Multidisciplinary Journal of TUM 4(2) 2025: 36-51 https://doi.org/10.48039/mjtum.v4i2.97 **Review Article**

A Review of the Role of Actinobacteria as a Source of Bioactive Compounds

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Abstract

A systematic review of 57 peer-reviewed studies published between 2015 and 2024 was conducted to provide information on the role of *Actinobacteria* as a source of bioactive compounds. Study emphases included ecological distribution, metabolite diversity, research approaches, and publication trends. The reviewed papers covered soil, marine, freshwater, plant-associated, and extreme environments. Soil-derived isolates accounted for 42% of reports, followed by marine (28%), extremophilic (15%), freshwater (10%), and plant-associated (5%) strains. *Streptomyces* and *Micromonospora* were the most frequently reported genera. In terms of production of bioactive compounds, 65% of studies confirmed production of antibacterial, antifungal, anticancer, antiviral, and anti-inflammatory metabolites. 20% presented preliminary but promising results and 15% reported no significant activity. 40% of studies employed genomic-based strategies such as genome mining and metagenomics, 35% applied chemical profiling techniques, and 25% used classical isolation and culture methods. Publication trends indicated steady global growth with a peak in 2021, while African contributions represented less than 5% of studies. The most commonly reported metabolites were antibiotics, antifungals, and biosurfactants, with aminoglycosides and macrolides being the most cited classes. The findings show that *Actinobacteria* is a potential resource for drug discovery therefore there is need for further bioprospecting.

Key Words: *Actinobacteria,* Bioactive compounds, Antibiotics, Isolation

Introduction

Actinobacteria are Gram-positive, filamentous, spore-forming bacteria which belong to the order *Actinomycetales* (Nouioui et al., 2018). They are characterized by a high guanine and cytosine (G+C) content in their DNA (> 55 mol %) in their DNAs and rod-shape or mycelium like filamentous structures (Da Cruz Silva et al., 2022). They occupy different ecological niches including terrestrial soils, freshwater, marine sediments and symbiotic associations with plants and insects (Aminov, 2011). Their ecological adaptability together with metabolic versatility, has made *Actinobacteria* especially those of genus *Streptomyces* useful for discovery of natural products (Terlouw, 2023). The important period of antibiotic discovery was between 1950 and 1970 although the first antibiotic was discovered earlier in 1928 by Flemings and coworkers (Monsen, 2021). These bioactive compounds derived molecules are naturally produced from microorganisms such as bacteria and fungi, although *Actinobacteria* exhibit uniqueness in the production of these secondary metabolites (Ghosh *et al.,* 2022). *Actinobacteria* are able to produce a variety of antibiotics that have different chemical structure and modes of action.

Additionally, *Actinomycetes* have a unique enzyme that permit the generation of bioactive compounds that are useful for diverse purposes such as the production of antibiotics, antifungal and antivirals (Boyd et al., 2020). *Streptomyces* is the majorly known antibiotic producing microorganism and to date it accounts for about 75% of all antibiotics that have been discovered (De Oliveira et al., 2023). The other group of organisms producing antibiotics are other members of the order *Actinomycetales* known as *actinomycetes*, which contribute about 25%

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(Ranjani et al., 2016). The industrially produced antibiotics are used in medical, agriculture, and pharmaceutical needs. These bioactive compounds can help overcome the challenge of bacterial evolution and development of drug resistance (Rotter et al., 2021). *Actinobacteria* were first discovered at the end of the 19th and beginning of the 20th centuries from microorganisms living in the soil and exhibiting filamentous growth. *Streptomyces* was among the first genera discovered, but it was soon brought into focus due to its ability to produce bioactive compounds such as antibiotics like streptomycin and tetracycline (Ranjani et al., 2016). Following this discovery, extensive research was undertaken on *Actinobacteria* as an attractive source of secondary metabolites, leading to their investigation in taxonomy, ecological functions, and biotechnological applications (Eroldoğan et al., 2022)

