



## **CHINMAYA DEGREE COLLEGE**

### **BHEL, HARIDWAR**

### **Criterion III**

### **Research, Innovations and**

### **Extension**

#### **3.3 Research Publication and Awards**

**3.3.1 Number of research papers published per teacher in the Journals notified on UGC care list during the last five years**

### **Documents Attached**

<b>Sr. No.</b>	<b>Document Name</b>
1.	Front Page of Published Research Papers

# Front Page of Published Research Papers

End-12/1

Original Research Paper

Volume - 11 | Issue - 08 | August - 2021 | PRINT ISSN No. 2249 - 555X | DOI : 10.36106/ijar

Biochemistry



## A STUDY ON KINETIC CHARACTERIZATION OF CHANNEL-BLOCKING MUTANTS IN BRADYRHIZOBIUM JAPONICUM UTILIZATION A

<b>Dr. Anand Shanker Singh</b>	Associate Professor, Department of Chemistry, Chinmaya Degree College, BHIL, Haridwar.
<b>Dr. G. Radhika</b>	MBBS, MD ( Biochemistry ), HOD , Department of Biochemistry, Sri .Venkateshwara Medical College and Hospital , Pondicherry.
<b>Dr. R. Praveen Kumar*</b>	MD ( Paediatrics ), MBBS, Assistant Professor, Department of Paediatric, Rajah Muthiah Medical College. *Corresponding Author
<b>Dr. Debarshi Jana</b>	Young Scientist, IPGMER and SSKM Hospital, Kolkata, WB.

**ABSTRACT** Proline utilization A (PutA) from *Bradyrhizobium japonicum* (BjPutA) is a bifunctional flavoenzyme that catalyzes the oxidation of proline to glutamate using fused proline dehydrogenase (PRODH) and  $\Delta 1$ -pyrroline-5-carboxylate dehydrogenase (P5CDH) domains. Recent crystal structures and kinetic data suggest an intramolecular channel connects the two active sites, promoting substrate channeling of the intermediate P5C from the PRODH domain to the P5CDH domain. In this work several mutations were made along the channel in an effort to block passage of P5C to the second active site. Analysis of several site-specific mutants in the substrate channel of BjPutA revealed an important role for D779 in the channeling path. BjPutA mutants D779Y and D779W significantly decreased the overall PRODH-P5CDH channeling reaction indicating that bulky mutations at residue D779 impede travel of P5C through the channel. Interestingly, D779Y and D779W also exhibited lower P5CDH activity, suggesting that exogenous P5C must enter the channel upstream of D779. Replacing D779 with a smaller residue (D779A) had no effect on the catalytic and channeling properties of BjPutA showing that the carboxylate group of D779 is not essential for channeling. An identical mutation at D778 (D778Y) did not impact BjPutA channeling activity. Thus, D779 is optimally orientated so that replacement with the larger side chains of Tyr/Trp blocks P5C movement through the channel. The kinetic data reveal not only that bulky mutations at residue D779 hinder passage of P5C to the second active site, but also P5C must use the channel to efficiently access the P5CDH domain. Moreover, these mutants may be used to learn more about the hydrolysis event that is thought to take place within the channel.

**KEYWORDS** : Proline utilization A, Kinetic Characterization, *Bradyrhizobium japonicum*.

### INTRODUCTION

Proline utilization A (PutA) catalyzes the conversion of proline to glutamate using two consecutive reactions. In the first step, proline dehydrogenase (PRODH) uses a flavin cofactor as an electron acceptor to remove two electrons from proline, resulting in  $\Delta 1$ -pyrroline-5-carboxylate (P5C). P5C then undergoes a non-enzymatic hydrolysis, which opens the pyrroline ring to create glutamate- $\gamma$ -semialdehyde (GSA).

GSA is a substrate for NAD<sup>+</sup>-dependent pyrroline-5-carboxylate dehydrogenase (P5CDH), where two additional electrons are removed generating glutamate. Proline and proline metabolism are important to all walks of life. For example, proline plays important roles in different all walks of life. For example, proline plays important roles in different all walks of life. For example, proline plays important roles in different all walks of life. For example, proline plays important roles in different all walks of life. For example, proline plays important roles in different all walks of life.

PutA occurs as a bifunctional enzyme in all Gram-negative bacteria and *Corynebacterium*<sup>1</sup>. A recent crystal structure of *Bradyrhizobium japonicum* PutA (BjPutA) revealed a tunnel connecting the two active sites<sup>2</sup>. Structural and kinetic results suggest P5C/GSA uses the channel sites<sup>3</sup>. Structural and kinetic results suggest P5C/GSA uses the channel sites<sup>3</sup>. Structural and kinetic results suggest P5C/GSA uses the channel sites<sup>3</sup>. Structural and kinetic results suggest P5C/GSA uses the channel sites<sup>3</sup>. Structural and kinetic results suggest P5C/GSA uses the channel sites<sup>3</sup>.

Several physiological benefits of substrate channeling versus free diffusion have been identified. Chiefly, channeling decreases transit time between active sites and prevents loss of intermediates by diffusion, making the overall reaction more efficient. Thus, channeling enzymes can operate at maximum rates even if cellular substrate concentrations are not at saturating levels. Also, labile intermediates can be concealed from solvent to prevent decay or interaction with other molecules. Finally, reaction intermediates from competing reactions can be kept separate, which dictates metabolic flux<sup>4</sup>.

As mentioned, a crystal structure of BjPutA revealed a tunnel connecting two active sites, which is thought to channel intermediate P5C/GSA. Theoretically, the channeling of P5C/GSA is physiologically reasonable, as P5C is a substrate of three competing reactions. It can be converted to glutamate via P5CDH, ornithine via ornithine aminotransferase, or back to proline via P5C reductase. Thus, channeling of P5C in proline catabolism may be necessary to retain proper metabolic flux and avoid metabolic cycling<sup>5</sup>. Besides enzyme competition, free P5C/GSA is reported to be an inhibitor of glutamine in three different *E. coli* enzymes including glucosamine-6-phosphate synthase, cytidine 5'-triphosphate synthase, and the amidotransferase domain of carbamoyl phosphate synthetase. Additionally, P5C was shown to form adducts with other important metabolic intermediates including oxaloacetic acid, pyruvic acid, and acetoacetic acid<sup>6</sup>. Considering the outcomes of liberated P5C/GSA, there appears to be a physiological advantage to sequester the intermediate during proline catabolism.

