Review Article

International Journal of Pharmaceutical Biological and Chemical Sciences

e-ISSN: 2278-5191

STUDY OF MEMBRANE FATTY ACIDS OF GRAM NEGATIVE BACTERIA AND ITS INFLUENCE TOWARDS THE TERRESTRIAL ECOSYSTEM

Lali Lingfa, Nathiya T, CH. VK Prudhvi, Sharmila R, Deepa R and Anand Prem Rajan*

Agricultural and Environmental Biotechnology Laboratory, School of Bio Sciences and Technology, VIT University, Vellore- 632014, India.

***Corresponding Author Email: aprdbt@gmail.com**

ABSTRACT:

Membrane fatty acids being the fundamental components of gram negative bacterial lipids contribute structural integrity, protection against the chemical and mechanical damage. Nature provides an enormous diversity in the composition of fatty acids to the different species of bacteria according to its habitat.Each bacterial species lives in different environment consist different grades and different types of fatty acid. With the help of some new and efficient analytical techniques the chemical complexity of fatty acid has been determined and it is now revealed that some polysaturated fatty acid, mono saturated fatty acids are found to be common amongst some groups of gram negative bacteria. This review indicates the recent year research done on many aspects of gram negative bacterial fatty acids and their influence towards the ecosystem. Some fatty acids discussed here may potentially be used as an active agent for recognizing certain important bacterium species in ecosystems.

KEYWORDS:

Gram negative bacteria, Fatty acids, Ecosystem.

1. INTRODUCTION

The fatty acid is an important carboxylic acid that exists either saturated or unsaturated in all the cell membrane of gram negative bacteria [1].Membrane fatty acid as part of lipids in gram negative bacteria plays important role in maintaining structural integrity and physiological functions of cell membrane [2]. Studies have mainly focused on maintaining different growth media for bacteria and methods for isolation of the fatty acids. Accumulation of knowledge regarding the chemistry of fatty acids has been lagging far behind the progress made in the studies of carbohydrates and proteins.

In recent year, membrane fatty acid has attracted attention of many researchers in both gram negative and gram positive bacteria [3, 4, 5, 6, 7, 8, and 9]. The biochemistry of the bacterium of fatty acids has been elaborated [10] till; there is a lacuna in the understanding the influence of membrane fatty acidspresent in the cell membrane of gram negative bacteria on terrestrial ecosystem.Therefore, the present study is to do comparative on fatty acid profile of gram negative bacteria as well as to understand the influence of towards terrestrial ecosystem.

2. MEMBRANE FATTY ACIDS

Biological membranes are not homogenous lipid mixtures, but rather, they are composed of dynamic lipid and proteins cluster referred to as micro domains that differ in their composition from their flanking regions [11]. Total fatty acid content in the most species of bacteria ranges between 1 to 10% of dry cell weight [12, 13]. Lipids are a large and diverse group of naturally occurring organic compound that share common physical properties, such as their solubility in non-polar organic solvent and in general insolubility in water. In terms of membrane composition, lipid can be classified into different groups: glycerolipids, sphingolipids and terpene- derived lipids. Fatty acid may contribute complex lipids, although they can be found as free entities in the membrane [14].

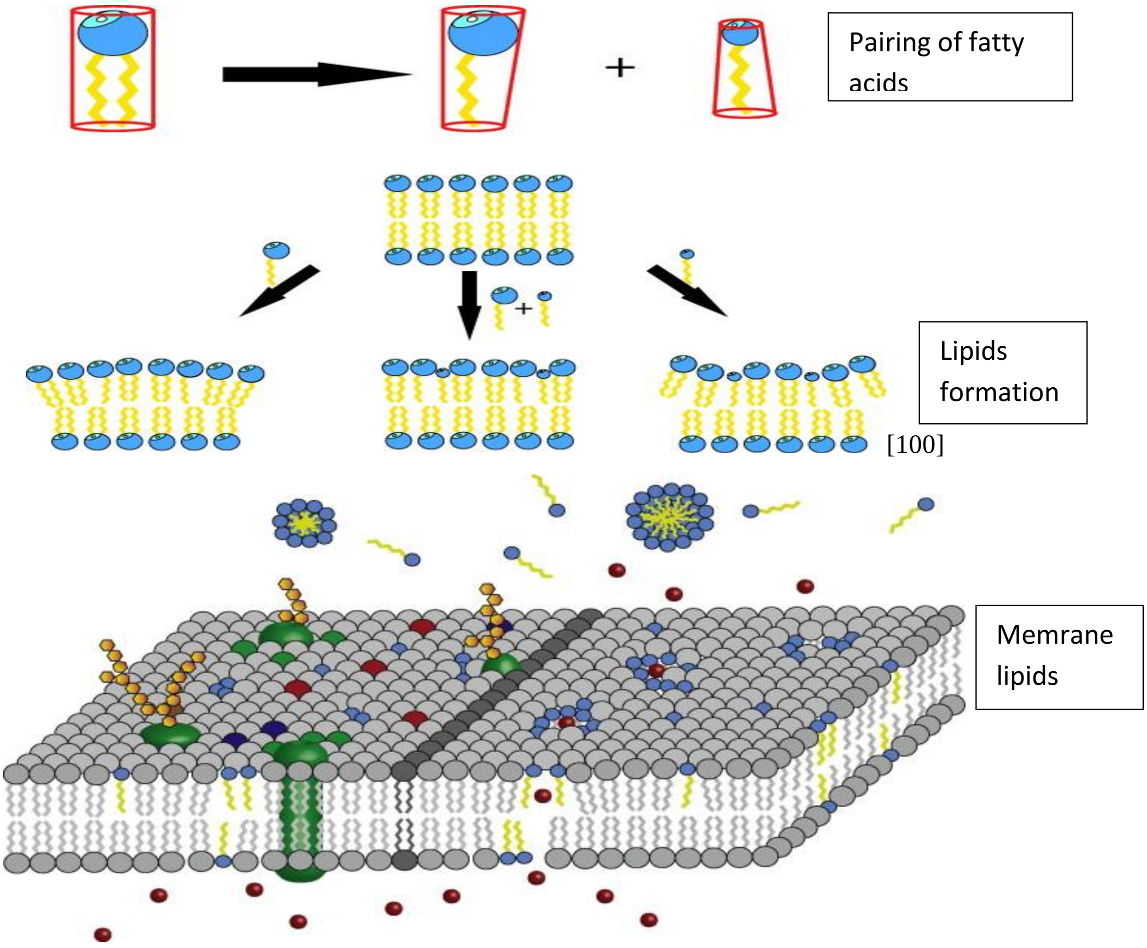


Fig 1.Cartoon illustration of the lipid complex membrane formation [100].

Lipid micro domainsform within the cell membrane has its unique composition that establishes environments that favor the activity of specific fatty acids and proteins [14].There isa compelling reason to believe that lipid domains exist, and they have been clearly demonstrated in model lipid monolayer and bilayer, their precise nature, compositions, size and dynamic in biological membranes still remain controversial [10].The number of fatty acids occurs in bacteria is vast.

According to the chemical nature and structural formula, fatty acids are categorized into many groups as shown in following figure:

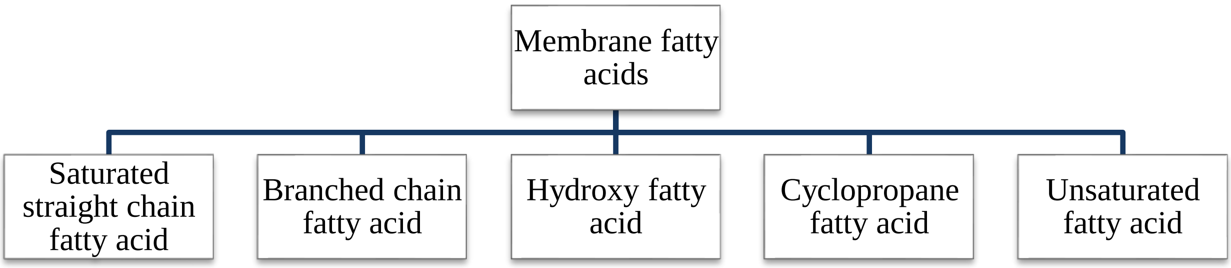


Fig 2. Types of membrane fatty acid present in every cell of bacteria

a. *Saturated straight chain Fatty acids*

Fatty acids having a chain of less than 12 carbon atoms have been detected in small amounts in virtually all species of gram negative bacteria. These fatty acids commonly found as follows acids: formic (C_1), acetic (C_2), propionic (C_3), butyric (C_4), caproic (C_6), Caprylic (C_8), and Capric (C_{10}). The higher fatty acids constitute a muchlargerproportion of the total fatty acid content of the cell. The acids included in this group are lauric (C), myristc (C_{12}), palmitic acid (C_{14}), steric (C_{16}), arachidic (C_{18}), behenic (C_{22}), lignoceric (C_{24}), and octaconsonoic (C_{28}). In bacteria palmitic acid occurs more frequently and usually in larger amount than any other saturated fatty acid found in the bacteria [15].There is less fatty acid reported to be having an odd number of carbon atom like evidence of C_{15} and C_{17} straight chain saturated acids in species *Pseudomonas aeruginosa*[16]. These fatty acids have yet to be identified with certainty [17].

