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Review Article

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

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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*.

Contents

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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-

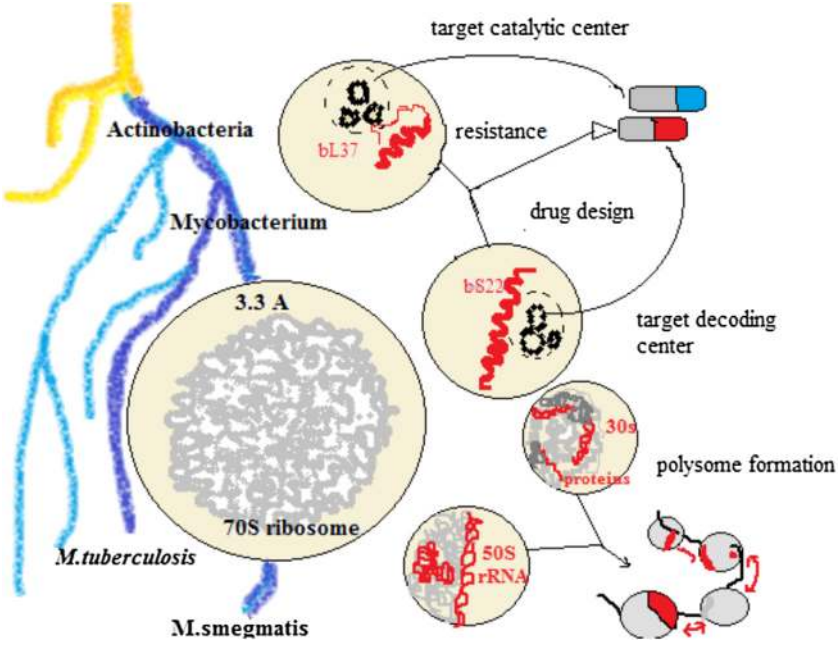

Fig. 1. Structure of *M. smegmatis* 70S ribosome.

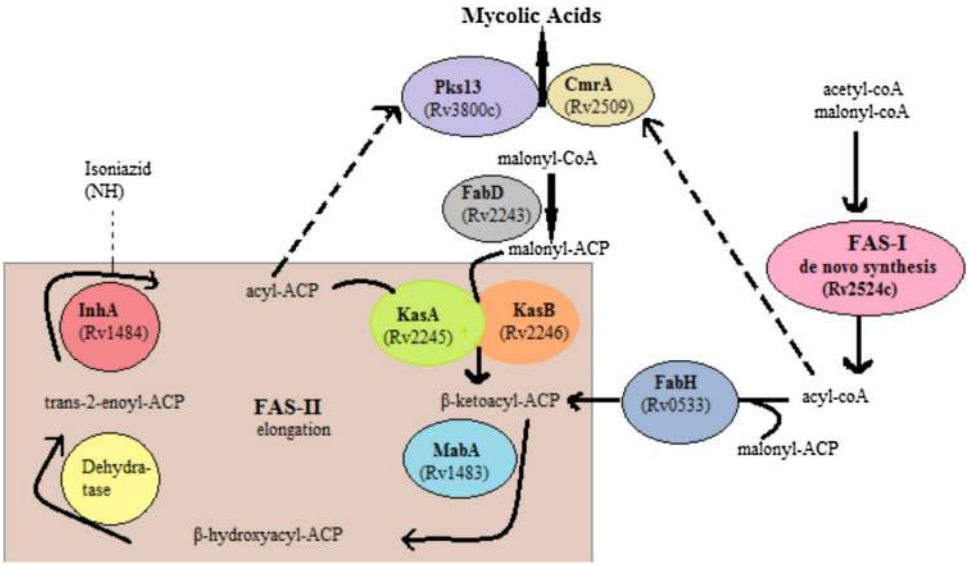

Fig. 2. Schematic representation of the mycolic acid chain.

