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Bio-Letters



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Bio-Letters

About Gurucharan College, Silchar

Gurucharan College, Silchar, the premier institute of North–Eastern region established in 1935, is undoubtedly playing a prime role in the cause of higher education for long eight decades. The college has established itself in every sphere of life, earning name and fame and has become one of the oldest citadels of higher education in the eastern part of India. The well-acclaimed reputation of the college pride to stand on its own feet with 25 Departments and 6 Research Centres funded by UGC, DBT, DST and Ministry of Culture, Govt. of India allied with impressive infrastructure facilities, self-financing courses supported by different cells playing a pivotal role for the promotion of curricular and co-curricular activities.

Institutional Biotech Hub

Institutional Biotech Hub (funded by, New Delhi) of Gurucharan College, Silchar was established in the year 2011 with a purpose to provide infrastructural facilities to the undergraduate students, research scholars and faculty members to carry out their research. Every year a good number of research papers are published and presented in seminars and conferences. Workshops/ hands-ontraining/ invited lectures and outreach programmes are conducted throughout the year on different topics of biological sciences. The Hub guides and provides laboratory facilities to the P.G students/ research scholars of nearby institutions and colleges. Institutional Biotech Hub also provides community services to the nearby villages by organizing programmes on awareness, education and health.

Bioinformatics Centre

The Bioinformatics Infrastructure Facility (BIF) of Gurucharan College, Silchar was established in 2009 with the sole purpose of imparting knowledge to students, researchers, scholars and faculty members for research and educational activities. The Bioinformatics Centre has constantly been achieving its objective by successfully conducting a significant number of trainings, seminars, demonstrations and outreach programmes. The centre has progressed steadily and has created adequate facility for study and exchange of biological information among the students, researchers. and faculties of nearby institutions. The centre has various collaborations with other BIFs of Assam and other north-eastern states for conducting seamless research activities and resource exchange for the benefit of students and teachers alike.



From Príncípal's Desk

Dr. Bibhas Deb *Principal,* Gurucharan College, Silchar



I am very much happy to know that Bioinformatics Centre and Institutional Biotech Нив (funded by DBT, New Delhi, India) of Gurucharan College, Silchar is going to release its 2nd issue of "Bio-Letters" 2018. As of 1st issue, this issue comprises the recent research activities carried out, utilizing the financial support of DBT, New Delhi. An invited article has been included. BioLetters-2018 also listed that have been the papers presented and semínars ín conferences, GenBank submissions and research papers that has been published in scientific journals.

I am confident that this newsletter will play a great role in showcasing and documenting all the activities of Bioinformatics Centre and Institutional Biotech Hub, and may enrich the future research activities in a greater depth.

I congratulate all the members associated with the publication of Bio-Letters-2018. I wish publication of this newsletter would be a grand success.

> Dr. Bibhas 1968 G. C. Frincipal Gurucharan College, Silchar

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Applications of Molecular Markers in Plant Genome Analysis - A study

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ABSTRACT

Genetic variation analysis and their recognition can help us to understand the molecular basis of various biological phenomena in plants. Elucidation of genetic variation of the entire plant kingdom cannot be covered under sequencing projects, but, molecular markers which may provide us the understanding of phenotypes with requisite landmarks. DNA based marker techniques such as RFLP (restriction fragment length polymorphism), RAPD (random amplified polymorphic DNA), SSR (simple sequence repeats) and AFLP (amplified fragment length polymorphism) are routinely being used in ecological, evolutionary, taxonomical, phylogenic and genetic studies of plant sciences. These techniques are well established. Their advantages and limitations have been well understood. With the advent of sciences, a new class of developed techniques has emerged, derived from a combination of earlier basic techniques. For the exposure of genetic discontinuity and distinctiveness, the advanced marker techniques tend to combine advantageous features of several basic techniques which are more sensitive and with more resolution power. The advanced marker techniques also utilize a newer class of DNA elements such as retrotransposons, mitochondrial and chloroplast-based microsatellites, thereby revealing genetic variation through increased genome coverage. Techniques such as RAPD and AFLP are also being applied to cDNA-based templates to study patterns of gene expression and uncover the genetic basis of biological responses. The study details with the account of techniques used in the identification of markers and their applicability in plant genome analysis in short.

Keywords: Molecular marker, Plant genome, Microsatellites.

