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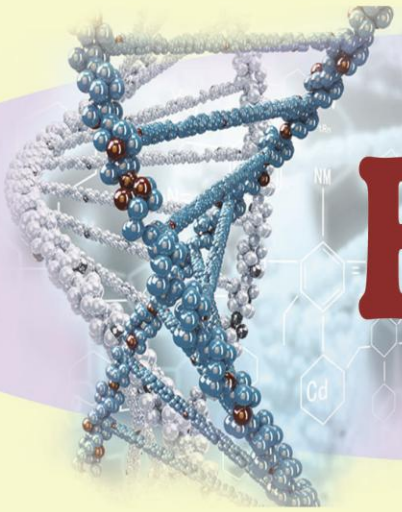

Bio-Letters

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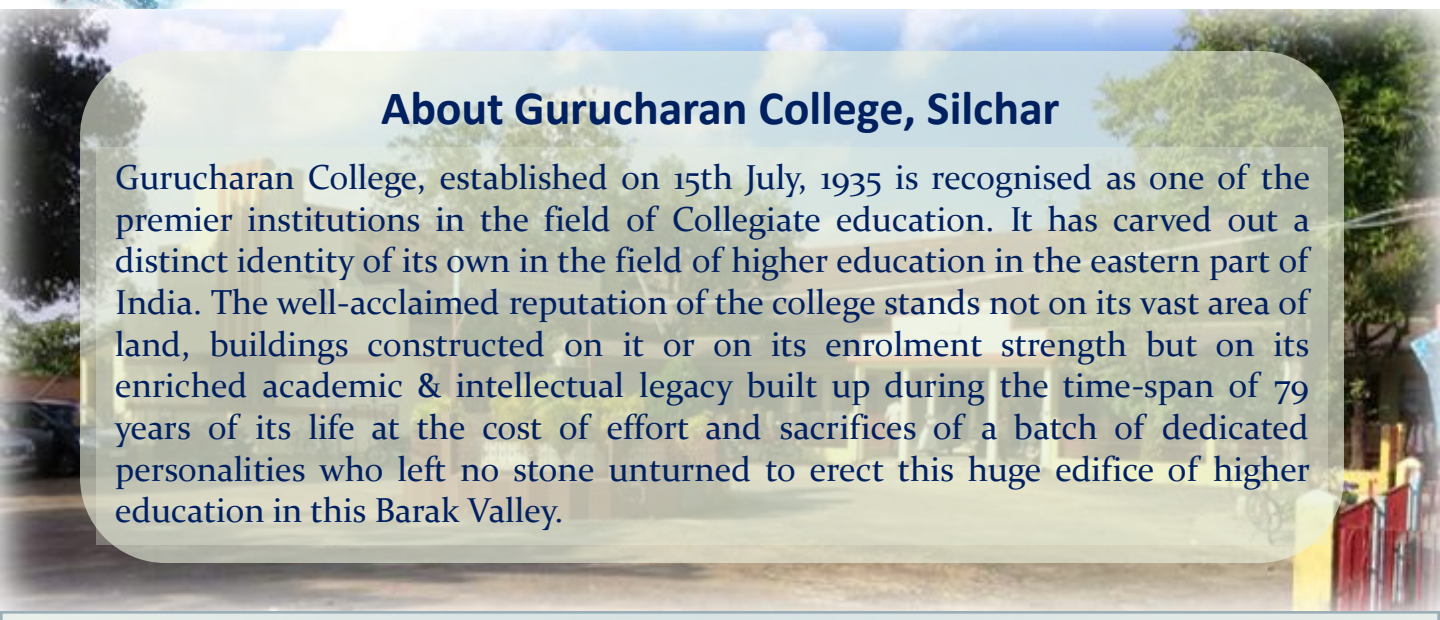
Bio-Letters



About Gurucharan College, Silchar

Gurucharan College, established on 15th July, 1935 is recognised as one of the premier institutions in the field of Collegiate education. It has carved out a distinct identity of its own in the field of higher education in the eastern part of India. The well-acclaimed reputation of the college stands not on its vast area of land, buildings constructed on it or on its enrolment strength but on its enriched academic & intellectual legacy built up during the time-span of 79 years of its life at the cost of effort and sacrifices of a batch of dedicated personalities who left no stone unturned to erect this huge edifice of higher education in this Barak Valley.

Institutional Biotech Hub

Institutional Biotech Hub, Gurucharan College Silchar was established in the year 2011 funded by Department of Biotechnology (DBT), New Delhi, India. The mandate of this centre is to provide infrastructural facilities to the undergraduate students, research scholars and teachers to carry out their research . A good number of research papers have been published by researchers and faculty members. Students are also presenting their project papers in conferences and seminars. Several workshops/ hands on training/ lecture and outreach programmes are conducted throughout the year on different topics of biological sciences. School students are also trained on the basic applications and scope of Biological research.

Bioinformatics Centre

The Bioinformatics Infrastructure Facility (BIF) of Gurucharan College, Silchar was established with the sole purpose of providing open access to students, researchers, scholars and faculty members for research and educational activities. Since its inception, the centre has marched forward steadily and has been achieving its goal by conducting trainings, seminars, demonstrations and outreach programmes. The centre has various collaborations with other BIFs of Assam and other north-eastern states for conducting seamless research activities and resource exchange. Since, the centre has collaborations with other Bioinformatics Centres and State Level & School Level Biotech Hubs; it is of paramount importance for providing training and imparting knowledge at various levels of education.

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From Principal's Desk

Dr. Bibhas Deb
Principal,
Gurucharan College, Silchar

I am very much happy to know that Bioinformatics Centre and Institutional Biotech Hub (funded by DBT, New Delhi, India) of Gurucharan College, Silchar will release its 1st issue of newsletter in the name of " Bio-Letters" 2017 in near future. It is the one and only mouthpiece of students, scholars and teachers of this college for sharing their new, innovative and review activities. In this age of fast changing scenario, documentation of each and every activities related to biological science is very much essential. I am confident that Bio-Letters will play a great role in this regard.

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

Dr. Bibhas Deb, M.Sc, M.Phil, Ph.D
Principal
Gurucharan College, Silchar

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INVITED ARTICLE

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Liver Cancer: A Journey through Genes

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Liver cancer, also known as hepatic cancer is a growing menace all over the globe. It comprises of various subtypes, including hepatocellular carcinoma (HCC), intrahepatic cholangiocarcinoma (ICCA), fibrolamellar carcinoma and hepatoblastoma. The most common form of liver cancer subtype in adults is hepatocellular carcinoma abbreviated as HCC, representing 90% of liver cancers. Cholangiocarcinoma is cancer of the bile ducts which accounts for 10% of liver cancers. Hepatoblastomas (childhood hepatic tumor), Hemangioendotheliomas (cancers of the blood vessels), Angiosarcoma (mesenchymal tumor of the liver usually occurs in elderly men) are some rare carcinomas of liver (Chuang et al., 2009; Sia et al., 2016, 2017).

