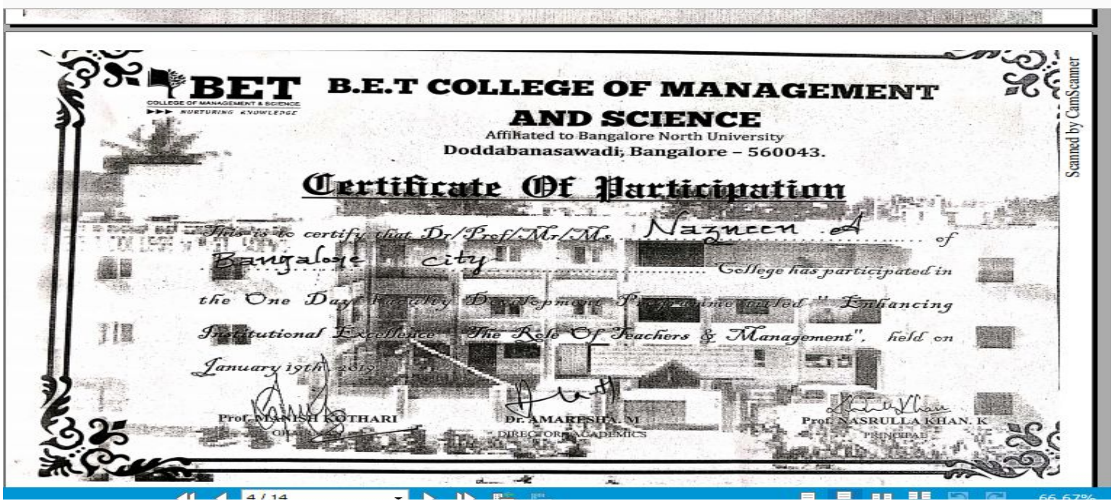
1, ROLE OF INSURANCE IN MINIMIZING BUSINESS RISK ON SMSE'S

Asst Prof . Nazneen.A



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Certificate Of Participation

This is to certify that Dr/Prof/Mr/Ms. Nazneen A of Bangalore city College has participated in the One Day Faculty Development Programme titled " Enhancing Institutional Excellence - The Role Of Teachers & Management", held on January 19th, 2019

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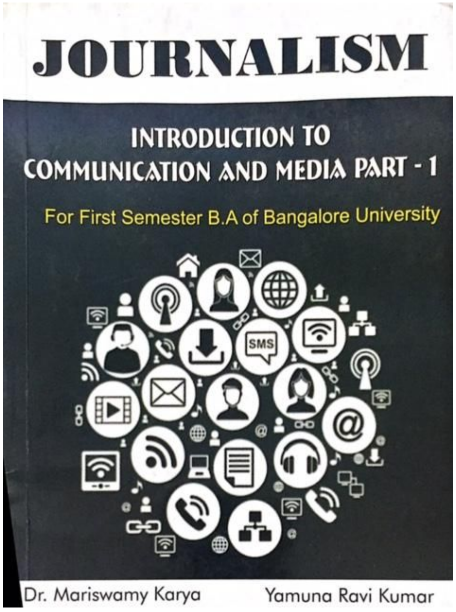
2. Introduction to communication and media part-1

(Dr. Mariswami Karya and Yamuna Ravi Kumar)



JOURNALISM

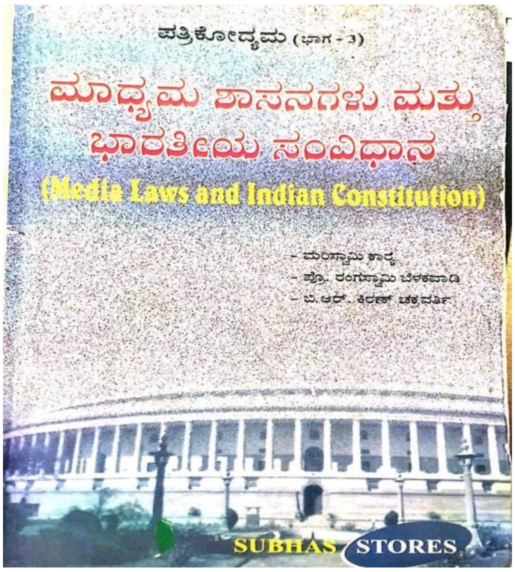
INTRODUCTION TO
COMMUNICATION AND MEDIA PART - 1

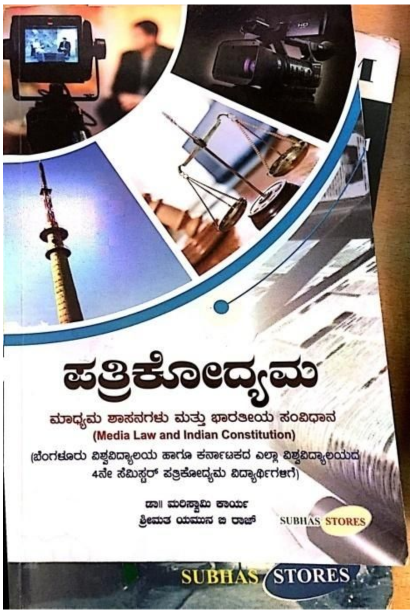
For First Semester B.A of Bangalore University