INTRODUCTION

The concept of genetic markers is not a new one, in the nineteenth century; Gregor Johann Mendel used phenotype-based genetic markers in his experiment. Later, the theory of genetic linkage was established on phenotype-based genetic markers for Drosophila. The limitations of phenotype based markers led to the development of more useful DNA based molecular markers or genetic markers. A molecular marker is defined as a particular segment of DNA that is representative of the differences at the genome level which may or may not correlate with the phenotypic expression of a trait. Molecular markers offer numerous advantages over conventional phenotype based alternatives as they are stable and detectable in all tissues regardless of growth, differentiation, development, or defense status of the cell are not confounded by the environment, pleiotropic and epistatic effects. Molecular marker technique should have the following criteria: (1) be polymorphic and evenly distributed throughout the genome, (2) provide adequate resolution of genetic differences (3) generate multiple, independent and reliable markers (4) simple, quick and inexpensive (5) need small amounts of tissue and DNA samples; (6) have linkage to distinct phenotypes and (7) require no prior information about the genome of an organism. Unfortunately, no molecular marker technique is ideal for every situation. Techniques differ from each other with respect to important features such as genomic abundance, level of polymorphism detected, locus specificity, technical requirements etc. Depending on the need, modifications in the techniques have been made, leading to a second generation of advanced molecular markers. In this study few techniques of recent advances made in molecular marker and their application in plant sciences have analyzed (Agarwal et al. 2008).



TYPES OF DNA MARKERS USED IN PLANT GENOME ANALYSIS

Different patterns of DNA-based molecular techniques (Botstein *et al.* 1980, Joshi *et al.*, 1999, Powell *et al.* 1996) are employed to evaluate DNA polymorphism. These are (1) hybridization-based methods, (2) polymerase chain reaction (PCR)-based methods and (3) sequencing-based methods.

Hybridization-based methods

Hybridization-based methods include RFLP (Botstein *et al.* 1980) and variable number tandem repeats (VNTRs) (Nakamura *et al.* 1987). Labeled probes such as random genomic clones, cDNA clones, probes for microsatellite (Litt et *al.* 1989) and minisatellite (Jeffrey *et al.* 1985) sequences are hybridized to filters containing DNA, which has been digested with restriction enzymes. Polymorphisms are detected by presence or absence of bands upon hybridization.

PCR-based methods

PCR-based markers involve *in vitro* amplification of particular DNA sequences or loci, with the help of specific or arbitrary oligonucleotide primers and the thermostable DNA polymerase enzyme which includes RAPD (Williams *et al.*, 1990, Welsh and McClelland, 1991), arbitrarily primed PCR (AP–PCR) (Welsh and McClelland, 1991) and DNA amplification fingerprinting (DAF) (Caetano-Anolles and Bassam, 1993). Intersimple sequence repeats (ISSRs) (Zietkiewicz *et al.*, 1993) polymorphism is a specific primer-based polymorphism detection system, where a terminally anchored primer specific to a particular simple sequence repeat (SSR) is used to amplify the DNA between two opposed SSRs of the same type. Other than that a recent approach known as AFLP (Vos *et al.*, 1999) is a technique that is based on the detection of genomic restriction fragments by PCR amplification.

Sequencing-based markers

DNA sequencing can also be used for identifying species. Variations due to insertion or deletion, transversion can be accessed directly, and information on a specific locus can be obtained. Genetic variation occurs extensively at the single nucleotide level. Direct sequencing can efficiently identify such single nucleotide polymorphisms that usually depend on how closely related are the organisms being compared. Other sequencing-based strategies include analysis of the variable internal transcribed spacer (ITS) sequences of ribosomal DNA (rDNA). The ITS region of 18s–26s rDNA has proved to be a useful sequence for phylogenetic studies in many angiosperm families. The level of ITS sequence variation suitable for phylogenetic analysis is found at various taxonomic levels within families, depending on the linkage. A number of researchers have also sequenced other regions of DNA such as trnK of chloroplast and spacer region of 5s rDNA as diagnostic tools for authentication purpose.

Applications of molecular markers

DNA-based molecular markers have proved their utility in fields like taxonomy, embryology, physiology, genetics, etc. As the science of plant genetics progressed, researchers have tried to explore these molecular marker techniques for their applications in commercially important plants such as crops, food, horticulture etc. and recently in the pharmacognostic characterization of herbal and traditionally used medicinal plants also.

Genetic variation/genotyping analysis

It has been well established that geographical conditions affect the active constituents of the medicinal plant and hence their activity profiles (Oleszek *et al.* 2002). Many researchers have studied geographical variation at the genetic level. Estimates of genetic diversity are also important in designing crop improvement programmes for the management of germplasm and evolving conservation strategies. RAPD-based molecular markers have been found to be useful in differentiating various accessions of Neem (Farooqui *et al.*, 1998), *Juniperus communis* (Adams *et al.*, 2002), *Taxus wallichiana* (Shasany *et al.*, 1999), *Codonopsis pilosula* (Fu *et al.*, 1999) collected from different geographical regions.