Hepatocellular carcinoma (HCC) is a malignant tumor originating from hepatocytes or their precursors. It is found predominantly in males; the sex ratio varies between 2:1 and 4:1, depending on the geographic region (Hefaiedh et al., 2013). HCC is now considered the fifth most prevalent malignancy. HCC ranks as the third leading cause of mortality in the world, resulting in almost 500000 deaths each year (Ghidini and Braconi, 2015; Hayes and Chayama, 2016; Mazzanti et al., 2016). Poor prognosis and limited therapeutic options lead to a lower five-year survival rate (Callegari et al., 2015). Most HCC cases are reported in the developing countries of Asia and Africa, but it is now fast becoming more prevalent in Western countries.

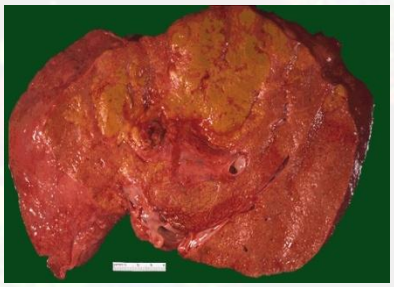

Figure**:** Hepatocellular carcinoma with a greenish yellow hue (Courtesy: Jain, 2015)

High genetic heterogeneity among patients is considered as one of the main challenges that are encountered in HCC treatment. HCC is a multifactorial disease with complex pathogenesis involving various risk factors. The major risk factors associated with HCC are briefly discussed below:

- ***Chronic hepatitis:*** The risk of liver cancer in individuals infected with both HCV (Hepatitis C virus) and HBV (Hepatitis B virus) is three times higher than with either alone.
- ***Cirrhosis:*** Cirrhosis is an important contributor to HCC. Male sex, age, and duration of cirrhosis are the major risk factors for HCC in patients with cirrhosis.
- ***Aflatoxin (chemical carcinogen):*** A group of mycotoxins is produced by the fungi *Aspergillus flavus*. Improper storage of peanuts and grains may cause contamination by this fungus. Dietary exposure to aflatoxin B1 is a prime risk factor for HCC. Aflatoxin can bind covalently with cellular DNA of hepatocytes and is source for a specific mutation of p53 tumor suppressor gene.
- ***Non-alcoholic steatohepatitis (NASH):*** Liver inflammation and destruction caused by a buildup of fat in the liver is termed as NASH.

Other risk factors include hemochromatosis, Wilson's disease, α1-antitrypsin deficiency, galactosidemia, oral contraceptives, cigarette smoking, fructosemia, obesity, and hypothyroidism. (Chuang et al., 2009); (Mazzanti et al., 2016). HCC is graded as well-differentiated, moderately differentiated, and undifferentiated (pleomorphic) forms (Mazzanti et al., 2016).

As majority of liver cancer patients are diagnosed in advanced stages, it accounts for lower survival rate (Liu et al. , 2016). A treatment modality for intermediate stage of HCC is chemoembolization. The only FDA-approved molecule for advanced HCC patients is the multikinase inhibitor sorafenib which improves survival rates by a few months(Anwar and Lehmann, 2014).

Genetics of Liver Cancer

Liver cancer, being a complex disease, develops through step-wise alteration of genetic and epigenetic condition. Genetic alteration includes somatic mutations, germline mutation, translocation, gene deletions and amplifications which are considered as important aspects in carcinogenesis(Knudson, 2002). Epigenetics refers to potentially heritable changes in gene expression without involving any DNA sequence changes. Epigenetic mechanisms include several distinct processes such as, DNA methylation, histone modification, and expression of non-coding RNA (Anwar and Lehmann, 2015).

Chromosomal aberrations : The most commonly observed chromosomal aberrations in HCC are deletions and copy number gains. Various studies have reported that gain in chromosome1q, 6p, 8q, 17q, and 20q and loss in 1p ,4q, 6q, 8p, 13q, 16p and17p is observed in HCC (Chen et al., 2010). Vital players of hepatocarcinogenesis are p53 and Rb. The gene p53 lies on chromosome 17p and Rb is located in chromosome 13q. However, sufficient details are not available to establish a connection between chromosomal aberrations and the clinical course of the HCC.

Gene mutations : It is reported that TP53 and CTNNB1 are the two most frequently mutated genes followed by a second group of genes (AXIN1 and ARID1A). Frequently these mutations affect various signaling pathways such as Wnt/b-catenin, p53, PI3K/Ras signaling, oxidative, endoplasmic reticulum stress pathways and chromatin remodeling. It is interesting to note that in HCC, frequent mutations result in loss of function rather than a gain of function of the crucial genes except for CTNNB1 mutations. Several genes annotated as associated with chromatin regulation show recurrent somatic mutations such as ARID1A, ARID1B, ARID2, MLL, MLL3, BAZ2B, BRD8, BPTF, BRE and HIST1H4B. Moreover, recurrent mutation is observed in some genes with higher transcript levels, engaging TP53 (18%), CTNNB1 (10%), KEAP1 (8%), C16orf62 (8%), MLL4 (7%) and RAC2 (5%). (Cleary et al., 2013).

P53: TP53 and RB1 are recognized as driver genes in HCC. Scientific investigation suggests that in HCC, p53 mutational differences vary with geographic areas, apparently reflecting differences in the occurrence of etiological factors. p53 point mutation (at the third position of codon 249) occurs in patients with Aflatoxin B1 exposure and the occurrence of chronic viral hepatitis. Mild to poorly differentiated HCC exhibits p53 mutations specifically along with or after p53 LOH.

Epigenetic deregulation : Epigenetic mechanisms associated with HCC are DNA methylation, post-translational histone modifications, chromatin changes and non-coding RNAs, micro-RNA expression and mutations affecting epigenetic regulatory genes.

***Hypomethylation*:** DNA hypomethylation is one of the most common molecular alterations known in HCC as well. A decrease in the number of methylated cytosine bases from the normal modulation level is called DNA hypomethylation. Multiple pathways are associated with hypomethylation of DNA. Extensive hypomethylation of LINE-1, ALU, and SAT2 repetitive elements in HCC is reported. Various hypo methylated tumor-promoting genes are reported in primary human HCC, such as UPA, HPA, SNCG, TFF3, MAT2A, HKII, CD147, and VIM.

***Hypermethylation*:** Genes like BLU, CFTR, GSTP1, HAI-2/PB, MTM1, OXGR1, SLIT2 and SOX17 are commonly silenced by DNA hypermethylation in primary hepatocellular carcinoma. In HCC, hypermethylation mainly affects tumor suppressor genes that are involved in cellular processes like cell proliferation, cell differentiation, DNA repair, cellular metabolism, cell adhesion and metastasis.