b. *Branched chain Fatty acids*

Branched fatty acid is also a common constitute of bacterial lipids. This type of complex fatty acid has been isolated fromthe corynebacteria[14, 18, and 19]. These include chronic and diptheric acids, both of which have the same empirical formula, $C_{35}H_{68}O_2$, although they appear different in their structural details. Several derivatives of this fatty acid have been found in the same bacterial organisms.

Hausmann and Craigh[24] have shown that isootanoic, or methylheptanoic, acid ($C_8H_{12}O_2$) is produced by *Bacillus polymyxa*as a component of polymyxin B.

Akashi and Saito [20] have detected a branched chain $C_{15}$and C_{17} acid in the lipids of strains of some gram positive bacterial strain like *sarcina, Bacillus subtilis and Bacillus natto.* This compound was tentatively namedsarcinic acid. In later studies in the *Bacillus* species, Saito [26, 27] showed that the C_{15} was 15-Methylhexadecanoic acid.

Asselineau[23] has reported another two branched fatty acid, whichin *Bacillus subtilis*, and a C_{15} compound and the other a C_{16} substance.Further characterization of this is not being reported yet. They have also reported the presence of C_{19} branched chain fatty acid in the gram negative bacterial strain *Pasteurelapestis*. The detailed study of this has not been made yet.

c. *Hydroxy fatty acids*

These are the fatty acid, which has carboxyl group and a hydroxyl group at different positions in the fatty acid chain [28]. Fatty acids like β- Hydroxybutyric, β-Hydroxydecanoic, β-δ-β Methyl valeric acid and Dihydroxysteric are some examples for hydroxyl fatty acid [29, 30, 31, 10, 32, 33, and 34]. Crowder and Anderson [34] have discovered the presence of Dihydroxystearic acid.Asselineau and Lederer[18] discussed detail about the fatty acid called Corynomycolic acid ($C_{32}H_{64}O_3$), and caorynolic acid, a dihydroxy compound also known as corynine ($C_{52}H_{104}O_4$). These substances, have many similarities to the mycolic acid found in mycobacteria [10].β-Hydroxybutyric fatty acid has been found in several bacteria including species of *Azabacter*[29,108], *Chromobacterium*[29], *Bacillus* [30, 31, and97], *Pseudomonas* [29], and *micrococcus* [98]. Mevalonic acid has been isolated from culture of lactobacilli and other microorganisms [137, 138]. β-Hydroxydecanoic fatty acid occur in *E.Coli*[32], *Serratia species* [33], and various species of *Pseudomanaspyocyanea*[99].

d. *Cyclopropane fatty acid*

Cyclopropane fatty acid is unique in its chemical structure by having a cyclopropane in fatty acid chain [25]. Earlier it was believed that only C_{19} cyclopropane occurred in bacteria. This belief was based on the fact that no other such acid had been encountered in all bacteria that had been studied [10]. However, after frequent use of more sensitive techniques and apparatus has shown that any cyclopropane does occur in bacteria. Most probably C_{17} fatty acid found in the lipids of *E. coli*in 1959 [38] might be the first cyclopropane to be isolated and studied successfully. However, Hofmann and Lucas [45] first reported the presence of cyclopropane fatty acid as cis-11, 12- methylene –octadecanoic acid [100, 101, 102, and 103]. Thereafter, Dauchy and Asselineau [44] showed that such acid was indeed present in *E. coli*bacteria. The location of the ring the fatty acid chain is still under study. Most of this fatty acid is found and studied in gram negative bacteria. It is studied in very few in gram negative bacteria i.e. *E. coli, P. pestis* and in *A. tumefaciens* [32, 38, 36 and 15] as compared with gram positive bacteria. It is not yet determined whether this acid occurs naturally as D or L form of isomer. Lactobacillus acid has been identified in *Latobacillusarabinosus*[36, 43], *Lactobacillus casei*[36, 105], *lactobacillus delbrueckii*[36], and *Agrobacterium tumefeciens* [36, 37]. The possible occurrence of shorter cyclopropane fatty acid having a carbon number C and C has also been reported in *C. butyricum*[39,104].

e. Unsaturated fatty acid

Unsaturated fatty acid constitutes the major portion of the bacteria in all cell bacteria. Most of this fatty acid is under C_{18}. Very few literatures are successfully studied and published on this unsaturated fatty acid. Unsaturated fatty acid like octadecenoic acid commonly known as mono-saturated C_{18} fatty acid "oleic acid" was isolated in the year of 1952 from *L. arabinosus*[43].It was reported in same paper that this octadecenoic acid is of two different types. These are cis-11-octadecenoic and cis-9-octadecenoic. Octadecenoic acid of *L. arbinosus*was actually in cis- vacccenic acid (i.e, cis-11-octadecenoic). Oleic acid is cis-9-octadecenoic acid [10]. The unsaturated fatty acid called cis-vaccinesaresole octadecenoic acids that present in *L. casei*[105] and in *A. tumefeciens* [37]. According to the study of Hofmann and Tausig [41], major octadecenoic acid present in the bacteria is cis- vessenic accompanied by small amount of oleic acid. Octadecenoic acid present in *E. coli* as cis-vecenic acid was reported by Law [32]. Unsaturated fatty acid having 16 carbons and less has also been reported by Asano and Takahasi [22] in *C. diphtheria* and C_{10} and C_{12} unsaturated fatty acid was reported to be present in *Brucellasuis* by Gubarev et al. [106]. Hexadecenoic acid was reported to be found in *streptococci species* [41]. Alimova [21] reported the presence of unsaturated fatty acid C_{18} and C_{20} in the corynebacteria. Later they have reported the presence of unsaturated fatty acid C_{21-28} [21, 22].

3. Fatty acids spectra of some gram negative bacteria

Fatty acid spectra usually are collection of all fatty acids information present in the particular microorganism [35]. At the present time there are not enough fatty spectra has been made. Here, I have referred some thorough fully characterized in this respect are *Thiobacillusthiooxidans*[10], *Agrobacterium tumifacian*[40, 37], *Escherichia coli*[38], *Clostridium butyricum*[15], *Streptococcus species*[36, 41], *Lactobacillus debruekii*[15], *Lactobacillus casei*[36, 71], and *Lactobacillus arabinosus*[15, 43]. Compare to information availability lipids have been somewhat less intensively studied in other gram negative bacteria as comparative to gram positive bacteria. These gram negative bacteria are easily found in different growth conditions in nature i.e. in terrestrial ecosystems.

The fatty acid composition of these organisms is shown in **Table 2**. But, before this table I would like to show the Fatty acidspectra of all common Grams negative is shown in following table [10].