tidoglycan is covalently connected with arabinogalactans that protects itself by a coating of mycolates. The mycolic corrosive layer shapes a powerful hindrance against the entry of both hydrophilic and hydrophobic mixes. It is thought to render mycobacteria impervious to anti-microbials even though they have relating drug-delicate targets. Mycolic acids are orchestrated as two alkyl anchors by compounds like those that collect unsaturated fats. These chains are joined and focus on different adjustments to produce a lipid group that are combined into the cell coat [26]. Mutant *M. smegmatis* damage the mycolate biosynthesis [27] which indicates the increased rate of affectability to erythromycin [28]. Moreover, a jumping gene modification in a mycolic corrosive synthesis by *M. tuberculosis* (kasB) made it delicate towards the antimicrobial proteins like lysozyme and defending [29]. Mass of mycobacterium is esterified to mycose in mycolic acid shows that can be cleared in natural solvents. Otherwise chemically associated with arabinogalactan within the cell divider. TDM enhance the positioning of expanded organisms' ("rope structures") within a gas or liquid medium otherwise on the outer surface. Esterification of mycolic acids is processed by batches of less than three similar compounds that provides enveloping action inside the cell wall. These exchanged proteins were at first reported as noteworthy antigens of *M. tuberculosis*, "the foreign substance 85 complex" [30]. Afterward, they are seen to be fibronectin-confining proteins (Fbp), a property at first said to be occupied within engulfment into macrophages [31]. These proteins were obtained to produce a mycolyl transferase response that is basic for compartment divider biogenesis [32] (Fig. 2).

Study of an M.TB mutant, shows that the basic was unnecessary for the growth however required for the improvement of compartment dividers [33] including Common measures of mycolic corrosive methyl esters MAMEs Both chenodeoxycholate, a

hydrophobic compound, and glycerine, a deliquescent compound, spread faster throughout the cell Co covering of the fbpC mutants. Inquisitively, secure from the restricted scope of antimicrobials attempted, was unaltered [34]. Genetic examination displayed that each one of the three M. T.B fbp qualities can be aggravated independently and that they believed abundance parts incompletely inside the cell divider synthesis. The way that a standard Fbp medium could suppress growth and cell divider synthesis, that shows these proteins have relative actions, and therefore targets for new antimicrobial drugs. Ligation between mycolic acids and supplementary segments of the mycobacterium cell divider constructs a hydrophobic, a tight water resistance that secures from lethal mixes. Ejected proteins FbpA, FbpB, and FbpC combine mycolic acids into arabinogalactan, delivering mycolic destructive methyl esters (MAME) or trehalose, producing trehalose dimycolate (TDM; conjointly known as line feature). The examinations of *M. smegmatis* displayed that interval of FbpA did not impact MAME levels but brought around 45% diminishment of TDM. The fbpA mutant indicated extended affectability on both face lines of tuberculosis-concentrated on medicine and in addition with a large amount of hostile to diseased persons by using medication therapy. The isolated, hydrophobic layer of different *M. smegmatis* gets damaged that becomes deliquescent and soft within the mutant. Whereas formation of *M. smegmatis* fbpA remodelled disfigurements of the deformity, heterogonous formation of tubercle bacillus fbpA quality was not as much of convincing.

A unique change in the *M. smegmatis* FbpA esterase space deactivates its ability of hostile to microbial activity. This fact shows that formation of TDM through FbpA is primary for the characteristic of anti-infective immunity and normal morphology of certain mycobacterium and support the thought that FbpA specific inhibitors, solitary or together with other hostile microbes, can produce an effective treatment for TB and other mycobacterium ailments. Most of the interrogative studies show that the isolation of the extent is mentioned as inert MTB cells. Their actual state was said to be accessing alkali. Still, generally they are 'non-culturable' microorganism in closed type wounds [35], and also sustained by enhancing inventories in the Cornell type of dormant tuberculosis. A team by, Khomenko along with his colleagues, invented screenable or smaller to the typical model of MTB that presides beneath the flesh of carvia porcellus even after anti-microbial TB treatment. In this treatment, functional tubercle bacillus would never again exist recognized through typical plating approach; Albert 2003, investigation of a homogenised organ is purified through 0.2–0.7 mm opened passage of thick electron pattern with a modified design and standard estimation of 0.25 mm [36]. Thus the establishment of these design to carvia porcellus processed the development of TB. After several methods, MTB can be isolated using specific culture methods [37].

