

Exploring Tuberculosis Evolution through Marine Sponge Bacteria

Hilpert Anam*

Department of Infectious Diseases, The University of Melbourne, Parkville, Australia

DESCRIPTION

Tuberculosis (TB) has been a scourge of human health for thousands of years. Despite centuries of scientific investigation, many mysteries remain about its evolution and the origins of this deadly pathogen. Surprisingly, recent studies have pointed to an unlikely source for insights into the evolution of TB: Marine sponges. These ancient organisms, which have thrived in the oceans for over 600 million years, harbor microbes that share genetic traits with the bacteria responsible for TB. The study of these marine sponge-associated bacteria is explaining on how *Mycobacterium tuberculosis* (*M. tb*) evolved into the pathogen we know today.

Role of marine sponges in microbial research

Marine sponges are among the oldest multicellular organisms on Earth. They live in a symbiotic relationship with a diverse range of microorganisms, including bacteria, fungi, and viruses. These symbiotic microbes play essential roles in the sponge's metabolism, defense mechanisms, and overall health. Because marine sponges house such a wide variety of microorganisms, they have become a focal point for researchers exploring the evolution of bacteria, including those with relevance to human health. In recent years, scientists have discovered that some bacteria living within sponges belong to the same broad family as the *Mycobacterium* genus, which includes *M. tb*. These sponge-associated microbes, while not pathogenic to humans, share key genetic features with *M. tb*. By studying these marine microbes, researchers are beginning to understand how environmental bacteria could have evolved into human pathogens over time.

Insights into the evolution of TB

The study of marine sponge bacteria offers several important clues about the evolutionary origins of TB. One important finding is that the ancestors of *M. tb* likely existed in environmental reservoirs long before they adapted to infect mammals. These ancestral bacteria may have lived in soil, water, or marine environments, where they formed symbiotic or

opportunistic relationships with different organisms. Researchers have also identified genes in marine sponge microbes that resemble those involved in the virulence of *M. tb*. For example, certain genes responsible for the production of mycolic acids a type of fatty acid that forms a waxy coat around *M. tb*, protecting it from the host immune system have been found in marine bacteria. This suggests that the protective features of *M. tb* may have evolved in response to environmental pressures long before the bacteria became specialized to infect humans.

Environmental to pathogenic shift

The evolutionary shift from an environmental bacterium to a highly specialized human pathogen like *M. tb* likely involved gradual adaptations that allowed the bacteria to survive and thrive within host organisms. Marine sponge bacteria, which live in close association with their host, provide a model for understanding how this transition may have occurred. In marine sponges, bacteria must compete with other microorganisms for resources and protection. These environmental pressures may have led to the development of defense mechanisms such as biofilms, protective coatings, and the ability to manipulate host immune responses traits that are also seen in pathogenic mycobacteria like *M. tb*. Over time, these traits may have been refined as certain bacteria adapted to life within mammals, eventually leading to the emergence of TB causing strains. Understanding the environmental origins of *M. tb* has important implications for modern TB research. For one, it highlights the adaptability of mycobacteria and their ability to survive in a wide range of environments. This adaptability is part of what makes TB so difficult to eradicate, as *M. tb* can persist in latent form within the human body for decades, only to reactivate under certain conditions. Moreover, studying marine sponge microbes could lead to the discovery of new antimicrobial compounds. Sponges and their symbiotic bacteria have evolved sophisticated chemical defenses to protect themselves from predators and infections. Some of these compounds have shown potential as new antibiotics, which could be important in the fight against drug-resistant TB.

Correspondence to: Hilpert Anam, Department of Infectious Diseases, The University of Melbourne, Parkville, Australia, Email: anahilp@yahoo.com

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CONCLUSION

The study of marine sponge-associated bacteria is opening new doors in our understanding of the evolution of tuberculosis. By tracing the environmental roots of *M. tb*, researchers are gaining valuable insights into how this deadly pathogen evolved and adapted to human hosts. The discovery that marine microbes

share genetic traits with TB causing bacteria provides a fascinating example of how life in the ocean may hold the key to solving some of humanity's most pressing health challenges. As we continue to explore these marine microbes, we may uncover not only the evolutionary history of TB but also new strategies for combating it in the future.