Substrate channeling in PutA was first kinetically described in *Salmonella typhimurium*; however, the structural and kinetic characterization of BjPutA have made this enzyme the prototype of PutA channeling. An X-ray structure of BjPutA revealed an irregularly-shaped cavity that spans 41 Å between the two active sites with a total volume of 1400 Å<sup>3</sup><sup>7</sup>. The majority of the volume (1325 Å<sup>3</sup>) of the tunnel comes from a large central chamber with dimensions 24 Å by 14 Å by 3-7 Å, which provides adequate space to accommodate P5C (102 Å<sup>3</sup>) or GSA (120 Å<sup>3</sup>)<sup>8</sup>.

Additionally, kinetic evidence comparing native BjPutA to an equal molar mixture of two complementary active site mutants (R456M, no



**A STUDY OF ORM EXPRESSION CHANGES FUMONISIN B1-INDUCED PERTURBATIONS OF SPHINGOLIPID HOMEOSTASIS AND DIFFERENTIALLY TOUCHES CERAMIDE SYNTHASE ACTIVITIES**

**Dr. Anand Shanker** Associate Professor, Department of Chemistry, Chinmaya Degree College, BHEL, Haridwar.

**Dr. G. Radhika** MBBS, MD ( Biochemistry ), HOD , Department of Biochemistry, Sri .Venkateshwara Medical College and Hospital , Pondicherry.

**Dr. Ankita Singh\*** DNB, DGO , MBBS. \*Corresponding Author

**Dr. Debarshi Jana** Young Scientist, IPGMER and SSKM Hospital, Kolkata, WB.

**ABSTRACT** Sphingolipid synthesis is tightly regulated in eukaryotes. This regulation in plants ensures sufficient sphingolipids to support growth, while limiting accumulation of sphingolipid metabolites that induce programmed cell death (PCD). Serine palmitoyltransferase (SPT) catalyzes the first step in sphingolipid biosynthesis and is considered the primary sphingolipid homeostatic regulatory point. In this report, Arabidopsis putative SPT regulatory proteins, orosomucoid-like proteins AtORM1 and AtORM2 were found to physically interact with the Arabidopsis SPT and to suppress SPT activity when co-expressed with Arabidopsis SPT subunits LCB1 and LCB2 and the small subunit of SPT in a yeast SPT-deficient mutant. Consistent with a role in SPT suppression, AtORM1 and AtORM2 overexpression lines displayed increased resistance to the PCD-inducing mycotoxin fumonisin B1 (FB1), with an accompanying reduced accumulation of long-chain bases (LCBs) and C16-fatty acid-containing ceramide accumulation relative to wild type plants. Conversely, RNAi suppression lines of AtORM1 and AtORM2 displayed increased sensitivity to FB1 and an accompanying strong increase in LCBs and C16 fatty acid-containing ceramides relative to wild-type plants. Overexpression lines were also found to have reduced activity of the Class I ceramide synthase that uses C16-fatty acid acyl-CoA and dihydroxy LCB substrates, but increased activity of Class II ceramide synthases that use very long-chain fatty acyl-CoA and trihydroxy LCB substrates. RNAi suppression lines, in contrast, displayed increased Class I ceramide synthase activity, but reduced Class II ceramide synthase activity. These findings indicate that ORM-mediation of SPT activity differentially regulates functionally distinct ceramide synthase activities as part of a broader sphingolipid homeostatic regulatory network.

**KEYWORDS :** Serine palmitoyltransferase, Sphingolipid synthesis, Ceramide Synthase Activities.

**INTRODUCTION**

Sphingolipids play critical roles in plant growth and development as essential components of endomembranes, including the plasma membrane where they comprise more than 40% of the total lipid.<sup>1,2</sup> Sphingolipids are also highly enriched in detergent insoluble membrane fractions of the plasma membrane that form microdomains for proteins with important cell surface activities, including cell wall biosynthesis and hormone transport.<sup>3</sup> In addition, sphingolipids, particularly those with very long-chain fatty acids (VLCFAs), are integrally-associated with Golgi-mediated protein trafficking that underlies processes related to the growth of plant cells.<sup>3</sup>

Furthermore, sphingolipids function through their bioactive long-chain base (LCB) and ceramide metabolites to initiate programmed-cell death (PCD), important for mediating plant pathogen resistance through the hypersensitive response (HR).

Sphingolipid biosynthesis is highly regulated in all eukaryotes. In plants, maintenance of sphingolipid homeostasis is vital to ensure sufficient sphingolipids for growth while restricting the accumulation of PCD-inducing ceramides and long-chain bases (LCBs), until required for processes such as pathogen-triggered HR.<sup>4</sup> Serine palmitoyltransferase (SPT), which catalyzes the first step in LCB synthesis, is generally believed to be the primary control point for sphingolipid homeostasis. SPT synthesizes LCBs, unique components of sphingolipids, by catalyzing a pyridoxal phosphate-dependent condensation of serine and palmitoyl (16:0)-CoA in plants. Similar to other eukaryotes, the Arabidopsis SPT is a heterodimer consisting of LCB1 and LCB2 subunits. Research to date has shown that SPT is regulated primarily by post-translational mechanisms involving physical interactions with non-catalytic, membrane-associated proteins that confer positive and negative regulation of SPT activity. These proteins include a 56-amino acid small subunit of SPT (ssSPT) in Arabidopsis, which was recently shown to stimulate SPT activity and to be essential for generating sufficient amounts of sphingolipids for pollen and sporophytic cell viability.<sup>4</sup>