Non-culturability

In recent years, the analytical analysis was performed to produce an in-vitro model of myco bacterial inactivity [38] particularly, inactive, 'non-culturable' tubercle bacillus cells were attained within invitro stage [39]. This MTB were recovered at early stationary state culture techniques of the same strain, was developed using phospholipids or 8 kDa of protein was introduced in the supernatant [40]. Besides, the importance of proteinaceous group recovery methods various (Rpf) produced by MTB for recovering of 'non-culturable' tubercle bacilli cells was cultured [41].Thus previously depicted the advancement of 'non-culturable' but, retainable cells of *M. smegmatis* [42] and MTB after late improvement in the stationary stage. While this bacterium indicated specific features that show inactivity, they might hang on during this condition for specific periods. MTB cells survive in the microaerophilic state and produce a hard cell divider surface in Wayne's model [43]. In any case, the researchers did not find any spore-like or round shape in a certain population [44]. A reagent like Ziehl distinctly recoloured the round cell and cell divider with excess outer coat design (differed using an electron microscope); they are assumed as L forms and stored at mycobacterium separated from in vivo state [38].

M. smegmatis mc2 155 could be a convertible strain that was separated from non-coatable ATCC 607 out of a 3 phase framework [45]. The two strains changes in the portion of their states, such as obnoxious converted for ATCC 607 in addition to mc2 155 [46]. ATCC 607 cells were identified of fivefold relatively to mc2 155. These phenotypic transformations do not show any importance in the growth rate of strains, because of their same age times (3–5 h within TS media). The colour congo red is absorbed on the cell surface property in mycobacterium [47,48], was used as a source of connection of these two strains. Similarly, more number of strain was absorbed in ATCC 607 cells as of this strain shows more colour than mc2 155. At the time when the layer motility of these strains on culture plates was stopped, cells from ATCC 607 strain was identified to show an increase in the corona constant, smaller than those from mc2 155 strains. Finally, the cell layer of ATCC 607 strain shows a more negative net charge than mc2 155. But no analytical contrast was identified within the strain when cell surface hydrophobicity was assessed by hexadecane structure [49]. The cell wall bilayer of *M. tuberculosis* contains phthiocerol dimycocerosates and *M. smegmatis* contains glycopeptidolipids. Chromosome arrangement of *M. smegmatis* is very similar to *M. tuberculosis*.

Dormancy

In the presence of environmental stress and immune responses from host, *Mycobacterium* will acquire a dormancy type which results in reduced metabolic activity and transcription rates. When favourable condition returns, significant changes in denova transcription, radioactive uracil incorporation will occur after the resuscitation of 24 h. Genes responsible for fatty acid synthesis such as fatty acid synthase system I and system II and transcription factor will be upregulated. After the second resuscitation phase of about 4 days, central metabolism genes will start encode ribosomal proteins, ATP-synthass, NADH dehydrogenases and cell division will be activated. A competitive study of *M. smegmatis* and *M. tuberculosis* showed that after resuscitation, the reactivation characteristic of both the microbe is highly similar. Based on this results we can suggest that *M. smegmatis* will be highly useful as a model organism to study dormancy of *Mycobacterium* species [50].

Ultrastructural highlights of the M. smegmatis *strains*

Cells of different strains ATCC 607 and mc2 155 of *M. smegmatis* was cultured in Sauton's medium that was observed by electron microscopy [50]. Ultrafine regions were coloured again with ruthenium red, counter strain that reacts with the layer of mycobacterium [51,52]. Investigation of a fine region that displayed for two strains shows the cell layer coat formed of (i) a plasma film, (ii) a theoretical 'periplasmic' gap, (iii) a rough interior electron thick surface, (iv) a fine electron-straightforward surface, challenging to identify in these fragments from an electron thick layer and (v) an electron-dense outer surface. This ultrastructure resembles that in recent mycobacterium species [53–55] and notably in *M. smegmatis* mc2 155, where the re-colouring of the electron-thick external coating. In *M. smegmatis*, electron-dense peptidoglycan layer and acid-containing electron transparent layer will be formed in the cell envelope during, whereas in *M. tuberculosis* septal electron dense peptidoglycan layer is not continuous in the cell envelope [56]. But both the microbe could be able to accumulate the lipid inclusions containing triglycerides under stress in vitro condition.

