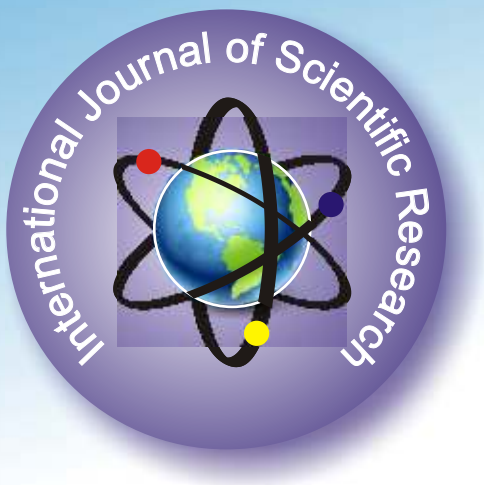
International Journal of Scientific Research

Listed in International ISSN Directory, Paris

Volume 1 | Issue 1 | June 2012



ISSN No. 2277 – 8179

A Multi-Subject Journal

Journal for All Subjects

ISSN No. 2277 – 8179

International Journal of Scientific Research

Journal for All Subjects

Advertisement Details

Position	B/W (Single Color)	Fore Color
Full Inside Cover	₹ 6250	₹ 12500
Full Page (Inside)	₹ 5000	-

Subscription Details

Period	Amount Payable
One Year (12 Issues)	₹ 3000
Two Year (24 issues)	₹ 5800
Three Year (36 issues)	₹ 8700
Five Year (60 issues)	₹ 14400

You can download the Advertisement / Subscription Form from website www.gra.in. You will require to print the form. Please fill the form completely and send it to the **Editor, International Journal of Scientific Research** along with the payment in the form of Demand Draft/Cheque at Par drawn in favour of **International Journal of Scientific Research** payable at Ahmedabad.

Editor-In-Chief

Khansa Memon
Editor, Sarah Publishing Academy

Editorial Advisory Board

Dr. Ashok S. Pawar
Associate Professor, Dept. of Economic
Dr. Babaasaheb Ambedkar
Marathwada.University, Aurngabad

Dr.(Prof) Vijay Kumar Soni
Principal,
Jai Meenesh College, Phagi,
Jaipur, Rajasthan

Dr. A.R. Saravankumar
Assistant Professor in Education
DDE, Alagappa University,
Tamilnadu

Dr.R.Ramachandran
Commerce Dde
Annamalai University
Tamilnadu India

Dr. R Ganpathy
Assistant Professor in Commerce
Directorate of Distance Education
Alagappa University Karaikudi.

Dr. Amit Bandyopadhyay
Assistant Professor
Department of Physiology
University of Calcutta

Dr. V. Kumaravel,
Professor and Head
Vivekanandha Buss. School for Women
Tiruchengode, Namakkal Dist

Dr. K. Prabhakar,
Professor,
Department of Manag. Studies,
Velammal Engg College, Chennai

Dr. Sunita J. Rathod
Maharashtra Education
Service Group-B
DIET Dist. Jalna

1. Thoughts, language vision and example in published research paper are entirely of author of research paper. It is not necessary that both editor and editorial board are satisfied by the research paper. The responsibility of the matter of research paper/article is entirely of author.
2. Editing of the **International Journal of Scientific Research** is processed without any remittance. The selection and publication is done after recommendations of atleast two subject expert referees.
3. In any condition if any National/International University denies accepting the research paper published in IJSR then it is not the responsibility of Editor, Publisher and Management.
4. Only the first author is entitle to receive the copies of all co-authors
5. Before re-use of published research paper in any manner, it is compulsory to take written permission from the Editor-IJSR, unless it will be assumed as disobedience of copyright rules.
5. All the legal undertaking related to **International Journal of Scientific Research** is subject to Ahmedabad Jurisdiction.
7. The research journal will be send by normal post. If the journal is not received by the author of research papers then it will not be the responsibility of the Editor and publisher. The amount for registered post should be borne by author of the research paper in case of second copy of the journal.