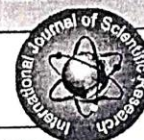
Evidence from yeast and mammalian research points to a more critical role for proteins termed ORMs in sphingolipid homeostatic regulation.<sup>5</sup> The *Saccharomyces cerevisiae* Orm1p and Orm2p negatively regulate SPT through reversible phosphorylation of these

polypeptides in response to intracellular sphingolipid levels.<sup>4</sup> Phosphorylation/de-phosphorylation of ORMs in *S. cerevisiae* presumably affects the higher order assembly of SPT to mediate flux through this enzyme for LCB synthesis. In this sphingolipid homeostatic regulatory mechanism, the *S. cerevisiae* Orm1p and Orm2p are phosphorylated at their N-termini by Ypk1, a TORC2-dependent protein kinase.<sup>5</sup> The absence of this phosphorylation domain in mammalian and plant ORM homologs brings into question the nature of SPT reversible regulation by ORMs in other eukaryotic systems.<sup>4</sup>

RNAi suppression of ORM genes in rice has been shown to affect pollen viability, but no mechanistic characterization of ORM proteins in plants has yet to be reported. Here we describe, two Arabidopsis ORMs, AtORM1 and AtORM2, that suppress SPT activity through direct interaction with the LCB1/LCB2 heterodimer.<sup>7</sup> We also show that strong upregulation of AtORM expression impairs growth. In addition, up- or down-regulation of ORMs is shown to differentially affect sensitivity of Arabidopsis to the PCD-inducing mycotoxin fumonisin B1, a ceramide synthase inhibitor, and to also differentially affect activities of Class I and II ceramide synthases as a possible additional mechanism for regulating sphingolipid homeostasis.

**METHODS**

Yeast Growth and Expression Plasmids. Yeast (*Saccharomyces cerevisiae*) strain TDY9113 (Mat a tsc3Δ::NAT lcb1Δ::KAN ura3 leu2 lys2 trp1Δ) lacking endogenous SPT was used for expression and characterization of the Arabidopsis thaliana SPT subunits and ORM proteins. The mutant was cultured in medium containing 15mM phyto-sphingosine and 0.2% (w/v) tergitol. The AtORM1 (Atlg01230) and AtORM2 (At5g42000) open reading frames were amplified by PCR and inserted into pPR3-N (Dualsystems Biotech) with HA tagged at N-terminus. The pAL2-URA was constructed for divergent constitutive expression of AtLCB1-FLAG and Myc-At LCB2a by replacing the GAL1 and GAL10 promoters of pESC-URA (Stratagene) with the yeast LCB2 and ADH promoters, respectively. The AtssSPTa cDNA open reading frame was inserted after the 3xHA tag in pADH1.<sup>4</sup> For deleting the first transmembrane domain (TMD1) of AtLCB1, an AvrII restriction site was inserted at codon 33 and 53 respectively by QuikChange II site directed mutagenesis (Agilent technologies). The deletion of TMD1 was achieved by cutting with AvrII and re-ligation. The deletion was confirmed by sequencing.



ASSOCIATION OF CARDIOVASCULAR RISK IN CHILDREN BORN WITH LOW BIRTH WEIGHT

Biochemistry

**Dr. Anand Shanker Singh\*** Associate Professor, Dept Of Chemistry, Chinmaya College of Sciences, Haridwar. \*Corresponding Author

**Dr . G . Radhika** MD Biochemistry, MBBS, HOD , Dept of Biochemistry, Sri. Venkateshwara Medical College And Hospital, Pondicherry

**Dr . R . Praveen Kumar** MD paediatrics , MBBS, Assistant Professor, Dept of Paediatric Rajah Muthiah Medical College

**Dr. Ankita Singh** DNB, DGO, MBBS

**Dr. Debarshi Jana** Young Scientist DST Department of Gynecology And Obstetrics Institute of Post-graduate Medical Education And Research, A.J.C. Bose Road, Kolkata-700020, West Bengal, India

ABSTRACT

**INTRODUCTION:** Most studies of early programming focus on very LBW or extremely LBW, even though the majority of all LBW children are born only with marginally LBW.<sup>1</sup> The pathogenesis behind CVD is multifactorial, and for health care providers to be able to assess the risk of each individual, we need to know more about this common subgroup.

**AIM:** Being born with LBW affects later cardiovascular risk.

**RESULT:** In Marginally LBW group, 4.7(0.6) patients had Fasting glucose(mmol/L), 2.7(2.3-3.8) patients had Fasting insulin( $\mu$ U/mL), 0.57(0.4-0.8) patients had HOMA-IR, 4.4(0.7) patients had Cholesterol(mmol/L), 0.50(0.2) patients had Triglyceride(mmol/L), 2.7(0.6) patients had LDL(mmol/L), 1.5(0.3) patients had HDL(mmol/L), 0.82(0.2) patients had ApoB(g/L), 1.4(0.2) patients had ApoA1 (g/L), 0.51(0.3) patients had ApoB/ApoA1 and 0.24(0.1-0.7) patients had hs-CRP(mg/L). In Controls group, 3.5(0.5) patients had Fasting glucose(mmol/L), 2.8(LD-3.5) patients had Fasting insulin( $\mu$ U/mL), 0.60(LD-0.7) patients had HOMA-IR, 5.5(0.8) patients had Cholesterol(mmol/L), 0.57(0.2) patients had Triglyceride(mmol/L), 2.9(0.7) patients had LDL(mmol/L), 1.4(0.3) patients had HDL(mmol/L), 0.71(0.2) patients had ApoB(g/L), 1.4(0.2) patients had ApoA1 (g/L), 0.57(0.1) patients had ApoB/ApoA1 and 0.18(0.1-0.5) patients had hs-CRP(mg/L).

**CONCLUSION:** Some risk factors originating from the fetal environment cannot be changed after birth, good cardiovascular health can be restored by influencing postnatal risk factors before adulthood. There were no significant differences in insulin, insulin resistance, hs-CRP or blood lipids between the marginally LBW children and controls.

KEYWORDS

Low Birth Weight, Cardiovascular Risk, Atherogenic Lipoproteins.

