INTERNATIONAL JOURNAL OF RESEARCH IN COMMERCE, IT & MANAGEMENT

IJRCM

A Monthly Double-Blind Peer Reviewed (Refereed/Juried) Open Access International e-Journal - Included in the International Serial Directories

Indexed & Listed at:

Ulrich's Periodicals Directory ©, ProQuest, U.S.A., EBSCO Publishing, U.S.A., Cabell's Directories of Publishing Opportunities, U.S.A., Google Scholar, Open J-Gage, India [link of the same is duly available at Inflibnet of University Grants Commission (U.G.C.)], Index Copernicus Publishers Panel, Poland with IC Value of 5.09 & number of libraries all around the world.

Circulated all over the world & Google has verified that scholars of more than **5000 Cities** in **187 countries/territories** are visiting our journal on regular basis.

Ground Floor, Building No. 1041-C-1, Devi Bhawan Bazar, JAGADHRI – 135 003, Yamunanagar, Haryana, INDIA

http://ijrcm.org.in/

CONTENTS

CALL FOR MANUSCRIPTS

We invite unpublished novel, original, empirical and high quality research work pertaining to the recent developments & practices in the areas of Computer Science & Applications; Commerce; Business; Finance; Marketing; Human Resource Management; General Management; Banking; Economics; Tourism Administration & Management; Education; Law; Library & Information Science; Defence & Strategic Studies; Electronic Science; Corporate Governance; Industrial Relations; and emerging paradigms in allied subjects like Accounting; Accounting Information Systems; Accounting Theory & Practice; Auditing; Behavioral Accounting; Behavioral Economics; Corporate Finance; Cost Accounting; Econometrics; Economic Development; Economic History; Financial Institutions & Markets; Financial Services; Fiscal Policy; Government & Non Profit Accounting; Industrial Organization; International Economics & Trade; International Finance; Macro Economics; Micro Economics; Rural Economics; Co-operation; Demography: Development Planning; Development Studies; Applied Economics; Development Economics; Business Economics; Monetary Policy; Public Policy Economics; Real Estate; Regional Economics; Political Science; Continuing Education; Labour Welfare; Philosophy; Psychology; Sociology; Tax Accounting; Advertising & Promotion Management; Management Information Systems (MIS); Business Law; Public Responsibility & Ethics; Communication; Direct Marketing; E-Commerce; Global Business; Health Care Administration; Labour Relations & Human Resource Management; Marketing Research; Marketing Theory & Applications; Non-Profit Organizations; Office Administration/Management; Operations Research/Statistics; Organizational Behavior & Theory; Organizational Development; Production/Operations; International Relations; Human Rights & Duties; Public Administration; Population Studies; Purchasing/Materials Management; Retailing; Sales/Selling; Services; Small Business Entrepreneurship; Strategic Management Policy; Technology/Innovation; Tourism & Hospitality; Transportation Distribution; Algorithms; Artificial Intelligence; Compilers & Translation; Computer Aided Design (CAD); Computer Aided Manufacturing; Computer Graphics; Computer Organization & Architecture; Database Structures & Systems; Discrete Structures; Internet; Management Information Systems; Modeling & Simulation; Neural Systems/Neural Networks; Numerical Analysis/Scientific Computing; Object Oriented Programming; Operating Systems; Programming Languages; Robotics; Symbolic & Formal Logic; Web Design and emerging paradigms in allied subjects.

Anybody can submit the **soft copy** of unpublished novel; original; empirical and high quality **research work/manuscript** ***anytime*** in ***M.S. Word format*** after preparing the same as per our **GUIDELINES FOR SUBMISSION**; at our email address i.e. infoijrcm@gmail.com or online by clicking the link **online submission** as given on our website (***FOR ONLINE SUBMISSION, CLICK HERE***).

GUIDELINES FOR SUBMISSION OF MANUSCRIPT

1. **COVERING LETTER FOR SUBMISSION:**

DATED: _____

THE EDITOR

IJRCM

Subject: **SUBMISSION OF MANUSCRIPT IN THE AREA OF _____.**

(e.g. Finance/Mkt./HRM/General Mgt./Engineering/Economics/Computer/IT/ Education/Psychology/Law/Math/other, please specify)

DEAR SIR/MADAM

Please find my submission of manuscript titled '_____' for likely publication in one of your journals.

I hereby affirm that the contents of this manuscript are original. Furthermore, it has neither been published anywhere in any language fully or partly, nor it is under review for publication elsewhere.

I affirm that all the co-authors of this manuscript have seen the submitted version of the manuscript and have agreed to inclusion of their names as co-authors.

Also, if my/our manuscript is accepted, I agree to comply with the formalities as given on the website of the journal. The Journal has discretion to publish our contribution in any of its journals.

NAME OF CORRESPONDING AUTHOR	:
Designation/Post*	:
Institution/College/University with full address & Pin Code	:
Residential address with Pin Code	:
Mobile Number (s) with country ISD code	:
Is WhatsApp or Viber active on your above noted Mobile Number (Yes/No)	:
Landline Number (s) with country ISD code	:
E-mail Address	:
Alternate E-mail Address	:
Nationality	:

* i.e. Alumnus (Male Alumni), Alumna (Female Alumni), Student, Research Scholar (M. Phil), Research Scholar (Ph. D.), JRF, Research Assistant, Assistant Lecturer, Lecturer, Senior Lecturer, Junior Assistant Professor, Assistant Professor, Senior Assistant Professor, Co-ordinator, Reader, Associate Professor, Professor, Head, Vice-Principal, Dy. Director, Principal, Director, Dean, President, Vice Chancellor, Industry Designation **etc**. ***The qualification of author is not acceptable for the purpose***.