Editor,
INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH
3, SUHANA, Nr. Rubi Apartment, B/H NID, Rajnagar Road,
Paldi – 380007. Ahmedabad-Gujarat. (INDIA)
Contact: +91 98247 02127, +91 88660 03636
Www.theglobaljournals.com | ijsr@theglobaljournals.com

Index

Sr. No	Title	Subject	Page. No.
1.	The Impact Of FIIs On Indian Stock Market *Dr. Vinod K. Ramani*	Accountancy	1-3
2.	Human Resource Management New Dimantion *Dr. Kishor V. Bhesaniya, A. R. Sakhida, C. C. Gediwala*	Accountancy	4-6
3.	Sequencing The Hypervariable Region V3 Of 16S RRNA Of Bacteria Isolated From RAM *V. S. Wadhai, Savitri R. Dewangan*	Biology	7-10
4.	Credit Rating Methodology for rating Small and Medium Enterprises A Comprehensive Outline *Dr. Bheemanagouda*	Commerce	11-13
5.	Growth And Performance Of Micro Small And Medium Enterprises (MSMES) In India *Dr. M. K. Maru*	Commerce	14-15
6.	Uses Of College Funds In Assam-with Reference To Lakhimpur District *Dr. Niranjan Kakati*	Commerce	16-17
7.	The Study On Awareness Of Solar Energy Products In House Holds, Coimbatore *Dr. M. Dhanabhakyam, T. Sumathi*	Commerce	18-20
8.	Connotation Of Systematised Warehouse Management System In Supply Chain Of Small Scale Firms *Dr. Vipul Chalotra*	Commerce	21-23
9.	Distribution Mix Straregy Of Jammu And Kashmir Co-operatives Supply And Marketing Federation Limited (JAKFED) In Jammu District Of J&k *Tarsem Lal*	Commerce	24-25
10.	A Study On Irrigation Projects In Maharashtra State *Dr. Pawar, Ashok S., Dr. Rathod Sunita J.*	Economics	26-27
11.	A Study Of Food Security In South Asia *Dr. Pawar, Ashok S., Dr. Rathod Sunita J.*	Economics	28-30
12.	Inter-District Variations In The Performance Of Self Help Groups (SHGS) In Tamil Nadu. *Dr. A. Shyamala*	Economics	31-34
13.	Challenges of Indian Agriculture and Rural Development *Dr. Sangappa. V. Mamanshetty*	Economics	35-36

14.	Enhancing Science Process Skills and Scientific Attitude and Analysing their Interactions. :- An Intervention through Inquiry Learning Approach *Sreetanuka Nath, Dr. Sybil Thomas*	Education	37-42
15.	Effect Of Piston Geometry On Combustion Efficiency A. B. Damor, I. H. Bhoraniya, V. H. Chaudhari	Engineering	43-45
16.	Multipoint Hand Gesture Recognition For Controlling Bot *Nishant M Labhane, Prashant Harsh, Meghan Kulkarni*	Engineering	46-48
17.	To Study the working conditions Level in Rajasthan Healthcare Department *Dr. Ashwin G. Modi, Sushman Sharma*	Healthcare	49-51
18.	Impact Of Nutrition Education On Nutritional Knowledge, Dietary Practices And Physical Endurance Of Amateur Badminton Players *Dr. Anjali A. Rajwade*	Home Science	52-53
19.	Impact Of Maternal Nutrition Education Module On Knowledge And Nutritional Status In Urban Pregnant Women *Dr. Anjali A. Rajwade*	Home Science	54-56
20.	Feminism and Gender Representation in Indian Writing in English *Bhaveshkumar B Rana*	Literature	57-59
21.	Impact of Grievances on Industrial Relations *Anuradha Averineni*	Management	60-61
22.	Bioactive Polyphenols Of Bombax Ceiba *K.Shakila, D. Sukumar, R. Priya, R.Rajaselvi*	Management	62-63
23.	A Study On Employee Motivation In Health Care Industry In A Private Multi-Speciality Organization *Dr. C. Swarnalatha, T. S. Prasanna*	Management	64-67
24.	Tax-advantaged Mutual Funds V/s. Rest of the Population *Dr. Deepak H. Tekwani*	Management	68-69
25.	Perception Analysis On Employees Motivation Techniques *Dr. M. Dhanabhakyam, R. Umadevi*	Management	70-73
26.	A Feasibility Study of Islamic Banking System in India Miles to Go *Dr. Sharif Memon*	Management	74-77
27.	Rural Marketing Practices in India: Emerging Issues *Kavita A. Trivedi*	Management	78-79
28.	Impact of Micro, Small and Medium Enterprises on Indian Economy using the ranking method in Today's Context *Vimal P. Jagad*	Management	80-81