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Similarly, different accessions of *Cannabis sativa* (Kojoma *et al.*, 2002) have been discriminated using ISSR markers and those of *Arabidopsis thaliana* L. Heynh (Barth *et al.*, 2002) have been differentiated using cleaved amplified polymorphic sequence (CAPS) and ISSR markers. Thus inter and intra-species variation has also been studied using DNA-based molecular markers.

The phylogenetic relationship has been studied among citrus and its relatives using SSR markers (Pang *et al.*, 2003). RAPD has been used to construct genetic linkage maps of *Eucalyptus grandis* and *Eucalyptus urophylla* (Grattapaglia, and Sederoff, 1994) An attempt has been made to develop a physical AFLP map of the complex *Arabidopsis* genome by combining gel-based AFLP analysis with *in silico* restriction fragment analysis using the published genome sequence (Peters *et al.*, 2001).

Authentication of medicinal plants

DNA-based techniques have been widely used for authentication of plant species of medicinal importance. This is especially useful in case of those that are frequently substituted or adulterated with other species or varieties that are morphologically and/or phytochemically indistinguishable.

Dried fruit samples of *Lycium barbarum* were differentiated from its related species using RAPD markers (Zhang *et al.*, 2001). The RAPD technique has also been used for determining the components of a Chinese herbal prescription, Yu Ping Feng San. In this study the presence of three herbs (*Astragalus membranaceous* (Fisch.) Bge., *Ledebouriella seseloides* Wolff and *Atractylodes macrocephala* Koidz) in the formulation have been detected using a single RAPD primer(Cheng *et al.*, 1998). Three RAPD primers have been identified that could successfully discriminate between three species of *Atractylodes*, from Chinese formulation purchased from local markets (Chen *et al.* 2001). In another study, three random primers were used to reveal the genetic variability of *Astragalus* medicine materials sold in the Taiwan market. SSCP analysis was also conducted on PCR products from the ITS-1 region of rDNA in order to differentiate the two *Astragalus* species (Cheng et al., 2000). Primers have been designed for hybridization with the hypervariable ends of microsatellite loci that could reveal DNA-polymorphism among five *Eucalyptus* species (Matsuda *et al.*, 1997). Some researchers have used a new approach called Direct Amplification of Length Polymorphism (DALP) for authentication of *Panax ginseng* and *Panax quinquefolius* (Ha *et al.*, 2001). Authentication of medicinal *Dendrobium* species by the internal transcribed spacer of rDNA has been done successfully (Lau *et al.*, 2001).

Detection of adulteration/substitution

RAPD technique was adopted to identify eight types of dried *Coptis* rhizomes and one type of *Picrorrhiza* rhizome, a substitute for the former in the Chinese herbal market (Cheng *et al.*, 1997). *P. ginseng* is often substituted by *P. quinquefolius* (American ginseng). Sequence characterized amplified region (SCAR), AP– PCR, RAPD, and RFLP have been successfully applied for differentiation of these plants and to detect substitution by other closely related species (Shaw *et al.*, 1995, Wang *et al.*, 2001).

Plant breeding system

ISSR–PCR has been found to be an efficient and reliable technique for the identification of zygotic plantlets in citrus interploid crosses (Tusa *et al.,* 2002). Molecular markers have been used as a tool to verify the sexual and apomictic offspring of intraspecific crosses in *Hypericum perforatum,* a well- known antihelminthic and a diuretic (Steck *et al.,* 2001).

Impact of molecular marker techniques

DNA-based molecular markers have been used extensively for a wide range of applications in food crops and horticultural plants (Sharma *et al.*, 2002). These applications include the study of genetic variation, identification of disease-resistant genes, identification of quantitative-trait loci, diversity analysis of exotic germplasms, sex identification of dioecious plants, phylogenetic analysis, cultivar identification, crossbreeding studies, etc. Recently, the application of DNA-based molecular markers is being explored in the field of nutraceuticals too.



According to the new European Council legislation, the labeling of food or food ingredients produced from, or containing licensed genetically modified organisms must indicate the inclusion of these ingredients where they are present at or above a level of 1%. In compliance with the labeling regulation for GM foods, several countries in Europe such as Germany and Switzerland have extensively developed PCR methods for both quantification and identification.

Traditionally, pharmacognosy mainly addressed quality related issues using routine botanical and organoleptic parameters of crude drugs. Pharmacognosy became more interdisciplinary because of subsequent advances in analytical chemistry. These developments added emphasis on chemo-profiling assisted characterization with chromatographic and spectroscopic techniques. The new pharmacognosy includes all aspects of drug development and discovery, where biotechnology-driven applications of advanced molecular markers will play a vital role.