NOTES:

a) The whole manuscript has to be in ***ONE MS WORD FILE*** only, which will start from the covering letter, inside the manuscript. ***pdf. version is liable to be rejected without any consideration***.

b) The sender is required to mention the following in the **SUBJECT COLUMN of the mail**:

New Manuscript for Review in the area of (e.g. Finance/Marketing/HRM/General Mgt./Engineering/Economics/Computer/IT/ Education/Psychology/Law/Math/other, please specify)

c) There is no need to give any text in the body of the mail, except the cases where the author wishes to give any **specific message** w.r.t. to the manuscript.

d) The total size of the file containing the manuscript is expected to be below **1000 KB**.

e) Only the **Abstract will not be considered for review** and the author is required to submit the **complete manuscript** in the first instance.

f) ***The journal gives acknowledgement w.r.t. the receipt of every email within twenty-four hours*** and in case of non-receipt of acknowledgment from the journal, w.r.t. the submission of the manuscript, within two days of its submission, the corresponding author is required to demand for the same by sending a separate mail to the journal.

g) The author (s) name or details should not appear anywhere on the body of the manuscript, except on the covering letter and the cover page of the manuscript, in the manner as mentioned in the guidelines.

2. **MANUSCRIPT TITLE:** The title of the paper should be typed in **bold letters**, **centered** and **fully capitalised**.

3. **AUTHOR NAME (S) & AFFILIATIONS**: Author (s) **name**, **designation**, **affiliation** (s), **address**, **mobile/landline number** (s), and **email/alternate email address** should be given underneath the title.

4. **ACKNOWLEDGMENTS:** Acknowledgements can be given to reviewers, guides, funding institutions, etc., if any.

5. **ABSTRACT**: Abstract should be in **fully Italic printing**, ranging between **150** to **300 words**. The abstract must be informative and elucidating the background, aims, methods, results & conclusion in a **SINGLE PARA**. ***Abbreviations must be mentioned in full***.

6. **KEYWORDS:** Abstract must be followed by a list of keywords, subject to the maximum of **five**. These should be arranged in alphabetic order separated by commas and full stop at the end. All words of the keywords, including the first one should be in small letters, except special words e.g. name of the Countries, abbreviations etc.

7. **JEL CODE:** Provide the appropriate Journal of Economic Literature Classification System code (s). JEL codes are available at www.aea-web.org/econlit/jelCodes.php. However, mentioning of JEL Code is not mandatory.

8. **MANUSCRIPT:** Manuscript must be in ***BRITISH ENGLISH*** prepared on a standard A4 size ***PORTRAIT SETTING PAPER***. *It should be free from any errors i.e.* ***grammatical, spelling*** *or* ***punctuation.*** *It must be thoroughly edited at your end*.

9. **HEADINGS:** All the headings must be bold-faced, aligned left and fully capitalised. Leave a blank line before each heading.

10. **SUB-HEADINGS:** All the sub-headings must be bold-faced, aligned left and fully capitalised.

11. **MAIN TEXT:**

THE MAIN TEXT SHOULD FOLLOW THE FOLLOWING SEQUENCE:

INTRODUCTION

REVIEW OF LITERATURE

NEED/IMPORTANCE OF THE STUDY

STATEMENT OF THE PROBLEM

OBJECTIVES

HYPOTHESIS (ES)

RESEARCH METHODOLOGY

RESULTS & DISCUSSION

FINDINGS

RECOMMENDATIONS/SUGGESTIONS

CONCLUSIONS

LIMITATIONS

SCOPE FOR FURTHER RESEARCH

REFERENCES

APPENDIX/ANNEXURE

The manuscript should preferably be in ***2000 to 5000 WORDS***, But the limits can vary depending on the nature of the manuscript.

12. **FIGURES & TABLES:** These should be simple, crystal **CLEAR**, **centered**, **separately numbered** & self-explained, and the **titles must be above the table/figure**. **Sources of data should be mentioned below the table/figure**. *It should be ensured that the tables/figures are referred to from the main text*.

13. **EQUATIONS/FORMULAE:** These should be consecutively numbered in parenthesis, left aligned with equation/formulae number placed at the right. The equation editor provided with standard versions of Microsoft Word may be utilised. If any other equation editor is utilised, author must confirm that these equations may be viewed and edited in versions of Microsoft Office that does not have the editor.

14. **ACRONYMS:** These should not be used in the abstract. The use of acronyms is elsewhere is acceptable. Acronyms should be defined on its first use in each section e.g. Reserve Bank of India (RBI). Acronyms should be redefined on first use in subsequent sections.

15. **REFERENCES:** The list of all references should be alphabetically arranged. ***The author (s) should mention only the actually utilised references in the preparation of manuscript*** and they may follow Harvard Style of Referencing. **Also check to ensure that everything that you are including in the reference section is duly cited in the paper**. The author (s) are supposed to follow the references as per the following:

- All works cited in the text (including sources for tables and figures) should be listed alphabetically.
- Use (**ed.**) for one editor, and (**ed.s)** for multiple editors.
- When listing two or more works by one author, use --- (20xx), such as after Kohl (1997), use --- (2001), etc., in chronologically ascending order.
- Indicate (opening and closing) page numbers for articles in journals and for chapters in books.
- The title of books and journals should be in italic printing. Double quotation marks are used for titles of journal articles, book chapters, dissertations, reports, working papers, unpublished material, etc.
- For titles in a language other than English, provide an English translation in parenthesis.
- ***Headers, footers, endnotes*** *and* ***footnotes*** *should* ***not be used*** *in the document.* However, **you can mention short notes to elucidate some specific point**, which may be placed in number orders before the references.