29.	Paradigm Changes in Healthcare Marketing *Dr Mahalaxmi Krishnan*	Marketing	82-84
30.	Evolution of New Consumer Class in India *Dr. Sanjeev Verma*	Marketing	85-86
31.	Socio-Economic and Demographic Determinants of Reproductive Tract Infections (RTIs). *Dr. K. JOTHY*	Social Sciences	87-89

ISSN : 2277 – 8179

June, 2012

Sequencing The Hypervariable Region V3 Of 16S RRNA Of Bacteria Isolated From RAM

* V. S. Wadhai ** Savitri R. Dewangan

Abstract

Bacterial 16S rRNA genes generally contain nine “hypervariable regions” (V1 V9) that demonstrate considerable sequence diversity among different bacterial species and can be used for species identification. Unknown bacteria is isolated from computer hardware by molecular detection and sequence analysis of 16S rRNA hypervariable region V3. The gene sequence obtained was studied in the region from V3-V6. Sequence similarity dendograms were created for hypervariable regions V3-V6. In present study it is determined that V3 is second best region to distinguish between different Bacillus subtilis species. Species-specific sequences within a given hypervariable region constitute useful targets for diagnostic assays and other scientific investigations. The 64 nucleotides long of V3 could distinguish among most bacterial species except enterobacteriaceae. Combination of V3 and V6 region may provide better understanding of further identification at subspecies level. Future studies on identification and analysis by hypervariable region V3 can be extended in biodegradation of toxic components in personal computer.

Keywords : 16S ribosomal, RNA, Hypervariable region (V3), Gene segments, Phylogenetic study

Introduction

Sequence analysis of the 16S ribosomal RNA (rRNA) gene has been widely used to identify bacterial species and perform taxonomic studies Clarridge et al.(2004) ; Munson et al.(2004); Petti et al. (2005); Schmalenberger et al., (2001). The primary structure of 16S rRNA is highly conserved. It is 1,542 nucleotides in length. Bacterial 16S ribosomal RNA (rRNA) is differentiated into conserved region and hyper variable region.

The genes coding for it are referred to as 16S rDNA and are used in reconstructing phylogenies Bacterial 16S ribosomal RNA (rRNA) genes contain nine “hypervariable regions” (V1 V9) that demonstrate considerable sequence diversity among different bacteria. Computers are not routinely disinfected the opportunity for the transmission of microorganism is potentially great. Therefore, it is very important to identify the microflora on computer hardware and analyze for its pathogenecity, if any. Thus, this research seeks to investigate what kinds of microorganisms, especially bacteria that actually can contaminate computer hardware. In our project we focused on identification of isolated bacteria from computer hardware by sequence analysis of 16S ribosomal RNA and focused on V3 hypervariable region. Detail studies on particular hypervariable region is one of the latest trend in molecular diagnosis of bacteria, as the total length of 16S rRNA is more than 1540 bases in general. Large size of this may resulted in flood of partial sequence submission to NCBI with BLAST results of any ambiguous region for any type of bacteria. Final outcome of this study may contribute specific detection of one studied bacteria from current studies by detail analysis of V3 region.

Ribosomes are molecular machines that make protein out of amino acids. The central dogma of biology is that DNA makes RNA, which then makes protein. Ribosomes read the information in this RNA and use it to produce proteins. In prokaryotes, 70S ribosomes are made from complexes of RNA and proteins. Ribosomes are divided into two subunits, one larger subunit (50S) & other smaller subunit (30S). The smaller subunit (30S) binds to the mRNA, while the larger subunit (70S) binds to the tRNA and the amino acids. The 30S ribosomal subunit has a 1540 nucleotide RNA subunit (16S) bound to 21 proteins.