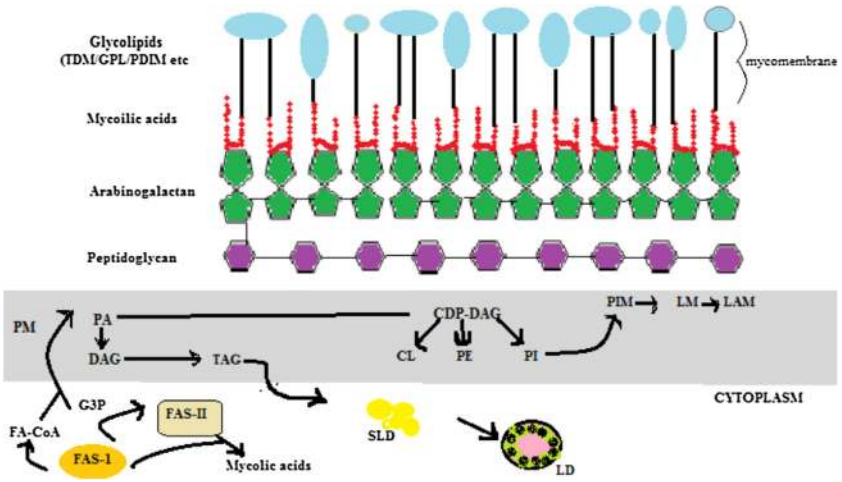

Fig. 3. Lipid layer of *M. smegmatis*.

M. smegmatis lipid

M. tuberculosis lives a long life in humans and it is said to be a slow-spreading pathogen inside the cell, it is the major cause for the global infective disease. The repetition of disease is based on the immune system of the host. To control TB, it is crucial to define the process of contact between pathogen present in the host and how it sustains in the host [57]. An appropriate as well as secure host-vector arrangement of a mycobacterium show is essential intended for it [58]. *M. smegmatis* is a quickly developing non-infectious microbe; it is commonly used for molecular investigation. However, the *M. smegmatis* mc2 155 strain is distinctly helpful since it has a huge rate of changing capacity [59,60]. Unfortunately, the c2 155 strain lives a shorter period in phagocytic cells. So, host-vector for the study of internal cell consistency is necessary. For the production of a host-vector framework in mycobacterium and the pure vector, pYT923, is duplicated in *M. smegmatis* J15cs and not in mc2 155 strains. The *M. smegmatis* J15cs strain has developed the sustainability of internal cell surface. Thus it can prolong for six days infective inside murine macrophage cell line J774, unlike different mycobacterial strains [61]. As well as, internal cell development of *M. smegmatis* is said to rely on the external layer as shown in Fig. 3. The J15cs strain produces a hard, brittle colony and displays a full, large electron surface in the cell wall on TEM analysis. The designation of various types of glycolipids and phospholipids decides the cell layer parts in the cell coat, cell wall stability, and phagocyte phenotype [62,63] changes. The durability of J15cs strain was supposed to be based on the shape of a cell wall. The J15cs cell line consists of high lipid content in the cell wall of fast alkali fast bacteria and continues for a long duration in the strain, and J774 corresponds to the adjustment of lipid compounds in the cell wall. Thus, the research reveals the lipid composition of J15cs and mc2 155 strains, and examined the results from their host cell.

M. smegmatis strain mc2 155 was usually utilized as a device for molecular investigation of mycobacterium to have a high rate of change. *M. smegmatis* is a quickly developing non-pathogenic mycobacterium. The strain, *M. smegmatis* J15cs that has the sustainability of living for 6 days in a murine vegetative cell. The J15cs strain creates a hard brittle segment, and prolonged life of J15cs strain was joined to cell wall segments. Thus, the lipid compounds of two strains were differentiated. The subdivisions and carbon types of the mycolic acids were fundamentally the same, as in addition tothe most imporrtant glycolipids along with phospholipids were indicated in the two strains. Polar glycopeptidolipids were eradicated from the J15cs strain. The accessibility of polar glycol peptide lipids provides the cell divider and design. Therefore, the polar glycol peptide lipids were identified by vegetative cells by use of toll like receptor 2 but not of 4. Thus authors have stated that non-aspect of polar glycol peptide lipids is a reliable component of J15cs strain, and alters its morphology and sustainability in a cell. Two parts were present in the outer membrane of Mycobacterium such as external and internal leaflets. Outer leaflets consist of various glycolipids like sulfolipids, phthiocerol dimycocerosate, glycopeptidolipids, phospholipids, trehalose 6,6′-dimycolate and trehalose monomycolate whereas inner leaflets consists majorly of mycolic acids. An envelope of the cell also contains other lipids such as phenolic glycolipids, polyacyltrehalose, triacyltrehalose and diacyltrehalose. Trehalose containing lipooligosaccharides will also be present in some fast growing Mycobacteria like *M. smegmatis*, *M. gordonae* and *M. canatti*. Lipids present in *M. tuberculosis* are sulfolipid, trehalose monomycolate, trehalose 6,6'-dimycolate, phenolic glycolipid, polyacyltrehalose and dimycocerosate. Biochemical characterization of *M. smegmatis* and *M. tuberculosis* with the addition of C16:0, a pyrazinamide and 5-chloro-pyrazinamide triggers C26:0 fatty acid from *M. tuberculosis* and C24:0 fatty acid from *M. smegmatis* [64].