Table 1.***Fatty acid of common gram negative bacteria***

Common name	**Systematic name**	**Carbon atom**
Higher straight chain saturated fatty acids		
Lauric	Dodecanoic	12
Myristic	Tetradecanoic	14
Palmitic	Hexadecanoic	16
Stearic	Octadecanoic	18
Arachidic	Eicosanoic	20
Behenic		
	Docosonoic	22
Lignoceric		
	Tetracosonoic	24
Montanic		
	Octacosanoic	28
Hydroxy acids		
	3- Hydroxybutanoic	4
β-Hydroxy-butyric		
Malvanic(β-δ-Dihydroxy-β-methyl-valeric)	3,5–Dihydroxy–3–methyl pantanoic	6
	β-Hydroxyoctanoic(3– Hydroxyoctanoic)	8
		10\12\14\18
β – Hydroxymyristci		
	β-Hydroxydecanoic(3-hydroxydecanoic)	
Dihydroxysteric Corynomycolic		
	β–Hydroxydodecanoic(3– Hydroxydodecanoic)	32
Corynomycolenic		
	3 – Hydrotetradecanoic	
Corynolic		
	Di –hydroxyoctadecanoic	32
	Methylheptanoic	52
Branched chain fatty acid		
	6-Methyloctanoic	8
Isootanoic		
		9

Table 1.–(*Continued*)

Common name	Systematic name	Carbon atom
	13 - Methytetradecanoic	15
	15 - Methylhexadecanoic	17
		35
		35
Corinnic		
Diphtheric		
		17
	Methylene – Hexadecanoic	
Cyclopropane fatty acids		
		19
	Cis – 11, 12 – Matylene–octadecanoic	
Lactobacillic		
	Tetradecenoic	
		14
	Hexadecenoic	
Unsaturated fatty acids		16
	cis-9-Hexadecenoic	
		16
	cis-11-Hexadecenoic	
		16
	Octadecenoic	
Palmitoleic		18
	cis-9-octadecenoic	
Palmitvacenic		18
	cis-11-Octadecenoic	
		18
	Eicosenoic	
Oleic		20
	Heneicosenoic	
Cis- Vaccenic		21
	Docosenoic	
		22
	Tetracosenoic	
		24
	Octacosenoic	
		28

4. Comparative fatty acid spectra of few representative gram negative bacteria

As I mentioned earlier, I have been referring only few gram negative bacteria, although the identification and isolation of fatty acids has been done successfully on many interesting bacteria. Reason behind this is because, very few bacterial spectra has full information about the fatty acids. In case of gram negative bacterial spectra it is even lesser than gram positive's fatty acids spectral. For example, the gram negative bacterial which have been most thoroughly characterized in this respect are *Escherichia coli* [44, 32, 38], *Thiobacillus*species [46], *Agrobacterium tumefacience, Streptococcus species* [62, 72], *Camonas species* [17], *Shewanellaputrefaciens* [48], *Cyclobacteriummarinus* [49], and *Shigellaflexneri* [50]. The fatty acid composition of these gram negative bacteria is shown in **Table 2**. There are many bacteria whose fatty acid study has been less intensively studied and according to me they have not given considerable information about the fatty acids. Here in **Table 2**, I have taken the quantitative measure as the center point regardless of their qualitative nature. The qualitative nature of growth media of bacteria often regulates the physiology of bacteria and may also cause the quantity of its components like fatty acid itself [45].

Table 2. ***Fatty acid of some gram negative bacteria***

Fatty acids	*Escheric-hia coli*	*Agrobac-teriumtumefaci- ence*	*Camona-s species*	*Shewane-llaputrefaciens*	*Cyclobcteriummarinus*	*Shigella- flexneri*	*Thiobaci-llusthiooxidans*
Common Ecosystem	*Tropical soil[52]*	*Normal Soil* [57]	*Normal soil [47]*	*Soil/water [48]*	*Coastal marine soil [49]*	*Soil [50]*	*Soil of low* pH*[46]*
Saturated							
C_{10}	0.3	0.9					
C_{12}	0.3	4.0					3.8
C_{14}	0.7	1.1					$+^d$
				11.4			
C_{16}		8.2	3.5			4	7.7
				3.6	26		
$C_{16}+C_{17}^c$	85.4		4.3			35	2.6
					26		
C_{18}			5.2			41	3.1
					6		
$C_{18}+C_{19}^c$	0.5					3	10.5
					8		
Unsaturated						13	
C_{16}							9.9
C_{18}							2.4
$C_{16}+C_{18}$	11.6	63.6					
Cyclopropane							
C_{13}							$+^d$
C_{15}							$+^d$
				8.9	34		
C_{17}	$+^d$					4	3.4
					$+^d$		
C_{19}	$+^d$	9.4	0.6				$+^d$

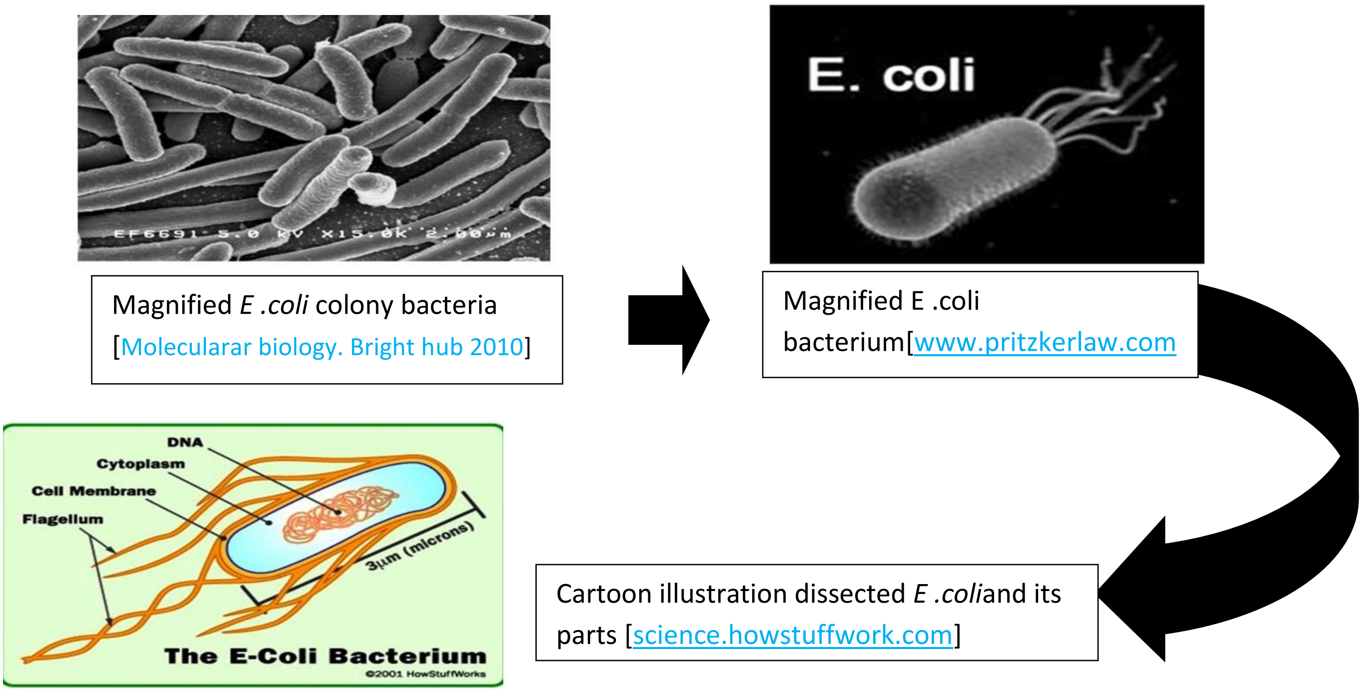
$+^d$ = Present but amount is either less than 1% or not determined.

^{c} = Cyclopropane acid.

4. Influence of bacteria to terrestrial ecosystem

a. *Escherichia coli*

Escherichia coli, commonly abbreviated as *E. coli* is a gram negative, facultative anaerobic, rod – shaped bacteria [51]. In terrestrial ecosystems, it is usually found in tropical soil having normal pH 5.8 -7 [52], temperature of 23 ^{0}C – 25 ^{0}C. It is reported [52] that when simple nutrients (Glucose and salts) were added to natural soil *E .coli* was shown to immediately increase by about three logs in its growth within 24 hours. The influence of the *E .coli* to habitat in tropical soil has not been fully studied. However, other related studies have been reported in many papers [38,53].