Extensive research on DNA-based molecular markers is in progress in many research institutes all over the world. In India, several agricultural universities and research institutes are actively involved in exploring DNA-based techniques in the gene-level analysis of medicinal plants. Although considerable progress has been made in DNA marker technology, applications of these techniques for characterizing semi-processed and processed botanical formulations to ensure that the desired quality remain under-utilized. This technique remains important in plant genome research with its applications in pharmacognostic identification and analysis.

Although DNA analysis is currently considered to be cutting-edge technology, it has certain limitations due to which its use has been limited to academia. In order to establish a marker for identification of a particular species, DNA analysis of closely related species and/or varieties and common botanical contaminants and adulterants is necessary, which is a costly and time-consuming process. Isolation of good-quality DNA suitable for analysis from semi-processed or processed botanicals is also a challenge. Another important issue is that DNA based markers will remain the same irrespective of the plant part used, while the phytochemical content will vary with the plant part used, physiology and environment. DNA markers ensure the presence of the correct genotype but do not reveal the contents of the active principle or chemical constituents. Hence DNA analysis and pharmacognostic techniques for chemo-profiling such as TLC, HPTLC, etc. will have to be used hand in hand rather than in isolation.

Several attempts have been made in recent years, to correlate DNA markers with qualitative and quantitative variations in phytochemical composition among closely related species. Proper integration of molecular techniques and analytical tools will lead to the development of a comprehensive system of botanical characterization that can be conveniently applied at the industry level for quality control of botanicals.

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Isolation and Identification of Cadmium and Copper Tolerant Bacteria from Soil

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INTRODUCTION

Contamination of agricultural soil by heavy metals has become a critical environmental concern due to their potential adverse ecological effects. Such toxic elements are considered as soil pollutants due to their widespread occurrence, and pose toxic effect on all organisms. Determination of microbial diversity plays an important role in assessing areas under anthropogenic stress. Quantification of species diversity and studying their tolerance ability has been done to monitor the environmental hazards.

METHODOLOGY

Bacterial tolerance towards cadmium (Cd) and copper (Cu) was determined by agar dilution method, which were added in the form of cadmium chloride and copper (II) sulphate pentahydrate. All the isolates were identified by morphological and biochemical characters. Predominant isolates were further identified by 16S rDNA sequence analysis, using Geneious R8 software package (Bio-matters Ltd., Auckland, New Zealand).

RESULTS

The present study showed that contaminated crop field nearby industrial discharge, brick industry, food industry etc. exerts pressure for the sustenance of microbial community. Subsequently, microbes develop resistance mechanism towards toxic metals and are able to withstand high concentration of Cadmium and Copper. The predominant isolates were identified as *Bacillus cereus* strain GCC-SO2 and *Chromobacterium pseudo violaceum* strain GCC-SO4.

CONCLUSION

B. cereus strain SO2 and *C. pseudo violaceum* strain SO4 are able to tolerate the presence of toxic heavy metals. These strains naturally bio-accumulates toxic metals, thereby reduces the amount of free ions in the soil. The study suggests that, bio-environmental interaction between soil-bacteria-metal-plant is of great significance for environmental clean-up and remediation of heavy metal-contaminated soil.

Keywords: Heavy metal; soil; bacteria; 16S rDNA; minimum inhibitory concentration



Bacteriological Analysis of Street Vended Fruit Juice in Silchar

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INTRODUCTION

Fruit juices have become an important part of the diet in today's world. They have several health and therapeutic benefits. In many tropical countries including India, freshly prepared fruit juices are sold at all public places and roadside stalls. The occurrence of food-borne illness has been reported due to the consumption of street vendor fruit juices The present study was conducted to analyze the quality of the juices available in the streets of Silchar. It was aimed at evaluating the safety of the squeezed juices following standard microbiological techniques.

METHODOLOGY

Five juice samples namely sugarcane juice, pineapple juice, orange juice, Bengal quince juice and lemon juice were studied. The collected samples wer taken to the laboratory and processed within an hour. Bacterial colonies were grown on Nutrient Agar and MacConkey Agar. The isolates were purified by sub-culturing and identified on the basis of morphological and biochemical characteristics.

RESULTS

The study showed that the juices were highly unhygienic and loaded with bacteria. The total bacterial count in the nutrient agar plates was in the range of 22.4×10⁴ CFU/ml-284.6×10⁴cfu/ml and the total bacterial count in the MacConkey agar plates was in the range of 17×10⁴cfu/ml-242×10⁴ CFU/ml for the juice samples.

CONCLUSION

The highest amount of contamination was found to be in sugarcane juice while the lowest in lemon juice. Thus the results imply that the fruit juices available in the streets of Silchar are a risk to human health and measures should be taken to educate the vendors and improve the quality of the juices. Regular monitoring of the quality of the fruit juices should be done.

Keywords: Fruit juice, contamination, bacteria, quality, health risk, hygiene.