Hypervariable region-

Regions present on light and heavy chains of immunoglobulin where most of the variation in amino acid sequences occurs. These are also sites of antigen binding. We focused on 16S rRNA's hyper variable region it's contain “9” hyper variable region. Bacterial 16S rRNA genes generally contain nine “hypervariable regions” (V1 V9) that demonstrate considerable sequence diversity among different bacterial species and can be used for species identification Van de Peer et al.(1996). Hypervariable regions are flanked by conserved stretches in most bacteria, enabling PCR amplification of target sequences using universal primers Baker et al. (2003); Lu et al. (2000); Mc Cabe et al.(1999); Munson et al. (2004). Hypervariable region is very short region also known as variable number tandem repeats or minisatellite. Once the DNA sequence is determined, we will compare the sequence to known sequences in a computer database. The obtained sequence was subjected to BLAST. BLAST2 of known sequence and 15 other Bacillus subtilis strain was performed and V3 hypervariable region determined. 16S rRNA is the best region to create phylogeny and obtain taxonomic relationships. The phylogeny tree was constructed by using neighbor joining method. For our investigation, we used the Bootstrap method with 500 times replicates and performing phylogeny.

The 16S rRNA genes of many bacterial species have already been sequenced, so that it is likely that the sequence of the 16S rRNA gene of your unknown is in the database. The 16S rRNA gene (1,500 bp) is large enough for bioinformatics purposes.

*, ** Department of Biotechnology,Sardar Patel Mahavidyalaya, Chandrapur

The 16S rRNA genes of many bacterial species have already been sequenced, so that it is likely that the sequence of the 16S rRNA gene of your unknown is in the database. The 16S rRNA gene (1,500 bp) is large enough for bioinformatics purposes.

Materials and Methods

Sample collection and Isolation of bacteria

The hard disk RAM from personal computer was collected in sterile conditions. One of the RAM of 512 MB, Number-8856, MM3-7B001855 was selected for the study. Para film was sterilized by ethanol and then by treatment for 15 minutes and was kept over RAM pressed and then kept over nutrient agar. Sterilized parafilm spreaded on agar plate. These plates were incubated at 37°C. After 18 hours parafilm was removed and again kept for incubation at 37°C. After desired growth, bacterial colonies were taken from the area occupied by the parafilm and subcultured to obtain pure culture. After 18 hrs isolated colonies were observed.

Bacterial DNA Extraction

Single isolated colonies were observed after 18 hrs of incubation. Bacterial colonies were inoculted from the pure culture and cultured in nutrient broth and incubated for 24 hrs.Growth was observed and DNA was extracted from the nutrient broth by Spin column method.The purified genomic DNA thus extracted was stored at 2-8° C.

Polymerase Chain Reaction (PCR) for 16S rRNA gene

After DNA extraction gradient PCR was done to obtain exact annealing temperature at which the DNA can be amplified. Amplification of DNA for further studies was done by PCR technique,where Gradient PCR is very important for finding exact annealing temperature for any new PCR with known primer set. DNA samples extracted from bacterial colonies grown in nutrient agar plates were subjected for amplification by gradient PCR to standardize annealing temperature of amplified DNA to obtain 1.5 kbp amplicon for further sequencing. Further scale up PCR was done t for increasing quantity of DNA for DNA sequencing.

DNA sequencing

After scale up PCR the amplified DNA was outsourced to Merck Specialists Pvt. Ltd; Bangalore for DNA sequencing. Briefly, PCR product was purified by Sanger Chain method, followed by cycle sequencing which was carried out by Sanger's modified method of DNA sequencing and after post cycle sequencing purification; sequenced products were read by ABI 3730 genetic analyzer. Cycle sequencing was carried out by modified by Sanger's Chain Termination method by adding TRRM (Termination reaction ready mix) along with Reverse and Forward primers (under cycle sequencing reactions). After cycle sequencing and post cycle sequencing purification, both the products were run on ABI 3700 DNA sequencer for generating chromatogram.

Applied Bioinformatics

Software used for data analysis-

BioEdit, BLAST, Reverse Complement, BLAST2, ClustalW, MEGA5.05

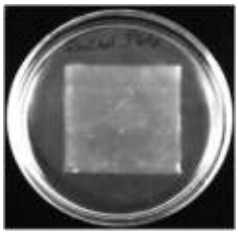
The received data after DNA sequencing was studied for clean sequences by bioinformatics analysis for interpretation.The DNA sequence was received and read using BioEdit. Reverse complement was used to convert the reverse sequence into the forward orientation. The raw DNA sequence was compared with the existing sequences in the GenBank database using the BLAST tool from NCBI for identification of the unknown bacteria isolate. The reverse sequences were subjected to BLAST2 to locate the region exhibiting sequence identity. Sequence was selected from BLAST result and clustalW was performed. Output file was saved in form of alignment as well as FASTA. Alignment file was used for showing multiple sequence alignment in colour and FASTA format file saved. FASTA format file was converted to MEGA and phylogenetic tree for hypervariable region of the different Bacillus subtilis species and the sequence obtained in ATG LAB was used by neighbour joining bootstrap method and the phylogeny image was created. Finally, a blast was conducted amongst Bacillus group of bacteria