INTRODUCTION

The World Health Organization defines low birth weight (LBW) as birth weight less than 2500 g. Being born with a birth weight below this cut off is associated with a range of poor health outcomes, both early and later in life. Today, these children accounts for approximately 15 % of all births, ranging from 4 % in developed countries to 16 % in developing countries.<sup>1,2</sup>

Most studies of early programming focus on very LBW or extremely LBW, even though the majority of all LBW children are born only with marginally LBW.<sup>1</sup> In Sweden, this accounts for over 2200 children every year. What these children potentially are at risk of is still unclear. Some studies have shown an inverse relationship between birth weight and cardiovascular risk, suggesting that also marginally LBW would be a risk factor, although lower. However, the pathogenesis behind CVD is multifactorial, and for health care providers to be able to assess the risk of each individual, we need to know more about this common subgroup.

Elevated levels of triglycerides and LDL (or Apolipoprotein B, [ApoB]) and lowered levels of HDL (or Apolipoprotein A1, [ApoA1]) are three markers included in the "lipid triad", a concept often used when discussing metabolic risk.<sup>3</sup> These are all related to atherosclerosis and CVD, a risk that increases with prolonged exposure.<sup>4,5</sup>

The atherogenic lipoproteins (LDL, very low-density lipoprotein [VLDL], intermediate-density lipoprotein [IDL]) are more prone to penetrate the vessel wall, where they bind to proteins in the extracellular matrix and triggers macrophages and inflammation. This process is the pathophysiological process that causes endothelial damage and atherosclerosis.<sup>1</sup> Furthermore, HDL is an anti-atherogenic lipoprotein that can bind to the vessel wall and remove fat molecules from cells, thereby protecting them from excessive storage.<sup>1</sup> On every atherogenic lipoprotein, there is a protein called ApoB, while every HDL particle contains ApoA1. Therefore, measuring these proteins correlates well to the lipid profile.<sup>6</sup>

Adipocytes in overweight and obese individuals become enlarged and saturated with lipids, which leads to impaired insulin sensitivity and release of FFA in the blood. The elevated levels of FFA further on result in an increased flux of FFA to hepatocytes in the liver, as well as increased storage in both the hepatocytes as well as in myocytes in muscle tissue. The FFAs in the liver are esterified to VLDL and IDL and released into the blood stream. The raised fat storage in the hepatocytes and myocytes damage the insulin sensitivity, further progressing the insulin resistance.<sup>7</sup>

Though less studied compared to insulin resistance, children and adults born with LBW have been suggested to have an adverse lipid profile, compared to those born with NBW, a correlation accentuated with increasing age.<sup>8</sup> However, the evidence is scarce, especially from prospective studies, and systematic reviews have not yet established a consensus.<sup>1</sup>

OBJECTIVE

The objective of the present thesis was to answer the following research question:

- How does being born with LBW affect later cardiovascular risk?

MATERIALS AND METHODS

This study was hospital based comparative study.

STATISTICAL ANALYSIS:

For statistical analysis data were entered into a Microsoft excel spreadsheet and then analyzed by SPSS (version 27.0; SPSS Inc., Chicago, IL, USA) and GraphPad Prism version 5. Data had been summarized as mean and standard deviation for numerical variables and count and percentages for categorical variables. Two-sample t-tests for a difference in mean involved independent samples or unpaired samples. Paired t-tests were a form of blocking and had greater power than unpaired tests. A chi-squared test ( $\chi^2$  test) was any statistical hypothesis test wherein the sampling distribution of the test statistic is a chi-squared distribution when the null hypothesis is true. Without other qualification, 'chi-squared test' often is used as short for



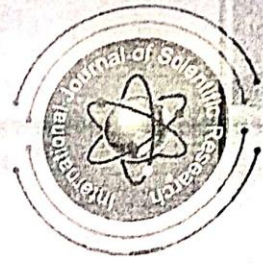


05/04/2022, 12:44

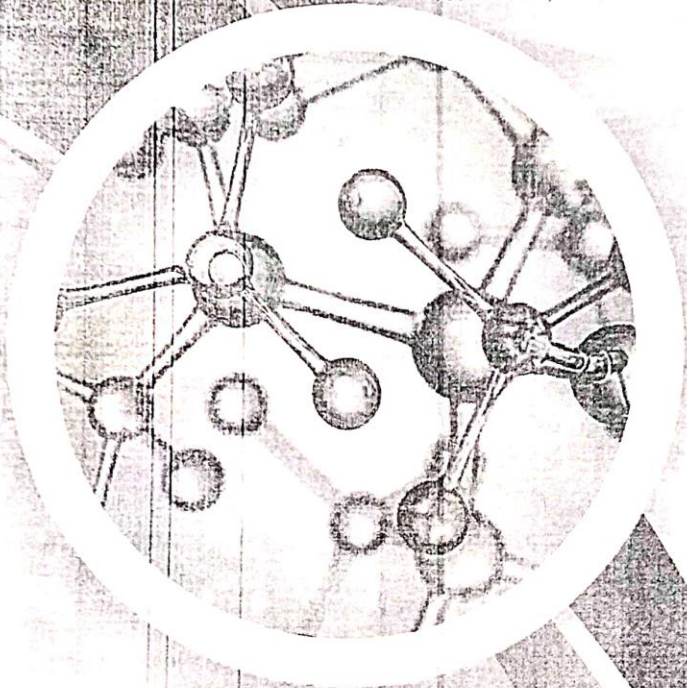
IMG\_0845.jpg

End-20/1

Print ISSN No. 2277 - 8179  
Journal DOI : 10.36106/ijsr



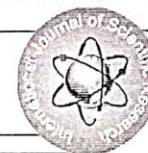
An International Journal  
A Medico Journal  
Volume-10 | Issue-11 | November-2021



# INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH

A Peer Reviewed, Referred,  
Refereed & Indexed  
International Journal

UGC Sr. No. 49217  
Impact Factor : 5.711  
₹ 500



ROLE OF LIPID AND LIPOPROTEIN IN FEMALE BREAST CANCER PATIENTS

Biochemistry

Dr. Anand Shanker Singh

Associate Professor, Department of Chemistry, Chinmaya College of Sciences.

Dr. G. Radhika

MD, HOD, Department of Biochemistry, Sri Venkateshwara medical college and hospital, Pondicherry.