***Histone modifications*:** The best characterized histone modifications in HCC are methylation and acetylation. Histone-modifying enzymes such as HDAC1, HDAC2, and HDAC3 and SIRT1 are reported in human HCC. HDACs-1, -2 and -3 are over-expressed in HCC.

***MicroRNAome alterations in human HCC*:** Study of non-coding RNAs (ncRNA) might be useful in identifying novel targets of therapies, early diagnostic and prognostic markers to improve the clinical management of HCC patients. In HCC, dysregulation of microRNA expression in various stages of liver cancer progression is documented in literature. Thus, miRNAs can serve as novel molecular targets for HCC therapy.

Table 1: List of miRNAs that are deregulated in hepatocellular carcinoma (HCC)

miRNA	Genome location	Expression in HCC	Targets
let-7g	3: 52302294–52302377 (−)	Down	BCL2L1, COLIA2
miR-1	20: 61151513–61151583 (+)	Down	MET, FOXP1, HDAC4
miR-23b	9: 97847490–97847586 (+)	Down	uPA, MET
miR-26a	3: 38010895–38010971 (+)	Down	CCND2, CCNE
miR-29	7: 130561506–130561569 (−)	Down	BCL2, MCL1
miR-34a	1: 9211727–9211836 (−)	Down	MET
miR-101	1: 65524117–65524191 (−)	Down	MCL1, FOS
miR-122	18: 56118306–56118390 (+)	Down	CCNG1, SRF, IGF1R, BCL2L2, ADAM10, ADAM17
miR-124	8: 9760898–9760982 (−)	Down	CDK6, VIM, SMYD3, IQGAP1
miR-125a	19: 52196507–52196592 (+)	Down	BMF, ERBB2, ERBB3
miR-125b	11: 121970465–121970552 (−)	Down	
miR-130a	11: 57408671–57408759 (+)	Down	ATXN1, PPARγ
miR-139	11: 72326107–72326174 (−)	Down	RHOK2
miR-145	5: 148810209–148810296 (+)	Down	FSCN1, IRS1, STAT1, YES, MYC, ESR1, KLF4, OCT4, SOX2, MUC1
miR-150	19: 50004042–50004125 (−)	Down	EGR2
miR-193b	16: 14397824–14397906 (+)	Down	MCL1
miR-195	17: 6920934–6921020 (−)	Down	CCND1, CDK6, E2F3
miR-199a-1	19: 10928102–10928172 (−)	Down	KRT7, SET, IKBKB, MAPK1, MET, HES1, Smad1, HIF1A
miR-199a-2	1: 172113675–172113784 (−)	Down	
miR-199b	9: 131007000–131007109 (−)	Down	
miR-200a	1: 1103243–1103332 (+)	Down	ZEB1, ZEB2, beta-catenin
miR-200b	1: 1102484–1102578 (+)	Down	
miR-223	X: 65238712–65238821 (+)	Down	Stathmin1
miR-375	2: 219866367–219866430 (−)	Down	YAP
miR-602	9: 140732871–140732968 (+)	Down	RASSF1A
miR-17-5p	13: 92002859–92002942 (+)	Up	NCOA3, E2F1, BCL2L11, CDKN1A, RBL2, MAPK14, STAT3, CCL1, DNAJC27, FBXO31, GPR137B, NPAT, OBFC2A, RAB12, YES1, ZNFX1, FN1, FNDC3A
miR-18a	13: 92003005–92003075 (+)	Up	NR3C1, CTGF, ESR1
miR-92a	13: 92003568–92003645 (+)	Up	HIF1A, STAT3, CDKN1A, MAPK14, ZBTB7A, E2F1, E2F2, E2F3
miR-106-25	7: 99691616–99691697 (−)	Up	CDKN1A, BIM
miR-21	17: 57918627–57918698 (+)	Up	FasL, SERPINB5, PDCD4, TIMP3, SPRY2, LRRFIP1, RECK, PTEN, BTG2, Peli1, HNRPK, TP63, MARCKS, TPM1
miR-30d	8: 135817119–135817188 (−)	Up	Galphai2
miR-151	8: 141742663–141742752 (−)	Up	RhoGDIA
miR-181b-1	1: 198828002–198828111 (−)	Up	CDX2, GATA6, NLK, TIMP3
miR-135a	3: 52328235–52328324 (−)	Up	APC
miR-221/miR-222	X: 45605585–45605694 (−)	Up	BMF, CDKN1B, CDKN1C, ESR1, ICAM1, KIT, PTEN, TIMP3, MET, DDIT4, FOXO3
miR-224	X: 151127050–151127130 (−)	Up	CD40, CDC42, CXCR4, KLK10, Smad4, API5
miR-373	19: 54291959–54292027 (+)	Up	MBD2, CD44, LATS2
miR-483-3p	11: 2155364–2155439 (−)	Up	BBC

Differential microRNA expression for predicting disease survival and recurrence in HCC have been documented (Ji et al., 2009). Both up-regulation and down-regulation, of miRNAs are involved with HCC (Pogribny and Rusyn, 2014).

Upregulated miRNAs in HCC comprise of miR-17-92 cluster, miR-21, miR-221, miR-222, and miR-224 whereas down regulated miRNAs are let-7 family, miR-29, miR-122, miR-124, miR-199a/b and miR-200 family. Growing evidence indicates that molecular networks such as Wnt/β-catenin, Ras, transforming growth factor-β(TGF-β), and JAK/STAT signaling pathways are activated due to the changes of microRNA expression in HCC (Borel et al., 2012). A good number of microRNA genes are located at fragile genomic sites which are frequently affected by copy number alterations (Calin et al., 2005). The EZH2 is over expressed in HCC. Well-characterized tumor-suppressor miRNAs, such as miR-139-5p, miR-125b, miR-101, let-7c, and miR-200b were epigenetically suppressed by EZH2 in human HCC(Knudson, 2002).

Uses of miRNA

Each mature miRNA potentially controls many gene targets. It is documented in numerous literature that aberrant expression of specific miRNAs is associated with the severity and poor prognosis of HCC (Huang, Wang et al. 2009). For example, in one study, HBV related HCC and HCV related HCC induced different sets of miRNAs, which could act as markers of disease progression.

1. *MiRNA in diagnosis* : Aberrant DNA methylation in microRNA genes is a useful parameter for the diagnosis of cancer, including HCC. Single locus hypermethylation of miR-129-2 acts as a marker for distinguishing HCC from non-cancerous liver disease (Lu, Lin et al. 2013). Quantification of circulating miRNA levels is an early cancer detector.