Dr. Mariswamy Karya
Yamuna Ravi Kumar

3. Media Laws and Indian constitution

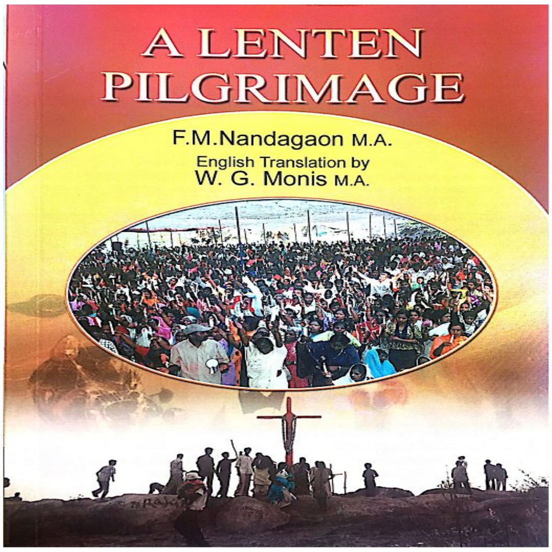
Dr. Mariswami Karya ,Prof.Rangaswami belakavadi, B.R. Kiran chakravarthi





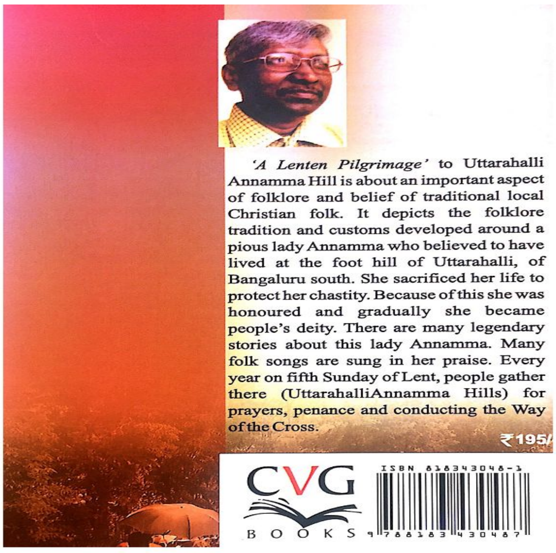
Alenten Pilgrimag

F.M.Nandagaon M.A. English translation by W.G.Monis M.A.



A LENTEN PILGRIMAGE

F.M.Nandagaon M.A.
English Translation by
W. G. Monis M.A.



'A Lenten Pilgrimage' to Uttarahalli Annamma Hill is about an important aspect of folklore and belief of traditional local Christian folk. It depicts the folklore tradition and customs developed around a pious lady Annamma who believed to have lived at the foot hill of Uttarahalli, of Bangaluru south. She sacrificed her life to protect her chastity. Because of this she was honoured and gradually she became people's deity. There are many legendary stories about this lady Annamma. Many folk songs are sung in her praise. Every year on fifth Sunday of Lent, people gather there (UttarahalliAnnamma Hills) for prayers, penance and conducting the Way of the Cross.

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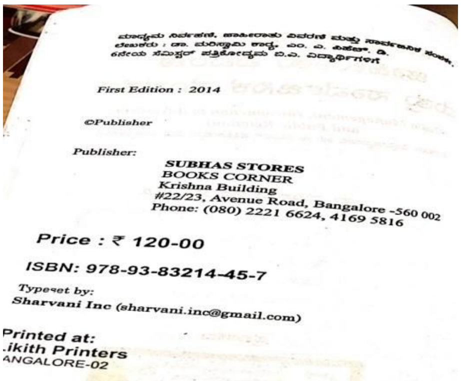
6. Media management , introduction to Advertising and Public Relation

Dr. Mariswami Karya and Yamuna Ravi Kumar



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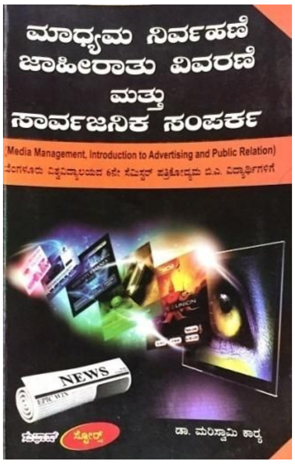