Allelopathic effect of Neem and Tulsi on the Growth and Germination of Mung Beans

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INTRODUCTION

Allelopathy was first coined by Austrian Professor Hans Molisch in 1937. It is the biological phenomenon by which an organism produces one or more biochemicals (allelochemicals) that influence the growth, survival, reproduction of other organisms. In this project, the allelopathic effect of Neem and Tulsi on the growth and germination of Mung beans were examined.

METHODOLOGY

Leaf extract of Neem and Tulsi were prepared by standard protocol. Cotton beds containing the extract were placed on sterilized petri plates. Mung beans were placed on the extract soaked cotton beds, sealed and kept for 10 days in an incubator. The changes were measured after 10 days of incubation. The experiment was carried out in triplicates.

RESULTS

Shoot length of Mung beans were found to be the least in the plate containing Neem extract (5.4 cm) and followed by Tulsi (23.6 cm). The control showed the maximum growth (25.94 cm).

CONCLUSION

From the experiment, it was observed that Neem exhibits strong phytotoxicity and allelochemicals to suppress the germination of Mung beans. Thus Neem can be used as an important source of natural herbicide to control weeds in a crop field.

Keywords: Allelopathy, Neem, Tulsi, Mung beans, Phytotoxicity.



Evaluation of Heavy Metal Stress in Bacteria and their Co-resistance Pattern with Antibiotics

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INTRODUCTION

Heavy metals and metalloids in soils are derived from the soil parent material (lithogenic source) and various anthropogenic sources. Large accumulation of heavy metals in organic layers of cultivable soils may adversely affect the structure and diversity of microbial communities. They are important environmental pollutants causing risks and hazards to humans and the ecosystem.

METHODOLOGY

The soil samples were taken from four different sites of Cachar district of Assam, India. Bacterial communities in the soil were screened and identified on the basis of morphological, biochemical and 16S rDNA sequence analysis. High concentrations of heavy metals negatively affected bacterial diversity and therefore, minimum inhibitory concentration for Pb and Fe was determined by agar dilution technique. Co-resistance of antibiotic resistance was also determined.

RESULTS

The isolates were identified as *Bacillus megaterium* strain GCC-SO1 and *Pseudomonas aeruginosa* strain GCC-SO3. 16SrDNA gene sequence of these isolates was submitted in the GenBank and was given accession numbers: MH109306 and MH109307. Maximum tolerance towards lead was shown by *Bacillus megaterium* strain GCC-SO1 and towards iron by *Pseudomonas aeruginosa* strain GCC-SO3. In antibiotics resistance test, it has been observed that both the isolates were resistant to methicillin and penicillin. *Pseudomonas aeruginosa* strain GCC-SO3, however, showed resistance to other antibiotics such as cefdinir, ampicillin, kanamycin, rifampicin, and vancomycin. Isolates of *Bacillus sp.* showed intermediate zone of inhibition against azithromycin, ceftriaxone, cefdinir, rifampicin, polymyxin, and co-trimoxazole.

CONCLUSION

The interaction between toxic metals and microbe may obstruct natural habitat, which may result in the evolution of new microbial strains and often shows resistance towards heavy metals, antibiotics, and other substances.

Keywords: Heavy metals; soil; 16S rDNA; bacteria; co-resistance.



Effect of Lead in the Germination and Shoot Growth of Kidney Beans

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INTRODUCTION

The increase in world population leads to increased threats to the environment. Rapid industrialization and urbanization processes have led to the incorporation of many chemical pollutants in the natural resources. In this project, we have summarized the effects of lead on seeds of the plant *Phaseolus vulgaris* (kidney beans) affecting the germination and the shoot growth process. Metal toxicity affects crop yields, soil biomass, and fertility.

METHODOLOGY

Pot experiments were carried out to study the effects of lead on seed germination and shoot growth of *Phaseolus vulgaris* (Kidney beans). Fresh seeds were collected, stored in moist conditions and transferred to glasses containing different concentrations of lead (0 mg, 8.2 mg, 16.2 mg, 32.8 mg, 65.6 mg, and 131.2 mg) in the form of lead nitrate. An average number of leaves and seed germinated were noted down. Shoot growth in each glass was noted for 15 days following inoculation.

RESULTS

The germination rate and shoot length were assessed at a time interval of 5, 10 and 15 days. It was seen that almost all the seeds germinated but however there was a gradual decrease in the shoot length of the plantlet with the increasing concentration of lead. At higher concentration, some plants failed to grow.

CONCLUSION

The study showed that lead is toxic to plant health. The shoot lengths of the plants were heavily affected by the applications of lead on high doses. The seed germination rate was also progressively reduced. Hence, it can be concluded that lead proves to be highly toxic in excessive dosage for the growth and productivity of *Phaseolus vulgaris* plant.