2. *MiRNAs in therapeutic role* : The miRNA therapeutics for HCC is still in its infancy and it earned limited rewarding results. Nevertheless, ongoing experiment is conducted in animal models with some promising candidates. Therapeutic strategy includes inhibition of tumor inducing miRNA using locked nucleic acids (LNA), antagomiRs and antimiRs. For example, miR-210 promotes hypoxia mediated tumor cell metastasis in HCC. Inhibition of miR-210 expression could lead to a reduction in HCC metastasis. A similar approach is designed for miR-30d, a miRNA associated with intrahepatic metastasis of HCC. The miRNA replacement by re-introducing miRNAs with tumor suppressor functions is another approach. A few miRNAs act as prognostic factor such as miR-26. Secondly, the loss of miRNA-122 function correlates with morbidity and mortality of liver cancer patients (Burchard, Zhang et al. 2010). Some miRNAs are reported to act as predictors of response to anti-cancer therapy in HCC. For instance, miR-193b can enable sorafenib-induced apoptosis in human HCC cell lines. Additionally, long non-coding RNAs have been found to be aberrantly expressed in HCC. It is reported that maternally expressed gene 3 (MEG3) is an imprinted ncRNA and is down regulated in human HCC. In HCC, mutation activates oncogenes such *as* β-catenin, Axin1, PI-3-kinase, K-*ras* and inactivate tumor suppressors gene like *p*53, Rb1, CDKN2A, IGF2R, PTEN(Taniguchi et al., 2002; van Malenstein et al., 2011).

Recent advances in molecular methods and insight into the complex signaling pathway have created opportunities for targeted agents and new therapeutic approaches for HCC. Network signaling pathway such as Wnt signaling pathway, TGFB pathway, *Ras* signaling and Rb pathway are associated with HCC.

Wnt signaling pathway : Like many other cancers, Wnt/ b-catenin signaling pathway is related to HCC as well. An activated Wnt signaling pathway suggests increased expression and nuclear accumulation of β-catenin. Development of HCC occurs, when oncogenic β-catenin mutations take place. In 90% of HCC cases, activation of β-catenin is noted (Waisberg and Saba, 2015). Wnt pathway is related to liver patho-biology though it is inactive in adult livers(Thompson and Monga, 2007). In HCC, early deregulation of the Wnt pathway has also been recognized. Proteins that are part of the Wnt signaling pathway are therapeutic targets in human hepatocellular carcinoma (Dahmani et al., 2011).

TGF β pathway : There is overproduction of transforming growth factor-beta 1 (TGF-beta 1) in human hepatocellular carcinoma (HCC). Expression of TGF β in liver tissues significantly reduces in patients with HCC compared to patients with other liver disease. In the liver tissue, in response to injury, TGF-β enhances hepatocyte destruction resulting in a wound-healing response. Experimental evidence suggests that TGF β levels in serum and urine correlate with poorer prognosis and increased tumor angiogenesis (Ito et al., 1995). Targeting of TGF-β pathway is needed in the right cell type at right time point to achieve therapeutic effects.

Ras signaling : Ras pathway activation in HCC involves various mechanisms/steps. H-*ras* is up-regulated during different steps of hepatocarcinogenesis and B-*raf* is over expressed in advanced tumors. Different mechanisms such as methylation of tumor suppressors and amplification of oncogenes (B-*raf*) account for Ras pathway activation in HCC(Newell et al., 2009). In advanced HCC, moderate therapeutic efficacy is noted when targeting Raf kinase with sorafenib.

Rb pathway : The tumor suppressor protein retinoblastoma protein (Rb) is vital for the development of several cancers including HCC. Rb is the target for phosphorylation by several kinases. In normal cell signaling, Rb prevents the cell from replicating damaged DNA. In 28% of HCCs, Rb has been reported to be inactivated in human HCC cell lines. Experimental evidence suggests that RB-loss correlates with the progression of HCC. Liver-specific RB-loss indicates increased proliferative gene expression and decreased immune function gene expression and thus cancer progression (Hutcheson et al., 2014).

Late diagnosis, poor prognosis and limited therapeutic approaches make HCC a deadly disease even deadlier. Hence, HCC is a growing concern among health enthusiasts and there is a need for further research in this area. In this regard, bioinformatics-based gene therapy approach demonstrates a promising role as an alternative therapeutic modality. As discussed earlier, some well-known genes which are over expressed can be silenced using miRNAs. Several examples based on modulation of miRNA activity could be a novel approach for treating HCC. Few examples of this approach are intravenous administration of specific antagomirs to silence miR-122 in the mouse liver; antimiR-221 molecules reduce proliferation of tumor cells in a mouse model of HCC. Restoration of tumor suppressor miRNAs is another strategy for treating cancer. Several lines of evidence have indicated that animal model studies are being investigated with strategies like miRNA inhibition and miRNA replacement. While miRNA-based approaches are not presently used in the clinic, the application needs larger preclinical studies to determine their potential efficacy in specific contexts.

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Screening of potential antibacterial properties of methanol extracts of some herbal plants and comparison with antibiotics

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Face colonizes enormous counts of bacteria, fungi, archaea of which some are beneficial, mutualistic, commensal while some are pathogenic. The emergence of anti-pathogenic activity has led to an urgent need of antibacterial drugs, especially from natural resources which are effective against skin microbiota. The herbal plants are in great focus for the solution to the skin disease and infection. There is a recent exponential growth in demand for herbal drugs due to their natural origin and less side-effects. Present study aims to isolate and identify facial bacteria and to evaluate the anti-bacterial efficacy of methanol extracts of some herbal plants. Eight herbal plants have been selected for this purpose, that were, *Azadirachta indica; Curcuma longa; Ocimum tenuiflorum; Santalum album, Aloe barbadensis Miller, Eucalyptus, Coriandrum sativum* and *Psidium guajava.* Significant zone of inhibition was found on neem, tulsi, eucalyptus and guava which may help in prevention of bacterial infections.

Effect of neem leaf extract on germination and seedling growth of tomato, okra and mung

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The plants have both inhibitory and stimulatory effects on other plants. The project was carried out to study the effect of neem leaf extract on seed germination and growth of *Solanum lycopersicum* L., *Abelmoschus esculentus* L. *and Vigna radiate* L. The seeds were treated with distilled water (control) and neem leaf extract on two separate petri plates. On the 10th day the seeds germinated were counted, roots and shoots were measured and analyzed. The results showed that the germination percentage of okra and mung in leaf extract is low whereas, in case of tomato, neem leaf extract has got more growth as compared to control. The reason is known for low growth of okra and mung i.e., allelochemicals inhibits growth of other plants. But the reason for the growth of tomato is not known. In future, neem could replace fertilizers specifically for tomato.