ಮಾಧ್ಯಮ ನಿರ್ವಹಣೆ
ಜಾಹೀರಾತು ವಿವರಣೆ
ಮತ್ತು
ಸಾರ್ವಜನಿಕ ಸಂಪರ್ಕ

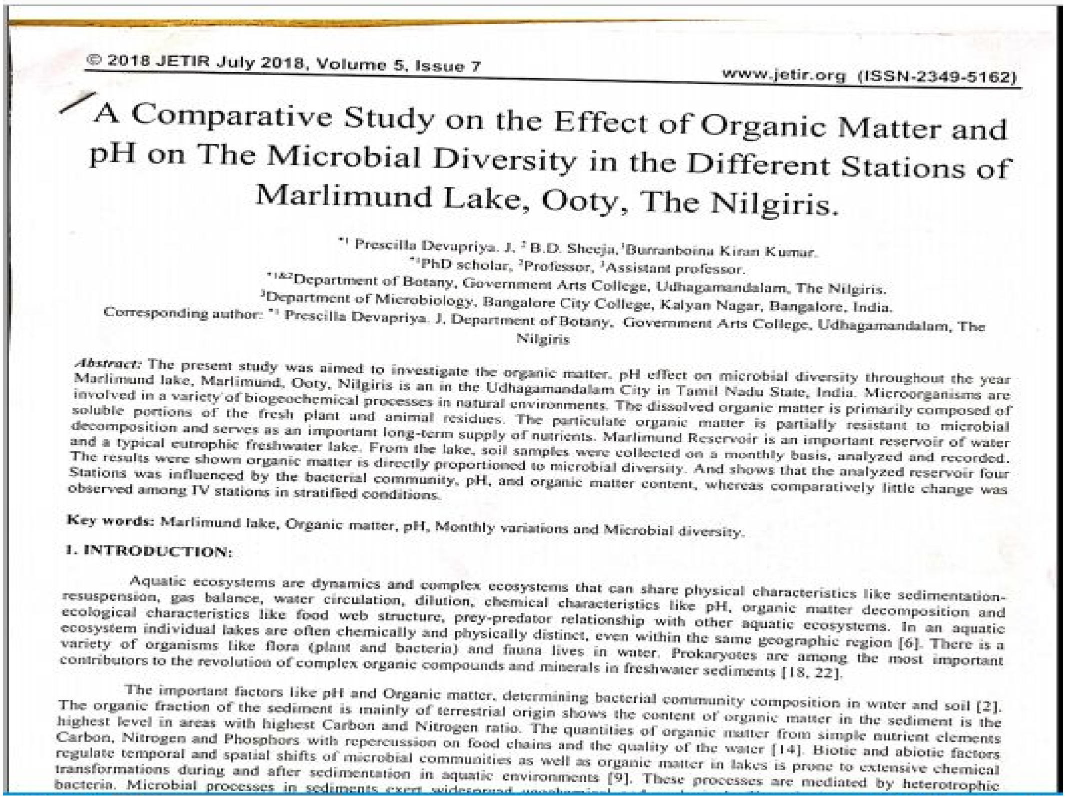
(Media Management, Introduction to Advertising and Public Relation)
ಬೆಂಗಳೂರು ವಿಶ್ವವಿದ್ಯಾಲಯದ 6ನೇ ಸೆಮಿಸ್ಟರ್ ಪತ್ರಿಕೋದ್ಯಮ ಬಿ.ಎ. ವಿದ್ಯಾರ್ಥಿಗಳಿಗೆ

ಸುಭಾಸ್ ಸ್ಟೋರ್ಸ್

ಡಾ. ಮರಿಸ್ವಾಮಿ ಕಾರ್ಯ

7. MVIT College_SOUVENIR NSIIE 29 -31 January, 2018

Prescilla Devapriya.J , Kirankumar.B, Ranjit Kumar



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A Comparative Study on the Effect of Organic Matter and pH on The Microbial Diversity in the Different Stations of Marlimund Lake, Ooty, The Nilgiris.

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*1PhD scholar, 2Professor, 3Assistant professor.
*1&2Department of Botany, Government Arts College, Udhagamandalam, The Nilgiris.
3Department of Microbiology, Bangalore City College, Kalyan Nagar, Bangalore, India.
Corresponding author: *1 Prescilla Devapriya. J, Department of Botany, Government Arts College, Udhagamandalam, The Nilgiris

Abstract: The present study was aimed to investigate the organic matter, pH effect on microbial diversity throughout the year Marlimund lake, Marlimund, Ooty, Nilgiris is an in the Udhagamandalam City in Tamil Nadu State, India. Microorganisms are involved in a variety of biogeochemical processes in natural environments. The dissolved organic matter is primarily composed of soluble portions of the fresh plant and animal residues. The particulate organic matter is partially resistant to microbial decomposition and serves as an important long-term supply of nutrients. Marlimund Reservoir is an important reservoir of water and a typical eutrophic freshwater lake. From the lake, soil samples were collected on a monthly basis, analyzed and recorded. The results were shown organic matter is directly proportioned to microbial diversity. And shows that the analyzed reservoir four Stations was influenced by the bacterial community, pH, and organic matter content, whereas comparatively little change was observed among IV stations in stratified conditions.

Key words: Marlimund lake, Organic matter, pH, Monthly variations and Microbial diversity.

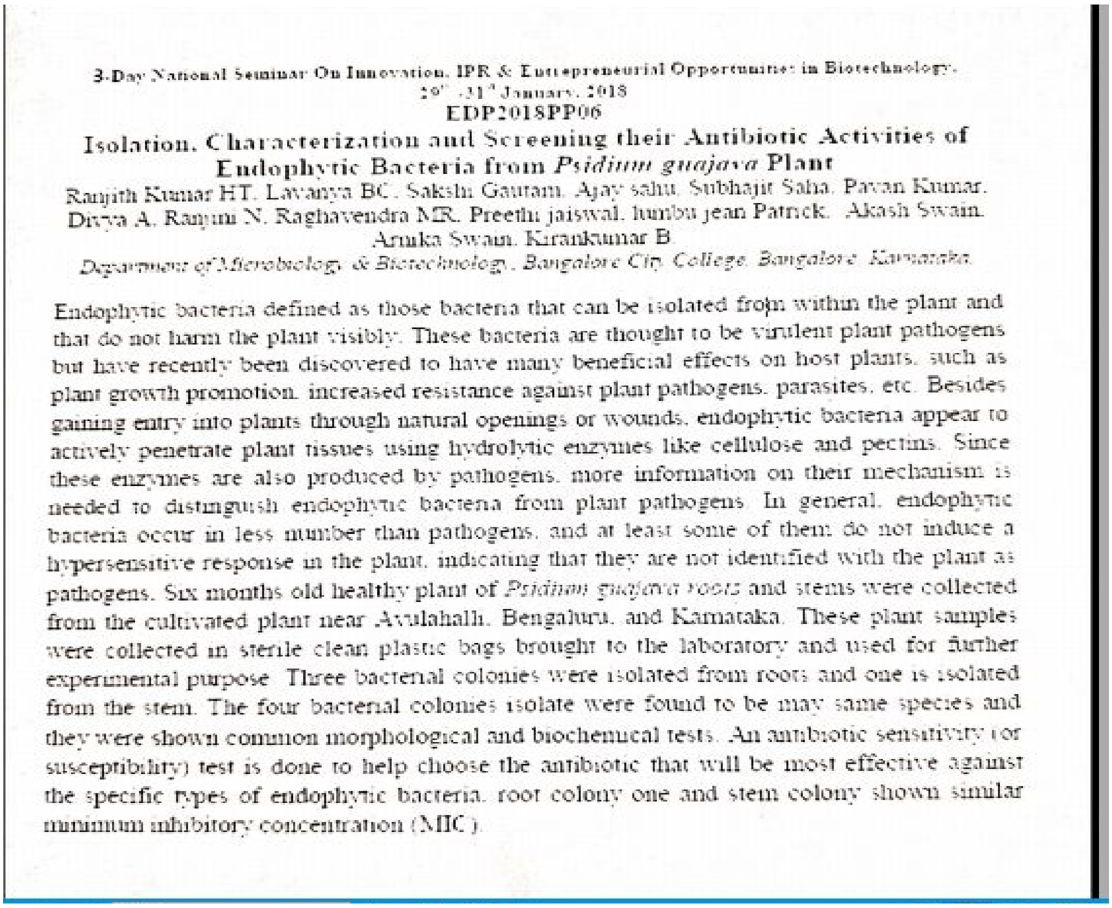
1. INTRODUCTION:

Aquatic ecosystems are dynamics and complex ecosystems that can share physical characteristics like sedimentation-resuspension, gas balance, water circulation, dilution, chemical characteristics like pH, organic matter decomposition and ecological characteristics like food web structure, prey-predator relationship with other aquatic ecosystems. In an aquatic ecosystem individual lakes are often chemically and physically distinct, even within the same geographic region [6]. There is a variety of organisms like flora (plant and bacteria) and fauna lives in water. Prokaryotes are among the most important contributors to the revolution of complex organic compounds and minerals in freshwater sediments [18, 22].

The important factors like pH and Organic matter, determining bacterial community composition in water and soil [2]. The organic fraction of the sediment is mainly of terrestrial origin shows the content of organic matter in the sediment is the highest level in areas with highest Carbon and Nitrogen ratio. The quantities of organic matter from simple nutrient elements Carbon, Nitrogen and Phosphors with repercussion on food chains and the quality of the water [14]. Biotic and abiotic factors regulate temporal and spatial shifts of microbial communities as well as organic matter in lakes is prone to extensive chemical transformations during and after sedimentation in aquatic environments [9]. These processes are mediated by heterotrophic bacteria. Microbial processes in sediments exert widespread

8. MVIT College_SOUVENIR NSIIE 29 -31 January, 2018

Kirankumar B, Ranjith Kumar HT, Lavanya BC, Sakshi Gautam.



3-Day National Seminar On Innovation, IPR & Entrepreneurial Opportunities in Biotechnology,
29th -31st January, 2018

EDP2018PP06

Isolation, Characterization and Screening their Antibiotic Activities of Endophytic Bacteria from *Psidium guajava* Plant

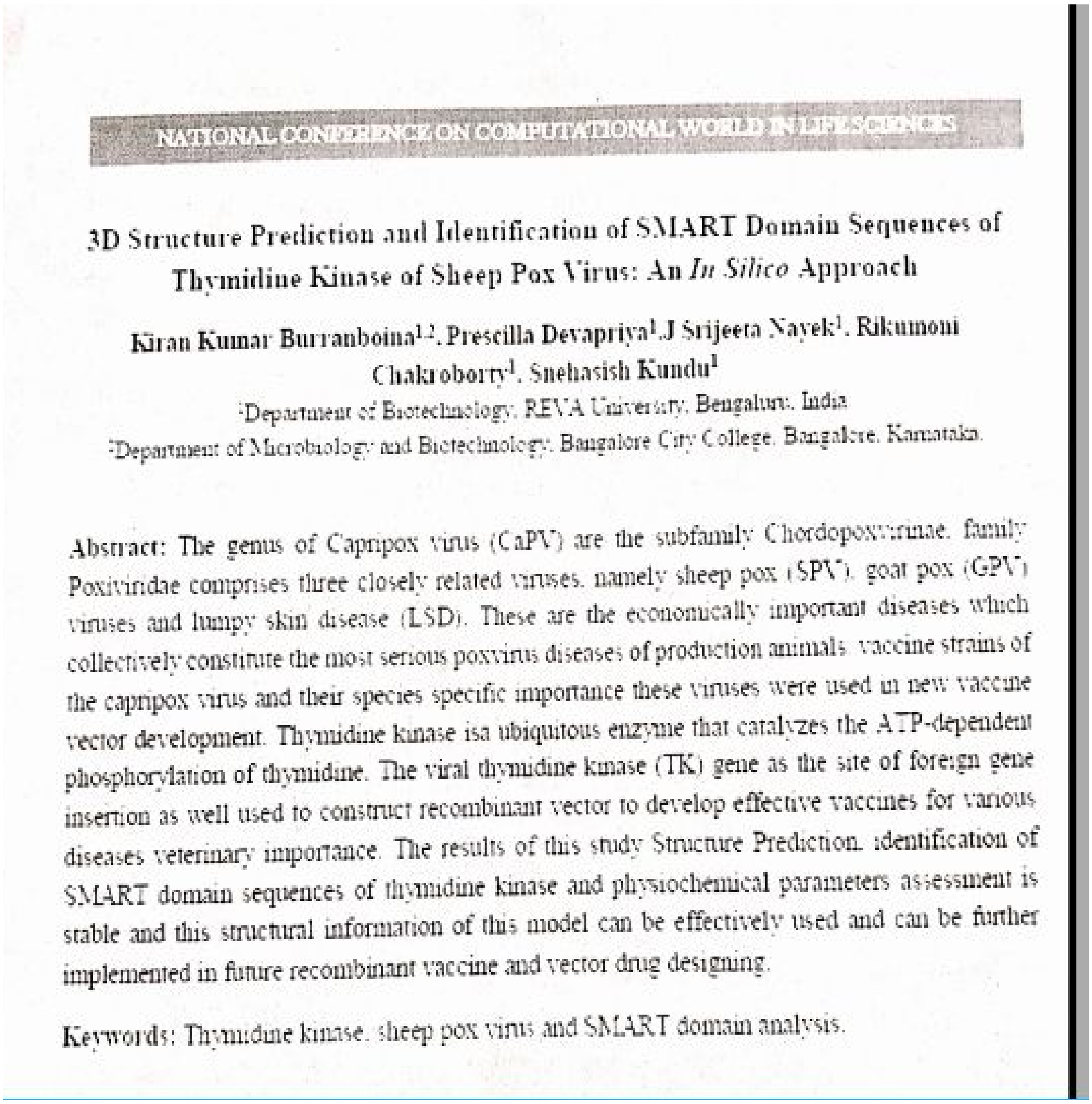
Ranjith Kumar HT, Lavanya BC, Sakshi Gautam, Ajay sahu, Subhajit Saha, Pavan Kumar,
Divya A, Ranjini N, Raghavendra MR, Preethi jaiswal, lumbu jean Patrick, Akash Swain,
Arnika Swain, Kirankumar B