Ecology

Biofilms of *M. smegmatis* could utilize sterol as a source of carbon from plants. The microorganisms will utilize the compound to a steroid hormone, androstenedione. If *M. smegmatis* utilizes expansive channel, which is the place it normally exists, at that point, the microbe will produce androstenedione. The steroid hormone inside the water affects the female mosquito, fish to identify male anatomical reproductive organ. [65].

Pathology

M. smegmatis does not consistently stay in any mammals, as well as does not cause contagious disease or infections. There are certain diseases that have changed superficial cases. There are enormous varieties of an organism that are pathogenic. Obligate pathogens, for example, *M. tuberculosis, Mycobacterium bovis*, and *Mycobacterium leprae* are highly pathogenic in nature. These organisms may cause TB, crippling, illness, etc., which will stay inside the host for long life. There are few likely pathogens in this classification such as *M. avium*, which stays outside the host state and cause harmful when it gets shrinked by the host. An Italian kid Tyke was affected by *M. smegmatis*, and he died when he was eight years old. After the examination of hereditary on tyke, states that four nucleotides were immersed, causing a shift and extreme change. The exons

Table 1
Significance and conviction of less, medium and high *MSM* and *MTB* framework level comparison.

Type of significance	Less conviction		Medium conviction		High conviction	
	MSM	*MTB*	*MSM*	*MTB*	*MSM*	*MTB*
Genome region	402	1163	1661	6972	836	4731
Gene bonding	86	337	16	52	6	99
Co-existance	316	1033	932	5862	369	1461
Trials	116	220	236	170	377	133
Statistical value knowledge	19	3	33	970	430	2002
Text removing	171	1174	224	722	38	93
Divided portion	0	0	42,805	20,915	6478	17,792
Chain relativity	0	8524	921	1345	244	77
Interologs	0	0	0	0	34	1701
PDB	0	0	0	5082	5487	864
Co expression	0	6538	3559	225	4523	4
Integrated score	55	6844	48,848	30,142	18,527	29,776

Table 2
Comparison of specification and estimations in *MSM* and *MTB* protein interactions.

Specifications	Estimations	
	MSM	*MTB*
Amount of proteins	4953	4136
Sum of functional junctions	66,543	59,919
Total junctions	755	201
Thickness	0.0054	0.007
Normal temperature	26	28
Normal length of short path	4.2224	3.62739
Sum of attached elements	166	23
Percentage of protiens in large elements	91.7%	98.7%

show an irregular stop of average protein production. But, the fact is that it shows typical pathogenic characters of *M. smegmatis*, this also reported that tyke has two mutants of an allele in his genome for microorganism that is especially harmful, overall, *M. smegmatis* is generally considered as non-pathogenic [66]. A heparin-binding hemagglutin protein called HbhA is usually present in pathogenic mycobacterium like *M. tuberculosis* and not in *M. smegmatis*. On the whole, *M. smegmatis* profoundly differs with *M. tuberculosis* in pathogenicity and virulence.

Frameworks level comparison in light of functional interaction network analysis

M. leprae may be an infective bacterium that causes disease, an affliction that impacts fundamentally the skin, peripheral nerves, eyes and mucous membrane of the respiratory tract [67]. *M. smegmatis* (MSM) combines with *M. tuberculosis* displays an opportunity to coordinate three mycobacterium with several genomes [68,69,70,71].