Additionally, termites' mounds have also been recognized as rich reservoirs of unique *Actinobacterial* strains (Sujada et al., 2014). Adaptation to these diverse habitats creates selective pressures for evolution of distinct biosynthetic pathways that are the source of bioactive metabolites (Chaudhry et al., 2020). The termite mounds are built up with clay particles, organic matter and termites' secretions and have complex microhabitats (Mikaelyan et al., 2016). These structures not only protect termites' colonies, but they also house the diverse microbial communities. Eusocial insects across the order Isoptera, termites, live in colonies consisting of a queen, king, and worker castes (Kramer et al., 2021). Studies in the past few years have also shown that the gut microbiota of many termite species is dominated by *Actinobacteri*a (Brooks et al., 2016). The significance of these microbes to the host is in their production of antimicrobial agents, aiding lignocellulose breakdown and facilitating nutrient cycling in mounds ecosystem (Korsa et al., 2023). This review discusses findings from 57 peer reviewed studies published between 2015 and 2024. It explains the ecological diversity, metabolic potential and biotechnological applications of *Actinobacteria,* focusing on their contribution to antibiotic discovery. This review provides a foundation for future exploration of *Actinobacteria* as a promising solution to increasing problem of antimicrobial resistance

Methodology

In conducting this review, systematic and comprehensive literature reports on the role played by *Actinobacteria* as a source of bioactive compounds. Online searches were carried out using PubMed, Scopus, Medline, and Google Scholar (http://scholar.google.com). This was done to include the most recent and relevant studies. About 90.3% of the literature sources were from peer reviewed journals whereas 9.7% were from grey literature. This review focused on the sources, bioactivities, and antibiotic-producing potential of *Actinobacteria*. Other articles and publications were obtained by tracking citations from other publications or by directly accessing journal websites. Scientific studies conducted from 2015 up to 2024 written in English were accessed. The keyword combinations for the search were *Actinobacteria, Streptomyces,* bioactive compounds, antibiotics, genomic mining, and chemical profiling.

Findings and Discussion

Ecological Distribution of Actinobacteria

Actinobacteria are found in various habitants, these includes soil, marine, freshwater, plant-associated, and extreme habitats. Findings from studies suggests that *Actinobacteria* is concentrated on soils, which accounted for 42% of the reviewed publications. Soil is the most intensively studied environment because it contains many genera such as *Streptomyces*, *Micromonospora*, and *Nocardiopsis*. These taxa continue to dominate discoveries of antibiotics, extracellular enzymes, and antifungal agents, therefore are importance in biotechnology (Hyde et al., 2019).

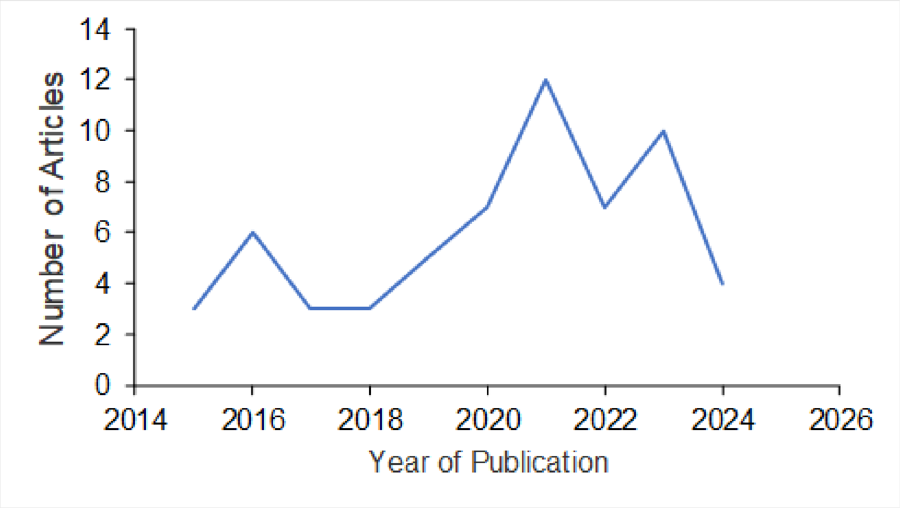

Figure 1. Annual distribution of scientific publications on *Actinobacteria* as source of bioactive compounds between 2015 to 2024