PLEASE USE THE FOLLOWING FOR STYLE AND PUNCTUATION IN REFERENCES:

BOOKS

- Bowersox, Donald J., Closs, David J., (1996), "Logistical Management." Tata McGraw, Hill, New Delhi.
- Hunker, H.L. and A.J. Wright (1963), "Factors of Industrial Location in Ohio" Ohio State University, Nigeria.

CONTRIBUTIONS TO BOOKS

- Sharma T., Kwatra, G. (2008) Effectiveness of Social Advertising: A Study of Selected Campaigns, Corporate Social Responsibility, Edited by David Crowther & Nicholas Capaldi, Ashgate Research Companion to Corporate Social Responsibility, Chapter 15, pp 287-303.

JOURNAL AND OTHER ARTICLES

- Schemenner, R.W., Huber, J.C. and Cook, R.L. (1987), "Geographic Differences and the Location of New Manufacturing Facilities," Journal of Urban Economics, Vol. 21, No. 1, pp. 83-104.

CONFERENCE PAPERS

- Garg, Sambhav (2011): "Business Ethics" Paper presented at the Annual International Conference for the All India Management Association, New Delhi, India, 19–23

UNPUBLISHED DISSERTATIONS

- Kumar S. (2011): "Customer Value: A Comparative Study of Rural and Urban Customers," Thesis, Kurukshetra University, Kurukshetra.

ONLINE RESOURCES

- Always indicate the date that the source was accessed, as online resources are frequently updated or removed.

WEBSITES

- Garg, Bhavet (2011): Towards a New Gas Policy, Political Weekly, Viewed on January 01, 2012 http://epw.in/user/viewabstract.jsp

COMPARATIVE STUDY OF FAME AND SEQUENCE ANALYSIS FOR IDENTIFICATION OF BACTERIA FROM INDUSTRIAL WATER OF KRIBHCO

N.J. NAIK
MANAGER
DEPARTMENT OF CHEMICAL LABORATORY
KRIBHCO
SURAT

ABSTRACT

There have been several systems developed in the past few years for rapid microbial identification. In the present study, two methods (GC FAME analysis and 16s rDNA sequencing) were compared for identification of bacteria. The results when compared, we found that the FAME results are equally similar to that of genotypic sequencing. five bacterial samples obtained from KRIBHCO plant and were analyzed, wherein FAME analysis, the automated system identified sample 1 to be Bacillus atrophaeus with 0.804 SI. The genotypic analysis also showed similar results, after BLAST the organism was identified to be Bacillus atrophaeus with 97% identity match. In case of sample 2, FAME analysis identified the organism to be Pseudomonas aeruginosa with 0.765 SI and sequencing also identified the organism to be Pseudomonas aeruginosa with BLAST showing 98% identity.

KEYWORDS
Bacteria, FAME, Sequencing, BLAST, Identification.

INTRODUCTION

Accurate identification of bacterial isolates is an essential task of the clinical microbiology laboratory. For many slow-growing and fastidious organisms, traditional phenotypic identification is difficult and time-consuming. Several commercial systems offer computer-assisted identification of a wide variety of bacterial organisms. The Biolog system (Biolog, Inc., Hayward, Calif.) was evaluated for the identification of strains likely to be encountered commonly in clinical laboratories [1,2], and the gas-liquid chromatography system developed by MIDI, Inc. (Newark, Del.), based on the cellular fatty acid profile. An automated cellular fatty acid (CFA) bacterial identification system, Microbial Identification System was compared with a conventional system for the species level identification of microorganisms. MIS identifications were based exclusively on the CFA composition. The MIS, as the first automated CFA identification system, is an accurate, efficient, and relatively rapid method for the identification of microorganisms [3,4].

Genotypic identification is emerging as an alternative or complement to established phenotypic methods. During the last decade, methods based on the analysis of DNA polymorphisms were added to this list of methodologies, for instance Random Amplified Polymorphic DNA (RAPD) [5], Arbitrarily Primed PCR (AP-PCR) [6] and micro satellite-primed PCR [7]. Polymerase chain reaction-mediated direct sequence determination can also be used as a rapid and reliable method for the identification of isolates in the clinical laboratory [8, 9]. The sequence of small-subunit rRNA varies in an orderly manner across phylogenetic lines and contains segments that are conserved at the species, genus or kingdom level [10, 11]. This method should be useful for increasing the amounts of bacterial 16S ribosomal DNA sequences for the purposes of sequencing and probing. This approach may make it possible to identify new, non-culturable organisms [12, 13]. The amplified segment is sequenced and compared with known databases to identify a close relative. The method is evaluated with respect to accuracy, sensitivity to modified nucleotides in the template RNA, and phylogenetic usefulness, by examination of several 16S rRNAs whose gene sequences are known [8,14]. In the present study, two methods, such as GC-FAME analysis and 16s rDNA sequencing were compared for identification of bacteria.