Magnified *E .coli* colony bacteria [Moleculararar biology. Bright hub 2010]

Magnified E .coli bacterium[www.pritzkerlaw.com

Cartoon illustration dissected *E .coli*and its parts [science.howstuffwork.com]

Fig 3.Scanning electron microscopy image and cartoon illustration of *E. coli* bacteria.

b. *Agrobacterium tumefaciens*

*Agrobacterium tumefaciens*is a gram negative rod shaped, flagellated, soil bacteria [54] that causes crown gal tumorsat wound sites of infected dicotyledonous plants which is characterized by a growth of tumor or gall on the infected plant, often the junction between the root and the shoot. [55].*Agrobacterium tumefaciens* is reported to be found in normal soil of neutral pH 7 [56].The influence of bacteria *Agrobacterium tumefaciens*to soil has not been fully understood. However, its important influence towards the agriculture biotechnology and its nature of pathogenicity is well described in many papers and references [54, 57]

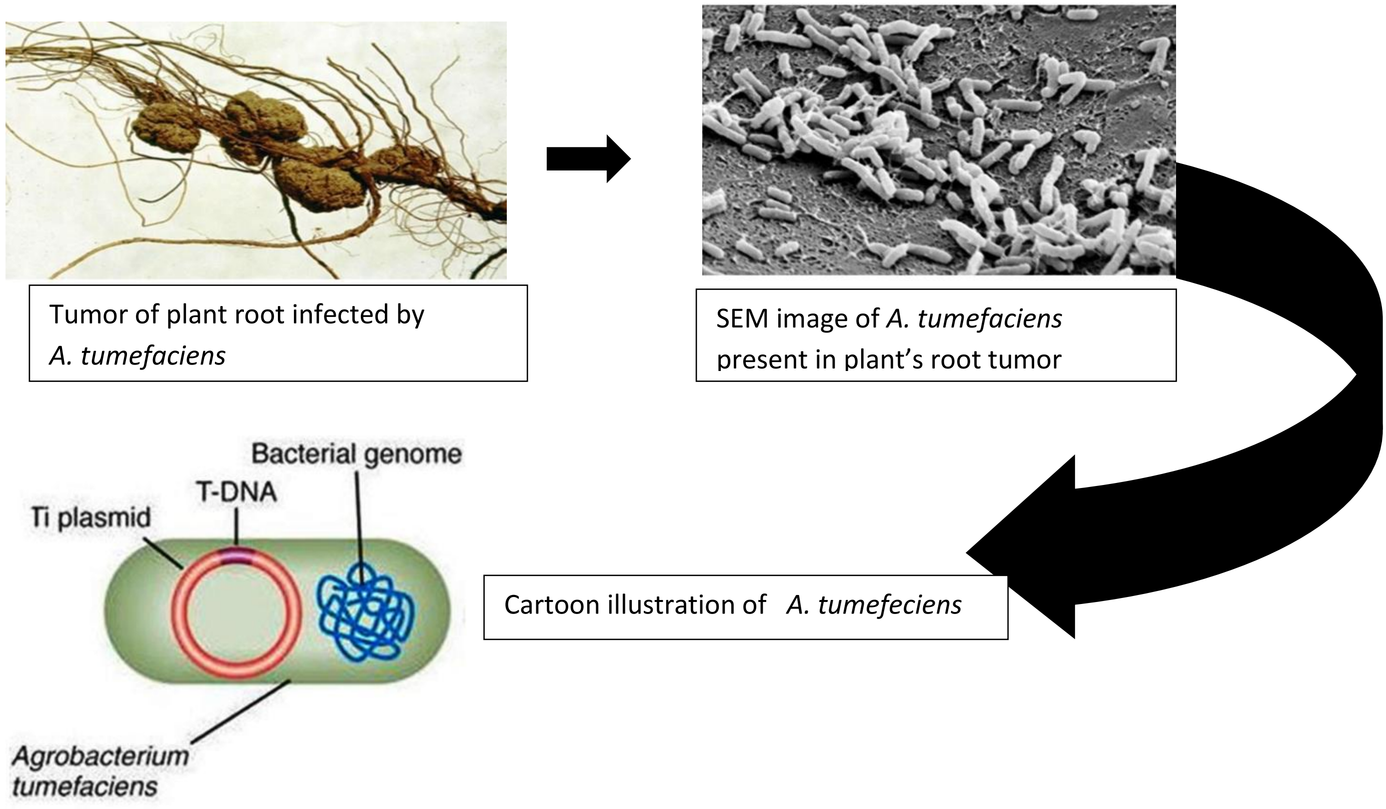


Fig 4. Scanning electron microscopic image and cartoon illustrated image of *Agrobacterium tumefaciens*[*International society of microbial cology*]

c. *Camonas*species

The *camonas*species is a strickly aerobic straight Gram – negative rod shapedpolarly flagellated bacteria [58, 59, and 60]. There are many types of *Camonas* species like *Camonaskoreensis, Camonastestosternai and Camonasacidovorans* but all of them share similar physical structure. These bacteria have attracted many researchers to study its influence to the terrestrial ecosystem and to the human health. Some paper has reported *Camonas*species to be opportunistic bacteriafor both plant and human [59, 61]. The genus *Camonas* includes many species [28, 34, 36, {411}] are reported to be successfully degraded the aromatic compounds and are considered to be an important species in biodegradation of toxic waste. The typical habitats of these species are in fresh water and marine habitat with low nutrient levels [58] but, some species like *Comanastestosternai* have been reported to be non - fermentative,chemoorgano–trophic bacteria that rarely attack sugars and well grow on organic acids and amino acids [62].

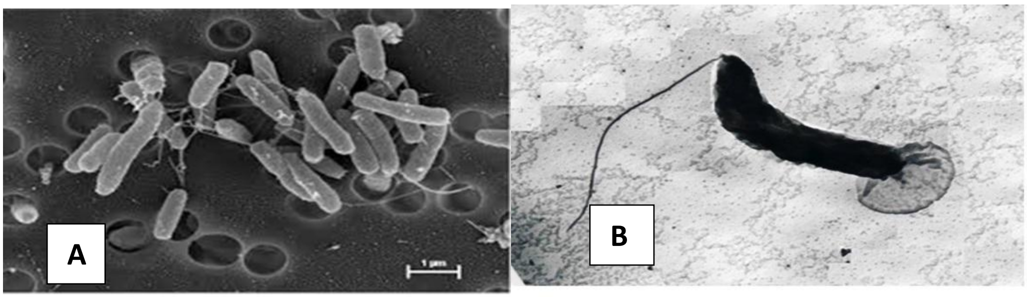


Fig 5. Scanning electron microscopic (SEM) image of *Casmanas* species

(A) Colony of *Camonas* species [111]

(B) Single polar flagelled*Camonas*species [222]

d. *Shewanellaputrefaciens*

*Shewanellaputrefaciens*are facultative anaerobic, gram negative, flagellated chemolithotrophicbacteria [63]. The natural habitat is usually in ground waste water, but, it is also found in ground soil,and in river [64]. The properties of being able to reduce metal by *Shewanella*species is reported [63, 64, 65, 66, 67 and 68]. *Shewanellaputrefaciens*are typical electro activechemolithotrophic bacteria [70], which can adsorb and transforms a range of metal ions [71, 72- 73] trough interaction of metal ions with outer membrane lipids [74, 75].

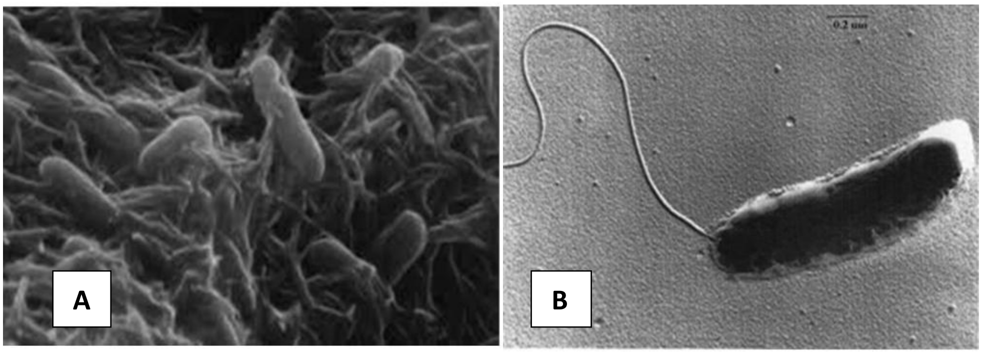


Fig 6.Scanning electron microscopic image of *Shewanellaputrefaciens*.