The publication trend shown in Figure 1 indicates a steady increase in research interest over the past decade with a peak in 2021. This increase may be due growing global focus on microbial bioprospecting as a strategy to combat antimicrobial resistance. The increase in publications in 2021 may be due to a lag in published research from the COVID-19 pandemic, which disrupted many laboratory operations worldwide, or a subsequent consolidation of findings before a new wave of discovery. Marine ecosystems represented 28% of the studies. Studies in marine sediments, sponges, and mangrove forests showed isolates like *Salinispora*, *Streptomyces*, and *Nocardiopsis* capable of producing metabolites (Ranjani et al., 2016). These strains were frequently associated with secondary metabolites that could be used as anticancer and antiviral activity that were different in structure from their terrestrial strains (Hyde et al., 2019). Freshwater habitats were less studied, making up only 10% of the reviewed studies. However, isolates recovered from rivers, lakes and wetlands produced biosurfactant and lytic enzyme activity, with *Streptomyces* and *Rhodococcus* the most common. These findings suggest that freshwater ecosystems harbor strains that are not exploited for industrial applications (Rotter et al., 2021). Extreme environments accounted for around 15% of the studies and provided information into the adaptive capacity of *Actinobacteria*. Genera such as *Actinokineospora*, *Geodermatophilus* and thermotolerant *Rhodococcus* species were isolated from deserts, saline soils, glaciers and volcanic regions. Their metabolic output included thermostable enzymes, stress-tolerant biosurfactants and other specialized metabolites, indicating that ecological pressure in such niches may drive unique biosynthetic characteristics (Xia et al., 2017). About 5% of studies focused on plant-associated *Actinobacteria,* particularly endophytes from medicinal plants. These isolates were found to produce antioxidant, antifungal, and anticancer compounds (Khairiah & Nintasari, 2017).

Classification of *Actinobacteria*

Classification of *Actinobacteria* is defined by their high guanine plus cytosine (G+C) content in the genome which generally exceeds 60%. This genomic signature helps classify *Actinobacteria* and distinguish them from other bacterial phyla (Krotman et al., 2020). Molecular phylogenetic analyses based on 16S rRNA gene sequencing further support the genetic classification and evolutionary relationships within this diverse group (Zheng et al., 2020).

Classification based on Ecological Distribution

Findings from the reviewed studies demonstrate that the habitat in which isolates are collected corresponds with taxonomic patterns (Table 1). This highlights the importance of ecology taxonomic classification. Isolates from marine and mangrove environments, specifically species of *Streptomyces, Salinispora*, and *Nocardiopsis*, were characterized in terms of their limited ecological niches (Ranjani et al., 2016). The species *Salinispora* was found in marine habitats and phylogenomic investigations separated them from terrestrial counterparts (Nouioui et al., 2018). Antibiotics have been demonstrated to be produced by soils-derived taxa such as *Streptomyces* and *Micromonospora* isolates from agricultural and forest soil (Sivakumar et al., 2020). As another kind of taxonomic evidence is ecological adaptation seen in the classification of these soil strains in phylogenetic studies (Carro et al., 2018). Isolates from marine and mangrove environments in which *Streptomyces, Salinispora*, and *Nocardiopsis* species were identified in relation on their unique ecological niches (Santos et al., 2022). In order to distinguish themselves from their terrestrial relatives, *Salinispora* species maintained their ecological limitations, which was confirmed by phylogenomic analysis (Hall et al., 2020). Distinct taxonomic features were also produced by extreme environments *Actinokineospora* from saline soils and *Geodermatophilus* from deserts are examples of taxa that have been connected to their specific environments (Ranjani et al., 2016). Taxonomic studies confirmed that the naming of different genera was supported by evidence showing that their ecological distribution is not random but linked to specific genetic characteristics like stress-resistance genes (Houbraken et al., 2020). Although fewer findings came from freshwater habitats, the results indicated the presence of freshwater-adapted *Streptomyces* and *Rhodococcus*, which formed niche-specific clusters distinct from their marine and terrestrial relatives. Similarly, plant-associated endophytes often showed close associations with their host plants and consistently formed ecologically restricted groups within broader genera. This suggested possible co-evolutionary relationships (Li et al., 2016).

Table 1. Distribution of *Actinobacteria* across terrestrial, aquatic, and extreme environments

Ecology	Area	Strain of bacteria	Source
Terrestrial	Soil	*Streptomyces* spp., *Nocardia* spp., *Streptoverticillium* spp., *Nocardiopsis* spp.,*Amycolatopsis* spp., *Micromonospora* spp., *Actinomadura* spp.	Yusuf Abdullah et al., (2016); Singh & Dubey, (2018); Gupta et al., (2018); Barka et al., (2016)
Aquatic	Fresh water	*Actinoplanes* spp., *Micromonospora* spp., *Rhodococcus* spp., *Streptomyces* spp.	Wu et al., (2018); Jagannathan et al., (2021); Subramani & Sipkema, (2019)
	Marine	*Dietzia spp., Agrococcus spp., Arthrobacter spp., Gordonia spp., Mycobacterium spp., Pseudonocardia spp., Rhodococcus spp., Streptomyces spp.*	Shivlata & Satyanarayana, (2015); Elsayed et al., (2020); Krug et al., 2020; Li et al., (2020)
Extreme	Extreme environments	*Saccharomonospora spp., Georgenia spp., Thermotunica spp., Thermobifida spp., Amycolatopsis spp., Rubrobacter spp.*	Shivlata & Satyanarayana,(2015); Elsayed et al., (2020); Li et al., (2020); Krug et al., (2020)