MATERIALS AND METHODS

The two cultures were obtained from soil sample and pure cultured onto Trypticase soya broth agar (TSBA) media at 28°C for 24 hours. The fatty acids were extracted and methylated to form fatty acid methyl esters (FAME). These FAME's were analyzed using Gas Chromatography (Agilent 6850 Series II) with the help of MIDI Sherlock software for FAME. Aerobic library was used. For DNA sequencing, the genomic DNA was extracted from the bacterial culture. The bioinformatics analysis was performed using NCBI BLAST (http://ncbi.nlm.nih.gov/blast) identifying the microorganism using online databases.

RESULTS AND DISCUSSION

We have analyzed two microbial cultures obtained from soil using FAME and sequencing approaches. On comparing FAME results with that of sequencing, it was found that both are similar to each other. Figure 1 shows peaks corresponding to the fatty acids identified through FAME analysis of bacterial sample one. The MIDI Sherlock microbial identification system using RTSBA 6 method identified the organism to be Bacillus-thuringiensis-kurstakii with 0.74 SI. The sequence analysis also showed similar results (Table 1).

TABLE 1: *BACILLUS-THURINGIENSIS-KURSTAKII* SEQUENCE ANALYSIS BY BLAST

	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus thuringiensis serovar konk	3.524e+05	8.702e+06	78%	0.0	99%	AE017355.1
Bacillus cereus F837/76, complete	3.049e+05	8.440e+06	77%	0.0	99%	CP003187.1
Bacillus cereus 03BB102, complete	3.045e+05	8.527e+06	78%	0.0	99%	CP001407.1
Bacillus anthracis str. H9401, comp	2.403e+05	8.912e+06	80%	0.0	99%	CP002091.1
Bacillus anthracis str. SVA11, compl	2.403e+05	8.887e+06	80%	0.0	99%	CP006742.1
Bacillus anthracis str. Sterne, comp	2.403e+05	8.925e+06	80%	0.0	99%	AE017225.1
Bacillus anthracis str. A0248, compl	2.403e+05	8.924e+06	80%	0.0	99%	CP001598.1
Bacillus anthracis str. 'Ames Ancest	2.403e+05	8.924e+06	80%	0.0	99%	AE017334.2
Bacillus anthracis str. Ames, compl	2.403e+05	8.924e+06	80%	0.0	99%	AE016879.1
Bacillus anthracis str. A16, complet	2.402e+05	8.923e+06	80%	0.0	99%	CP001970.1
Bacillus anthracis str. CDC 684, cor	2.402e+05	8.933e+06	80%	0.0	99%	CP001215.1
Bacillus anthracis str. A16R, compl	2.402e+05	8.921e+06	80%	0.0	99%	CP001974.1
Bacillus cereus AH820, complete g	2.313e+05	9.346e+06	82%	0.0	99%	CP001283.1

After the completion of BLAST analysis, the organism was identified to be Bacillus-thuringiensis-kurstakii with 97% identity match. Figure 2 depicts the chromatogram with fatty acid peaks identified through the FAME analysis of the second bacterial sample. The automated system identified the organism to be Pseudomonas aeruginosa with 0.765 SI. The sequence analysis also identified the organism to be Ps. aeruginosa with 98% identity match after BLAST (Table 2).

TABLE 2: *PSEUDOMONAS AERUGINOSA* SEQUENCE ANALYSIS BY BLAST

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain C gene island PAGI-4(C) sequence	63522	63522	100%	0.0	100%	AY258138.1
Pseudomonas aeruginosa plasmid Rms148 transposon Tn4661 DNA, comple	23462	23462	36%	0.0	100%	AB375440.1
Pseudomonas aeruginosa strain PACS88 clone fa1398, complete sequence	23255	23255	36%	0.0	99%	EU595754.1
Pseudomonas aeruginosa PA7, complete genome	23255	54692	93%	0.0	99%	CP000744.1
Pseudomonas aeruginosa strain PACS171b clone fa1386, complete sequence	23254	23254	36%	0.0	99%	EU595748.1
Pseudomonas aeruginosa PA38182, complete genome	22676	59779	96%	0.0	99%	HG530068.1
Pseudomonas aeruginosa UCBPP-PA14, complete genome	20332	60022	97%	0.0	97%	CP000438.1
Pseudomonas aeruginosa SCV20265, complete genome	20325	61291	96%	0.0	97%	CP006931.1
Pseudomonas aeruginosa DK2, complete genome	20194	64969	98%	0.0	99%	CP003149.1
Pseudomonas aeruginosa M18, complete genome	19752	20449	32%	0.0	99%	CP002496.1
Pseudomonas aeruginosa RP73, complete genome	19664	34631	58%	0.0	99%	CP006245.1
Pseudomonas aeruginosa c7447m genome	19642	22656	36%	0.0	99%	CP006728.1
Pseudomonas aeruginosa LES431, complete genome	19640	20336	32%	0.0	99%	CP006937.1
Pseudomonas aeruginosa LESB58 complete genome sequence	19640	20336	32%	0.0	99%	FM209186.1
Pseudomonas aeruginosa PAO1-VE13 genome	19631	22734	36%	0.0	99%	CP006832.1

Species level identification of microbes is possible through MIDI Sherlock microbial identification. Abel and colleagues first suggested that microorganisms could be classified by gas chromatographic analysis [16]. These concepts found application in the form of the Sherlock system. The Sherlock microbial identification system is solely based on computer comparison of the unknown organism's fatty acid methyl ester profile with the profiles of a predetermined library of known isolates with pattern recognition software. Identification of bacteria by conventional methods usually requires 48 h after a discrete colony has been isolated. Two weeks are required for the identification of many slow-growing and fastidious organisms by conventional methods. In some circumstances, no identification can be made after weeks of analysis, even by an experienced technologist [17].