Results

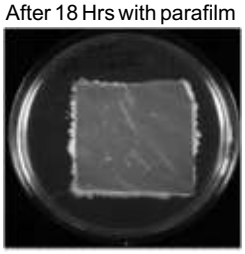
1. Culture of isolated bacteria

Bacterial Colonies Isolated from RAM

Control Plate



After 18 Hrs with parafilm

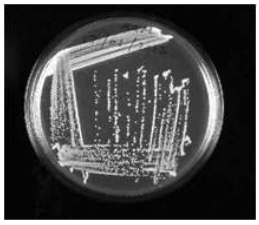


After 24 Hrs without parafilm

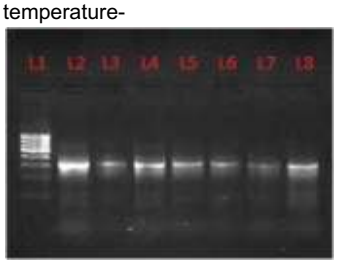


2.. Subculture of isolated bacteria

Pure culture of bacteria



3. 16S rRNA Gradient PCR for standardization of annealing temperature-



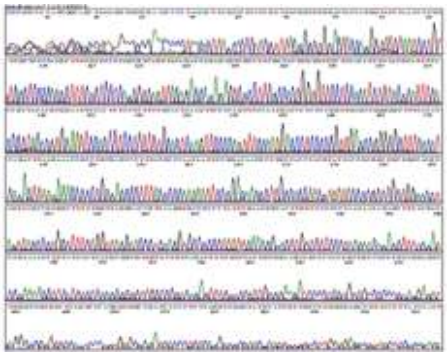
Gradient PCR: Lane 1: Molecular wt. marker 500 bp ladder; Gradient Temperature- Lane 2: 56°C; Lane 3: 54.2°C; Lane 4: 52.0°C; Lane 5: 50.1°C; Lane 6: 48.8°C; Lane7: 48°C; Lane 8 (Genomic DNA was isolated by DNAzol method)

4. Scale up PCR for amplification of 1.5kbp DNA product-



Scale up PCR: Lane 1: Molecular weight marker 500 bp ladder; Lane 2: 5µl of PCR product; Lane 3: 25 µl of PCR product both amplified at 56° C.

5. Chromatogram generated by 900R primer



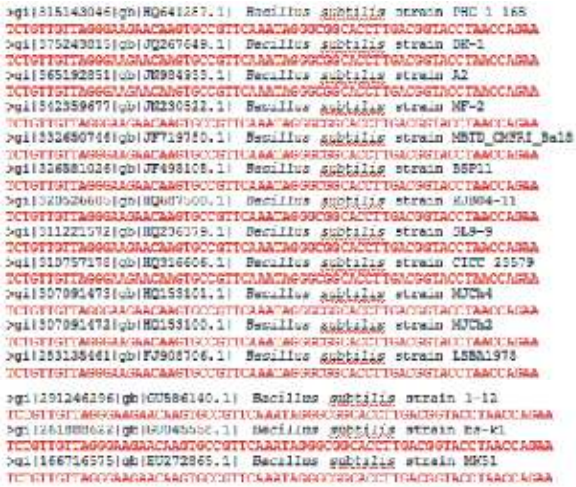
The reverse sequence was subjected to BLAST, after BLAST analysis it was confirmed that the unknown bacteria was Bacillus Subtilis with 99% identity.