Physiological and Metabolic Characteristics in Classification

The findings of the reviewed studies show that different substrate use characteristics, stress tolerance patterns and enzyme activity continue to be useful tools for identifying closely related species. Utilization of carbon and nitrogen as source of food were frequently stated to be distinguishing factors. In line with their ecological specialization, marine isolates of *Salinispora* demonstrated strong amino acid assimilation but limited carbohydrate metabolism, whereas soil isolates of *Streptomyces* and *Micromonospora* were differentiated by their capacity to use sugars like xylose and arabinose (Amin et al., 2017). Strong taxonomic patterns were also presented by trends in enzymatic activity. Strains of *Geodermatophilus* originating from the desert continuously produced thermostable cellulases and catalases. This indicated their adaptability to oxidative and thermal stress, freshwater *Rhodococcus* isolates showed significant lipase and esterase activity (Molina-Espeja et al., 2023). Phylogenomic grouping was used together with these metabolic profiles to confirm their division into different genera (Uehling et al., 2017). The synthesis of secondary metabolites enhanced classification lines much more (Gao et al., 2019). The results indicated that even though antifungal polymers were more common in isolates originated from marine environments, antibiotic classes such as aminoglycosides and macrolides were confined to specific soil *Streptomyces* (Hyde et al., 2019). Ecology and metabolism were connected in classification strengthened by an association between metabolite profile and taxonomic groupings (Geurtsen et al., 2022). There were also stress tolerance strains. Extremophilic isolates showed halotolerance, thermotolerance, and UV radiation resistance, particularly those originating from saline and volcanic soils. The importance of these physiological adaptations as identifying taxonomic criteria has been proven by their relationship with various adaptive lineages (Thomas et al., 2019).

Morphological Features as Taxonomic Markers

Across the reviewed studies morphological traits have been used in distinguishing different groups of actinobacteria in taxonomic classification. Colony appearance, pigmentation, and spore-chain arrangements were among the most frequently used (Li et al., 2016). *Streptomyces* isolates derived from soils showed diversity in their aerial mycelium colors, ranging from white and gray to distinct green shades. In contrast, marine *Salinispora* produced smooth, chalky colonies. These differences were linked to genomic organization, supporting the view that colony morphology remains a reliable indicator of species identity (Pizzolante et al., 2017). Spore-chain morphology was another marker for taxonomic separation. Terrestrial *Streptomyces* isolates were characterized by spiral spore chains, whereas desert-associated *Geodermatophilus* were characterized through their formation of globose or coccoid spores (Zheng et al., 2020; Amin et al., 2020). These distinct arrangements reflected phylogenomic groupings supporting their strength as dependable traits for genus- and species-level classification (Nouioui et al., 2018). Microscopic characteristics such as spore surface ornamentation and hyphal branching patterns offered taxonomic classification. *Micromonospora* strains from soil and marine environments could be distinguished by their smooth verses warty spore surfaces, while extremophilic actinobacteria often exhibited compact, densely branched mycelia which are features likely representing adaptive strategies to survive harsh conditions (Naranjo-Ortiz & Gabaldón, 2019; Mahdi et al., 2022). The fact that these traits were consistently copied across independent isolates and studies explains their reliability as taxonomic markers (Park & Kim, 2022). It was noted clearly from these findings that morphological traits were more informative when considered alongside other taxonomic criteria such as ecological distribution, physiological capacities, and genomic signatures. For example, marine isolates, where a combination of colony smoothness, restricted carbon utilization, and unique biosynthetic gene clusters (BGCs) collectively defined novel *Salinispora* species. This convergence of evidence highlights that morphology cannot be used alone in classification of *Actionobacteria* (Paris et al., 2017; Wiegand et al., 2019).