Keywords: Lead, toxicity, kidney beans, seed germination, shoot length.



16S rRNA based Sequence Analysis of some Plant Growth Promoting *Bacillus* species

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INTRODUCTION

Plant pathogens are responsible for many plant diseases, resulting in economic losses. The use of bacterial agents is an excellent option to fight against plant pathogens and an alternative to the use of chemicals, which are offensive to the environment and to human health. Some of the biocontrol agents such as *Bacillus subtilis*, Bacillus pumilus M4 are members of the *Bacillus* genera that are used as an antagonist against pathogens like Colletotrichum *gloeosporioides and* Colletotrichum langearium respectively. These bacterial genera have important traits such as plant growth-promoting properties.

METHODOLOGY

The present study was conducted to analyze the evolutionary relationship and their divergence of 20 bacterial species. This was achieved by studying the 16s rRNA sequences. Nucleotide sequences were collected from GenBank (NCBI) and Multiple Sequence Alignment (MSA) was done by using Geneious R8. The phylogenetic tree was also prepared using the Neighbor-Joining method.

RESULTS

Inference was made on different species of genus *Bacillus*, which diverged from their clade and cluster with different species of same genus *Bacillus*. The mean GC% of all the sequences was found to be 54.94%. It was observed that *B. amyloliquefaciens* and its variant *B. velezensis* strain BCRC 17467 cluster together in the middle of the tree. However, *B. velezensis* strain BPR 189 forms a different branch with *B. methylotrophicus* strain DA16-5. *B. velezensis* strain BCRC 17467 was proposed to be a heterotypic synonym of *B. amyloliquefaciens* because of DNA relatedness ranging from 74% to 89%.

CONCLUSION

The presence of plant growth promoting *Bacillus* species in the rhizospheric region and their role has been investigated. Results of the present study demonstrated that the diversity of *Bacillus* species pose a positive effect on plants, thereby providing opportunities for better seedling growth, root and shoot development, fruiting etc. for plant growth promotion.

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12. Sample_SO4														
14. MG041385.1_(Chromobacterium_spstrain_56AF)														
22 ME4424281 (Chromoharterium inseudoviolaceum strain														



Sodium arsenite induced Morphological, Behavioural, Hematological and Histopathological Abnormalities in *Labeo rohita*

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INTRODUCTION

Toxic metals have contaminated the aquatic ecosystems to a large scale and eventually enter human systems by contaminated air, food, water, and soil. Arsenic toxicity has become an alarming concern around the globe. Dissolved Arsenic in Barak Valley is many folds higher than the permissible limit of WHO and BIS of $10\mu g/l$ and $50\mu g/l$ respectively and ranges between $100-1000 \mu g/l$. Fishes are the major dwellers of the aquatic ecosystem and serve as good bio-indicators for determination of health status of an aquatic ecosystem.

METHODOLOGY

Labeo rohita (n=10) of similar size and weight were exposed to sodium arsenite at concentrations 100 μ g/l and 250 μ g/l along with controlled set up for 10 days. The morphological and behavioral aspects were observed daily while hematological and histopathological changes were evaluated at the end of the experiment.

RESULTS AND DISCUSSION

Fishes exposed to Sodium arsenite showed irregular ocular movement, fin movement, swimming pattern and loss in scales with higher prominence in 250 μ g/l of the arsenic group than those at 100 μ g/l. The hematological indices revealed a decrease in RBC count and increase in WBC count in both sodium arsenite exposed groups. The histopathological study of the liver revealed parenchymal disorganization and atypical residual body in both sodium arsenite treated groups. Results obtained showed major damages to fishes due to contamination with sodium arsenite. These fishes, when consumed by humans, leads to an increase in several thousand folds of sodium arsenite by means of biomagnification.

CONCLUSION

High exposure of arsenic in human through fishes leads to several disorders. The possible way of eradicating sodium arsenite entry into humans is banning fishing activities in highly contaminated aquatic ecosystems. Community education and local participation are also essential to get a fruitful outcome.

Keywords: Sodium arsenite, Labeo rohita, Hematological, Morphological, Anemic.



Research Paper Published

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- Bhattacharjee S, Singha PB, Yadav R, Deb B, Nath A and Nath S (**2017**) Antibacterial efficacy of ethanol extract of some herbal plants. *Chemical Journal of Karimganj College* 2(1): 47-52
- Biswas R and Nath S (2017). Effect of paper mill effluents on morphological and hematological indices of Anabas testudineus. *International Journal of Current Trends in Science and Technology*, 7(11): 20383-20387.