(A) Colony of *Shewanellaputrefaciens*[112]

(B) Single flagellated*Shewanellaputrefaciens* bacterium[www.x-divers.ru/aricles/technologies/36/full.html]

The *Shewanella*species have a very interesting ability for human welfare i. e known as bio electrochemical system [76, 77]. The bio electrochemical system is able of microorganism to create an electrochemical potential by transferring electron to extracellular electron acceptor [78-79]. *Shewanella*species in terrestrial ecosystem have a great deal of interest in their application for recalcitrant wastewater remediation using microbial fuel cells and microbial electrolysis cell [80] by reducing metal like gold, cobalt and ferrous to its corresponding anions. The process it follows to complete bio electrochemical is by using electrode as electron donors or electron donors for respiration, electron transfer of microbial cells, coupled with the reduction of pollutant leading to their reduced mobility and sequestration [63]. Furthermore, this species can live at extreme pH up to 2 and interestingly inorganic contaminants act as electron acceptors while in its bio electrochemical system [71, 81].*Shewanella* species are reported to be pathogenic both for fish and human health [80] other than bio electrochemical system.

e.Cyclobcteriummarinus

*Cyclobacteriummarinas*are gram negative, Oxidative chemoorganotrophic bacteria, mostly found in soil, marine water and in oil [83, 84]. The *Cyclobacterium*species have a very unique ring like and mostly non - flagellated [811]. Studies have reported *Cyclobacterium*species to be growth on red algae and other marine life [86]. *C. marinus*required NaCl for growth and variety of organic compound in seawater for its growth [85]. The influence of these bacteria like pathogeneticity, the property of being able to reduce metal and other influences on terrestrial system is not clearly understood yet. The lipid composition of the *Cyclobacterium*has been studied thoroughly and reported to be having mostly polar lipidsi.e. glycolipid type.

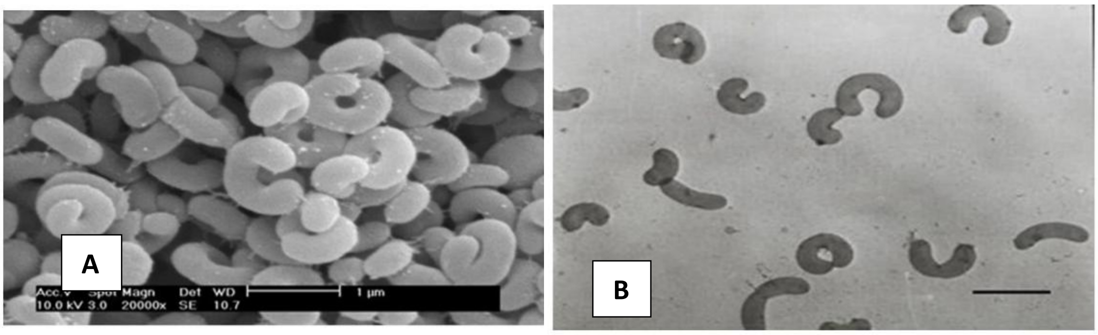


Fig 7.*Cyclobacterium* species SEM, scanning electron micrograraph image

(A) Scanning electron micrograph image of *Cyclobacteriummarinus*[109]

(B) Transmission electron microscopy image of*cyclobacteriummarinus*[110]

e. *Shigellaflexneri*

*Shigellaflexneri*is a rod shaped,lactose fermenting, non-spore forming, non-motile, facultative anaerobic Gram negative bacteria [88]. Naturally *Shigellaflexneri*are found in a low pH environment, 37 ^{0}C of temperature [87]. The required conditions not easy to find in terrestrial ecosystems hence, the *ShigellaFlexneri*israrely found in soil. *Shigellaflexneri* are found in the human gastrointestinal tract, which seems to be fulfilling the require environment for its growth [87]. The influence of *Shigellaflexneri* to terrestrial ecosystem is not clearly studied, but, its influence of the human health has been studied far enough.

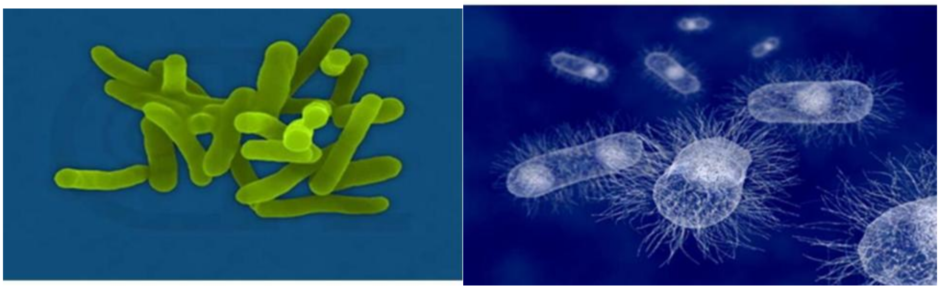


Fig 8. Transmission electron microscopic image of *Shigellaflexneri* [$^{©}$Dennis Kunkel Microscopy, Inc]

The *Shigella* species have been reported to be pathogenic for human health like *Shigelladysenterriae*, one of four *Shigella species*, that causes classic bacillary dysentery, which is most severe form of shigellosis (an enterobacterium disease) [89]. The same paper reported that *Shigellaflexneri*and *Shigellaboydii*can cause mild or severe infections. It is further need to study on *Shigella* species and its interaction with the terrestrial ecosystem.

f. *Thiobacillus*species

Most of the *Thiobacillus*species share same basic physical property. *Thiobacillus species* have been reported to be very important gram negative bacteria that present mostly in extreme environments like in low pH environments [90].*Thiobacillus species* have high economic importance in bioleaching which helps in the recovery of the lost minerals like ferrous, suphate and suphur. These bacteria usually use in leaching out of acid drainage situation. These bacteria use in the extraction of metals from ores [90]. The extraction of minerals from the ores by means of bioleaching is more environmental friendly [91]. There are different bioleaching techniques to extract ores from different source like hydrometallurgical for extraction of metal from solid ores. *Thiobacillus species* usually attach to the surface of ore during the bioleaching[92]. During mineral extraction by the use of *Acidithiobacillusferroxidans* formation of crystal boundaries around ore restrict the attachment of bacteria often [93]. Later the formation of the biofilm takes place. The Layer is formed as continuous extracellular polymeric substance in a few weeks after the initial attachment of cells and the extraction of minerals is done by bioleaching. These extracellular polymeric substances are the LPS which consist of fatty acids **[**94, 95, and 107**]**.

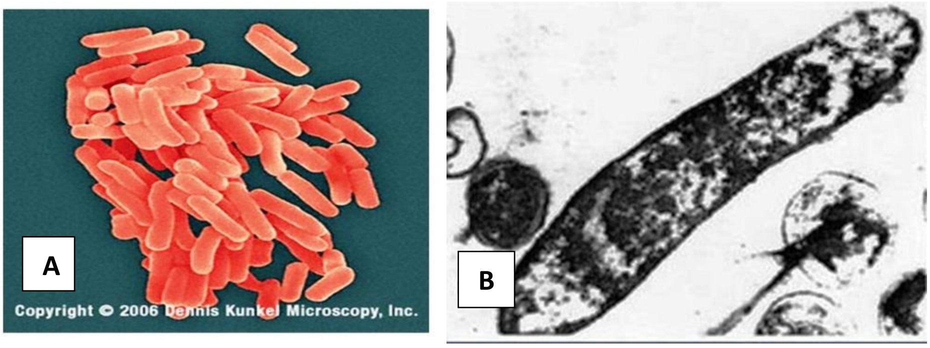


Fig 9. (A) Scanning electron microscopic image of *Thiobacillusferrooxidans*[$^{(c)}$ Dennis Kunkel Microscopy, Inc]
(B) Highly magnified microscopic image of *Thiobacillusferrooxidans* [109].

4. CONCLUDING REMARKS

The study of membrane fatty acids has become one of the important fields in research of membrane lipids. Habitate of gram negative bacteria and its ability to show various characteristic like chemolithotrophic, chemoorganotrophic, pathogenicity, autotrophic and symbiotic has influence some researcher to do study details about the mechanism of the bacteria to performed these property and bioproduct that often involved in the mechanism. Most of the time membrane lipids have been reported to be involved in the reaction, protection and interaction with the specific substance or host of the gram negative bacteria. The fatty acids study of the gram negative bacteria is present in varying concentration and in varying types according to its corresponding bacteria. Different bacteria having little similarity in its fatty acid profile show almost similar characteristic and show similar influence to the terrestrial ecosystem for example: *Shewanellaputrefaciens, shigellaflexneri, camonas* species *and thiobacllus species* share similarity in having unsaturated fatty acid and cyclopropane fatty acids all of them can be grown in low pH environment.*Shewanellaputerfaciens* and *Thiobacillus* species also share similarities in saturated fatty acids, thus, possibly both of them share similar properties of reducing and oxidizing the metals.