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Nuclear abnormalities in exfoliated buccal epithelial cells in healthy individuals and stone crusher workers by buccal cytome assay

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The Buccal Micronucleus Cytome (BMCyt) assay deals with most frequently used in hazard identification and risk assessment process. In the present study, exposure assessment studies carried out in the Cachar district, Assam on several air pollutants released from Stone Crusher. The stone crushing industry has been growing rapidly due to increasing infrastructure activities across countries. The stone contains approximately 100% free silica and the stone crushing process release high level of respirable crystalline silica dust in the working environment. These pollutants leads to itching in the eyes, lung and skin infections and other health hazards. The exposure possesses a risk to human health and development of several types of diseases and cancers. We collected 10 samples from Bricks industry workers and 10 control samples in the age group of 17 to 35 years. A questionnaire based survey was conducted and buccal smears were collected from oral cavity and analyzed for nuclear abnormalities. A higher frequency of micronucleus was observed among workers at stone crusher (6.21 ± 0.46) than control (0.36 ± 0.14). Significant increase in nuclear buds (5.25 ± 0.52) and binucleated cells (4.23 ± 0.54) were observed among workers of stone crusher in comparison to control participants. This evidence strongly suggests that exposure at stone crusher industry increase the percentage of cellular damage of individuals working there.

Evaluation of micronucleus and other nuclear anomalies in individuals exposed to toxic pigments- a biomonitoring study

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The Buccal Micronucleus Cytome Assay deals with most frequently used in hazard identification and risk assessment process. The exposures possess a risk to human health and development of several types of cancers. A total of 10 exposed individuals and 10 control participants in the age group of 20 to 40 years were recruited, a questionnaire based survey was conducted and buccal smears were collected from oral cavity and analyzed for nuclear abnormalities. A higher frequency of micronucleus was observed among Painters exposed to toxic pigments (4.70 ± 0.38) than control (0.50 ± 0.14). Significant increase in nuclear buds (4.32 ± 0.54) and binucleated cells (6.25 ± 0.72) were observed among painters in comparison to control participants. Toxic pigments enhanced micronucleated cells and other nuclear abnormalities in buccal cells in Painters. Significant differences in nuclear anomalies were observed in painters populations who are in service for longer periods.

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Effect of pesticides on the growth parameters of *Coriandrum sativum* and to study their rhizospheric microflora

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Pesticides are the only lethal compounds that are deliberately applied to debar pests. The present investigation aims to study the effects of three pesticides Fenvalerate, Cypermethrin and Chlorpyriphos on the growth of *Coriandrum sativum*. Pot experimental study was carried out for 35 days by applying pesticides preceding and exceeding the recommended dosage. The growth parameters like shoot-root length, maturation and mortality of stressed plants were compared with control. This was followed by isolation, enumeration and characterisation of pesticide resistant rhizobacteria which were further identified as *Bacillus* spp., *Pseudomonas* spp., *E. coli,* and *Staphylococcus* spp. Antibiotic susceptibility test infers that all isolates were resistant to Cefixime, susceptible to Levofloxacin while *Bacillus* spp. and *Staphylococcus* spp. showed intermediate zone against Meropenem. Chlorpyriphos showed deleterious effect on the plant growth and mortality was seen even before maturity. Student's t-test and ANOVA revealed that plants at permissible limit showed better growth than plants grown in control on applying Fenvalerate and Cypermethrin. Finally, it may be concluded that reckless pesticide usage retards plant physiology and is unfit for consumption.

Effect of pesticides on the bacterial endophytic diversity of *Coriandrum sativum*

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The present study was conducted on the plant *Coriandrum sativum* to analyse the effect of pesticides on its bacterial endophytic diversity of the leaves. The plants were grown in pot culture and three pesticides, namely Ustaad (Cypermethrin), Tatafen (Chlorpyriphos) and Tricel (Fenvalerate) were applied on three pots each and two pots were kept as control, in which only cow dung was applied as manure. The pesticides were applied at the optimum level and the leaves were collected three days after the application of pesticides. The leaves were then surface sterilised and cultured. The isolated bacteria were then pure cultured and each culture colony was subjected to a series of biochemical tests and gram staining. Four different genera of bacteria were identified, namely *Bacillus* sp., *Staphylococcus* sp., *Pseudomonas* sp. and *Salmonella* sp. It was observed that on application of pesticides, the bacterial diversity changed in each case, except for Cypermethrin, which was same as control. Hence, it was clear from the study that application of pesticides has a huge impact on the bacterial endophytic diversity of plants, showing the occurrence of a variety of bacteria including highly pathogenic ones.

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Callus induction in Black Ginger (*Kaempferia parviflora*): An endangered medicinal plant

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Kaempferia parviflora is a Thai herb and its rhizomes were used in ancient times as folk medicines. The present study aimed to induce callus initiation of *Kaempferia parviflora* (Black ginger) in Murashige and Skoog media supplemented with various growth regulators. The callus was initiated using rhizome as an explant. Initially callus formation was checked in controlled media; followed by evaluating the effect of varied concentrations of NAA (auxin) and BAP (cytokinin). Maximum fresh weight (1.30g) of callus was observed in the media having NAA and BAP together in equal concentration (1.5mg l^{-1}). In most of the combinations, the color of callus was creamy, while other observations gave pale greenish color. Results were recorded after five weeks of inoculation of rhizome.

Callus formation in Black Turmeric (*Curcuma caesia*) through *in vitro* culture of rhizome bud

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Curcuma caesia (Black turmeric) belonging to family Zingiberaceae is an important traditional medicinal plant and is categorized as an endangered plant. Turmeric is vegetatively propagated exclusively through underground rhizomes and multiplication rate is very low. In the present study, the species *Curcuma caesia* have been propagated through tissue culture using rhizome bud. Rhizome buds used as explants were cultured on Murashige and Skoog (MS) medium containing different concentration of NAA (1-Napthaleneacetic acid) alone or in combination with the single concentration of BAP (6-Benzylaminopurine). The result showed that optimum callus formation was obtained from MS medium containing 0.5 mg/l BAP + 1.5 mg/l NAA. In this growth regulator condition, the explants produced maximum callus weighing 2.20 g after 5 weeks of culture. The calluses, thus obtained, in various hormone concentration and combination were compact and friable in texture; greenish, pale greenish and creamy in color.

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Phylogentic analysis of plant growth promoting rhizobacteria

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Plant Growth Promoting Rhizobacteria (PGPR) are present in the rhizosphere which can enhance plant growth through a wide variety of mechanisms like phosphate solubilization, siderophore production, biological nitrogen fixation, production of 1-Aminocyclopropane-1-carboxylate deaminase (ACC), quorum sensing (QS) signal, interference and inhibition of biofilm formation, phytohormone production, exhibiting antifungal activity, production of volatile organic compounds (VOCs), induction of systemic resistance, promoting beneficial plant-microbe symbioses, interference with pathogen toxin production etc. The study was done to understand the evolutionary relationships among thirty-eight different PGPR species on the basis of their 16s rRNA conserved sequences. Data was collected from NCBI Gen-Bank, multiple sequence alignment was done using ClustalX, nucleotide sequence and conserved sites were seen using BioEdit, and phylogenetic tree was constructed using MEGA 4. The phylogenetic tree revealed homology relations amongst the various PGPR which formed different clades on the basis of their similarity or dissimilarity with each other. Most of the PGPR strains formed clades with their own genus. However, two PGPR species formed cluster with different genus of PGPR species rather than its own genus. Inference can be drawn from the phylogenetic characterisation of the various PGPR that a deeper understanding can be developed to figure out the mechanisms underlying the symbiotic association between different PGPR strains and varied plant species.