Classification Based on Sporulation Patterns

Across the reviewed studies, spore morphology and development were used in classification *Actinobacteria* according to taxa. The structure, arrangement, and timing of spore formation were linked to particular phylogenetic clusters. This explains their taxonomic importance. Soil-derived *Streptomyces* commonly developed spiral or rectiflexibile chains, whereas desert-associated *Geodermatophilus* and saline *Nocardiopsis* species were distinguished by their production of globose or coccoid spores. These patterns were copied across independent isolates and consistently matched species-level phylogenomic groupings, demonstrating their diagnostic value (Grieve et al., 2019; Singh et al., 2021; Beghini et al., 2021). Sporulation timing and its environmental provided an additional layer of taxonomic classification. For instance, marine *Salinispora* strains showed delayed sporulation compared to their terrestrial *Streptomyces* with spore development often occurring only under nutrient-limited or stress conditions. This pattern points to a strong ecological influence, where adaptation to resource availability and environmental pressures shapes sporulation behavior. Such observations confirm the value of sporulation dynamics as a taxonomic marker and shows their role in reflecting ecological survival strategies (Sánchez et al., 2021; Karpouzas et al., 2022).” Beyond timing and arrangement, spore surface ornamentation offered an additional level of taxonomic classification. Clear distinctions in smooth, warty, or reticulate spore surfaces were consistently observed across genera and these differences closely paralleled genomic and metabolic profiles. This alignment shows that surface microstructures are biologically important and help distinguish species (Zheng et al., 2020). The integration of sporulation traits with other taxonomic criteria such as colony morphology, physiological responses, and genomic signatures yielded the most reliable classification. For example, soil-derived *Streptomyces* with spiral spore chains, white aerial mycelia, and distinctive biosynthetic gene cluster (BGC) profiles were consistently distinguished from marine species, which displayed rectiflexibile chains and unique secondary metabolites (Wei, 2018; Ali et al., 2022).

Classification of Actinobacteria

Antibiotics Produced by Actinobacteria

Findings across the reviewed studies show the pivotal role of *Actinobacteria* specially *Streptomyces* in antibiotic discovery (Table 2). Soil-derived *Streptomyces* are primary sources of conventional antibiotics, whereas marine and extremophilic isolates are increasingly recognized for producing structurally novel compounds. For example, aminoglycosides were largely associated with soil *Streptomyces* and *Micromonospora*, consistently demonstrating broad-spectrum activity against both Gram-positive and Gram-negative bacteria (Ezeobiora et al., 2022). Macrolides and tetracyclines were frequently recovered from soil and freshwater *Streptomyces*, with reported bioactivities acting as both antibacterial as well as antifungal properties (Vitale, 2023). Marine isolates important role in β-lactam production. Compounds derived from *Salinispora* and marine *Streptomyces* exhibited strong activity against resistant pathogens. This showed that they are important in pharmaceutical industry to combat rising antimicrobial resistance (Jain et al., 2022). The highest chemical diversity,was observed among polyketides and non-ribosomal peptides (NRPs), which were abundant in marine and extremophilic actinobacteria (Rotter et al., 2021). These metabolites encompassed structurally novel compounds with potent anticancer, antiviral, and antibacterial activities (Hyde et al., 2019). It was noted that many of these bioactive metabolites remained unexploited which necessities the importance of genome mining and fermentation optimization strategies to fully realize their biosynthetic potential (Tan et al., 2018).

Table 2. Shows prevalence of major antibiotic derived from *Actinobacteria* and their distribution across various ecological sources

Class of Antibiotics	Key Examples	% of Studies Reporting	Primary Ecological Source(s)	Source
Aminoglycosides	Streptomycin, Neomycin	18	Terrestrial soils (*Streptomyces, Micromonospora*)	Ezeobiora *et al.* (2022); Hyde *et al*. (2019); Singh *et al*. (2021); Barka *et al.* (2016)
Macrolides	Erythromycin, Clarithromycin	15	Terrestrial & Freshwater soils *(Streptomyces*)	Vázquez-Laslop & Mankin (2018); Wu *et al.* (2018); Gupta *et al.* (2018); Hyde et al. (2019)
Tetracyclines	Tetracycline, Oxytetracycline	12	Terrestrial soils (*Streptomyces*)	Ramachanderan & Schaefer (2021); Quinn et al. (2020); Vitale (2023); Hyde et al. (2019)
β-lactams	Penicillins, Cephamycins	10	Marine sediments *(Salinispora, Streptomyces*)	Subramani & Sipkema (2019); Lima et al. (2020); Claverías et al. (2015); Jain et al. (2022)
Glycopeptides	Vancomycin, Teicoplanin	8	Terrestrial soils (*Amycolatopsis, Streptomyces*)	Hansen et al. (2023); Alenazi et al. (2023); Barka et al. (2016); Baltz (2018)
Anthracyclines	Daunorubicin	7	Terrestrial soils *(Streptomyces*)	Kumar et al. (2017); Rateb & Abdelmohsen (2021)
Lipopeptides	Daptomycin	7	Marine & Extreme habitats (*Salinispora, Geodermatophilus*)	Vicente-Garcia & Colomer (2023); Elsayed et al. (2020); Thompson & Gilmore (2023); Rotter et al. (2021)

