., 2025)
Marine sediment, marine sponge (Spheciospongia mastoidea) and sea-sand	The Red Sea, Ras Mohammed and The Mediterranean Sea (Marsa Matruh)	*Actinobacterial strains EGY1, EGY34, RA2 and EG25*	partial 16S rRNA and agar media	Sharkquinone, Resistomycin, Undecylprodigiosin, Butylcyclopentylprodigiosin, Elloxizanone A, Elloxizanone B, Carboxyexfoliazone and Exfoliazone	Jurkat, HCT116, MDA-MB-231	colorectal cancer and breast cancer	(Elmallah et al., 2020)
marine sponge (Spongia irregularis)	The Red Sea (Ras Mohammed)	*Rhodococcus sp. UR21, Streptomyces sp. UR32 and Micromonospora sp. UR44*	M1, ISP 2, oligotrophic medium 91 (OLIGO), and marine agar	crude extract	CACO-2, HepG2, MCF-7	colon cancer, liver cancer and breast cancer	(Abdelaleem et al., 2023)
marine sediment	The Red Sea(Marsa Allam)	*Streptomyces vinaceusdrappus AMG31*	starch nitrate broth	titanium dioxide nanoparticles (TiO_2-NPs) of cell-filtrate	Caco-2, PANC-1	colon cancer and pancreas cancer	(Ghareeb et al., 2025)
			Marine and Soil				
marine habitats (Ain Sokhna sediment, Ras Sedr sediment, and Hurghada sea water) and soil habitats (Mansoura)	The Red Sea and Dakahlia	*Streptomyces sp. 22SH*	starch nitrate agar	cis-9-Octadecenoic acid	HepG2, MCF-7	liver cancer, breast cancer	(Hassan et al., 2025)
marine water, sediment and plants	The Red Sea (Hurghada), (Sharm El Sheikh) and The Mediterranean Sea (Alexandria), (Marina)	*Streptomyces sp. and Brevibacterium sp.*	Starch Casein Agar, Kuster's agar and ISP-2 agar	3-Hydroxy-3-[(4-methoxyphenyl) methyl]-1,4-dimethyl-2,5-piperazine-dione, 3'-N-Formyl Fusarochromanone and Nb-(5-Methylhexanoyl) tryptamine	HCT-116, MCF-7	colon cancer and breast cancer	(Abdel-Razik et al., 2025)
soil and sea water	Giza, Dakahlia, Gharbia, The Mediterranean Sea (Alexandria) and the The Red Sea (South Sinai)	*Streptomyces sp. strain 5 M*	starch nitrate agar	L-glutaminase	HepG2, HeLa, MCF-7	liver cancer, cervix cancer, breast cancer	(Hassan, El-Sayyad, et al., 2025)
			Extremophilic Environments				
groundwater , ancient stones , desert rocks , medicinal plants, and industrial wastewater	Not specified	*Micromonospora sp1*	Starch Casein broth	Palitantin and SAdenosyl-L-methioninamine	HepG2	liver cancer	(Nafie et al., 2021)

cave soil	Beni-Suef	*Actinobacteria Am 139* and *Am 152*	yeast extract/malt extract (ISP2), and MM media	crude extract	MCF-7, HepG2, JURKAT	breast cancer, liver cancer, T lymphocyte leukemia	(Abdel-Fattah et al., 2024)

Table 3. Diversity and different antitumor activities of actinomycetes isolated from various environments in Egypt

other biological activities

In addition to their well-documented antimicrobial and anticancer effects, secondary metabolites produced by actinomycetes have been shown to possess a wide range of other bioactivities. These include antiparasitic, antioxidant, antihyperglycemic, and anti-inflammatory properties. Some compounds have also demonstrated anti-trypanosomal potential, antibiofilm effects, and even the ability to promote vitamin D production. These diverse biological functions highlight the broad therapeutic potential of actinomycete-derived compounds, as outlined in **Table 4**.