Among the gram bacterial fatty acids profile *Thiobacillus*species have more types of fatty acids and it is followed by Shigella*putrefacien*and Escherichia coli and *Agrobacterium tumefaciens*. *E.coli*, *Agrobacterium tumefacies*and *Camonas* species share similar fatty acid profiles of saturated and unsaturated fatty acids. *Camonas*species havea minimum fatty acid type, it shows highest tolerant to the salt water. Some of these bacteria have been reported been reported to be pathogenic to human, marine life and some have been reported to be pathogenic to plant. Hence, there is a lacuna in understanding the specific fatty acid functions in contributions of the bacterial physiological action on its environment. The study of various fatty acids distribution in the gram negative bacteria has revealed the presence of varying types of fatty acids in different gram negative bacteria but, the major accomplishment in the study of fatty acid and its influence to the variousecosystems are still to be reported.

Acknowledgement

We would like to acknowledge the funding and support for the project "Differential membrane lipid profile and fluidity of *Acidithiobacillus ferroxidans* during the process of adhesion to minerals" under SERB Scheme, DST- with the reference of DO No. SR/S3/ME/0025/2010. The author wants to thank Dr. Preston Devasia for his support in manuscript discussion and improvement

3. REFERENCES

1. Jame Oliver O., and Rita Colwell. Extractable lipids of Gram-Negative Marine Bacteria: Fatty-Acid Composition. Systematic Biotechnology. 23 (1973) 442-458.
2. Dubois-BrissonnetF., MalgrangeC., Guerin-Mechin .L, Heyd .B and Leveau .J. Y. Effect of temperature and physiological state on fatty acid composition of *Pseudomaonasaeuruginosa*. Food microbiology. 55 (2000) 79-81.
3. Jiangwei.Y and Charles Rock .O. Phospholipid acid synthesis in bacteria. BiochimicaetBysiophysica Acta., 1831 (2013) 495-502.
4. Josef.E and Gerrad.L. Application of stable isotopes to investigate the metabolism of fatty acids, glycerophospholipid and sphingolipid. Progress in Lipid Research. 54 (2014) 14-31.
5. Carol Fischer .L, Derek Blanchette .R, Kim Brogden .A, Deborah Dawson .V, David Drake .R, Jeniffer Hill .R, Philip Wertz .W. The role of cutaneous lipids in defense. BiochimitaetBiophysicaActa. 1841 (2014) 319-322.
6. Enrica .C, Elenora .M, Veleria .B, Massimiliano .G, Victoria .V, Stefania De .L. Pectin functionalized with natural fatty acids as antimicrobial agent. International Journel of biological Macromolecules. 68 (2014) 28-32.
7. David J. Sanabria-Ros, Yaritza – Torres, Gamalier Maldonado-Dominguez, Idializ Dominguez, Camille Rios, Damarith Diaz, Jose W. Rodriguez, Joanne S. Altieri-Rivera, Eddy Rios-Olivares, Gabriel Clinton, Nasblymonatno, Nestor M. Carbelleira. Antibacterial activity of 2-alkynoic fatty acids against multidrug resistant bacteria. Chemistry and Physics of Lipids. 178 (2014) 84-91.
8. MaitaneIbarguren, David J. Lopez, Pablo V. Escriba. The effect of natural and synthetic fatty acids on membrane structure, microdomain organization, cellular functions and human health. BiochimicaetBiophysicaActa. 1838 (2014) 1518-1528.
9. Joshua B. Parsons, Charles O. Rock. Bacterial lipids: Metabolis and membrane homeostasis. Progress in Lipid Research. 52 (2013) 249-276.
10. William M. O'Leary. Fatty acid of bacteria. Bacteriol Rev. 26 (1962) 421-442.
11. Herbert .D. Chemical composition of micro-organism as function of their environment, Microbial Reaction to Enviroment. In G. G. Meynell and H. Gooder edition (1961) 391-416.
12. Knaysi .G. Chemistry of bacterial cell. Bacterial Physiology. In C. H. Werkman and P. W. Wilson edition (1951) 1-27.
13. Porter .J .R. The chemical composition of microorganisms. Bacterial chemistry and Physiology. John Willey and Sons, inc. (1946) 352-450.
14. Asselineau .J. Application of chromatotpgraphy to fatty acids. Chim .Anal. 39 (1957) 375-383.
15. Hofman .K, Henis .D .B and Panos .C. Fatty acid interconversion in lacto bacilli. J. Biol. Chem. 228 (1957) 349- 355.

16. James .A .T and Martin .J .P. The separation of and identification of saturated and unsaturated unsaturated fatty acids formic acids to n-Octadecanoic acids. Gas Liquid Chromatography. 63 (1956) 144-152.
17. Goldfine .H and Bloch .K. On the origin of unsaturated fatty acids in *Closridia*. J. Biol. Chme. 236 (1961) 2596-2601.
18. Asselneu .J, and Lederer .E. Chemistry and metabolism of bacterial lipids. Lipid metabolism. In Bloch .K edition. (1960) 337-406.
19. Gabarev .E .M, Lubenets E. K. Kanchukh A. A, and Galarev .Y .V. Fractionation and composition of lipid fraction of diphtheria bacteria. Biochimya 16 (1958) 139-145.
20. Akashi .S, and Saito .K. A branched saturated C_{15} acid (sarcinic acid) from *Sarcina*phospholipids and similar acids from several microbial lipids. J. Biochem. 47 (1960) 222-229.
21. Alimova .E .K. The distribution of lipids between the cell membrane and other components parts of the cell in diphtheria microbes. Biochemistry (U. S. S. R). 23 (1960) 193-198.
22. Asano .M and Takahasi .H. Bacterium components of *Corynobacterium diphtheria*. I. Studies of fats. J. Pharm. Soc. 65 (1945) 17-19.
23. Asselineau .J. Sur queleques application de la chromatogarphie en phase gas bacteriens. Ann. Inst. Pasteur. 100 (1961) 109- 119.
24. Hausmann .W and Craig .C .L. Polymyxin B_1: fractionation, molecular weight determination, amino acid and fatty acid composition. J. Am. Chem. Soc. 76 (1954) 4892-4896.
25. Allen Marr G and John L. Ingraham. Effects of temperature on the composition of fatty acids in *Escherichia coli*, J. Bacteriol 84 (1962) 1260-1267.
26. Saito .K. Chromatogarphic studies on bacterial fatty acids. J. Biochem. 47 (1960) 699-709.
27. Saito .K, Studies on bacterial fatty acids; the structure of subtilpendetadecanoic and subtilohepdetadecanoic acids. J. Biochem. 47 (1960) 710-719.
28. Miller L. T. Single derivatization method for routine analysis of bacteria whole-cell fatty acid esters, including hydroxy acids. Journal of Clinical Microbilogy 16 (1982) 584-586.
29. Forsyth .W .G .C, Hayward .A .C and Robert .J .B. Occurance of poly –β- hydroxybutyrc acid in aerobic gram negative bacteria. Nature. 182 (1958) 800-801.
30. Lemoigne .M, Delaporte .B and Croson .M. Contribtion a I’etudebotaniqueetbiochimique des bacteriens du genre *Bacillus*. Ann. Ints. Pasteur. 70 (1944) 224-233.
31. Weibull .C. the lipids of a lysozyme sensitive *Bacillus* species. Acta chem. Sacnd. 11 (1957) 881-892.
32. Law .J .H. Lipids of *Escherichia coli*. Bacteriol. Proc (1961) 126.
33. Cartwright .N .J. The structure of serratamic acid. Biochem .J. 67 (1957) 663-669.
34. Crowder .J .A and Anderson .R .J. A contribution to the chemistry of Lactobacillus acidophilllus. III. The composition of phosphatide fraction. J. Biol. Chem. 250 (1960) 487-495.
35. Myron Sasser. Indentification f bacteria by Gas chromatography of cellular fatty acids. MIDI.Technical Note 101 (2001).
36. Hof,ann .K, Henis .D .B and Panos . The estimation of fatty acids inter conversion into lactobacilli. J. Biol. Chem. 217 (1955) 49-60.
37. Hofmann .K, and Taousic .F. On the identity of phytomonic and lactobacilllic acids. A reinvestigation of fatty acid spectrum of *Agrobacterium tumefaciens*. J. Biol. Chem. 213 (1955) 425-432.
38. O’Leary .W .M. Involvement of methionine in bacteria lipid synthesis. J.Bacteriol. 78 (1959) 709-723.