Dr. Ankita Singh

Dr. Debarshi Jana

Young Scientist (DST), Institute of Post-Graduate Medical Education and Research, A.J.C. Bose Road, Kolkata-700020, West Bengal, India.

ABSTRACT

**Introduction:** The lipid profile status among breast cancer patients at initial diagnosis and during chemotherapy remains controversial. The aim of this study is to study the status of lipid and lipoprotein in female breast cancer patients at initial diagnosis and during chemotherapy.

**Methods:** We conducted a retrospective cohort study of the status of the lipid and lipoprotein in 1054 primarily diagnosed breast cancer patients and 2483 normal controls with age stratification, from July 2015 to October 2016. At the same time, the status of lipid and lipoprotein were also analyzed among 250 breast cancer patients before and after adjuvant chemotherapy.

**Results:** The incidence of dyslipidemia was significantly lower in breast cancer group (41.82%) compared to normal group (55.26%) ( $P < 0.001$ ). The levels of total cholesterol (TC), triglycerides (TG), HDL cholesterol (HDL-C), LDL cholesterol (LDL-C) among breast cancer group were significantly lower compared to normal control group ( $P < 0.05$ ). With age stratification, the levels of TC and LDL-C in breast cancer group were still significantly lower than those in control group ( $P < 0.001$ ). And the levels of TC, TG, LDL-C, apolipoprotein B were significantly higher among post-chemotherapeutic patients compared to prechemotherapeutic patients, however HDL-C and Apo-A1 levels were contrary.

**Conclusions:** Breast cancer patients have lower incidence of dyslipidemia compared to normal populations. However, the situation of dyslipidemia may become worsened after chemotherapy. Therefore, lipid monitoring and dyslipidemia prevention and treatment should be conducted for breast cancer patients at initial diagnosis and during chemotherapy.

KEYWORDS

Breast cancer, Dyslipidemia, Adjuvant chemotherapy.

INTRODUCTION

Breast cancer is the most general diagnosed cancer and the second leading cause of cancer-related death among women worldwide<sup>1</sup>. The female breast cancer mortality is down to 36% from peak rates due to early diagnosis and treatment. However, it is still crucial to investigate the relative hazardous factors and methods to improve prognosis.

An unbalanced lipid profile with high total cholesterol (TC), low-density lipoprotein-cholesterol (LDL-C), triglycerides (TG), and low high-density lipoprotein-cholesterol (HDL-C), apolipoprotein AI (Apo-AI), apolipoprotein B (Apo-B) is an established risk factor of cardiovascular diseases. LDL-C has been successfully treated by lipid-lowering therapies. Apolipoproteins are crucial for the development of HDL and LDL lipoprotein complex. Moreover, Apo-B is considered as a better indicator of cardiovascular disease (CVD) compared to LDL-C<sup>2</sup>. Apo-AI binding protein accelerates cholesterol efflux from endothelial cells and regulates angiogenesis. Plasma lipids and lipoproteins are influenced by environmental factors, including weight and diet, and are closely associated with breast cancer risk factors which suggest the role of lipids in causing breast cancer. A study suggested that higher mammographic density considered to be a strong risk factor of breast cancer<sup>3</sup>, which is associated with increased HDL-C levels and decreased LDL-C levels. Furthermore, HDL-C level is associated with several other breast cancer risk factors. Several studies have reported the association between lipids and breast cancer. However, the results are controversial. Some prospective clinical studies reported that high levels of TC and HDL-C may increase breast cancer incidence<sup>4</sup>. However, others have suggested that low TC and HDL-C levels could increase breast cancer risk<sup>5</sup>. Few researchers have studied the status of lipid in breast cancer patients before and after chemotherapy. Derya H B et al. reported that adjuvant chemotherapy may contribute to an increased risk for metabolic syndrome in breast cancer patients and these changes are more profound in pre-menopausal patients<sup>6</sup>. The aim of this study is to investigate the status of serum lipids and lipoproteins in breast cancer patients and normal controls and their changes during chemotherapy.

MATERIAL AND METHODS

Subjects

The clinical data of blood lipid status of 250 primarily diagnosed breast

cancer patients and 1200 normal women (as controls) were collected from the electronic medical records of Breast Cancer Center. Also the blood lipid status of 250 breast cancer patients was comparatively analyzed before and after chemotherapy. Key exclusion criteria included the patients with history of other malignancy and tumor recurrence and with no pathological reports.

Evaluate Parameters

This study compares the status of lipids among breast cancer patients and normal people. The status of lipid and apolipoprotein of 250 breast cancer patients were evaluated before and after chemotherapy. The biochemical parameters related to dyslipidemia TC, TG, HDL, LDL, Apo A-1, Apo-B were categorized using cut-off values as follows: TC with 5.20 mmol/L, TG 1.7mmol/L, HDL-C 0.9 mmol/L, LDL-C 3.1 mmol/L. Dyslipidemia was considered when TC > 5.2 mmol/L or TG > 1.7 mmol/L or LDL-C > 3.1 mmol/L or HDL-C < 0.9 mmol/L.

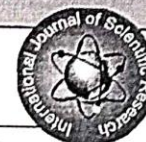
Statistical Analysis

The data were analyzed using the Statistical Package for Social Sciences (SPSS) software version 22.0. Mean (x) and standard deviation (SD) were evaluated using student t-test for the comparison between control and patient groups.  $P < 0.05$  was considered statistically significant. The incidence of dyslipidemia among both groups was compared using Chi-square test. The mean values of lipids among both groups were compared using independent sample T test. Finally, the status of blood lipids and apolipoproteins in breast cancer patients before and after chemotherapy were compared using paired-sample T test.

RESULT

No significant difference was observed in the mean age of breast cancer group ( $41.03 \pm 11.31$  years) and control group ( $51.10 \pm 11.09$  years). In our study, We observed the prevalence of preobese or obese (BMI  $\geq 25$ ) was 24.50% in breast cancer patients and 20.45% in control population, respectively.