Specimen type	Isolation site/ Study area	Isolated strains	Actinomycetes Isolation (*Serial dilution on selective media)*	Bioactive/chemical compound(s)	Biological Activity	Reference
			Soil			
Agricultural soil	El-Menoufia	*Streptomyces enissocaesilis BS1*	starch nitrate agar	silver-nanoparticles (Ag-NPs) of cell-filtrate	Antibiofilm	(Shaaban et al., 2024)
local soil	Not specified	*Actinomyces hyovaginalis A11-2*	purchase	laboratory fermenter	Vitamin D 3 bioconversion	(Abbas et al., 2023)
soil	Not specified	*Streptomyces MDMMH4*	purchase	extracellular L-methioninase	Antioxidant	(Abdelraof et al., 2023)
soil	Mansoura	*Streptomyces sp. ASM19*	starch nitrate agar	gold nanoparticles (Ac-AuNPs) of cell-filtrate	Antibiofilm	(Aati et al., 2025)
			Rhizosphere Soil			
Wild desert valley soil (olive and Banat vineyard)	Marsa Matrouh (Al Najila, Matrouh and Ras El-Hikma)	*Streptomyces sp. AMM1*	starch nitrate agar	crude extract	Anti-tyrosinase	(Bast et al., 2024)
			Marine			
Marine sponges (Coscinoderma mathewsi)	The Red Sea (North of Hurghada)	*Micromonospora sp. UA17, Gordonia sp. UA19* and *Nocardia sp. UA 23*	M1, ISP2, and Marine Agar	crude extract of Nocardia sp. UA 23 (Anti-Trypanosomal)	Anti-Trypanosomal	(Shamikh et al., 2020)
Marine sponges (Sarcophyton glaucum)	The Red Sea (North of Hurghada)	Micromonospora sp. UA17, Gordonia sp. UA19 and Nocardia sp. UA 23	ISP2 agar	Desferrioxamine B (3), bafilomycin D (10) and bafilomycin A1 (11)	Anti-Trypanosomal	(Gamaleldin et al., 2020)
Marine sponges (Sarcophyton convolutum)	The Red Sea (Makadi bay, Saphaga)	*Streptomyces sp. MORSY 17 and MORSY 22*	ISP2 medium	Crude extract	Antiviral	(El-Gendy et al., 2021)
marine sediment	The Red Sea	Actinomyces sp. AW6	starch nitrate agar with 50% salt water	C1: umbelliferone, and C2: 1-methoxy-3-methyl-8-hydroxy-anthraquinone.	Antioxidant	(Agour et al., 2022)
marine water	The Red Sea (Hurghada)	*Streptomyces sp. SMGL39*	starch-casein agar	iron oxide nanoparticles (FeNPs) of cell-filtrate	Antibiofilm	(Attea et al., 2024)
Marine shore sediment	The Red Sea (Hurghada)	*Streptomyces sp. NRCG4*	starch nitrate agar	exopolysaccharide	Antioxidant, anti-Alzheimer, anti-tyrosinase	(Mahmoud et al., 2023)

					and anti-inflammatory	
marine sediments	The Mediterranean Sea, Alexandria (Abu-Qir coast)	*Streptomyces tunisiensis W4*	starch casein agar with sea water	MT573222 pigment	Antiviral and antioxidant	(Ibrahim et al., 2023)
marine water	The Mediterean Sea,(Western Harbour of Alexandria)	*Streptomyces albidoflavus strain EgyAB2*	Not specified	2-D N-methyl imidazole, 2-nonadecene, 1-D-2-methyl imidazole and propane dinitrile	Antioxidant	(Shata et al., 2025)
marine sponge (Spongia irregularis)	The Red Sea (Ras Mohammed)	*Streptomyces sp. UR32 and Micromonospora sp. UR44*	M1, ISP 2, oligotrophic medium 91 (OLIGO), and marine agar	crude extract	Antiviral	(Abdelaleem et al., 2023)
marine sediment	The Red Sea (Marsa Allam)	*Streptomyces vinaceusdrappus AMG31*	starch nitrate broth	titanium dioxide nanoparticles (TiO_2-NPs) of cell-filtrate	Antibiofilm, antioxidant, wound healing, anticoagulant activity and antidiabetic	(Ghareeb et al., 2025)
marine sponge (Callyspongia siphonella)	The Red Sea	*Streptomyces sp. US4*	M1, ISP-2 medium and Oligotrophic medium (OLIGO) media	quinones, saframycin Y3 (5) and juglomycin E (1)	Antimalarial	(Gamaleldin et al., 2023)
			Marine and Soil			
marine habitats (Ain Sokhna sediment, Ras Sedr sediment, and Hurghada Sea water) and soil habitats (Mansoura)	The Red Sea and Dakahlia	*Streptomyces sp. 22SH*	starch nitrate agar	cis-9-Octadecenoic acid	Antibiofilm	(Hassan et al., 2025)
			Freshwater			
lake sediment	Alexandria(Lake Mariout "main basin")	*Streptomyces fulvissimus EM1 and Streptomyces mediolani EM2*	ISP2 agar	AgNPs Combined with Crude extract	Antibiofilm	(Eltarahony et al., 2021)
lake sediment	Wadi El-Natron (El-Hamara Lake)	*Streptomyces thinghirensis WAE1*	starch nitrate agar	crude extract	Antioxidant and anti-inflammatory	(Osman et al., 2024)

Table 4. Diversity and different biological activities of actinomycetes isolated from various environments in Egypt.