We have generated functional protein–protein interaction networks for *M. leprae*, *M. smegmatis* and used an updated *M. tuberculosis* network. In this interpretation, they made helpful protein–protein interactions frameworks for *M. leprae*, *M. smegmatis* and *M. tuberculosis* network [72]. The three frameworks were analysed by using a three-way approach such as MTB (slow grower) vs MSM (fast grower); MLP (slow grower) vs MSM fast grower) and MTB (slow grower) vs MLP (slow grower). The Exploitation of orthologous as portrayed as shown in Table 1.

The uncommon functional interactions and proteins among the 1001 set of proteins were removed from the original networks of three. This finding showed that the subnetworks of MLP and MTB were highly similar when compared to the subnetworks of MSM vs MLP and MSM vs MTB. Table 2 shows the comparison of protein interactions of MSM and MTB.

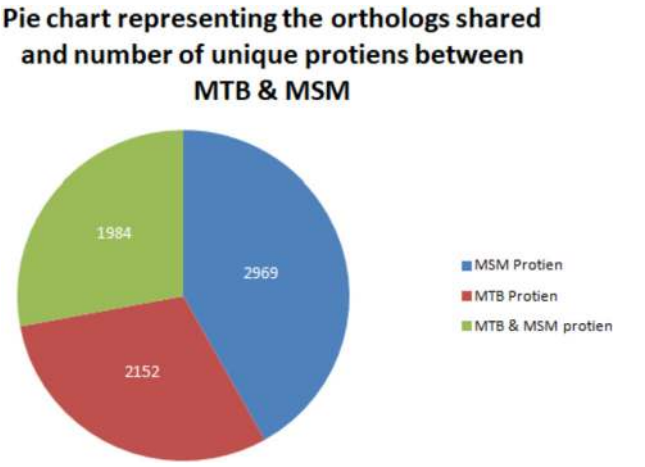

Fig. 4. Pie chart representing the orthologous and number of unique protein shared between *MSM* and *MTB*.

Recombinant *M. smegmatis* against *M. tuberculosis*

A set of mycobacterial gene and esx-3 region involved in killing *M. tuberculosis* by innate immunity. This esx-3 genes from orthologous *M. tuberculosis* was introduced in mutant *M. smegmatis* and found to be susceptible for killing by innate immunity and also have the ability to arouse the bactericidal immunity against virulent *M. tuberculosis*. This finding determined the role of esx-3 region in endorsing the virulence of mycobacterium and also identified as a supreme candidate which has a potential as a vaccine vector for *M. tuberculosis*. The orthologous and number of unique protein shared between *MSM* and *MTB* is shown in Fig. 4 [73–75]. Thus recombinant *M. smegmatis* can exert immunotherapy effects on the *M. tuberculosis* infection

X-beam analysis of M. smegmatis

Dps (deoxyribonucleic acid-restricting macromolecule as of predatory cells, involved in protecting the DNA from damage due to excess of oxygen when diet measures were low as depicted in *Escherichia coli* [76]. The rare crystal structures of the macromolecule from *M. smegmatis* make sure that deoxyribonucleic acid particles will embrace areas within the pattern without revealing the idea of dodecamer molecule [77–79]. The crystal structures of *M. tuberculosis* and *M. smegmatis* had been analysed in a study [80]. They found that RecA with its complexes such as dATP, ADP and ATPγS possess an increased site for binding similar to *M. tuberculosis*, but has a slight difference in their proteins and also its mode of binding with nucleotide.

Prosthetic total knee arthroplasty by M. smegmatis *and* M. tuberculosis

Staphylococci is the primary cause of prosthetic knee joint disease, which has been observed widely in living beings. Such as arthroplasty infection with unusual micro pathogens. Due to abnormal of mycobacterial prosthetic joint infection, diagnose and managing of strange disease reports laboratory test. A woman at the age of 71 years old, post agent after 40 days of combined knee arthroplasty was admitted in a hospital for left knee torment and doubted that arthroplasty infection. She had an outcome of disease and gave antimicrobial treatment orally for schematic ulcer; and oral antimicrobials for clinical postoperative septic bursitis. Finally, incision arthroplasty with patient's tissue of harmful bacteria shows growth of *M. smegmatis* association. Post-operative done with the oral doxycucline and levofloxacin that successfully ended up a supplanting arthroplasty with medical and microbial analysation of infections. Collecting the data on a survey of three existing instance of knee arthroplasty infections are mainly affected by *M. smegmatis* associations. Accordingly, to the thought of surgical techniques and antimicrobial determination, the foremost diagnose is composed of two types of surgical treatment. After the vast antimicrobial treatment, drawn by ideas of grafting arthroplasty. In this case, it demonstrates about maintaining unusual mycobacterial infections in post agent arthroplasty disease, which does not respond to usual surgical methods and antimicrobial. For an arthroplasty infection combining the atypical *M. smegmatis* gathering, two types of arthroplasty alteration [81,82]. Another study [83] showed the presence of *M. tuberculosis* in the tissues of joint arthroplasty affected patients. Hence both the microbe found to be associated with the knee arthroplasty.