Microbial Strains Identified

Sl. No.	Name of the Microorganism	GenBank Ac. No.	Year	Submitted by
1.	Acinetobacter johnsonii strain SB_SK	MH482927	2018	Bhattacharjee S, Nath S and Deb B.
2.	Bacillus cereus strain SN_SA	MH482928	2018	Nath S, Bhattacharjee S and Deb B.
3.	Bacillus megaterium strain GCC-SO1	MH109306	2018	Bhattacharjee S, Nath S, Paul P, Roy R and Deb B.
4.	Bacillus cereus strain GCC-SO2	MH109312	2018	Paul P, Roy R, Bhattacharjee S, Nath S and Deb B.
5.	Pseudomonas aeruginosa strain GCC-SO3	MH109307	2018	Roy R, Paul P, Bhattacharjee S, Nath S and Deb B.
6.	<i>Chromobacterium pseudoviolaceum</i> strain GCC-SO4	MH109305	2018	Nath S, Bhattacharjee S, Roy R, Paul P and Deb B.

* 16S ribosomal RNA gene sequence of all the above isolates can be downloaded from https://www.ncbi.nlm.nih.gov



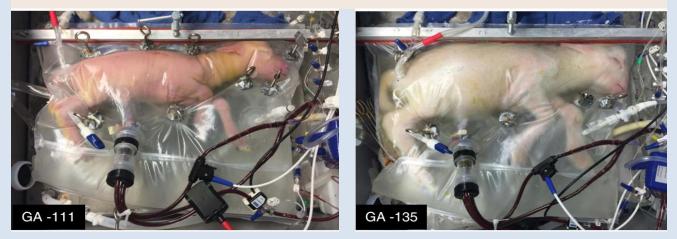
Paper Presented (2017-18)

- Nath B, Deb B and Nath M (2018) Phyto-Oncobank: A database of medicinal plants in Cachar district with anticancerous properties. International Symposium on "Biodiversity and Biobanking BIODIVERSE 2018
- Paul S, Deb B and Nath M (2018) In Silico study of G460W polymorphism in ADD1 gene associated with hypertension. "Biodiversity and Biobanking BIODIVERSE 2018"
- Nath M and Deb B (2018) Bacterial Biochemical Identification Platform (BBIP): An in silico tool for identification of bacteria through biochemical analysis. International Symposium on "Biodiversity and Biobanking BIODIVERSE 2018"
- Nath B, Nath M and Deb B (2018) In silico analysis of medicinal plants having anti-carcinogenic properties: A regional study. National Seminar on "Frontiers of Research in Physical Sciences"
- Nath A, Sharon M and Bhattacharjee C R (2018) Low temperature synthesis and antioxidant activity of multiwalled carbon nanotubes and nanowhiskers from natural precursors. National conference on Emerging Materials (NCEM-2018)
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- Sinha K, Choudhury SM, Dey H, Modak BK, Nath A (2018) Synthesis and antimicrobial efficacy of copper oxide nanoparticles from thermal decomposition of copper (II) complex. National Seminar on frontiers of Research in Physical Sciences (NSFRPS, 2018)
- Nath B, Singha Y S, Nath M and Deb B (2017) Phytochemical Study on some plants in Silchar having anti-cancer properties. National Seminar on Bio-Resource Utilization: Special emphasis on ethnic population of North-East India"
- Paul B, Mohanta S, Nath M and Deb B (2017) Plant growth promoting rhizobacteria and 16s rRNA phylogenetic analysis National Seminar on "Bio-Resource Utilization: Special emphasis on ethnic population of North-East India"
- Nath M, Singha K H B, Nath S and Deb B (2017) In-silico analysis of Tissue non-specific alkaline phosphatase (TNAP) gene mutations and its implication in Hypophosphatasia. National Seminar on "Recent Trends in Basic Science Researches"
- Nath M, Dey S and Deb B (2017) Computational Screening of Various Natural Compounds as Potential Drug Candidates against Sickle Cell Anemia. National Seminar on "Recent Trends in Biodiversity Conservation and Bioresource Utilization"
- Nath M, Nath A, and Deb B (2017) Comparative Study on High Content Biological Image Analysis. "International Conference on Sophisticated Instruments in Modern Research"
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- Biswas R, Nath S (2017) Effect of paper mill effluent on morphological and hematological indices of *Anabus* testudineus. National Seminar on Recents trends in biodiversity conservation and bioresource utilization
- Nath S, Das N, Roy R (2017) Isolation and characterization of Iron bacteria from underground water. National Seminar on Recents trends in biodiversity conservation and bioresource utilization
- Singha PB, Bhattacharjee S, Nath S and Deb B (2017) Antibacterial activity of methanol extracts of some herbal plants on bacteria and to study their antibiotic resistance pattern. National Seminar on "Resent Trends in Biodiversity Conservation and Bioresource Utilization"

LAMB-IN-A-BAG: AN ARTIFICIAL WOMB SUSTAINS

In April 2017, a team of physicians from the Children's Hospital of Philadelphia published a study in the journal *Nature Communications* that detailed the successful use of an artificial womb.