39. Goldfine .H. Fatty acid metabolism in closteridiumbutiricum. Federation proc. 20 (1961) 273.
40. Hofmann .K, Hsio .C .Y, Henis .D .B and Panos .C. The estimation of fatty acid composition of bacterial lipids. J. Biol. Chem. 217 (1955) 49-60.
41. Hofmann .K, and Tausig .F. The chemical nature of fatty acids a group C Streptococcus species. J. Biol. Chem. 213 (1955) 415-423.
42. Hofmann .K and Sax .S .M. The chemical nature of the fatty acids of *Lactobacillus casei*. J. Biol. Chem. 205 (1953) 55-63
43. Hofmann .K, Lucas .R .A and Sax .S .M. The chemical nature of fatty acid of *Lactobacillus arabinosus*. J. Biol. Chem. 195 (1952) 473-485.
44. Dauchy .S and Asselineau .J. Sur les acides lipids de *Escherichia coli*.Existence d' unacide $C_{17}H_{32}O_{32}$ contenant un cycle propanique. Compt. Rend. 250 (1960) 2635-2637.
45. Hofmann .K, O'Leary .W .M, Yoho .C .W and Liu .T .Y. Further observation of lipids stimulation of bacterial growth. J. Biol. Chem. 234 (1959) 1672-1677.
46. Richard Levin .A. Fatty acid of *ThiobacillusThiooxidans*.Journel of Bacteiology. 108 (1971) 992-995.
47. Cory Lytle .A, Mark Fuller .E, Ying Dong Gan .M, Aaron Peacock, MaryDeFlaun .F, TullisOnstott .C and David White .C. Utility of hig performance liquid chromatography/electrospray/mass spectrometry of polar lipids in specifically Per-^{13}C labeled Gram – negative DA001 as a tracer for accelation of bioremediation in the surface. Journal of Microbiological Methods. 44 (2001) 271-281.
48. Mark Teece .A, Marilyn Fogel .L, Michael Dollhopf .E and KennetNealson .H. Isotopic fractionation associated with biosynthesis of fatty acid by a marine bacterium under oxic and anoxic conditions. Organic Geochemistry. 30 (1999) 1571-1579.
49. StanislavBatrackov .G, Denis Nikitin .I, Vladimir Sheichenko .I, AlexandrRuzhitsky .O. A novel sulfonic-acid analogue of cermide is major extractable lipids of gram-negative marine bacterium Cyclobacteriummarinus WH. Biochimicaet Biophysical Acta 1391 (1998) 79-91.
50. Anders Kussak and Andrej Weintraub. Quadrupole ion-trap mass spectrophotometry to locate fatty acids on lipids A from Gram-negative bacteria. Analytical Biochemistry. 307 (2002) 131-137.
51. Ivan Sondi and BrankaSalopek –Sondi. Silver nanoparticles as antimicrobial agent: a case study on *E. coli* as a model for gram negative bacteria.Jornal o colloid and interface science 275 (2004) 177-182.
52. Byappanahalli .M .N and Fujioka .R .S. Evidence that tropical soil environment can support the growth of *Escherichia coli*. Water Science and Technology. 38 (1998) 171-174.
53. Mollie WindfieldD, and Eduardo Groisman A. Role of NonhostEnviroments in the Lifestyles of *Salmonella* and *Escherichia coli*. Apllied and Enviromental Microbiology 69 (2003) 3687-3694.
54. RolaJadallah and Nasser Sholi. Isolation and detedtion of *Agrobacterium tumefaciens*from soil. Natural science 14 (2012) 77-84.
55. Marcel de Groot .J .A, Paul Bundock, Paul Hooykaas .J .J and Alice Beijersbergen G .M. *Agrobacterium tumefaciens*-mediated transformation of filamentous fungi. Nature Biotechnology. 16 (1998) 839-842.
56. Van Larebeke N, Engler G, Hostlers M, Van Den Elsacker S, Zaenen I, Schilperoort and Schell J. Large plid in agrobacterium tumefaciens essential for gall –inducing ility. Nature 252 (1974)169-170.
57. Hoekema .A, Hirsch .P .R, Hooykaas .J .J .P and Schilproort .R .A. Nature. 303 (1983) 179-180.
58. LinedaAitTayeb, Martine Lefevre, VirginePasset, Laure Diancourt, Sylvain Brisse and Patrick

Grimont A. D. Comparative phylogenies of *Burkholderia, Ralstonia, Comamnas, Brevundimonas*and realated organisms derived from *rpoB, gyrB*and *rrs*gene sequences. Research in Microbiology 159 (2008) 169-177.

59. Shengnan Shi, Xuwang Zhang, Fang Ma, Tieheng sun, Ang Li and Jiti Zhou. Cometabolic degradation of dibenzofuran by *Comamonas*sp. MQ. Process Biochemistry 48 (2013) 1553-1558.
60. Nishanth Kumar S, Moahandas C, BalaNambisan. Purification, structural elucidation and bioactivity of tryptophan containing diketopiperazines, from *Comamonas testosterone* associated with a rhabditidentomopathogenenic nematode against major human-pathogenic bacteria. Peptides 53 (2014) 48-58.
61. Tung-Li Tsui, Shih-Ming Tsao, Ken-Sen Liu, Tzy-Yen Chen, Ya-lin Wang, Ying-Hock Teng and Yuan-Ti Lee. *ComamonasTestosteroni*infection in Taiwan: Reported two cases and literature review. Journal of Microbiology, Imminology and Infection 44 (2011) 67-71.
62. Wei Ji, Yuanan Chen, Hao Zhang, Ziyi Li and Yuanhua Yu. Cloning, expression and characterization of a putative 7alpha-hydroxysteroid dehydrogenase in *Comamonas testosterone*. Microbiological Research 169 (2014) 148-154.
63. Alessandro Carmona-Martinez A, Falk Hanisch, Ute Kuhlicke and Thomas Neu R. Electron transfer and biofilm formation of *Shewanellaputrefaciens* as function of anode potential. Bioelectrochemistry 93 (2013) 23-29.
64. ZeynepAydinSinirlioglu, DenizSinirlioglu and FahriAkbas. Preparation and characterization of stable cross-linked enzyme aggregates of novel laccase enzyme from *ShewanellaPutrefaciens*and using Malachite green decolorization. Bioresource Technology 146 (2013) 807-811.
65. Ellen Martin Taratus, Sean G. Eubanks, Thomas J. DiChristina. Design and application of a rapid screening technique for isolation of selenite reduction-deficient mutants of *Shewanellaputrefaciens*. Microbiol,Res. 155 (2000)79-85.
66. Lopez-Caballero M. E, Sanchez-Fernandez J .A, Moral A. Growth and metabolic activity of *Shewanellaputrefaciens*maintained under different CO_2 and O_2 concentrations. International Journelof Food Microbiology 64 (2001) 277-287.
67. Yan Qiao, Xiao-Shuai Wu and Chang Ming Li. Interfacial Electron transfer of *Shewanellaputrefaciens* Enhanced by Nanoflaky Nickel Oxide Array in Microbial Fuel cells, Journel of Power source, doi: 10. 1016/jpowsour 2014. 05. 015.
68. SungjunBae, Yoonhwa Lee, man Jae Kwon, Woojin Lee. Riboflavin – mediated putrefaciens CN32 and Lepidocracite. Journal of Hazardous Materials 274 (2014) 24-31.
69. JeetVaria C, Susana Silva Martinez, Sharon Velasquez-Orta and Steve Bull. ElectrochimicaActa 115 (2014) 344-351.
70. Caccavo F. Jr, Lonergan D. J, Lovley D. R, Davis M, Stolz J. F and Mclnerney M. J. Geobactersulfurreducens sp. Nov., Hydrogen-and acetate-Oxidizing dissimilatory metal-reducing microorganism. Appl, Environ, Microbiol, 60 (1994) 3752-3759.
71. Masuda M, Freguia S, Y-F Wang, Tsujimura S and Kano K. Flavin contained in yeast extract are exploted for anodic electron transfer bu*Lactococcuslactis*, Bio-electrochemistry 78 (2010) 173 – 175.
72. Malvankar N. S, Vargas M, Nelvin K. P, Frank A. E, Leang C, Kim B-C, Mester T, Covalla S. F. Johnson J. P, Rotello V, M, Tuominen M. T, Lovley D. R, Tunabel metallic-likeconductivity in microbial nanowire networks, Nat. Nanotechnology 6 (2011) 573-579.
73. Inoue K, Leang C, Frank A. E, Woodard T. L, Nevin K.P, Lovley D. R. Specfic localization of the

c-type cytochrome omcZ at the anode surface in current-producing biofilm of*GeobacterSulfurreducens*. Enviro, Microbiol, Rep 3 (