Bioinformatics tools in sequence analysis: A review

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The revolutionary growth in the field of computation has fuelled a new era in the analysis of biological data. Sequence analysis refers to subjecting a DNA, RNA or peptide sequence to any of a wide range of analytical methods to understand its features, function, structure, or evolution using sequence alignment, searches against biological databases and others. The rate of addition of new sequences to the databases increased exponentially with the development of methods of high-throughput production of gene and protein sequences. A wide variety of alignment algorithms and software have been developed over the past few years. In this review, we highlight the current development of these algorithms and also consider future development of alignment algorithms with respect to emerging long sequence reads.

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Assessment of popular street vended food (panipuri) and inhibitory effect of neem and garlic against bacterial growth

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This study aims to investigate the hygiene condition of the vendors and microbial quality of street food particularly panipuri. Different samples of panipuri water were aseptically collected from different locations of Silchar city. The samples were analyzed within an hour of procurement. Isolation, enumeration and identification of the prevalent bacteria and fungi were carried out following the standard procedures. The results obtained revealed that total bacterial count ranged from $7.6x10^6$to $2.40x10^7$cfu/ml. Bacteria isolated includes *E. coli, Staphylococcus sp., Salmonella sp., Streptococcus sp., and Pseudomonas sp.* Fungi like *Aspergillus sp. and Penicillium sp.* were also found. It was found that their food handling practices were very poor. Food hawkers in India are generally unaware of food regulations and have no training in food-related matters. They also lack supportive services such as water supply of adequate quality and disposal systems, which hamper their ability to provide safe food. It is suggested that proper hygienic and sanitary conditions should be maintained both personally and institutionally to avoid any food borne pathogenic outbreaks in India, especially in children who are tempted to such food. The critical control points should be taken as safe limit by authorities to reduce the cases of food contamination. Antibacterial activities of two medicinal plants were also established on the pathogens isolated from panipuri water. Among the medicinal plant studied, garlic had shown maximum antibacterial activity. Antibacterial efficacy showed that garlic was comparatively of superior quality than neem in killing food borne pathogen. The present study is a prerequisite in understanding the significance of pathogenic microorganisms in street foods and use of medicinal plant as both antibacterial agents and food preservatives.

Isolation and identification of endophytic bacteria from *Oscimum sanctum* and antibacterial activity of tulsi against food-borne microbial pathogens

Sagarika Mohanta, Parveen Sultan Laskar* and Bibhas Deb
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The aims of this study were to isolate and identify endophytic bacteria from *Oscimum sanctum* and to investigate the antibacterial potential of *O. sanctum* against four food borne pathogens. A total of 9 bacterial endophytes were obtained from the healthy leaves of *O. sanctum* in which *Bacillus sp.* was found in highest concentration. Aqueous, ethanol, acetone leaf extracts and commercialized products from *O. sanctum* were investigated for their antibacterial activities at various concentrations against *Escherichia coli, Staphylococcus aureus* and *Pseudomonas aeruginosa* using standard method. The plant extracts and essential commercialized oil showed various levels of antibacterial activity against food borne pathogens. Antimicrobial studies indicated that the Ethanol leaf extracts of *O. sanctum* were found comparatively more effective against these bacteria than any other extract tested while aqueous extract being the least effective against the tested microbes. The antimicrobial activity of the ethanol leaf extract was more pronounced against test microbes than the other solvent extracts. Since, *S. aureus*, *P. aeruginosa* and *E. coli* are major pathogens causing skin and stomach infections, Tulsi essential oil could be a valuable topical antimicrobial agent for management of skin and stomach infections caused by these organisms. The study revealed that the plant possessed antimicrobial properties and could be potential source of antimicrobial agent in treatment of bacterial infections.

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In vitro micropropagation of pineapple (*Ananas comosus* L. var. Queen)

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Micropropagation can be designated as the process of development of elite variety of plants from meristematic tissue or somatic cells of plants with superior quality. It can also be defined as the generation of genetically identical clones of a cultivar by the method of asexual reproduction. The Queen variety of pineapple (*Ananas comosus*) has been selected for the propagation due to its increased demands in Assam, especially Cachar district. The aim of this study was to establish an efficient micropropagation protocol for the cultivar. The crown has been selected as explant and grown in Murashige and Skoog (MS) medium supplemented with NAA and BAP. The concentration of BAP that was found best for shoot elongation is 2.0mg/l and the shoot length is 2.6 cm while the combination of hormones NAA and BAP produced best results (shoot length of 1.9 cm) at a concentration of 2mg/l. Furthermore, both at increased and decreased concentration of BAP alone and also in combination of BAP and NAA, there occurred a decline in the shoot elongation.

Assessment of water quality after storage in different containers

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Safe drinking water is one of the major necessity of healthy life, but waterborne disease is still a major cause of death in many parts of the world. In recent times, most of the people store water in clay pot in some rural areas. It is believed to have health benefits. Based on this fact the aim of this study was to assess the chemical and microbiological parameters of water stored in different vessels. Water samples were collected from deep tube well and stored in different containers viz copper, steel, glass, clay, aluminum and plastic for further analysis. pH of the water stored in clay decreased to 5.9 which was lower than the standard limit given by WHO, ISI and ICMR while TDS, Turbidity, Hardness, Nitrate, Iron, Fluoride and Chloride test showed significant result. Water stored in copper and clay vessels showed minimum colonies of bacteria, while other vessels showed negligible effect on microbial reduction. Thus, storing water in clay and copper container may inhibit the bacterial growth and is safe for drinking purpose.

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Cytological Study of Tea Garden Workers of Khaspur, Cachar District

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Genotoxicity is one of the important endpoints for risk assessment of various lifestyle factors. The study is the report on the genotoxic effect associated with exposure to pesticide and chewing tobacco in Barak valley, Southern Assam. In the present cytogenetic monitoring study, analysis of micronucleus, nuclear buds and binucleated cells were performed in the exfoliated buccal cells. We collected 10 samples from individuals having chewing habit and 10 control samples. Significant increase in the frequency of micronucleus were found in tobacco chewers (5.15 ± 0.48, $P < 0.001$), as compared to the unexposed control group (0.20 ± 0.09). Tea garden workers showed significant increase (4.75 ± 0.52, $P < 0.001$) in the frequency of binucleated cells as compared to the control group (0.40 ± 0.19). Statistically significant increase ($P<0.001$) in cells with nuclear bud (3.36 ± 0.42) was found in the exposed group in comparison to control group (0.15 ± 0.08). We suggest that analysis of other degenerative nuclear changes in addition to micronucleus can provide valuable information while evaluating potential genotoxic agents.