The incidence of dyslipidemia was significantly lower in breast cancer group compared to control group ( $P < 0.001$ ). The levels of TC and LDL-C in breast cancer group were significantly lower than those in control group ( $P < 0.001$ ). With age stratification, the levels of TC and



**LIPID PROFILE ALTERATION IN RHEUMATOID ARTHRITIS PATIENTS**

**Biochemistry**

<b>Dr. Anand Shanker Singh</b>	Associate Professor, Department of Chemistry, Chinmaya College of Sciences.
<b>Dr. G. Radhika</b>	MD, MBBS, HOD, Department of Biochemistry, Sri. Venkateshwara Medical College And Hospital, Pondicherry
<b>Dr. Ankita Singh</b>	DNB, DGO, MBBS
<b>Dr. Debarshi Jana</b>	Institute of Post-graduate Medical Education And Research, A.J.C. Bose Road, Kolkata-700020, West Bengal, India

**ABSTRACT**

**INTRODUCTION:** It has been proved that rheumatoid arthritis (RA) is linked to dyslipidemia and the risk of cardiovascular complications is higher in these patients. The aim of this study was to evaluate dyslipidemia in RA patients.  
**MATERIAL AND METHODS:** In this study, RA patients were enrolled regarding the inclusion and exclusion criteria. Their demographic information and medication profiles were evaluated. Clinical assessments were performed by evaluation of disease activity score (DAS28) and visual analogue scale. Moreover, laboratory investigations of lipid profile including triglycerides (TG), total cholesterol (Chol), low-density lipoprotein (LDL), and high-density lipoprotein (HDL) were performed.  
**RESULT:** Total of 150 patients with the mean age of 53.8±15.7 years, 64.4% were diagnosed with dyslipidemia. Females in menopausal ages had a higher prevalence of dyslipidemia as well as patients with longer disease duration. Considering DAS28, 100% of the patients with high disease activity were diagnosed with dyslipidemia.  
**CONCLUSION:** According to the results, patients under treatment with prednisolone and methotrexate were more affected by dyslipidemia than those with prednisolone, methotrexate, and hydroxychloroquine. In the patients under prednisolone, methotrexate, and leflunomide treatment, the prevalence of dyslipidemia was significantly lower than those used only prednisolone and methotrexate. Altogether, it is necessary to have more clinical suspicion towards dyslipidemia and its complications in the patients with a greater number of affecting factors.

**KEYWORDS**

Rheumatoid arthritis, Dyslipidemia, Lipid profile, Cardiovascular diseases

**INTRODUCTION**

Rheumatoid arthritis (RA) is a chronic systemic disease diagnosed mostly by presenting articular manifestations. This pathology with a prevalence of 0.5- 1% in general population is more common in females<sup>1</sup>. So far, the main pathogenesis of RA is unknown, but it seems that both genetic and environmental factors are involved<sup>2</sup>. Similar to other chronic diseases, RA is accompanied by inflammation which has made the main target for therapeutic agents<sup>3</sup>. Although RA is mostly known for its particular presentations, skin, ocular, and cardiac manifestations are also expectable<sup>4</sup>.

Nowadays, cardiovascular diseases (CVD) are known as the leading cause of death worldwide<sup>5</sup>. The most common type of CVD is atherosclerosis which is a chronic inflammatory condition. Interestingly, it has been showed that both CVD and RA have similar pathways of inflammation<sup>6</sup>. Furthermore, mortality caused by CVD is more common (up to 50% higher) in RA patients compared to a normal population which makes it the most common cause of death among these patients. This increase in mortality rate is caused by the higher risk of myocardial infarction (MI) and stroke in RA population which is attributed to CVD and mainly atherosclerosis<sup>7</sup>. Furthermore, it has been shown that MI risk due to CVD in RA patients is 200% (2 folds) higher compared to age and sex-matched controls<sup>8</sup>. Taken together, it seems that CVD is a serious issue in patients diagnosed with RA since it increases the risk factors involved<sup>9</sup>. Remarkable risk factors for atherosclerosis are male gender, high serum total cholesterol (Chol), low-density lipoprotein (LDL), low serum high-density lipoprotein (HDL), aging, diabetes, high blood pressure, and smoking.

**MATERIALS AND METHODS**

**Clinical assessments**

Patients' demographic information, disease duration, drug history, and disease activity score (DAS28) were evaluated. For calculation of DAS28 score, we considered swollen and tender joints, erythrocytes sedimentation rate (ESR) and visual analogue score. In this evaluation any score ≤2.6, 2.6 < score ≤3.2, 3.2 < score ≤5.1, and <5.1 were considered as remission, low disease activity (DA), moderate DA and high DA, respectively.

**Para-clinical assessments**

Laboratory makers such as serum total Chol, triglyceride (TG), LDL and HDL were evaluated after 12- hour fasting. Normal values

considered as follows: LDL <100 mg/dl, TG <150 mg/dl, total cholesterol <200 mg/dl, and HDL >50 mg/dl. Also, both ESR and C-reactive protein (CRP) serum levels were evaluated. All the laboratory tests were done by the same laboratory expert using the same kits and methods for each parameter. All the kits were provided from Merck Chemi Co<sup>TM</sup>.

**RESULTS AND DISCUSSION**

According to the literature, patients with RA are more susceptible to dyslipidemia and atherosclerosis (and its complications such as CVD) due to the impaired lipid profile in comparison to the normal population<sup>10</sup>. Thus, it is very important to investigate any possible mechanism that may affect lipid profile in them. In this study, we intended to assess dyslipidemia in RA patients by categorizing them into the different groups according to the different variables such as age, sex, disease duration, and types of medications consumed. It is important to consider all the variables such as age in this study since it has been proved to significantly increase CVD<sup>10</sup>. As the results showed, the patients' mean age in the current study was 54.9±16.8 which was the same as the other studies<sup>11,12</sup>. Also, 87.33% and 12.66% of patients were female and male, respectively. This clearly affirms that RA is more common in women than men as expected. Moreover, according to the epidemiological investigations, females, especially those in menopausal status, are more susceptible to impaired lipid profile which strongly increases the risk of atherosclerotic events. In this study, it was shown that 92% and 100% of females with the age ranges of 56-65 and 66-75, respectively (menopausal ages) were diagnosed with dyslipidemia. In a general aspect, the prevalence of dyslipidemia in our patients was 65.3% which was similar to Nisar *et al.*'s study<sup>13</sup>. Also, the serum levels of HDL, LDL, TG, and total cholesterol almost were similar to another study by Vijaykumar *et al.*<sup>14</sup>. The cause of changes in lipid profile is still unclear, but there are some hypotheses proposed to describe this phenomenon. It seems that different polymorphisms such as REL (c-Rel) polymorphism have been shown to affect LDL levels. Also, interleukin 6 (IL-6) which is an inflammatory cytokine is able to induce lipoproteins abnormalities. This interleukin has been shown higher in RA patients with lower HDL levels.