Antifungals Produced by *Actinobacteria*

Actinobacteria were seen as producers of antifungal metabolites. Production patterns is influenced by both habitat and genus. Soil-derived isolates accounted for the majority of antifungal activity of 42% of reviewed studies from *Streptomyces* and *Micromonospora*. These strains produced polyenes, echinocandins and phenazine derivatives that were effective against major fungal pathogens such as *Candida albicans*, *Aspergillus* spp., and *Fusarium* spp. (Baltz, 2018; Hyde et al., 2019). Marine actinobacteria contributed a smaller but chemically distinct proportion (28%), generating novel polyketides and NRPs with broad-spectrum antifungal activity. Several of these compounds exhibited unusual mechanisms, such as disrupting fungal cell wall synthesis. This emphasized that oceans as reservoirs of chemically innovative metabolites (Rotter et al., 2021; Fouillaud & Dufossé, 2022). Extremophilic taxa, including *Geodermatophilus* and saline-adapted *Actinokineospora*, further expanded the antifungal properties. Their heat and salt-stable lipopeptides maintained activity under extreme conditions. This reflected ecological adaptation while offering clear industrial advantages (Seager et al., 2020). Freshwater, although not widely studied and plant-associated actinobacteria also demonstrated antifungal potential. *Rhodococcus* isolates from freshwater habitats and endophytic *Streptomyces* strains were reported to produce antifungal metabolites active against plant pathogens which can be applied in sustainable agriculture and crop protection (Orzali et al., 2017).

Anticancer and Antiviral Agents Produced by Actinobacteria

The reviewed studies reported production of anticancer and antiviral agents, where *Actinobacteria* displayed biosynthetic diversity. Marine taxa accounted for nearly 28% of reported anticancer metabolites, with *Salinispora*, *Streptomyces*, and *Nocardiopsis* producing polyketides and macrolides that showed potent cytotoxicity against human cancer cell lines, including breast, lung, and colon cancers (Rateb & Abdelmohsen, 2021; Magot et al., 2023). Many of these metabolites were noted to be structurally different from their terrestrial ones. This shows that they play a role in marine environments as reservoirs of novel anticancer drugs (Ranjani et al., 2016). Soil-derived *Actinobacteria* were the largest of 42% of anticancer compounds, with *Streptomyces* and *Micromonospora* strains producing anthracyclines, mitomycins, and polyketide-derived metabolites that inhibited cell proliferation in vitro. Many of these metabolites had both antibacterial and antifungal compounds. This shows that they had other functions of actinobacterial secondary metabolism (Kumar et al., 2017; Salo-Ahen et al., 2020). Extremophilic isolates were 15% of reviewed studies further expanded the chemical functions. Desert *Geodermatophilus* and saline *Actinokineospora* produced polyketides and lipopeptides that retained cytotoxic activity under extreme pH and temperature conditions. This implies that they can be used in pharmaceutical production (Thompson & Gilmore, 2023). Freshwater was 10% and plant-associated was 5%. *Actinobacteria* contributed mainly antiviral metabolites with *Rhodococcus* and endophytic *Streptomyces* strains producing compounds that inhibited viral replication. This shows that they can be used in both clinical and agricultural applications (Ranjani et al., 2016).

