OPEN ACCESS Freely available online

Mycobacterial Diseases

ISSN: 2161-1068

Opinion Article

Evolution and Ecological Spread of Mycolactone-Producing Mycobacteria

Daglia Siculella*

Department of Microbiology and Immunology, National University of Singapore, Singapore

DESCRIPTION

Mycobacterium species are a diverse group of bacteria, many of which are associated with significant human and animal diseases, including tuberculosis and leprosy. However, a lesser-known subset of this genus is characterized by their production of mycolactone, a potent macrolide toxin that plays a pivotal role in their pathogenicity. The best-known mycolactone-producing *Mycobacterium* is *Mycobacterium ulcerans*, the causative agent of Buruli ulcer, a debilitating skin disease that primarily affects people in tropical and subtropical regions. Nevertheless, research in recent years has shown that *M. ulcerans* is not the only species capable of producing mycolactone. A number of other Mycolactone-Producing Mycobacteria (MPMs) have been identified, revealing a diverse group of organisms with varying ecological niches, geographical distributions, and pathogenic profiles.

Mycolactone and its biological function

Mycolactone is a cytotoxic and immunosuppressive lipid-like molecule that serves as the primary virulence factor for *M. ulcerans* and other MPMs. It is responsible for the characteristic painless skin ulcers in Buruli ulcer by causing cell necrosis and suppressing the immune response. This immunomodulatory effect is central to the pathogenesis of Buruli ulcer, allowing the bacteria to evade detection and destruction by the host immune system. Structurally, mycolactone is a polyketide-derived macrolide that includes a core lactone ring attached to various side chains. Different mycolactone-producing mycobacteria produce slightly different variants of mycolactone, which may affect their virulence and the types of lesions they cause. The gene cluster responsible for mycolactone synthesis (the *mlsA* and *mlsB* genes) is located on a large plasmid within the bacteria, suggesting horizontal gene transfer as a possible mechanism for the dissemination of mycolactone-producing capabilities across different species.

Diversity among mycolactone-producing mycobacteria

While *Mycobacterium ulcerans* is the most prominent MPM, other species have been found to produce mycolactone or mycolactone-like compounds. These species include *Mycobacterium marinum*, *Mycobacterium pseudoshottsii*, *Mycobacterium liflandii*, and *Mycobacterium shinshuense*, among others. These species are typically found in aquatic environments, such as slow-moving rivers, wetlands, and estuarine ecosystems, and they are often associated with fish, amphibians, and other aquatic animals. *Mycobacterium ulcerans* as the best-known mycolactone producer, M. ulcerans primarily affects humans, leading to Buruli ulcer. It is believed to have evolved from the fish pathogen *Mycobacterium marinum* through the acquisition of the mycolactone-producing plasmid. *M. ulcerans* has a reduced genome compared to *M. marinum*, which reflects its adaptation to a more specialized niche, particularly in tropical and subtropical regions of Africa, Australia, and the Western Pacific. *Mycobacterium marinum* known primarily as a pathogen of fish and amphibians, *M. marinum* can also infect humans, typically causing skin lesions after exposure to contaminated water. Some strains of *M. marinum* produce mycolactone, though in lesser quantities than *M. ulcerans*. This organism is often found in temperate and tropical aquatic environments and can cause a disease similar to Buruli ulcer in cold-blooded animals. *Mycobacterium pseudoshottsii* species is closely related to *M. marinum* and was initially isolated from diseased fish in the Chesapeake Bay. Like *M. ulcerans*, it carries a plasmid encoding mycolactone, though its pathogenicity and ecological role are less well understood. It serves as a reminder of the diversity of environmental mycolactone producers that have yet to be fully characterized. *Mycobacterium liflandii* is another aquatic pathogen, *M. liflandii* is associated with amphibian die-offs, particularly in captive settings.

Ecological and evolutionary implications

The diversity of mycolactone-producing mycobacteria suggests that the ability to produce this toxin is not confined to a single lineage but is distributed across several species, likely due to horizontal gene transfer of the plasmid responsible for mycolactone synthesis. These bacteria thrive in a variety of ecological niches, particularly in aquatic environments, and affect a broad range of hosts, including humans, fish, and amphibians. Understanding the diversity of MPMs is important for tracking the spread of diseases like Buruli ulcer and for comprehending

Correspondence to: Daglia Siculella, Department of Microbiology and Immunology, National University of Singapore, Singapore, Email: dagsicue@gamil.com

Received: 03-Jul-2024, Manuscript No. MDTL-24-33690; **Editor assigned:** 05-Jul-2024, PreQC No. MDTL-24-33690 (PQ); **Reviewed:** 19-Jul-2024, QC No. MDTL-24-33690; **Revised:** 26-Jul-2024, Manuscript No. MDTL-24-33690 (R); **Published**: 02-Aug-2024, DOI: 10.35248/2161-1068.24.14.489.

Citation: Siculella D (2024). Evolution and Ecological Spread of Mycolactone-Producing Mycobacteria. Mycobact Dis.14:489.

the evolutionary forces driving the emergence of new pathogens. Moreover, the identification of new MPMs in different geographic regions suggests that the public health impact of mycolactone-related diseases could be broader than previously thought, necessitating further surveillance and research into these enigmatic bacteria.

CONCLUSION

The discovery of diverse mycolactone-producing mycobacteria reveals an intricate web of ecological relationships and evolutionary pathways within this genus. While *Mycobacterium ulcerans* remains the most prominent species due to its impact on human health, other species such as *M. marinum*, *M. pseudoshottsii*, *M. liflandii*, and *M. shinshuense* demonstrate the widespread nature of mycolactone production in the environment. As research continues to uncover new species and variants, the full scope of mycolactone's role in the pathogenicity of mycobacteria remains an exciting field of study with significant implications for both human and animal health. It produces a mycolactone variant similar to that of *M. ulcerans* but is primarily a pathogen of frogs and toads. Its capacity to produce mycolactone highlights the environmental distribution of this virulence factor across different species and hosts. *Mycobacterium shinshuense* was identified in Japan, *M. shinshuense* causes skin lesions in humans, similar to M. ulcerans. However, this species is geographically distinct, and its mycolactone production suggests an independent evolutionary adaptation to produce this toxin. Its discovery emphasizes the global distribution of MPMs beyond Africa and Australia.