In older age groups, the prevalence of dyslipidemia has been increased.





ASSOCIATION OF LIPID PROFILE AMONG THE HYPERTENSIVE IN COMPARISON TO NORMOTENSIVE PATIENTS IN OUR INSTITUTION

Biochemistry

**Dr. Anand Shanker Singh** Associate professor, Department of Chemistry, sciences College of Chinmaya.

**Dr. G. Radhika** MD, MBBS, HOD, Department of Biochemistry, Sri. Venkateshwara Medical College And Hospital, Pondicherry.

**Dr. Debarshi Jana** Institute Of Post-graduate Medical Education And Research, A.J.C. Bose Road, Kolkata-700020, West Bengal, India.

ABSTRACT

**Introduction:** Hypertension and dyslipidemia are associated with oxidative stress and are major causes of cardiovascular disease amounting to 30% of global death rate. It is widely accepted that cardiovascular disease is associated with hypertension and increased blood levels of low-density lipoprotein (LDL), total cholesterol (TC), and triglycerides. In contrast, a low level of high density lipoprotein (HDL) is a risk factor for mortality from cardiovascular disease. Hypertension is a major public health problem in developed and developing countries.

**Methods:** This study was a cross sectional study in which 159 diagnosed hypertensive patient and 75 with normal blood pressure (normotensive) were enrolled. These patients sought a through health check up including blood pressure assessment between May 2020 to April 2021

**Results:** The mean of Systolic blood pressure and Diastolic blood pressure of hypertensive were higher than normotensive ( $p < 0.001$ ). The serum levels of total cholesterol, triglyceride and LDL-C in hypertensive subject were higher than normotensive and statistically significant ( $p < 0.001$ ). Serum HDL-C was significantly lower ( $p < 0.001$ ) in hypertensive patients than in normotensive.

**Conclusion:** Hypertensive patients have been found to have close association with dyslipidemia. Hypertensive patients need measurement of blood pressure and lipid profile at regular interval to prevent heart diseases and stroke.

KEYWORDS

Hypertension, Lipid profile, Total cholesterol, Triglyceride, LDL-C, HDL-C.

INTRODUCTION:

Hypertension is a major public health problem in developed and developing countries. Hypertension and dyslipidemia are associated with oxidative stress and are major causes of cardiovascular disease amounting to 30% of global death rate.<sup>1</sup> It is widely accepted that cardiovascular disease is associated with hypertension and increased blood levels of low-density lipoprotein (LDL), total cholesterol (TC), and triglycerides. In contrast, a low level of high density lipoprotein (HDL) is a risk factor for mortality from cardiovascular disease.<sup>2</sup> Epidemiological studies have established a strong association between hypertension and coronary artery disease (CAD). Hypertension is a major independent risk factor for the development of CAD, stroke and renal failure. Non-communicable disease risk factor survey Bangladesh 2010 studies have estimated that among adults, the prevalence to range from 16% to 20%.<sup>3</sup> Nutrition, health and demographic survey of Bangladesh 2011 have estimated that among adults, the prevalence of hypertension was 34%. Urban subjects had a higher prevalence of hypertension 37% while for rural prevalence was significantly lower at 33% ( $p < 0.001$ ).<sup>4</sup>

The Seventh report of the Joint National Committee on Prevention, Detection, Evaluation and Treatment of High Blood Pressure (JNC-7) classifies BP as normal (Systolic BP < 120mmHg and Diastolic BP < 80mmHg). Pre hypertension (Systolic BP 120-139mmHg and Diastolic BP 80-89mmHg), Hypertension stage 1 (Systolic BP 140-159mmHg and Diastolic BP 90-99mmHg and hypertension stage 2 (Systolic BP 160mmHg and Diastolic BP 100mmHg) respectively.<sup>5</sup>

Atherosclerotic diseases are a leading cause of disability and death worldwide and two third of these are associated with dyslipidemia. Worldwide, there is a wide variation in mean population lipid profiles levels. Increased serum total cholesterol (TC), triglyceride (TG), low density lipoprotein (LDL-c) level and decreased high density lipoprotein (HDL-c) are associated major risk factors for cardiovascular disease (CVD). Dyslipidemia comprising altered ratio of high to total cholesterol level and isolated evaluation of the low density lipoprotein or triglycerides is usually associated with rising blood pressure levels. There are strong and relations between total LDL cholesterol concentrations and coronary heart disease risk. In Bangladesh consumption of saturated fat and red meat is injurious to health and a known risk factor for CVD especially hypertension.<sup>6</sup>

METHODS:

This study was a cross sectional study in which 159 diagnosed hypertensive patient and 75 with normal blood pressure

(normotensive) were enrolled. These patients sought a through health check up including blood pressure assessment between May 2020 to April 2021. All the subjects were residents of the surrounding areas and aged 30-60 years. Patients with features of any cardiac or renal complication and major medical problem were excluded. For statistical analysis data were entered into a Microsoft excel spreadsheet and then analyzed by SPSS 24.0 and GraphPad Prism version 5. A chi-squared test ( $\chi^2$  test) was any statistical hypothesis test wherein the sampling distribution of the test statistic is a chi-squared distribution when the null hypothesis is true. Without other qualification, 'chi-squared test' often is used as short for Pearson's chi-squared test. Unpaired proportions were compared by Chi-square test or Fischer's exact test, as appropriate.  $p$ -value  $\leq 0.05$  was considered for statistically significant.

Table - Distribution Of Age: Hypertensive And Normotensive Patients.