Department of Microbiology & Biotechnology, Bangalore City College, Bangalore, Karnataka.

Endophytic bacteria defined as those bacteria that can be isolated from within the plant and that do not harm the plant visibly. These bacteria are thought to be virulent plant pathogens but have recently been discovered to have many beneficial effects on host plants, such as plant growth promotion, increased resistance against plant pathogens, parasites, etc. Besides gaining entry into plants through natural openings or wounds, endophytic bacteria appear to actively penetrate plant tissues using hydrolytic enzymes like cellulose and pectins. Since these enzymes are also produced by pathogens, more information on their mechanism is needed to distinguish endophytic bacteria from plant pathogens. In general, endophytic bacteria occur in less number than pathogens, and at least some of them do not induce a hypersensitive response in the plant, indicating that they are not identified with the plant as pathogens. Six months old healthy plant of *Psidium guajava roots* and stems were collected from the cultivated plant near Avulahalli, Bengaluru, and Karnataka. These plant samples were collected in sterile clean plastic bags brought to the laboratory and used for further experimental purpose. Three bacterial colonies were isolated from roots and one is isolated from the stem. The four bacterial colonies isolate were found to be may same species and they were shown common morphological and biochemical tests. An antibiotic sensitivity (or susceptibility) test is done to help choose the antibiotic that will be most effective against the specific types of endophytic bacteria. root colony one and stem colony shown similar minimum inhibitory concentration (MIC).

9. REVA College_ SOUVENIR _12 january, 2019.

Kiran Kumar Burranboina, Prescilla Devapriya.



NATIONAL CONFERENCE ON COMPUTATIONAL WORLD IN LIFE SCIENCES

3D Structure Prediction and Identification of SMART Domain Sequences of Thymidine Kinase of Sheep Pox Virus: An *In Silico* Approach

Kiran Kumar Burranboina[1,2], Prescilla Devapriya[1], J Srijeeta Nayek[1], Rikumoni Chakroborty[1], Snehasish Kundu[1]

[1]Department of Biotechnology, REVA University, Bengaluru, India

[2]Department of Microbiology and Biotechnology, Bangalore City College, Bangalore, Karnataka.