The device, a specialized transparent biobag filled with a fluid that allows it to imitate the environment inside a uterus, successfully housed a 23-week old lamb. This artificial womb can help save the lives of premature babies. The team working on the technology expects it to soon be ready for human use.



Reference: Partridge, E.A., Davey, M.G., Hornick, M.A., McGovern, P.E., Mejaddam, A.Y., Vrecenak, J.D., Mesas-Burgos, C., Olive, A., Caskey, R.C., Weiland, T.R. and Han, J., 2017. An extra-uterine system to physiologically support the extreme premature lamb. *Nature communications*, *8*, 15112.

ARTIFICIAL LEAF HARNESSES SUNLIGHT FOR EFFICIENT FUEL PRODUCTION

- Generating and storing renewable energy, such as solar or wind power, is a key barrier to a clean-energy economy.
- Fusing living cells with light-harvesting technology could lead to cyborg factories for clean energy and new compounds.
- These cost-effective green machines can produce fuels, using only sunlight, water, and carbon dioxide, mimicking the natural process of photosynthesis in plants and storing energy in the form of chemical fuels for use on demand.

Green machines

During the day, plants take in water

and carbon dioxide. They use light

convert these into oxygen and sugar

ROTON

and a menagerie of enzymes to

WATER

OX YGEN

Bio-Letters

A new generation of sunlight harvesters will be more useful than ever before

CARBON DIOXIDE

SUGAR

Natural leaf

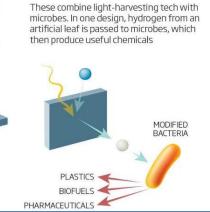
LIGHT

Artificial leaf

Synthetic leaves have a semiconductor to generate electrons from light, and a catalyst to steal protons from water. These are combined to make hydrogen

SEMICONDUCTOR

Bionic leaf



Source: https://www.scoopnest.com/user/newscientist/852227480064860164

HYDROGEN

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CAREER OPTIONS

AFTER GRADUATING IN BIOTECHNOLOGY

Biotechnology is a field of study, that has emerged into the scientific world as a result of revolutions in Biology, Chemistry, Informatics, Engineering and technology. Due to the growing demand for biotechnologists in India and abroad, candidates who successfully completes this course have a good career opportunities.

Here are few career options one may choose after completing the graduation in Biotechnology.

Option 1: Higher studies in Biotechnology

Pursue Ph.D from universities and research institutes in India and abroad. Candidates, who wish to join as a research fellow (JRF/ SRF/ RA) can apply for the post under the guidance of scientist/ faculty of any universities or research organizations.

Option 2: Opportunities in Academia

Teaching profession provides opportunities and one can enter into the job as professors, lecturers etc in universities, colleges etc. for that they need a post graduation. They also need to pass examinations like NET, SET etc. and/or having doctoral degree (Ph.D). To start a career as teacher in schools, they should have a B. Ed along with their basic degree.

Option 3: Intellectual Property Research and Patenting

Biotech students can join patent firms in India. Few jobs available for fresher's in IPR industry are Patent analyst, patent docketing officer, Patent agent, IP proofread etc.

Option 4: Government sector and Research and Development (R&D) jobs

Apply for various posts in public health centers and autonomous institutes in India. Join as a scientist in R&D sectors like DBT, DST, CSIR, ICAR, FSSAI, ICMR etc.

Option 5: Private sector

The rapid advancement in Biotechnology has generated some of the best careers in science and pharmacology. Fresh graduates can apply in private sectors like food and pharmaceuticals industry as a quality control officer.

Option 6: Entrepreneurship

Biotech start ups is a thriving economy in India. So if you are inventive and creative, search for available funding from the Indian Government and present your own Biotech innovation.

Option 7: Laboratory Technician/Assistant

Private and government universities/ colleges offer a variety of jobs for lab managers and technical assistant. Most of these fields would require applicants to at least have a Bachelor's Degree in Biotech. That means you don't even have to get a Ph.D. in Biotech to get hired.



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Department of Biotechnology Biotechnology Information System Network Ministry of Science & Technology, Govt. of India

Incentive Awards for publications - 2017

This Certificate is Awarded to **Bioinformatics Infrastructure Facility (BIF),** Gurucharan College, Silchar for getting the second Position in the category of BIF (Colleges) for publication of papers in the journals of high repute in the year 2016

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Suman Mallik Member, Incentive Awards Committee

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Dr. T. Madhan Mohan Adviser, DBT

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K. Vijayladar

Dr. K. Vijay Raghavan Secretary, DBT

