Ranjith N. Kumavath et al., J Pet Environ Biotechnol 2012, 3:7
http://dx.doi.org/10.4172/2157-7463.S1.007

OMICS Group Conferences
Accelerating Scientific Discovery
Global Biofuels & Bioproducts Summit
November 19-21, 2012 Hilton San Antonio Airport, USA

Bacterial diversity for cellulose producing gene(s) from Western Ghats of India and their biological potentials in tissue engineering

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Microorganisms are ubiquitous; they form communities in different natural as well as manmade habitats. The activity of these microbial communities plays an important role in human welfare and the ecology of the whole planet. The major objective of this study will be to look into microorganisms that produce cellulose. Cellulose is the most abundant natural polymer in the biosphere during human history for industrial use such as energy, materials, paper, clothes and foods. Bacterial cellulose has been successfully used in a wide range of applications, including wound dressings, scaffolds for tissue growth, food additives, and flexible screen displays. Recent reports toward incorporating particles, enzymes, growth factors and antibiotics into bacterial cellulose scaffolds, which will improve their utility in tissue regeneration, biosensors and wound dressings. *Gluconacetobacter xylinum (*formerly called *Acetobacter xylinum)* has served as the model organism for elucidating the basic features of cellulose biosynthesis in bacteria. The production of cellulose has also been described in *Agrobacterium tumefaciens* and *Rhizobium leguminosarum* bv. Trifolii, some species of cyanobacteria, and the gram-positive bacterium *Sarcina ventriculi*. Recent studies on the biofilm formation process of *Salmonella enterica* ser. Typhimurium (S. Typhimurium) and *E. coli* have revealed that these bacteria, as well as many other species of the Enterobacteriaceae family, such as *Citrobacter* spp., *Enterobacter* spp., and *Klebsiella* spp., produce cellulose as a crucial component of the bacterial extracellular matrix. Synthesis of bacterial cellulose, which has mainly been examined in G. xylinus, remains poorly understood. Therefore it is still a pristine topic which needs to be probed thoroughly before we explore the potentialities of microbial cellulose. As part of the technical programme of the research work planned, extensive sampling covering different geographical areas have been carried out and eight strains of bacteria were identified which had shown diverse response positively in the production of cellulose. This diverse response was determined by various means. It includes morphological characteristic studies, microbiological media inoculation and their response to various media which are specific to cellulose production, biochemical assays, and enzymatic assays. This has prompted to study the genetic diversity of these strains and hence PCR amplification of 16 S RNA genes was carried out and the sequences obtained were used to construct a phylogenetic tree using the MEGA5. Also the primer amplification of cellulose synthase gene using gene specific primer is attempted from the organism which showed maximum production under cultural conditions.

Biography

Ranjith N.Kumavath received Ph.D in Microbial Biochemistry (University of Hyderabad). Before joining Central University of Kerala (CUK) in September, 2011. He had been a Post- Doctoral Fellow at Mercer University, Georgia, USA. at Nanyang Technological University (NTU), Singapore and a UGC-Dr. DSKothari Post Doctoral Fellow at the Central University of Hyderabad. He received Bio-Asia Innovation for young scientist award and was invited to give lectures at the Ben-Gurion University of the Negev, Israel and The Management Development Institute of Singapore (MDIS), School of Life Science, Singapore. He has been awarded the Fast Track Young Scientists award by DST, Govt. of India. Presently, he is operating two major research projects funded by UGC-Startup grant and DST. He is the reviewer for many prestigious science journals and has published 1 Book; 1 Book chapter and 12 Research papers, discovered 4 Novel enzymes (Enzymes Code assigned by IUBMB) and made 8 national and 5 international presentations. He has research collaboration with Central University of Hyderabad; Institute of Integrative Omics and Applied Biotechnology (IIOAB) West Bengal and San Diego State University, USA. His research interests are Microbial Genomics and Metagenomics (MGM), Human Pathogenic Infective Diseases; Integrative Omics Based Markers and Target Drug Discovery, Cancer Pharmacogenomics and Proteomics.

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