6. BLAST outputs for 900R
Subject: E coli
Query: B. subtillis (our sequence)
>lcl|44291
Length=1541
Score = 455 bits (246), Expect = 9e-132
Identities = 483/594 (81%), Gaps = 29/594 (5%)
Strand=Plus/Plus

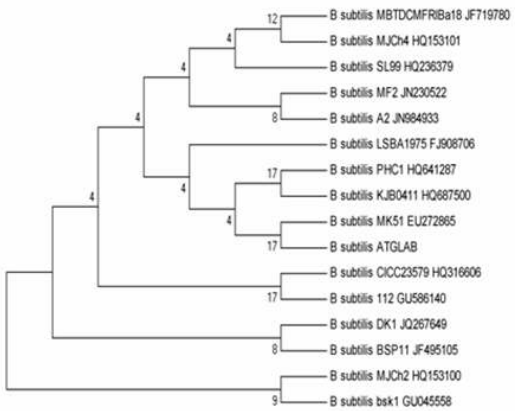


V3 hypervariable region
>B_subtilis_ATGLAB
TCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAGGG
CGGCACCTTGACGGTACCTAACCAGAA

7. Sequence similarity on hypervariable region V3 of 16S rRNA in Bacillus subtilis strain V3 (HVR) bp



8. MEGA structure (Molecular Evolution Genetic Analysis)-
Phylogenetic Analysis of hypervariable region V3 by MEGA 5.05 (Neighbour Joining Bootstrap method)
Figure: Phylogenetic analysis of V3 region by MEGA 5. Phylogenetic trees showing the relationship among 16S rDNA gene sequences of Bacillus subtilis. Construction of phylogenetic trees was carried out by the neighbour-joining bootstrap method.



Discussion

The bacterial 16S rRNA gene is increasingly being used to identify bacterial species in clinical practice and scientific investigations. Species specific sequences can be identified very rapidly in assays that combine nucleic acid amplification.

Molecular identification of bacteria by 16S rRNA is frequently used. The RAM was selected as source and bacteria isolated. Number of colonies appeared on plate of which single isolated colony was subcultured to obtain pure culture, the property that one bacteria can generate a colony. The aim of the current study was to characterize V3 hyper variable segments of the 16S rRNA gene bacterial to examine hyper variable sequences that would be most beneficial for identifying specific bacterial species & strains.

Then, DNA was extracted, PCR was performed for gene amplification, and then sequencing was done. The obtained sequence was subjected to BLAST where it was confirmed that the unknown bacteria was Bacillus subtilis. BLAST2 of known sequence and 15 other Bacillus subtilis strain was performed and V3 hypervariable region determined. 16S rRNA is the best region to create phylogeny and obtain taxonomic relationships.

The phylogeny tree was constructed by using neighbor joining method. The robustness for individual branches was estimated by bootstrapping with 1000 replicates. For our investigation, we used the Bootstrap method with 500 times replicates &performing phylogeny.

In present study it is determined that V3 is second best region to distinguish between different Bacillus subtilis species. Species-specific sequences within a given hypervariable region constitute useful targets for diagnostic assays and other scientific investigations. The 64 nucleotides long of V3 could distinguish among most bacterial species except enterobacteriaceae. V3 is also noteworthy for being able to differentiate among all CDC-defined select agents including Bacillus anthracis and B.cereus. Combination of V3 and V6 region may provide better understanding of further identification at subspecies level.

Conclusion

The presence of micro organisms in our surroundings, public places is identified in every research. Some are beneficial while others are detrimental. It is virtually impossible to eliminate all harmful microbes, but with same precautionary measures. Therefore, it is very important to identify the microflora on computer hardware and analyze for its pathogenecity, if any, so that some precautionary measures can be taken.

Numerous studies have identified 16S rRNA hypervariable region sequences that identify a single bacterial species or differentiate among a limited number of different species or genera. Based on available 16S rRNA, it contains conserved and hypervariable regions. This study has focused on hypervariable region of 16S rRNA and especially on V3 region and how about its analysis we can identify unknown bacteria and create relationship and make phylogeny among closely related bacterial species.

The present finding suggests that the bacteria Bacillus subtilis is present on the personal computer component surface, RAM. Many explorations can be derived from this finding including carbon and energy source for bacteria, degradation of particular component, which is otherwise pose problem due to e-waste. Future studies can be extended in biodegradation of toxic components in personal computer.