Challenges and Future Perspectives

5.1 Challenges in Culturing and Screening

Despite the promising potential of Egyptian actinomycetes, several barriers hinder their full exploitation. Many strains remain "silent" or uncultivable under standard laboratory conditions, as conventional methods often fail to mimic the biochemical and ecological conditions needed for growth. This limits the discovery of novel metabolites, since a significant proportion of biosynthetic gene clusters (BGCs) remain inactive. In addition, metabolomic profiling frequently leads to the re-isolation of known compounds, highlighting the redundancy problem that slows down novel drug discovery.

Economic and infrastructural limitations present further challenges. Large-scale fermentation and downstream processing require advanced equipment, high-resolution analytical platforms, and sustained funding—resources that are not always readily accessible in Egypt. These constraints restrict the ability to scale promising laboratory findings into industrially viable products.

Finally, the regulatory pathway for developing new antimicrobial agents is long and costly, adding

further complexity to translating actinomycete research into therapeutic applications (Hamed et al., 2023 and Helmi, 2025).

5.2 Future Trends and Opportunities

Advancements in modern biotechnology offer promising solutions to these challenges. Genome mining, metagenomics, and omics-driven approaches (genomics, transcriptomics, proteomics, and metabolomics) can help unlock cryptic BGCs and reveal metabolites that remain inaccessible through conventional cultivation. Synthetic biology and CRISPR-based strategies provide powerful tools to activate silent pathways and enhance metabolite production.

On the applied side, continuous fermentation, metabolic engineering, and nanotechnology-based drug delivery systems are opening new opportunities to improve compound yield, stability, and therapeutic efficacy. Expanding bioprospecting into Egypt's underexplored ecosystems—such as deserts, caves, mangroves, and extreme aquatic niches—may uncover unique strains with enhanced biosynthetic capacity. Beyond antimicrobials, actinomycete-derived metabolites hold promise for oncology, immunotherapy, agriculture, and other fields, underscoring their broad biotechnological potential.

Importantly, sustainable bioprospecting practices and collaborative efforts uniting microbiology, biotechnology, and pharmaceutical research will be crucial for translating Egyptian actinomycete diversity into clinically relevant therapeutics (Osama et al., 2022, Hamed et al., 2023 and Helmi, 2025).

6.conclusion

Actinomycetes remain a vital reservoir of bioactive compounds with broad applications in medicine, agriculture, and biotechnology. This review highlights their presence across Egypt's diverse ecosystems—including agricultural soils, rhizospheres, marine sediments, freshwater habitats, deserts, and caves—each serving as a potential source of novel strains with unique biosynthetic capacities. The studies discussed here affirm that these microorganisms are capable of producing a wide array of secondary metabolites with antibacterial, antifungal, anticancer, and immunomodulatory activities. While *Streptomyces* continues to dominate metabolite discovery, contributions from rare and underexplored genera are becoming increasingly recognized, underscoring the hidden potential within Egypt's microbial biodiversity.

Nevertheless, challenges remain. Many actinomycetes are difficult to culture under standard laboratory conditions, and a significant proportion of their biosynthetic gene clusters remain silent. Redundancy in metabolite discovery, limited access to advanced screening technologies, and resource constraints further hinder progress. Overcoming these barriers will require the integration of modern tools such as genome mining, metagenomics, synthetic biology, and CRISPR-based activation of cryptic pathways. At the same time, optimizing fermentation processes, applying nanotechnology-based drug delivery systems, and ensuring sustainable bioprospecting practices are crucial for translating laboratory findings into industrially and clinically viable products.

Looking ahead, future research in Egypt should prioritize interdisciplinary partnerships among microbiologists, biotechnologists, and pharmaceutical industries. Expanding exploration into under-investigated niches—such as deserts, caves, and extreme aquatic habitats—will likely uncover strains with novel bioactivities. With targeted investment, advanced molecular approaches, and sustainable development strategies, Egyptian actinomycetes could contribute significantly to the global fight against antimicrobial resistance and pave the way for next-generation therapeutics.

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