74. Reguera G, McCartthy K. D, Mehta T, Nicoll J. S, Tuominen M. T and Lovley D. R. Extraction of cellular electron transfer via microbial nanowires. Nature 435 (2005) 1098-1101.
75. El-Nagger M. Y, WangerM .Y, Leung. T. D, Yuzvinsky T. D, Southam G, Yang G, Lau W. M, Nealson K. H, Gorby Y. A. Electrical transport along bacterial nanowires from *Shewanellaoneidensis* MR-1, Proc, Natl. Acad. Sci. 107 (2010) 18127-18131.
76. Rabaey K, Angenent L, Schroder U and Keller J. Bioelectrochemical systems: from Extracellular Electron Transfer to Biotechnological application. IWA Publishing, London 2010.
77. Rabaey K, Rozendal R. A. Microbial electrosynthesi-revisiting the ecletrical route for microbial production. Na. Rev. Microbiol. 8(2010) 706 – 716.
78. Hernandez M. E, Newman D. K. Extracellualar electron transfer, cell. Mol. Life sci 58 (2001) 1562-1571.
79. Watanabe K, Manefield M, Lee M, Kouzuma A. Electron shuttles in biotechnology. Curr. Opin. Biotechnol 20 (2009) 633-641.
80. Schroder U. Discover the possibilities: microbial bioeclectrochemical system and the revival of 100-year-old discovery. J. Solid State Electrochem 15 (2011) 1481-1486.
81. Ducommun R, Favre M-F, Carrad D, Fisher F. Outward electron transfer by *Saccharomyces cervisiae* monitored with a bi-cathodic microbial fuel cell-type activity sensor, yeast 27 (2010) 139-148.
82. Raj H. D and Paveglio K. A. Contributing carbohydrates catabolic pathways in *Cyclobacteriummarinus*.Journal of Bacteriology. 153 (1983) 335-339.
83. Raj H. D. *Microcylus*and realated ring-forming bacteria. Crit. Rev. Microbiol. 5 (1977) 243-269.
84. Raj H. D. The genus *Microcyclus* and related bacteria. Springer-Verlag Inc., New York (1981) 630- 644.
85. Raj H. D. A new species –*MicrocylusMarinus*. Int. J. syst. Bacterion 26 (1967) 528-544.
86. Sieburth J. M, Pratt H. L, Johnson P. W and Scales D. Microbiol Seascapes- a pictorial assay of marine microorganisms and their enviroments. Univerity Park Press, Baltimore. 1975.
87. Cotter R. J, Honovich J, Qureshi N, Takayama K. Structural determination of lipids A from Gram-Negative bacteria using laser desorption mass spectrometry, Biomed. Environ. Mass spectrum. 14 (1987) 591-598.
88. Aussel L, Brisson J. R, Perry M. B and Caroff M. Structure of the lipid A of *Bordetellahinzii*ATCC51730, Rapid column. Mass Spectrom 14 (2000) 595-599.
89. Gloria Tetteh L and Larry BeuchatR.Survival, growth, and inactivation of acid – stressed *Shigellaflexneri*as affected by pH and temperature. International Journa; of Food Microbiology 87 (2003) 131-138.
90. XingQing .Z, Rucheng .W, XiangCai .L, Jianjun .L, ChengXiang .L and Juan .L. Bioleaching of chalcopyrite by *Acidithiobacillusferroxidans.* Minerals Engineering. 53 (2013) 184-192.
91. Crundwell .F.K. How do bacteria interact with minerals? Hydrometallurgy. 73 (2003) 75-81.
92. Wiertz .J .V, Pedro Moya, Angel Sanhueza, Tomas Vargas. Influence of substrate polarization on activity of *Thiobacillusferrooxidans* in bioleaching. Hydrometallurgy. 94 (1994) 395-405.
93. Dong –Jin K., Debrata P., Kyung-Ho P., Jong-Gwan A., and Seoung-Won L. Effect of pH and Temerature on Iron Oxidation by Mesophilic Mixed Iron oxidizing Microflora, 49 (2008) 2389-2393.

94. Marlen .B, Eugenia .J, and David Holmes .S. Identification of a gene cluster for the Formation of Extracellular Precursors in Chemolithoautotroph*Acidithiobacillusferrooxidans,* Appl Environ Microbiol.,71 (2005) 2902-2909.
95. Barbara .V, Miao .C, Russell Crawford .J and Elena Ivanova .P. Bacterial ExtracellualarPollysaccharides Involved in Biofilm Formation. Molecules. 14 (2009) 2535-2554.
96. Renukadevi K.P., Angyarkanni J., Karunakaran J.G. Extraction and characterization of lipopolysaccharides from serratiarubidaea and its cytotoxicity on lungs cancer cell line –NCL-H69, 2 (2012) 2067-3809**.**
97. Williamson D. H, and Wilkinson J. F. The siolation and estimation of the poly-β-hydroxybutyrateinclussion of *Bacillus* species. J. Gen. Microbiol. 19 (1959) 198-209.
98. Smithies W. R, Gibbons N. E and Bailey S. T. The chemical composition of the cell and cell wall of some halophilic bacteria. Can. J. Microbiol 1 (1955) 605-613.
99. Bergstorm S, Theorell S. H, and Divide H. Pyolipid acid, a metabolic product of *Pseudomonas Pyocyanea*, active against *Myobacterium tuberculosis*. Arch. Biochem. 10 (1946) 165-166.
100. Hofmann. K, Jucker. W, Miller W. R, Young A. C and Tousig F. On the structure of lactobacillic acid. J. A. Chem. Soc. 76 (1954) 1799-1804.
101. Hofmann K, Marco G. J, and Jeffrey G. A. Studies on structure of lactobacillic acid. III. Position of the cyclopropane ring. J. Am. Chme. Soc 80 (1958)1672-1677.
102. Hofmann K, and Orochena S. F and Yoho C. W. An equivocal synthesis of DL –cis-9, 10-methyleneoctadecanoic acid (dihydrosterculic acid) and DL-cis-11, 12-Soc. 79 (1957) 3608.
103. Hofmann K and Panos C. The biotin-like activity of lactobacillic acid and related compounds. J. Biol. Chem. Soc210 (1954) 687-693.
104. Goldfine H and Bloch K. On the origin of unsaturated fatty acid in *Clostridia*. J. Biol. Chem. 236 (1961) 2596-2602.
105. Hofmann K and Panos C. The chemical nature of fatty acids of lactobacillus casie. J. Biol .Chem 205 (1953) 55-63.
106. Gubarev E. M, Bolgova G. D and Alimova E. A study of free lipids bound faction of The *Brucell*type *suis*44 by methods of chromatography. Biochemistry (U. S. S. R) 24 (1959) 185-289.
107. Renukadevi K.P., Angyarkanni J., Karunakaran J.G. Extraction and characterization of lipopolysaccharides from serratiarubidaea and its cytotoxicity on lungs cancer cell line –NCL-H69, 2 (2012) 2067-3809.
108. LemoigneM, and Girard H. Reserve lipidique β-hydroxybutyriques. Comt. Rend 217 (1943)557-559.
109. Hnry Lutz Ehrlich,Geomicrobiology, 2nd edition 1990.
110. Olga Nedashkovskaya,Seung Bum Kim, MyungSookLee,MyungSoo Park, Kang Kyun Lee, Anatoly Lysenko M, Hyun Woo Oh, Valery Mikhailov V and Kyung Sook Bae. *Cyclobacter iumamurskyense* sp. Nov., a novel marine bacterium isolated from sea water. International journel of Systematic and Evolutionary Microbiology. 55 (2005) 2391-2394.
111. Ying J.-Y , Wang B.-J., Yang S.-S, and Liu S.-*J. Cyclobacteriumlianum* sp. nov., a marine bacterium isolated from sediment of an oilfield in the south china a, and embeded description of the g*enus Cyclobacterium*. 56 (2014)2927-2930.
112. Liza Gross. Cultivating Bacteria's Taste for Toxic waste. Biology. Doi:10.1371/jurnal.pbio.0040282.

Corresponding author** ***Email address:
aprdbt@gmail.com