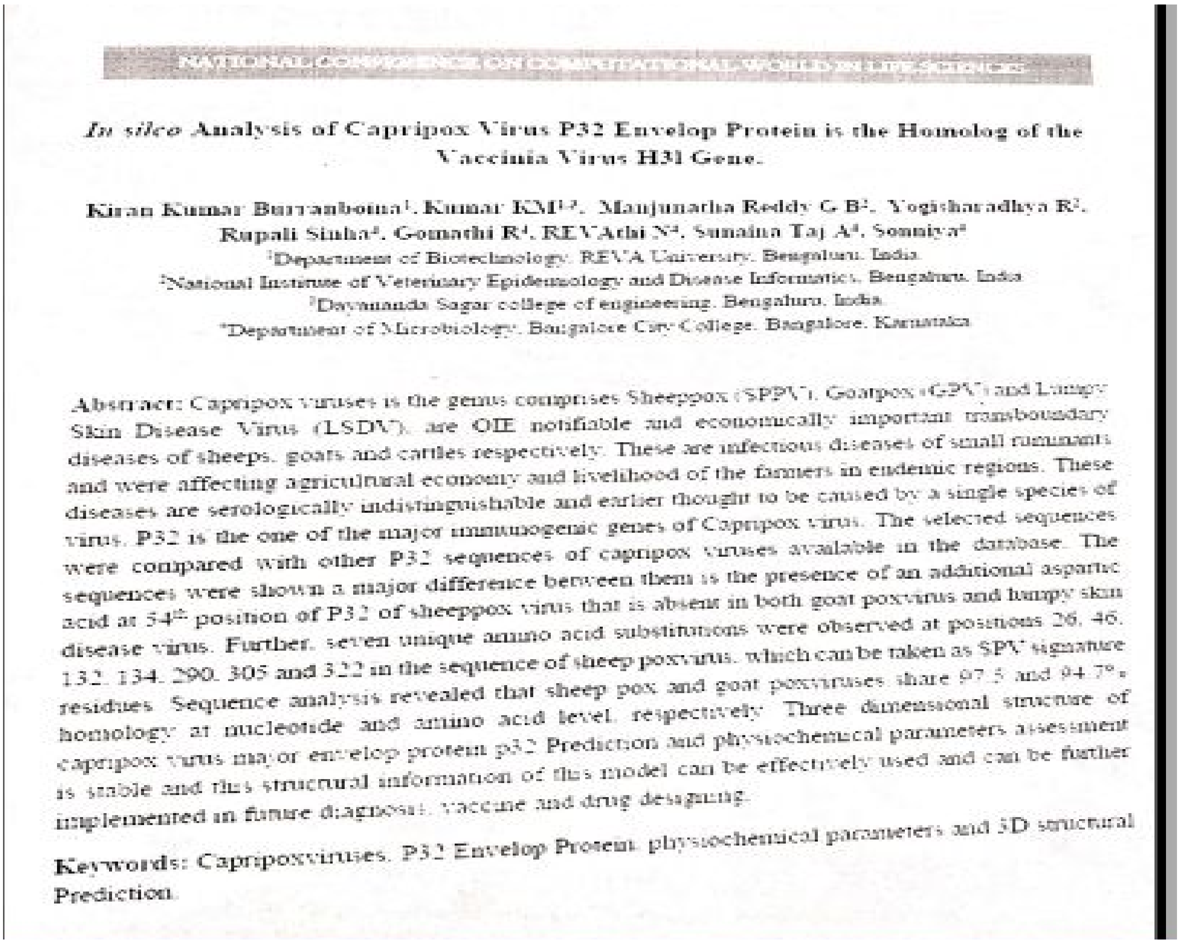
Abstract: The genus of Capripox virus (CaPV) are the subfamily Chordopoxvirinae, family Poxiviridae comprises three closely related viruses, namely sheep pox (SPV), goat pox (GPV) viruses and lumpy skin disease (LSD). These are the economically important diseases which collectively constitute the most serious poxvirus diseases of production animals. vaccine strains of the capripox virus and their species specific importance these viruses were used in new vaccine vector development. Thymidine kinase isa ubiquitous enzyme that catalyzes the ATP-dependent phosphorylation of thymidine. The viral thymidine kinase (TK) gene as the site of foreign gene insertion as well used to construct recombinant vector to develop effective vaccines for various diseases veterinary importance. The results of this study Structure Prediction, identification of SMART domain sequences of thymidine kinase and physiochemical parameters assessment is stable and this structural information of this model can be effectively used and can be further implemented in future recombinant vaccine and vector drug designing.

Keywords: Thymidine kinase, sheep pox virus and SMART domain analysis.

10. In silco Analysis of Capripox Virus P32 Envelop Protein is the Homolog of the Vaccinia Virus H3l Gene.

REVA College_ SOUVENIR _12 january, 2019.

Kiran Kumar B



NATIONAL CONFERENCE ON COMPUTATIONAL WORLD IN LIFE SCIENCES

In silco Analysis of Capripox Virus P32 Envelop Protein is the Homolog of the Vaccinia Virus H31 Gene.

Kiran Kumar Burranboina[1], Kumar KM[1,2], Manjunatha Reddy G B[2], Yogisharadhya R[2], Rupali Sinha[4], Gomathi R[4], REVAthi N[4], Sunaina Taj A[4], Sonniya[4]

[1]Department of Biotechnology, REVA University, Bengaluru, India

[2]National Institute of Veterinary Epidemiology and Disease Informatics, Bengaluru, India