Effects of drinking arsenic contaminated water on human buccal epithelial cells

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Arsenic is a naturally occurring metalloid trace element with potent toxic and mutagenic effects. It is present ubiquitously in the environment and is released from both natural and man-made sources. 20 Individuals donated buccal mucosa cells extracted by slightly scraping the oral cavity with a cotton swab. Every participant filled out a questionnaire about the exposure period and arsenic concentration. 10 Individuals who consumed arsenic contaminated water and 10 samples are healthy individuals, considered as control. Additionally, information on age, gender, body weight, smoking status, medication and nutrition was retrieved. Micronuclei and other markers were evaluated in 1000 cells per individual at the microscope. Individuals drinking high concentration of arsenic in water leads to a significantly increased ($P<0.001$) frequency of micronuclei (4.20 ± 0.41), nuclear buds (3.36 ± 0.42), binucleated cells (4.75 ± 0.52) as compared to control.

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Effect of Anemia among pregnant woman – a case study

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Anemia is one of the most frequent complications related to pregnancy. It is a medical condition in which the red blood cell count or haemoglobin (Hb) is less than normal. Anemia is caused by either a decrease in production of red blood cells or haemoglobin, or an increase in loss (usually due to bleeding) or destruction of red blood cells. Normal physiologic changes in pregnancy affect the haemoglobin, and there is a relative or absolute reduction in Hb concentration. The relationship of anemia as a risk factor for low birth weight and less hemoglobin content were analyzed by using cross-sectional, longitudinal and case-control studies because randomized trials were not available for analysis. The study was conducted at the Civil Hospital, Silchar. The major pregnancy complications and perinatal outcome were compared between mothers with and without anaemia and adjusted for parity. The incidence of multiparity was significantly higher in the 25 anaemia patients compared to the 25 non-anaemia patients, but there was no difference in the incidence of other major antenatal complications, type of labour or mode of delivery, incidence of preterm delivery, or perinatal mortality or morbidity, after adjusting for parity. Antenatal anaemia, defined as a maternal haemoglobin of < 10 g/dl and low birth weight of child does not adversely affect pregnancy outcome. A case study was conducted and a definite correlation established between the anaemia patients and low birth weight and less percentage of haemoglobin content.

Metastasis-inducing neo-angiogenesis is the major contribution for patients developing chronic tumors

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Angiogenesis the recruitment of new blood vessels is an essential component of the metastatic pathway. These vessels provide the principal route by which tumor cells exit the primary site and enter the circulation. For many tumors, the vascular density provides a prognostic indicator of metastatic potentiality with the highly vascular primary tumors than the poorly vascular tumors. Tumor angiogenesis is regulated by the production of angiogenic stimulators including members of Fibroblast Growth Factors and Vascular Endothelial *Growth Factors* families. In addition, tumors can activate angiogenic inhibitors like *Angiostatin* and *Endostatin* that can modulate angiogenesis both at the primary and at the downstream sites of metastasis. Angiogenesis factors are found in various body fluids, the most compelling correlation between angiogenesis and tumor metastasis has been in a large number of studies in which vascular density of a tumor has been correlated with metastasis and with patient outcome.

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Primary Autosomal Recessive Microcephaly: A Global Review

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Autosomal recessive primary microcephaly (MCPH) is a neuro-developmental disorder that is characterized by microcephaly present at birth and non-progressive mental retardation. Microcephaly is the outcome of a smaller but architecturally normal brain; the cerebral cortex exhibits a significant decrease in size. MCPH is a neurogenic mitotic disorder, though affected patients demonstrate normal neuronal migration, neuronal apoptosis and neural function. Seven MCPH loci (MCPH1-MCPH7) have been mapped to date from various populations around the world and contain the following genes: Microcephalin, WDR62, CDK5RAP2, ASPM, CENPJ and STIL. It is predicted that MCPH gene mutations may lead to disease phenotype due to a disturbed mitotic spindle orientation, premature chromosomal condensation, signaling response as a result of damaged DNA, microtubule dynamics, transcriptional control or a few other hidden centrosomal mechanism that can regulate the number of neurons produced by neuronal precursor cell. Additional findings have further elucidated the microcephaly aetiology and pathophysiology, which has informed the clinical management of families suffering from MCPH. The provision of molecular diagnosis and genetic counseling may help to decrease the frequency of this disorder.

In-silico analysis of Tissue non-specific alkaline phosphatase (TNAP) gene mutations and its implication in Hypophosphatasia

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Hypophosphatasia (HPP), a rare form of genetic disorder, results in the defective mineralization of teeth and bones due to mutation in alkaline phosphatase gene (ALPL; OMIM#171760) encoding the tissue-nonspecific alkaline phosphatase (TNAP). TNAP mainly cleaves extracellular substrates such as inorganic pyrophosphates (PPi), pyridoxal-5′- phosphate (PLP), phosphoethanolamine (PEA) and nucleotides. Till date, 334 distinct mutations have been reported in the ALPL gene which consists mostly of missense mutations. Severe forms of Hypophosphatasia are found to have mutations primarily within the active site of TNAP enzyme. Computational analysis of the 3D-model of TNAP by studying the reported mutations causing severe Hypophosphatasia revealed certain changes in terms of bonding type, bond angles and bond lengths. The most observable change was the intermolecular hydrogen bond interactions amongst the amino acids which varied with mutational variations. Better understanding of the TNAP structural and functional changes would provide further insight in developing curative treatment strategies for the disorder.

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Establishment of Biotech Park

A **Biotech Park** has been developed with the cumulative efforts of the Department of Biotechnology, Institutional Biotech Hub and Bioinformatics Centre of Gurucharan College, Silchar. During last NAAC visit to this college (in 2016), Peer team appreciated the whole effort and activities and ultimately the **College is re-accreditated with 'A' grade**.

