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Review Article

Features of the biochemistry of *Mycobacterium smegmatis*, as a possible model for *Mycobacterium tuberculosis*

Joseph Antony Sundarsingh T, Ranjitha J, Aiswarya Rajan, Vijayalakshmi Shankar*

CO2 Research and Green Technologies Centre, VIT University, Vellore-14, India

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ABSTRACT

An alternate host for mycobacteria is *Mycobacterium smegmatis* which is used frequently. It is a directly budding eco-friendly organism not emulated as human infection. It is mainly useful for the investigation of various microorganisms in the sort of *Mycobacteria* in cell culture laboratories. Some Mycobacterium species groups that is normal, unsafe ailments, likely to *Mycobacterium leprae, Mycobacterium tuberculosis* and *Mycobacterium bovis*. At present, various laboratories are clean and culture this type of species to make an opinion that fascinating route of harmful *Mycobacteria*. This publication provides aggregate data on cell shape, genome studies, ecology, pathology and utilization of *M. smegmatis*.

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* Corresponding author.
E-mail address: vijimicro21@gmail.com (V. Shankar).

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Introduction

In 1884, Lustgarten isolated the species named as *Mycobacterium smegmatis*. Lehmann and Neumann gave the name *M. smegmatis* in 1889. This microbe mainly lives in the layers of the cells and all the cells will join together in a group is known as a biofilm. *M. smegmatis* was commonly found in the soil, water and plants. They are found in sixteen States, Australia, Russia, Canada, and Switzerland [1]. *M. smegmatis* is usually known as saprophytic group that rarely causes disorder and is not susceptible to live in mammals. When developing on available supplements, this microbe will be velvety white and finely wrinkled. As soon as the *M. smegmatis* started developing for about forty-eight hours, the growth will beabudant, and the colour of shading will be changed to non-pigmented velvety yellow from white colour. The surface morphology of this microbe will be shiny, smooth, finely wrinkled or coarsely collapsed [2]. *M. smegmatis* is found to non-pathogenic and rapidly developing than other *Mycobacterium* species [3]. The organism is aerobic, which donates the final electrons to oxygen during respiration. The maximum amount of energy for this bacteria will be obtained by oxidative phosphorylation. Although Mycobacteria are strict aerobes, sometimes oxygen may not require during infection as it undergoes anaerobic respiration for certain virulent *Mycobacterium* sps. Mycobacterial DNA-binding protein 1 is critical for long term survival of *M. smegmatis* and simultaneously coordinates cellular functions. The microbe will be eliminated by identifying a proper treatment, especially by hindering the mycolic biosynthesis pathway, which is more critical for the cell division of bacteria [4]. After the invention of streptomycin, chemotherapy has been identified as the treatment for tuberculosis. For active and latent tuberculosis infection, it takes from 6 to 9 months for the therapy respectively, which results in the generation of drug-resistant strains [5]. The barriers in identifying the drug for the infection is its slower growth rate, contagious, higher virulence, impermeable and hydrophobic cell envelope [6]. As the tuberculosis infection is life-threatening, identifying a potential drug is highly essential in controlling the disease. There are various similarities between *M. smegmatis* with other harmful, infectious *Mycobacterium* species like *Mycobacterium tuberculosis* [7]. The Major similarity is the mycothiol biosynthesis for the production of basic thiol, which is highly needed for the growth of the *Mycobacterium* sps.

Structure of *M. smegmatis* 70S ribosome

The ribosome does the amalgamation of proteins in each living cell. It slowly focuses on hostile to microbial treatment. *M. tuberculosis*, a structure that reveals two extra ribosomal macromolecules and prohibits them to the part of medication target destinations in both the reactant focus and the interpreting site of the ribosome. Likewise, actinobacterium-particularly RNA and protein developments that generally alters the ribosomal layer with the help of polysomes. Oxazolidinones refer to a novel class of anti-infection agents that detaches the peptidyl-transferase focus inside the 50S large ribosomal subunit [8]. The oxazolidinone linezolid shows growth impacts in the treatment of multi-sedate safe microbes, for example, *Staphylococcus aureus* [9] yet in addition to *M. tuberculosis* [10].