[3]Dayananda Sagar college of engineering, Bengaluru, India

[4]Department of Microbiology, Bangalore City College, Bangalore, Karnataka

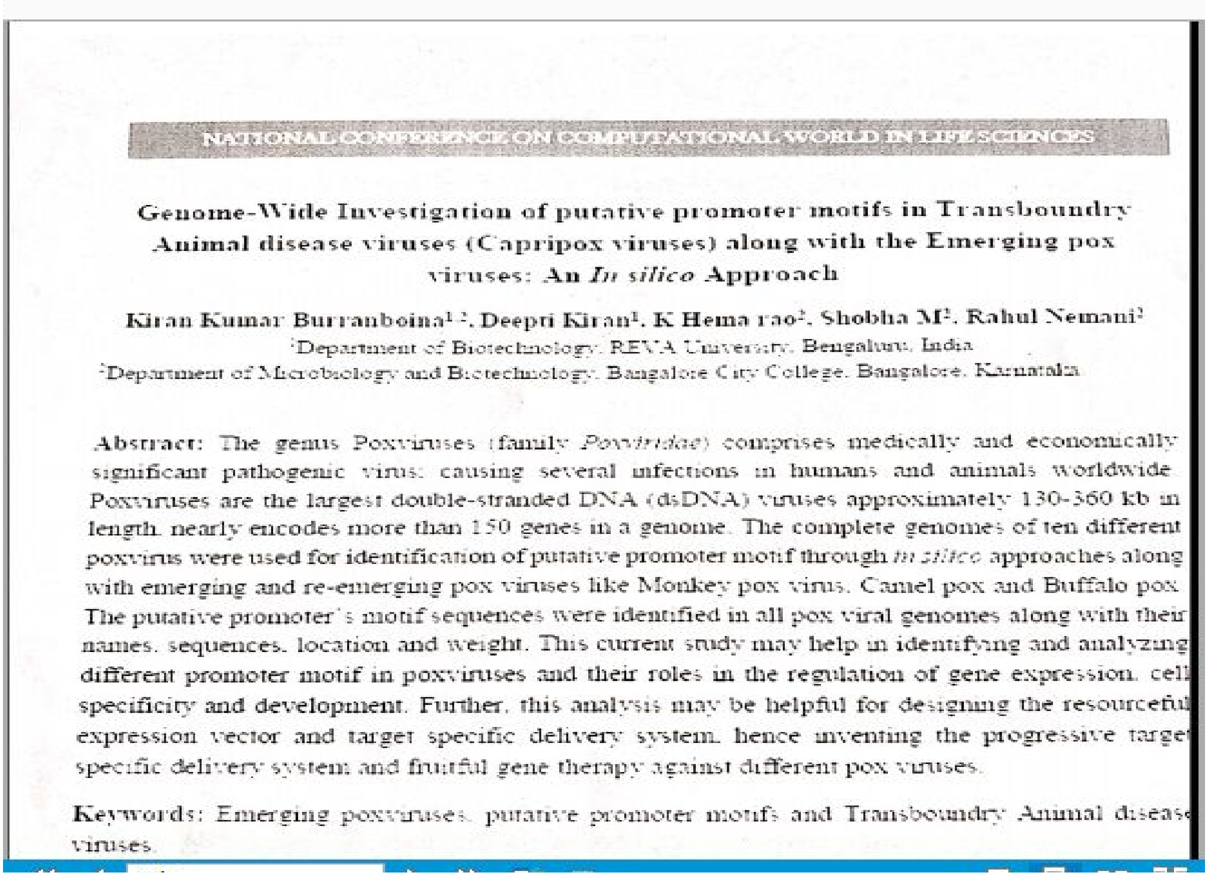
Abstract: Capripox viruses is the genus comprises Sheeppox (SPPV), Goatpox (GPV) and Lumpy Skin Disease Virus (LSDV), are OIE notifiable and economically important transboundary diseases of sheeps, goats and cattles respectively. These are infectious diseases of small ruminants and were affecting agricultural economy and livelihood of the farmers in endemic regions. These diseases are serologically indistinguishable and earlier thought to be caused by a single species of virus. P32 is the one of the major immunogenic genes of Capripox virus. The selected sequences were compared with other P32 sequences of capripox viruses available in the database. The sequences were shown a major difference between them is the presence of an additional aspartic acid at 54th position of P32 of sheeppox virus that is absent in both goat poxvirus and lumpy skin disease virus. Further, seven unique amino acid substitutions were observed at positions 26, 46, 132, 134, 290, 305 and 322 in the sequence of sheep poxvirus, which can be taken as SPV signature residues. Sequence analysis revealed that sheep pox and goat poxviruses share 97.5 and 94.7% homology at nucleotide and amino acid level, respectively. Three dimensional structure of capripox virus major envelop protein p32 Prediction and physiochemical parameters assessment is stable and this structural information of this model can be effectively used and can be further implemented in future diagnosis, vaccine and drug designing.

Keywords: Capripoxviruses, P32 Envelop Protein, physiochemical parameters and 3D structural Prediction.

11. Genome-Wide Investigation of putative promoter motifs in Transboundry Animal disease viruses (Capripox viruses) along with the Emerging pox viruses: An In silico Approach.

REVA College_ SOUVENIR _12 january, 2019.

Kiran Kumar B



NATIONAL CONFERENCE ON COMPUTATIONAL WORLD IN LIFE SCIENCES

Genome-Wide Investigation of putative promoter motifs in Transboundry Animal disease viruses (Capripox viruses) along with the Emerging pox viruses: An *In silico* Approach

Kiran Kumar Burranboina[1,2], Deepti Kiran[1], K Hema rao[2], Shobha M[2], Rahul Nemani[2]
[1]Department of Biotechnology, REVA University, Bengaluru, India
[2]Department of Microbiology and Biotechnology, Bangalore City College, Bangalore, Karnataka

Abstract: The genus Poxviruses (family *Poxviridae*) comprises medically and economically significant pathogenic virus, causing several infections in humans and animals worldwide. Poxviruses are the largest double-stranded DNA (dsDNA) viruses approximately 130-360 kb in length, nearly encodes more than 150 genes in a genome. The complete genomes of ten different poxvirus were used for identification of putative promoter motif through *in silico* approaches along with emerging and re-emerging pox viruses like Monkey pox virus, Camel pox and Buffalo pox. The putative promoter's motif sequences were identified in all pox viral genomes along with their names, sequences, location and weight. This current study may help in identifying and analyzing different promoter motif in poxviruses and their roles in the regulation of gene expression, cell specificity and development. Further, this analysis may be helpful for designing the resourceful expression vector and target specific delivery system, hence inventing the progressive targe specific delivery system and fruitful gene therapy against different pox viruses.

Keywords: Emerging poxviruses, putative promoter motifs and Transboundry Animal diseas viruses.