Microbial Strains Identified

Sl. No.	Name of the Microorganism	GenBank Ac. No.	Year of Submission	Submitted by
1.	*Klebsiella* sp. AU_SC5_M	JN375552	2011	Mohanta S, Sharma GD and Deb B
2.	*Bacillus* sp. AU_SW3_M	JN375551	2011	Mohanta S, Sharma GD and Deb B
3.	*Klebsiella pneumoniae* strain SMEND03	JF838291	2011	Mohanta S, Sharma GD and Deb B
4.	*Burkholderia caribensis* strain SDSA-I10/1	GU372342	2011	Deb Roy B, Deb B and Sharma GD
5.	*Acinetobacter johnsonii* strain SDSA-I19/1	GU372343	2011	Deb Roy B, Deb B and Sharma GD
6.	*Gluconacetobacter liquefaciens* strain SDSA-I28/1	GU372344	2011	Deb Roy B, Deb B and Sharma GD
7.	*Azospirillum amazonense* strain SDSA-I14/1	GU372345	2011	Deb Roy B, Deb B and Sharma GD
8.	*Beijerinckia indica* strain SDSA-I30/2	GU372346	2011	Deb Roy B, Deb B and Sharma GD
9.	*Azotobacter chroococcum* strain SDSA-I12/2	GU372347	2011	Deb Roy B, Deb B and Sharma GD
10.	*Pseudomonas aeruginosa* strain SN1	KF031122	2013	Nath S, Sharma I, Deb B and Pandey P
11.	*Pseudomonas aeruginosa* strain SN3	KF031123	2013	Nath S, Deb B, Sharma I and Pandey P
12.	*Pseudomonas aeruginosa* strain SN4	KF447770	2013	Nath S, Deb B and Sharma I
13.	*Pseudomonas aeruginosa* strain SN5	KF447771	2013	Nath S
14.	*Bacillus cereus* strain SN6	KM489153	2014	Nath S
15.	*Bacillus cereus* strain SN7	KM489154	2014	Nath S
16.	*Bacillus cereus* strain GCC7	KT347590	2015	Deb K, Pandey P and Deb B
17.	*Bacillus cereus* strain GCC12	KT347591	2015	Deb K, Deb B and Pandey P

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

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- Naha A, Roy BS, Paul B, Chakraborty S, Nath S and Deb B (**2016**) Impact and adversity of some orally administered drugs. Published in proceedings of DST sponsored National Seminar on "*Computational Research and its Development in Experimental Sciences"*. Pp. 7.

MinION

Portable, real-time biological analyses

MinION is a portable, real time device for DNA and RNA sequencing. It streams data in real time so that analysis can be performed during the experiment and workflows are fully versatile. The MinION weighs under 100g and plugs into a PC or laptop using a high speed USB 3.0 cable. No additional computing infrastructure is required and can be used in diverse areas, ranging from environmental microbiology to viral epidemics.

Johnson, S. S., Zaikova, E., Goerlitz, D. S., Bai, Y., & Tighe, S. W. (2017). Real-Time DNA Sequencing in the Antarctic Dry Valleys Using the Oxford Nanopore Sequencer. Journal of Biomolecular Techniques: JBT.

Synthetic Yeast genome

Working as part of an international research consortium, a multidisciplinary team at The Johns Hopkins University has completed the design phase for a fully synthetic yeast genome termed *Saccharomyces cerevisiae* 2.0, or Sc2.0.

The design plan for the Sc2.0 genome is about 8 percent smaller than the natural yeast genome, with noncoding "junk" DNA removed and other genetic sequences relocated that can make DNA unstable and prone to mutations.

The synthetic genome also is designed for customization, so scientists can study questions related to the structure, function and evolution of chromosomes.

Source: http://www.hopkinsmedicine.org/news/media/releases/first_fully_artificial_yeast_genome_has_been_designed

THE LANCET Gastroenterology & Hepatology

The mesentery: structure, function, and role in disease

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Summary: Systematic study of the mesentery is now possible because of clarification of its structure. Although this area of science is in an early phase, important advances have already been made and opportunities uncovered. For example, distinctive anatomical and functional features have been revealed that justify designation of the mesentery as an organ. Accordingly, the mesentery should be subjected to the same investigatory focus that is applied to other organs and systems. In this Review, we summarise the findings of scientific investigations of the mesentery so far and explore its role in human disease. We aim to provide a platform from which to direct future scientific investigation of the human mesentery in health and disease.

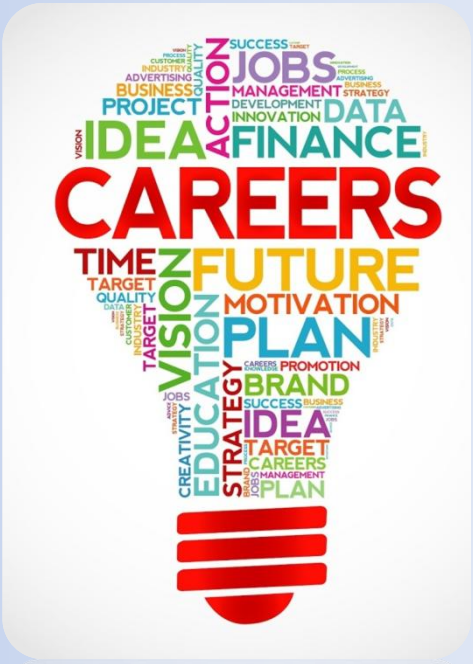
Lancet Gastroenterol Hepatol. 2016 Nov;1(3):238-247. doi: 10.1016/S2468-1253(16)30026-7

Biotechnology combines biological sciences with engineering technologies to manipulate living organisms and biological systems to produce products that advances healthcare, medicine, agriculture, food, pharmaceuticals and environment control.

Scope of Biotechnology for B.Sc. students

It is highly recommended to pursue M.Sc. in a specialised discipline after attaining basic graduation. The job opportunities for B.Sc. graduates in a highly research oriented field like biotechnology is very less. India is a major hub for some excellent masters programme such as JNU, DU, IISc, TIFR, IITs etc. With an M.Sc. degree, most students tend to work in research labs and industries as research assistants where the pay package is quite less. Thus, it is advisable to do M.Sc. in a reputed institution for good campus placements and job opportunities.

Master students may also opt to pursue their Ph.D. degrees in Biotechnology and allied fields which opens up more avenues both in India and worldwide. A Ph.D. degree will give you the ability to start your own research projects and venture in start-up entrepreneurship or may create some opportunities to become a professor in colleges/universities or research scientist in R&D organizations.



List of companies, universities and research institutions that are renowned in India and worldwide for their work in Biotechnology and allied fields

Pharmaceuticals: Biocon, Orbees Medical, Invitrogen, GlaxoSmithKline, Reliance Life Sciences, CTS Life Sciences, Dr. Reddy's Labs, Cipla, Jubilant Life Sciences, Wockhardt, Torrent Pharma, Cadila Healthcare, Sun Pharma, Lupin Pharma, Pfizer, Patanjali, Himalaya, Novartis etc.

Universities and Technical institutions: IISc, TIFR, JNU, DU, IITs, IISERs etc.

Research institution: Center for Cellular and Molecular Biology (CCMB), Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), National Centre for Biological Sciences (NCBS), Institute of Genomics and Integrative Biology (IGIB), National Institute of Plant Genome Research (NIPGR), National Institute of Oceanography (NIO), National Brain Research Centre (NBRC) , National Environmental Engineering Research Institute (NEERI), National Chemical Laboratory (NCL), National Centre for Cell Science (NCCS), National Institute of BioMedical Genomics (NIBMG), Rajiv Gandhi Centre for Biotechnology (RGCB), Institute of Microbial Technology (IMTech) , MS Swaminathan Research Foundation (MSSRF), All India Institute of Medical Sciences (AIIMS), National Institute of Immunology (NII), AU-KBC Research Centre, Centre for Stem Cell Research (CSCR) etc.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