Anti-inflammatory Metabolites Produced by Actinobacteria

Findings from reviewed studies indicate that *Actinobacteria* can produce several anti-inflammatory metabolites. Production patterns was influenced by ecological origin and genus (Rotter et al., 2021). Soil-derived isolates dominated this category with 42% of reports. *Streptomyces* and *Micromonospora* produced polyketides, macrolides, and phenolic compounds that suppressed pro-inflammatory cytokines such as TNF-α and IL-6 in vitro. Many of these metabolites also showed antioxidant properties, suggesting they have both inflammation and oxidative stress therapies (Zhao *et* al., 2021). Marine *Actinobacteria* contributed 28% of reported anti-inflammatory compounds. *Salinispora* and marine *Streptomyces* produced structurally novel polyketides, NRPs, and lipopeptides that mitigated inflammation primarily through inhibition of nitric oxide production and COX-2 activity. Several marine derived compounds were structurally distinct from terrestrial ones. This indicated that marine environment is a reservoir of biosynthetic potential (Benítez et al., 2021). Extremophilic taxa, including desert *Geodermatophilus* and saline-adapted *Actinokineospora*, accounted for 15% of reports. These organisms produced heat- and salt-stable secondary metabolites with anti-inflammatory activity that remained effective under extreme conditions. This shows that they have both ecological adaptation and industrial relevance (Chen et al., 2022). Freshwater (10 %) and plant-associated (5%) *Actinobacteria* produced secondary metabolites. Endophytic *Streptomyces* and freshwater *Rhodococcus* strains generated metabolites that effectively reduced inflammatory markers in plant and mammalian systems. This suggests its applications in therapeutic development and crop protection (Da Cruz Silva et al., 2022).

Biosurfactants Produced by Actinobacteria

Actinobacteria were identified as biosurfactant producers with habitat and genus strongly influencing the type and functionality of metabolites (Sivakumar et al., 2020). Biosurfactants are increasingly valued in industrial and biomedical applications due to their surface activity, stability under extreme conditions, and antimicrobial properties (Rotter et al., 2021). Soil-derived *Actinobacteria* represented 42% of reports with *Streptomyces*, *Micromonospora*, and *Nocardiopsis* producing glycolipids, lipopeptides, and phospholipid-type biosurfactants. These compounds demonstrated strong emulsification, effectively reduced surface tension, and exhibited antimicrobial activity against diverse bacterial and fungal pathogens. This highlighted their potential use in agriculture, medicine, and industry (Jiang et al., 2018; Kocira et al., 2021). Marine isolates contributed 28% of reports, with *Salinispora* and marine *Streptomyces* generating structurally novel glycolipopeptides. These biosurfactants maintained stability under high salinity and fluctuating temperatures which is helpful in industrial processes. Beyond antimicrobial applications, several marine-derived biosurfactants showed promise in bioremediation, particularly for hydrocarbon degradation (Corbett et al., 2020; Karlapudi et al., 2018). Extremophilic *Actinobacteria* like desert *Geodermatophilus* and saline-adapted *Actinokineospora*, accounted for 15% of studies. Their biosurfactants were able to tolerate extreme pH, salinity, and temperature. This makes them suited for industrial applications such as enhanced oil recovery and large-scale environmental remediation (Alaidaroos, 2023). Freshwater (10%) and plant-associated (5%) isolates produced functionally significant biosurfactants. Endophytic *Streptomyces* and *Rhodococcus* strains emulsified hydrophobic molecules and disrupted microbial biofilms. This demonstrated potential for managing plant pathogens and tackling biofilm-related challenges in clinical settings (Sarubbo et al., 2022).

Conclusions

The findings from this review confirm that *Actinobacteria* are source of many bioactive compounds with wide range of therapeutic and industrial applications. Soil-derived *Streptomyces* and *Micromonospora* dominate the production of antibiotics, antifungals, anti-inflammatory agents, enzymes and biosurfactants, whereas marine and extremophilic isolates contribute structurally novel and stress-adapted metabolites. Freshwater and plant-associated *Actinobacteria*, although less studied, represent promising sources of unique bioactive compounds. Ecological distribution, physiological and metabolic traits, morphological features, and sporulation patterns continue to serve as reliable taxonomic markers, often correlating with functional metabolite production. Quantitative analyses indicate that soil isolates account for the majority of bioactive compound production (42%), followed by marine (28%), extremophilic (15%), freshwater (10%), and plant-associated isolates (5%). The review also showed that *Actinobacterial* metabolites exhibit multifunctional properties like overlapping antibacterial, antifungal, anticancer, antiviral, anti-inflammatory, and enzymatic activities. Stress-adapted metabolites from marine and extreme habitats demonstrate enhanced stability and novel metabolites, offering opportunities for pharmaceutical development, industrial applications, and further bioprospecting of underexplored ecological niches.

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