References

Baker, G.C., Smith, J.J., & Cowan, D.A. (2003). Review and re-analysis of domain-specific 16S primers. J Microbiol Methods. (55) , 54155. | Becker, K., Harmsen, D., Mellmann, A., Meier, C., Schumann, P., Peters, G., and von Eiff C. (2004). Development and evaluation of a quality-controlled ribosomal sequence database for 16S ribosomal DNA-based identification of Staphylococcus species. J Clin Microbiol. (42) 498895. | Clarridge, J.E. (2004). 3rd Impact of 16S rRNA gene sequence analysis for identification of bacteria on clinical microbiology and infectious diseases. Clin Microbiol Rev.(17) 84062. | Fogel, G.B., Collins, C.R., Li, J., & Brunk, C.F. (1999). Prokaryotic Genome Size and SSU rDNA Copy Number: Estimation of Microbial Relative Abundance from a Mixed Population | Harayama, Yamamoto, and Aman et al. Molecular characterization of the mosquitocidal Bacillus subtilis strain(VCR CB 471) | Kataoka, M., Ueda, K., Kudo, T., Seki, T., and Yoshida, T. (1997). Application of the variable region in 16S rDNA to create an index for rapid species identification in the genus Streptomyces. FEMS Microbiol Lett. (151), 24955. | Marchesi, J.R., Sato, T., Weightman, A.J., Martin, T.A., Fry, J.C., Hiom, S.J., Dymock, D., and Wade, W.G. (1998). Design and evaluation of useful bacterium-specific PCR primers that amplify genes coding for bacterial 16S rRNA. Appl Environ Microbiol. (64), 795799. | Maynard, C., Berthiaume, F., Lemarchand, K., Harel, J., Payment, P., Bayardelle, P., Masson, L., and Brousseau, R. (2005). Waterborne pathogen detection by use of oligonucleotide-based microarrays. Appl Environ Microbiol.(71) 85488557. | McCabe, K.M., Zhang, Y.H., Huang, B.L., Wagar, E.A., and McCabe, E.R. (1999). Bacterial species identification after DNA amplification with a universal primer pair. Mol Genet Metab. (66) 205211. | Munson, M.A., Banerjee, A., Watson, T.F., and Wade, W.G. (2004). Molecular analysis of the microflora associated with dental caries. J Clin Microbiol .(42) 30233029. | Petti, C.A., Polage, C.R., & Schreckenberger P. (2005). The role of 16S rRNA gene sequencing in identification of microorganisms misidentified by conventional methods. J Clin Microbiol. (43) 61236125. | Rothman, R.E., Majmudar, M.D., Kelen, G.D., Madico, G., Gaydos, C.A., Walker, T.,and Quinn T.C. (2002). Detection of bacteremia in emergency department patients at risk for infective endocarditis using universal 16S rRNA primers in a decontaminated polymerase chain reaction assay. J Infect Dis. (186) 16771681. | Schmalenberger, A., Schwieger, F., & Tebbe, C.C. Effect of primers hybridizing to different evolutionarily conserved regions of the small-subunit rRNA gene in PCR-based microbial community analyses and genetic profiling. | Soumitesh Chakravorty. (2007) May. A detailed analysis of 16S ribosomal RNA gene segments for the diagnosis of pathogenic bacteria. J microbial methods. | Stefan, Bertilsson., Colleen, M., Cavanaugh and Martin F. Polz. (2002). Sequencing-independent method to generate oligonucleotide probes targeting a variable region in bacterial 16S rRNA by PCR with detachable primers. 68(12) 6077-6086.| Li ,Ting., Wang, L.T., Lee, F.L., Tai, C.J., Kasai, H. (2007). Comparison of gyrB gene sequences, 16S rRNA gene sequences and DNA-DNA hybridization in the Bacillus subtilis group | Van de Peer, Y., Chapelle, S., & De, Wachter R. (1996). A quantitative map of nucleotide substitution rates in bacterial rRNA. Nucleic Acids Res. (24) 33813391. | Yang, S., Lin, S., Kelen, G.D., Quinn, T.C., Dick, J.D., Gaydos, C.A., and Rothman, R.E. (2002). Quantitative multiprobe PCR assay for simultaneous detection and identification to species level of bacterial pathogens. Journal of Clinical Microbiology. (40) 34493454.



Sara Publishing Academy
INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH
Journal for All Subjects

Editor,
INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH
3, SUHANA, Nr. Rubi Apartment, B/H NID, Rajnagar Road,
Paldi – 380007. Ahmedabad-Gujarat. (INDIA)
Contact: +91 98247 02127, +91 88660 03636
Www.theglobaljournals.com | ijsr@theglobaljournals.com

Printed at Unique Offset, Novatsing Rupam Estate, Opp. Abhay Estate, Tavdipura, Shahibaug, Ahmedabad