The peptide anti-microbial capreomycin focuses on the 30S little ribosomal subunit and interfere with interpretation and translocation [11–13]. *M. smegmatis* is referred as a valuable model organism for mycobacterium investigation because of its close association with *M. tuberculosis* concerning biochemical properties and genetic information. It has been widely used to determine anti-microbial activity and biochemical protection [14]. Redevelopment of *M. smegmatis* 70S ribosome to 12 A° and redevelopment of *M. tuberculosis* 50S ribosomal subunit to 9 A° a portion of the broadened surface highlights of the mycobacterium ribosome [15,16].

Therefore, results should motivate researchers to include the genetic loci of bL37 and bS22 (Mt Rv0500B) for antibiotic resistance, as shown in Fig. 1. The reorganization of rRNA and protein elements on the mycobacterium surface suggests unique implications for the geometry and function of polysomes. *M. tuberculosis* is susceptible to various antibiotics like, isoniazid, rifampicin, pyrazinamide, ethambutol, streptomycin, kanamycin, capreomycin, ethionamide, fluroquinolones, P.aminosalicylic acid, cycloserine, clofazimine, oxazolidinones, B.lactams, bedaquiline, nitroimidazoles, SQ109, phenothiazines and benzothiazinones, whereas *M. smegmatis* is resistant to various antibiotics like ampicillin, erythromycin, amoxicillin and streptomycin and sensitive to iifampicin, pyranizimide, ethambutol and isoniazid.

Cell construction and metabolism

It is a Gram-positive microbe, depicted by the internal cell layer with the dense cell wall. This has a unique characteristic feature of more Guanine–Cytosine content when compared to Adenine-Thymine content. It is utilized because of the rough calculation of comparability of various types of microbes. This microbe has some kind of character that is different from the other gram-positive microbe. Its cell division consists of mycolic acids, fanned unsaturated fats that are ordinarily present in slide microorganisms. The cell division remains additionally strange because it is rarely broad for a gram-positive microbe and its hydrophobicity. This element, despite its moderate cell development in contrast with most other microscopic organisms to *M. smegmatis*, results in a low reaction to anti-infection agents. *M. smegmatis* is a high-impact living being; it may give its last electrons in high-impact breath to oxygen using a single of three fatal oxidases. In vigorous breath, and the microorganisms experience oxidative phosphorylation to give way the most important measures of life. The microscopic organisms may also utilize methanol intended for its only basis for carbon and vitality. Similarly, this bacterium requires an extraordinary unsaturated fat biosynthesis to generate the mycolic acids that are accessible in cells divider. This bacterium has no motility and no arrangement of endospores [17–19]. Although *M. smegmatis* include the comparative auxiliary highlights of *M. tuberculosis*, while *M. smegmatis* develops considerably rapid when compared to *M. tuberculosis*. Oxygen is necessary for the growth of Mycobacterium because of its aerobic nature but some pathogenic mycobacterium may grow in anaerobic condition. The major similarity in *M. tuberculosis* and *M. smegmatis* is the presence of *N*-acetylmuramic acid (MurNAc) and *N*-glycolylmuramic acid (MurNGlyc), and its presence improved the lysozyme resistant to both microbe. Thus, *M. smegmatis* possess similarities in cell structure and metabolism with *M. tuberculosis*.

Cell surface characteristics

Mycolate biosynthesis

Mycobacteria are renowned for its extraordinary degree measures of absolute pharmaceutical protection, generally results in the direction of an impermeable, hydrophobic cell covering. The guideline segments that cover are determined falsely and approved in an auxiliary model proposed by Minnikin [20] in 1982. After which, various biophysical, biochemical and fine electron examinations had developed this model [21–23]. Mycobacterium plasmocyte film and peptidoglycan layer resemble with other gram-positive microorganisms [24,25]. The external cell layer was found to be similar in related genera such as Actinomycetales biological group, includes Cornebacterium, Nocardia, Gordona, Rhodococcus, as well as Mycobacteria. Within mycobacteria, pep-