Differentiating between live and dead M. smegmatis

To invent the fastest and powerful characteristic method for TB was attempted by Roy et al. It is generally crucial to analyse the patient retort to diagnose later, similarly the modified principle of a multi drug resistant tuberculosis safe (MDR) and extensively drug resistant (XDR) TB. Utilizing sputum spread microscopy, culture, and Gene expert, the culture could check properties of mycobacteria. That may cause up to one and a half months to culture *M. tuberculosis*, the patient may respond for the treatment otherwise the mycobacteria are still viable on the ground, and the patient has MDR or XDR TB. In this situation, diagnosing makes the victim helpless to have clinical impacts, such as liver injury. A fluorescent co-enzyme was usually found in mycobacteria known as co-enzyme factor 420 (F420) with an existing peak of 420 nm and production peak of 470 nm. Using *M. smegmatis*, they presented that live and dead pathogens observed various rate of photobleaching for 2 min. These preliminary survey suggested that particular photobleaching rates can be used analyze the patient's response to TB treatment. [84–86]. Both *M. smegmatis* and *M. tuberculosis* utilizes F420 coenzyme which provides intrinsic fluorescent property. By utilizing the F420 auto-fluorescent intensity measurements, the viability can be determined for both *M. tuberculosis* and *M. smegmatis*.

Effects of nutrition on growth

M. smegmatis mostly cultured using shaken culture in carbon, nitrogen and iron restricted media, composed with slowdown rate within the normal duration. The growth stage was concise; later deceleration stage might be due to the development of granular type growth. Media restricted culture showed a late development. In all the cultures with the presence of a higher proportion of riboxy nucleic acid/nitrogen sows elevated growth at the beginning and after reaching maximum growth, it will start declining. The deoxyribonucleic acid/nitrogen proportion additionally declined in the iron restricted cultures, yet expanded relatively in the nitrogen constrained cultures and, after a concise decrease, developed notably within the carbon-constrained cultures. In all cultures the dissolvable deoxyribonucleotide pool sustained within the range of 10–5 μm/g of nitrogen, as the aggregate dissolvable nucleotide media ranges from 1000 to 250 μm/g of nitrogen because of the low developmental rate. Mycobacteria has not investigated widely, and a region of obtainable research has affected by inability to identify some problems relieved in the evaluation of nucleic acid in these organisms. Such as, few results on the RNA molecule of mycobacteria [87] based on the use of pentose test for evaluation. Some techniques for the evaluation of nucleic acid in mycobacterium have prepared to retain far from these problems [88–90]. Tepper [91] observed change in DNA content during the growth of *Mycobacterium phlei* in some medium. Winder and Rooney [92] published regarding the DNA molecule *of M. tuberculosis* H37Ra from cultures at different incubation time, while Newton and Fahey [3] investigated both RNA and DNA molecule of tubercle bacillus BCG under the range of different growth conditions. The behaviour of segments of the dissoluble nucleotide media of this creature. Tuberculosis in natural conditions were studied in detail by Reutgen and Iwainsky and Carlberg and Jann [9394] gave information about the effect of phage infection on DNA molecule of *M. smegmatis*. Youmans and Youmans [89] examined the alterations in deoxyribonucleic acid as well as riboxynucleic acid in respect to macromolecules within this species along the growth restriction, zinc protected and 'metal-sufficient' media. Harris [95,96] changed this effort, using inactive cultures. For transporting carbohydrate, *M. tuberculosis* contains five significant transporters in the inner membrane, while 28 such transporters were found in *M. smegmatis*. Transporters for sulfate, phosphate and some amino acids have also been identified in the inner membrane of both the Mycobacterium. Nutrient uptake for both the microbe will be through the outer-membrane channel proteins. Porins set was also found to be different for *M. smegmatis* and *M. tuberculosis*.