ECL Deviation: 0.006 Reference ECL Shift: 0.016 Number Reference Peaks: 10

Total Response: 442595 Total Named: 414136

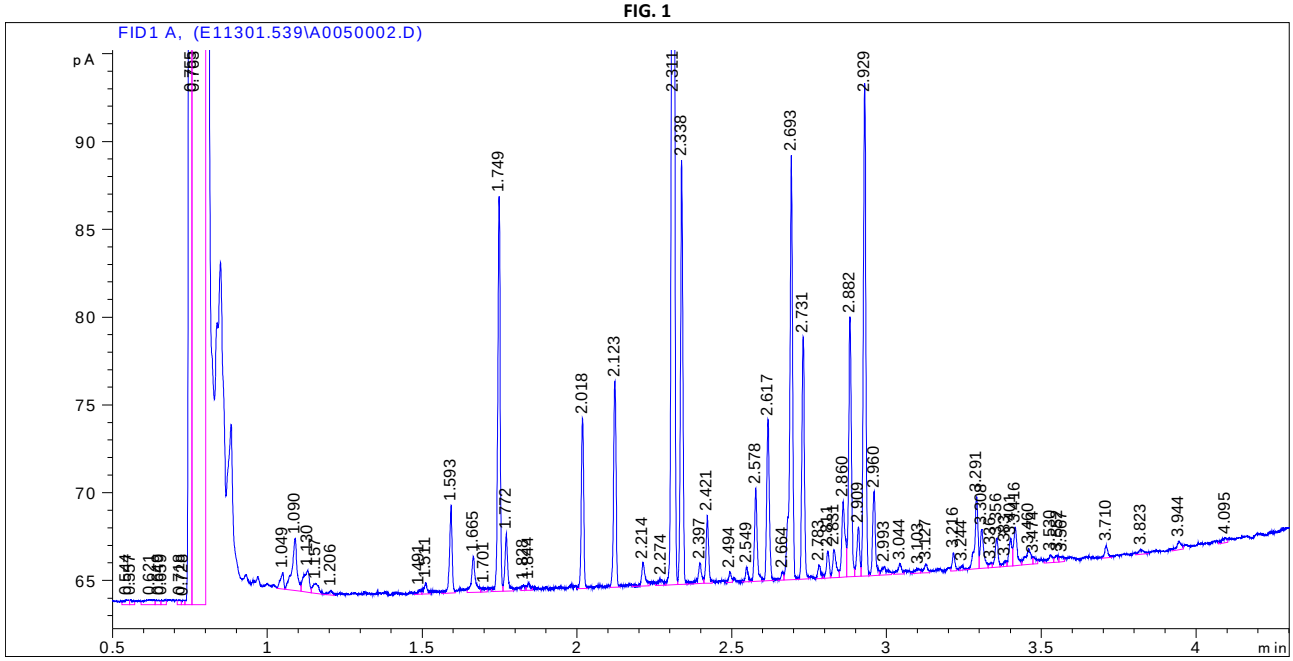
Percent Named: 93.57% Total Amount: 394254

Matches

TABLE 3

Library	Sim Index	Entry Name
RTSBA6 6.00	0.605	Bacillus-cereus-GC subgroup A
	0.370	Bacillus-thuringiensis-kurstakii