12. Screening of Selected Medicinal Plant Compounds against Sheeppox Virus using Molecular Docking Studies.

REVA College_ SOUVENIR _12 january, 2019.

Kiran Kumar B

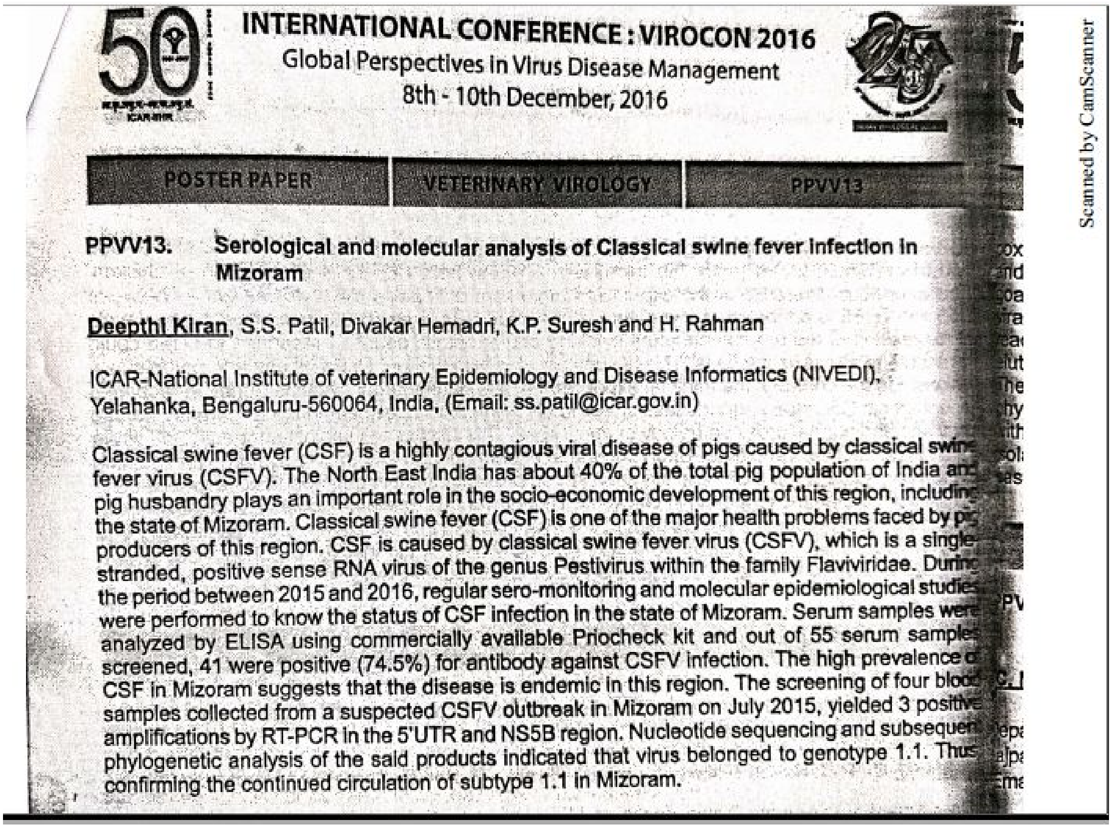
13. **Phylogeographic Analysis of Transboundry Animal Disease Virus (Capripox viruses) Based on Major Envelop protein P32: An In silico Approach.**

REVA College_ SOUVENIR _12 january, 2019.

Kiran Kumar B

14. VIROCON 2016

Deepthi Kiran*, S.S. Patil, Divakar Hemadri, K.P. Suresh, H. Rahman



INTERNATIONAL CONFERENCE : VIROCON 2016

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8th - 10th December, 2016

POSTER PAPER	VETERINARY VIROLOGY	PPVV13

PPVV13. Serological and molecular analysis of Classical swine fever infection in Mizoram

Deepthi Kiran, S.S. Patil, Divakar Hemadri, K.P. Suresh and H. Rahman

ICAR-National Institute of veterinary Epidemiology and Disease Informatics (NIVEDI),
Yelahanka, Bengaluru-560064, India, (Email: ss.patil@icar.gov.in)

Classical swine fever (CSF) is a highly contagious viral disease of pigs caused by classical swine fever virus (CSFV). The North East India has about 40% of the total pig population of India and pig husbandry plays an important role in the socio-economic development of this region, including the state of Mizoram. Classical swine fever (CSF) is one of the major health problems faced by pig producers of this region. CSF is caused by classical swine fever virus (CSFV), which is a single-stranded, positive sense RNA virus of the genus Pestivirus within the family Flaviviridae. During the period between 2015 and 2016, regular sero-monitoring and molecular epidemiological studies were performed to know the status of CSF infection in the state of Mizoram. Serum samples were analyzed by ELISA using commercially available Priocheck kit and out of 55 serum samples screened, 41 were positive (74.5%) for antibody against CSFV infection. The high prevalence of CSF in Mizoram suggests that the disease is endemic in this region. The screening of four blood samples collected from a suspected CSFV outbreak in Mizoram on July 2015, yielded 3 positive amplifications by RT-PCR in the 5'UTR and NS5B region. Nucleotide sequencing and subsequent phylogenetic analysis of the said products indicated that virus belonged to genotype 1.1. Thus confirming the continued circulation of subtype 1.1 in Mizoram.

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16. IOT and Health Care System for Helderly

Mrs. Innahai Anugrahan

17. IOT and Health Care System for Helderly

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