Growth inhibition of M. smegmatis *and* M. tuberculosis *by mycobacteriophage-derived enzymes*

The capability of mycobacteriophage-inferred endolysins is to suppress the growth of *M. smegmatis*. The modified Lys B as mycobacteriophage Bxz2 was compared its action with exhaustive Lys B as mycobacteriophage Ms6. Interpretation of Lys B-treated *M. smegmatis* cells and LysB-treated filtered cell divider through spectroscopy confirmed the water eliminating action of that compound [97–100]. A study was conducted with *M. smegmatis* and *M. tuberculosis* for the effect of mycobacteriophage derived enzyme on its growth. It showed that both the microbe showed inhibition of concentration with the presence of these enzyme. They identified that LysB is a inhibitor of both the microbe which particularly act on mycobacterium because of its ability to attack mycolylarabinogalactan esterase leads to the hydrolyses of ester linkages joining the arabinogalactan with outer membrane which is rich in mycolic acid [101].

Effect of liposomes on growth of M. smegmatis

The collision of the liposome type of isoniazide (IN) and liposomes without IN on the Growth of *M. smegmatis* were considered. A Fluorescent test resulted that the portion of liposome that combined with *M. smegmatis* added up to 1–3%. A primary incubation of mycobacteria along with liposome caused declining in their reactivity to IN. Surprisingly an equivalent to impact was inspected while culturing *M. smegmatis* with oleic corrosive. It was said that

the relative protection of *M. smegmatis* to the anti-infection was depicted when using lipids as a carbon source because of some modification in operator digestion and it should be studied, when examining the in vitro liposomal types of anti-infection agents [102]. Similarly, *M. tuberculosis* when grown in the presence of liposomes partially inhibited its growth [103]. Thus, *M. smegmatis* and *M. tuberculosis* have a similar type of reactivity for liposomes.

Application studies

Several *M. smegmatis* are used to produce a compound, Xylitol. It is an impermeable sugar substance that is used as an alternate for entrepreneurial nutritional sugars to stop tooth decay and decrease plaque. It is likely imbedded slowly in the passage system, so it keeps unfavourable impacts of normal sugar level. It is used as a nutritional option for diabetics. It also has advanced drugs for osteoporosis and other respiratory disease. The D-xylulose sugar produced by *M. smegmatis* to give a useful xylitol compound [104].

M. smegmatis is also utilized to convert L-ribulose to L-arabinose along with the compound L-arabinose isomerises. *M. smegmatis* is responsible for producing L-arabinose during sugar digestion. This L-arabinose is used by various biotechnological organizations to produce chiral medicines. An investigator uses L-arabinose as a segment for some material culture medium. It is also used for making nutrition for the Maillard response to produce bread, brewed, etc. Like other microbial genera, the various species of Mycobacterium includes both saprophytic and pathogenic organisms. Pathogen type of mycobacterium includes *M. tuberculosis* and *M. leprae* the entire genome sequence of *M. tuberculosis* and *M. leprae* has resolved. At any cause attempted to differentiate the determinants of pathogenicity of these microorganisms. The Institute for Genomic Research (TIGR) had sequenced the genome of *M. smegmatis* and found that this microbe does not contain any pathogenic properties like *M. tuberculosis*. Thus the *M. smegmatis* differs with *M. tuberculosis* in pathogenicity. Another difference for *M. smegmatis* is its genome is 1.7 times greater than *M. tuberculosis* [105].

In spite of full *M. smegmatis* genome sequence is still being collected and is not been elaborated, the primary data showed 12 out of 19 *M. tuberculosis*'s pathogenic qualities were shared with homologues in *M. smegmatis*. Such qualities are primarily displayed in *M. tuberculosis*, assisting theory that they are specifically related with this microbe. At any point *M. tuberculosis* must process other hazardous qualities, or phenotypic alterations of these regular qualities. *M. smegmatis* can be used to differentiate the accurate aspect of these qualities, and it is frequently a prohibited type for some part of pathogenic characters of mycobacteria.

Based on this review we can conclude that *M. smegmatis* is a good model for studying the general biological properties of mycobacteria such as physiological conditions, responses to stress, reactivation from a non-culturable state, but it is not suitable for studying pathogenicity and virulence.

Competing interests

No Conflict of interest

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