FIG. 1

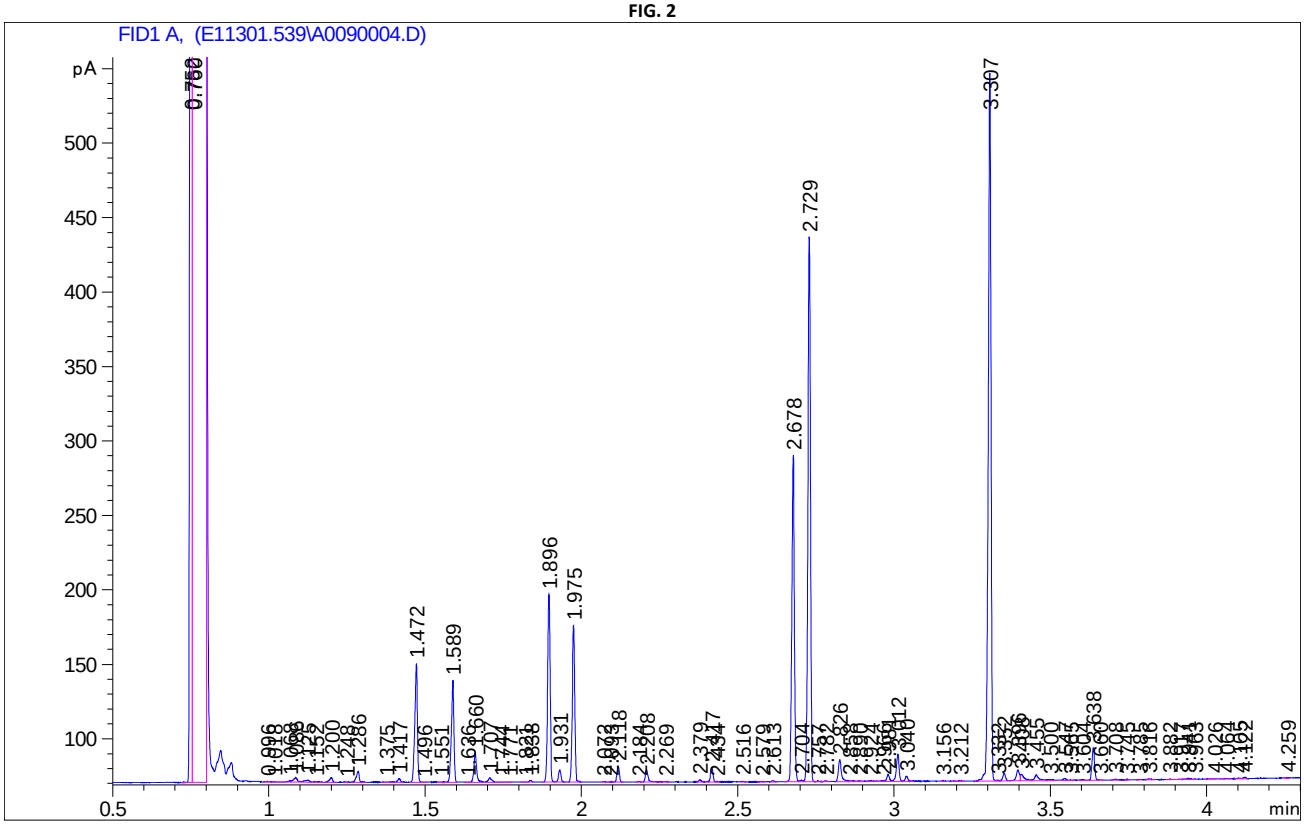


ECL Deviation: 0.006 Reference ECL Shift: 0.007 Number Reference Peaks: 15
Total Response: 1904747 Total Named: 1791748
Percent Named: 94.07% Total Amount: 1719475
Matches

TABLE 4

Library	Sim Index	Entry Name
RTSBA6 6.00	0.765	*Pseudomonas-aeruginosa*

FIG. 2

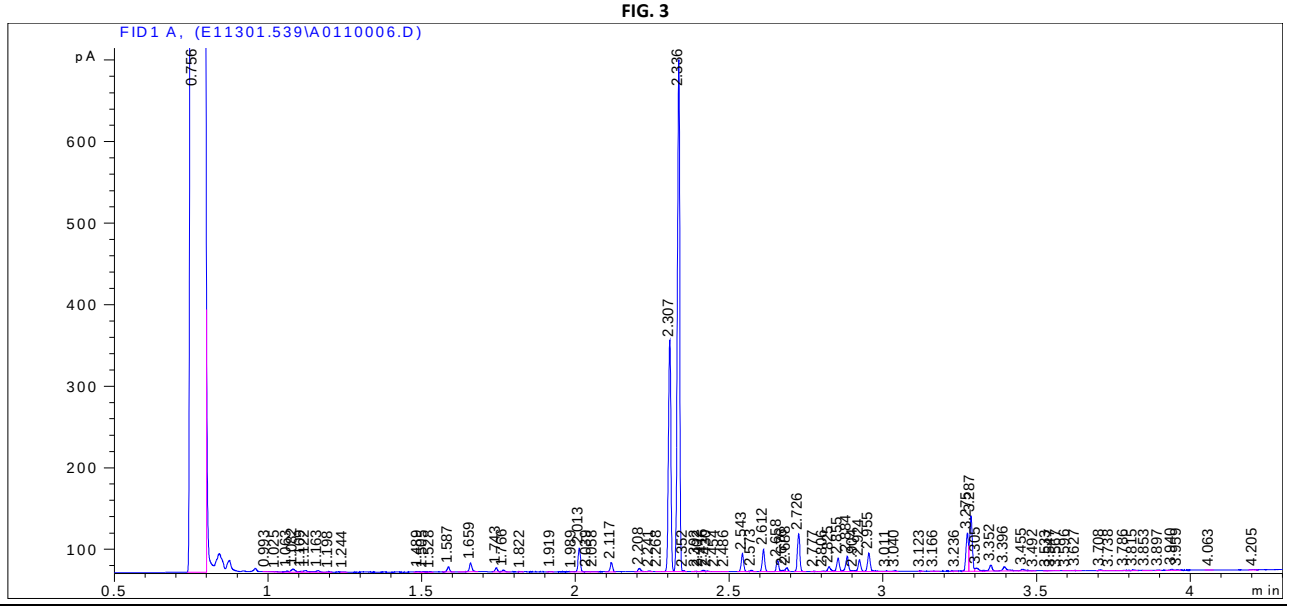


ECL Deviation: 0.004 Reference ECL Shift: 0.009 Number Reference Peaks: 18
Total Response: 1483894 Total Named: 1414122
Percent Named: 95.30% Total Amount: 1351343
Matches:

TABLE 5

Library	Sim Index	Entry Name
RTSBA6 6.00	0.716	*Bacillus-megaterium-GC subgroup A*

FIG. 3

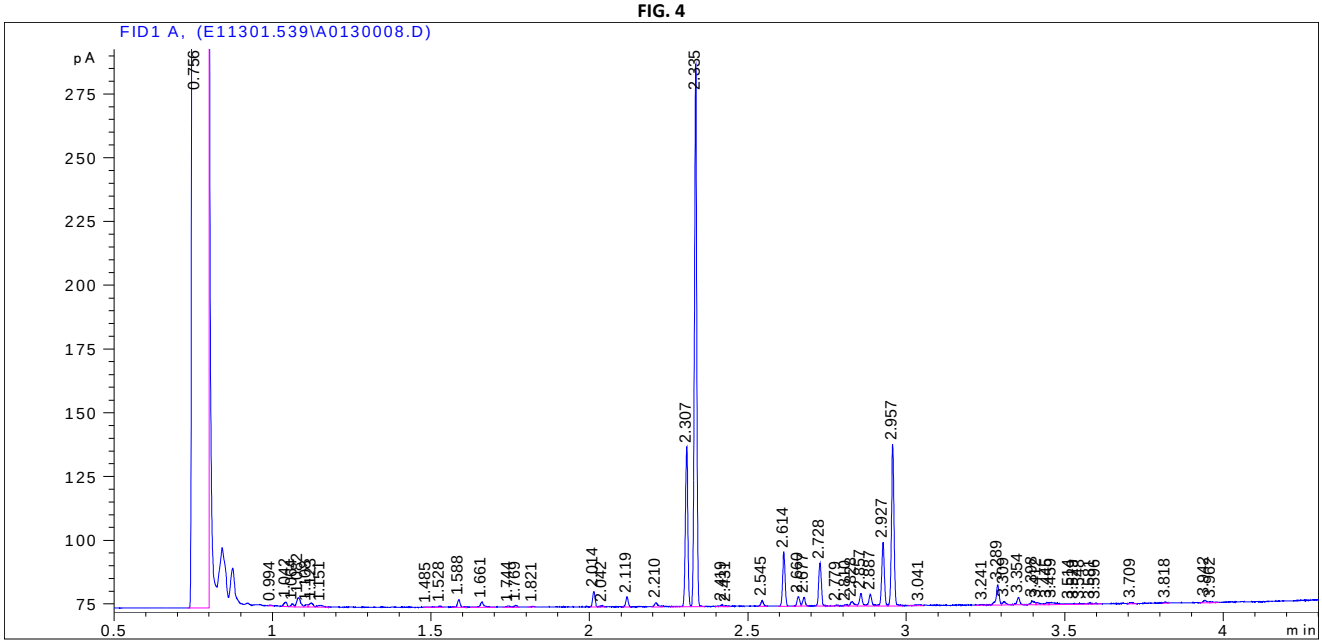


ECL Deviation: 0.004 Reference ECL Shift: 0.005 Number Reference Peaks: 20
Total Response: 532865 Total Named: 505577
Percent Named: 94.88% Total Amount: 482369
Matches:

TABLE 6

Library	Sim Index	Entry Name
RTSBA6 6.00	0.804	*Bacillus-atrophaeus*

FIG. 4

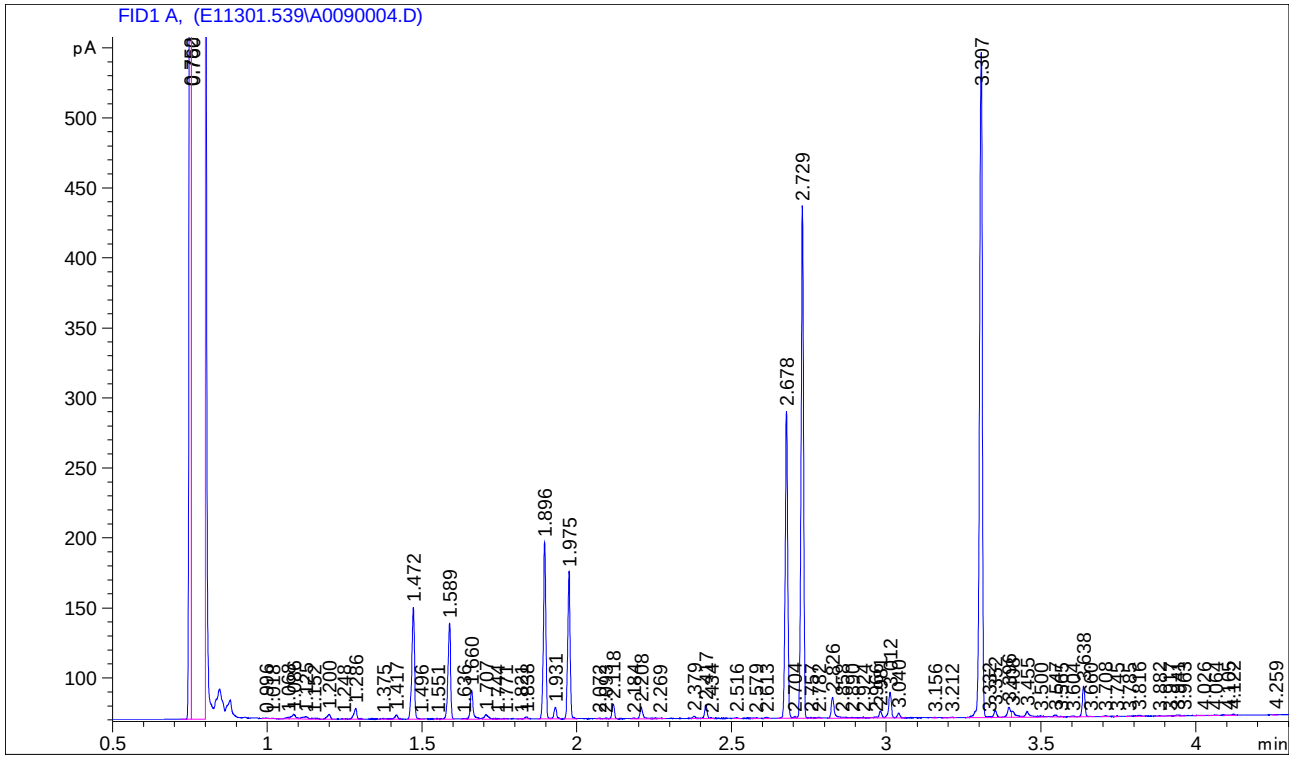


ECL Deviation: 0.006 Reference ECL Shift: 0.007 Number Reference Peaks: 15
Total Response: 1904747 Total Named: 1791748
Percent Named: 94.07% Total Amount: 1719475
Matches:

TABLE 7

Library	Sim Index	Entry Name
RTSBA6 6.00	0.765	*Pseudomonas-aeruginosa*

FIG. 5



Direct sequence determination of 16S rRNA gene fragments represents a versatile method for identification of bacteria to the species level. But one of the potential limitations of the 16S rDNA sequencing application is the inability to assign a species for recently diverged species [18,19]. Cost is a critical issue in the evaluation of 16S rDNA sequence analysis as a diagnostic tool. Driven in part by the technology underlying the human and microbial genome projects, sequencing costs will probably continue their rapid trend upward.

CONCIUSION

Through the above study we can conclude that FAME analysis is equally reliable and cost effective as compared to sequencing. Identification of bacteria through FAME is rapid, accurate and less expensive, thus this technology should be brought within the reach of microbiologists and into routine practice.

REFERENCES

1. Holmes B, Costas M, Ganner M, et al. J. Clin. Microbiol. 1994, 32:1970-1975.
2. Miller JM, Rhoden DL. J. Clin. Microbiol. 1991, 29:1143-1147.
3. Osterhout GJ, Shull VH, Dick JD. 1991. J. Clin. Microbiol. 29:1822-1830.
4. Von Graevenitz A, Osterhout G, Dick J. Acta Pathologica, Microbiologica et Immunologica Scandinavica 1991, 99:147-154.
5. Williams JGK, Kubelik AR, Livak KJ, et al. Nucl. Acids Res. 1990, 18:6531-6535.
6. Welsh J, McClelland M. Nucl. Acids Res. 1990, 18:7213-7218.
7. Longato S, Bonfante P. Mycol. Res. 1997, 101:425-432.
8. Kirschner P, Springer B, Vogel U, et al. J. Clin. Microbiol. 1993, 31:2882-2889.
9. Relman D A, Loutit JS, Schmidt TM, et al. N. Engl. J. Med. 1990, 323:1573-1580.
10. Wilson KH, Blitchington RB, Greene RC. J. Clin. Microbiol. 1990, 28:1942-1946.
11. Woese CR, Kandler O, Wheelis ML. Proc. Natl. Acad. Sci. USA 1990, 87:4576-4579.
12. Chen K, Neimark H, Rumore P, et al. FEMS Microbiol. Lett. 1989, 48:19-24.
13. Weisburg WG, Barns SM, Pelletier DA, et al. J. Bacteriol. 1991, 173:697-703.
14. Lane DJ, Pace B, Olsen J, et al. Proc. Natl. Acad. Sci. USA 1985, 82:6955-6959.
15. Lambert LH, Cox T, Mitchell K, et al. Int. J. Sys. Bact. 1999, 48:511-518.
16. Abel K, de Schmertzing H, Peterson JI. J. Bacteriol. 1963, 85:1039-1044.
17. Tang YW, Ellis NM, Hopkins MK, et al. J. Clin. Microbiol. 1998, 3674-3679.
18. Wolff K, Sperka S, Stern A. Nucl. Acids Res. 1992, 20:4657.
19. Fox GE, Wisotzkey JD, Jurtshuk P, et al. Int. J. Syst. Bacteriol. 1992, 42:166-170.

REQUEST FOR FEEDBACK

Dear Readers

At the very outset, International Journal of Research in Commerce, IT & Management (IJRCM) acknowledges & appreciates your efforts in showing interest in our present issue under your kind perusal.

I would like to request you to supply your critical comments and suggestions about the material published in this issue, as well as on the journal as a whole, on our e-mail **infoijrcm@gmail.com** for further improvements in the interest of research.

If you have any queries, please feel free to contact us on our e-mail **infoijrcm@gmail.com**.

I am sure that your feedback and deliberations would make future issues better – a result of our joint effort.

Looking forward to an appropriate consideration.

With sincere regards

Thanking you profoundly

Academically yours

Sd/-
Co-ordinator

DISCLAIMER

ABOUT THE JOURNAL

In this age of Commerce, Economics, Computer, I.T. & Management and cut throat competition, a group of intellectuals felt the need to have some platform, where young and budding managers and academicians could express their views and discuss the problems among their peers. This journal was conceived with this noble intention in view. This journal has been introduced to give an opportunity for expressing refined and innovative ideas in this field. It is our humble endeavour to provide a springboard to the upcoming specialists and give a chance to know about the latest in the sphere of research and knowledge. We have taken a small step and we hope that with the active co-operation of like-minded scholars, we shall be able to serve the society with our humble efforts.

Our Other Journals