	Hypertensive = 159		Normotensive = 75	
	Male (n=88)	Female (n=71)	Male (n=40)	Female (n=35)
Age groups (years)				
<=30	12 (80)	3 (20)	16 (59)	11 (41)
31 - 40	18 (51)	17 (49)	9 (43)	12 (57)
41 - 50	24 (53)	21 (47)	7 (54)	6 (46)
51 - 60	21 (49)	22 (51)	6 (75)	2 (25)
61 - 70	9 (75)	3 (25)	2 (33)	4 (67)
>=71	4 (44)	5 (56)	0(0)	0(0)

Table 2: Serum Lipid Profile Of Hypertensive And Normotensive Patients.

Indicator s(mg/dl)	Hypertensive = 159		Normotensive = 75		P-Value
	Mean (SE)	CI	Mean (SE)	CI	
Total Cholesterol	248.31 (2.16)	211.01 - 242.5	177.01 (4.26)	183.62 - 191.51	0.001
Triglyceride	179.34 (1.84)	169.51 - 181.1	151.47 (2.83)	136.72 - 143.13	0.001
HDL-cholesterol	42.23 (1.09)	39.23 - 46.36	43.38 (1.82)	45.65 - 48.91	0.001
LDL - cholesterol	139.22 (1.65)	137.13 - 165.3	120.32 (2.33)	106.63 - 113.97	0.001



EVALUATION OF SERUM LIPID PROFILE IN PATIENTS OF CORONARY ARTERY DISEASE

**Dr. Anand shanker Singh** Associate professor in Chinmaya College of sciences. Chemistry Department.

**Dr. Ankita Singh** DNB, DGO , MBBS

**Dr. R. Praveen kumar** MD ( Paediatrics) , MBBS, Assistant professor, Department of paediatric, Rajah Muthiah medical college.

**Dr. Debarshi Jana\*** Institute Of Post-graduate Medical Education And Research, A.j.c. Bose Road, Kolkata-700020, West Bengal, India. \*Corresponding Author

**ABSTRACT** Background: Coronary heart disease (CHD) or cardiovascular diseases are recognized to be one of the most important reasons of morbidity and mortality and imposes tremendously heavy socioeconomic burden worldwide. There are varieties of risk factors in the literature which increases the incidence of CHD such as hyperlipidemia. By the year 2020, World Health Organization (WHO) is predicting more than 11.1 million deaths from CHD. Coronary heart disease occurs when cholesterol accumulates on the artery walls, creating plaques. Reduced blood flow occurs when one or more of these arteries become partially or completely blocked. The four primary coronary arteries are located on the surface of the heart are: right, left main coronary artery, left circumflex artery and left anterior descending artery.

**Material and Methods:** The present study was done on 100 patients with acute or severe coronary heart diseases. Serum levels of total cholesterol, HDL cholesterol, LDL cholesterol, and triglycerides were examined by using biochemical kits.

**Results:** The Total Serum Cholesterol to High density lipoprotein-Cholesterol and Low density lipoprotein-Cholesterol ratios also were significantly higher in cases than in controls, whereas the rise in Triglycerides to High Density Lipoprotein-Cholesterol ratio was not found to be significant.

**Conclusion:** It was found that the total cholesterol, HDL cholesterol, LDL cholesterol and triglycerides concentrations were significantly higher in coronary heart disease patients.

**KEYWORDS :** Coronary Heart Diseases, Lipid Profile, Triglycerides, Cholesterol

**INTRODUCTION**

Coronary heart disease (CHD) or cardiovascular diseases are recognized to be one of the most important reasons of morbidity and mortality and imposes tremendously heavy socioeconomic burden worldwide. There are varieties of risk factors in the literature which increases the incidence of CHD such as hyperlipidemia. By the year 2020, World Health Organization (WHO) is predicting more than 11.1 million deaths from CHD. It is projected that the annual number of million deaths due to cardiovascular disease will increase from 17.5 million in 2012 to 25 million in 2030. Approximately out of 14 million Indians affected with coronary heart disease (CHD), 1.5 million develop Acute Myocardial Infarction (AMI), and 500,000 of these individuals die annually. This increase is due to industrialization, urbanization and related lifestyle changes which is called epidemiologic transition.<sup>12</sup> Coronary heart disease occurs when cholesterol accumulates on the artery walls, creating plaques. Reduced blood flow occurs when one or more of these arteries become partially or completely blocked. The four primary coronary arteries are located on the surface of the heart are: right, left main coronary artery, left circumflex artery and left anterior descending artery.<sup>1</sup>

CHDs are the most predictable cause of sudden death. For many years, CHD prevalence was believed to be relatively low in developed countries. Recent studies have indicated a remarkably high proportion of mild to severe CHD in a number of patients. CHD is more prevalent in men than in women. However its prevalence interrelates with age. It is about 0.7% in 18 to 45 year olds. Whereas 13.3% in the 55 years and onwards. According to the Global Burden of Disease study estimate of age-standardized CVD death rate of 272 per 1,00,000 population in India is higher than the global average of 235 per 100,000 population.<sup>4,5</sup>

According to the guidelines of the American Heart Association, the following values are prescribed for the above-mentioned risk factors for cardiovascular disease: total cholesterol: <200 mg/dL; triglycerides: <200 mg/dL; HDL: >40 mg/dL; and LDL: <130 mg/dL.<sup>6</sup>

The term cardiovascular diseases are a group of disorders of the heart or blood vessels, and include mainly ischemic heart disease, rheumatic heart disease and cerebrovascular disease or strokes. The lipid profile is a group of tests that are often done together to identify the risk of

heart disease. These tests are good indicators of whether someone is likely to have a heart attack or stroke caused by the blockage of blood vessels or hardening of the arteries. The lipid profile usually includes: high levels of cholesterol in blood circulation are strongly associated with progression of heart disease. For a person of about 68 kg typical total blood cholesterol synthesis is about 1g (1000mg) per day.<sup>7,8</sup>

CHD requires an integrated approach to the reduction of its risk factors. Identification and management of risk factors are essential for preventing CHD in asymptomatic individuals mainly over 40 years of age as primary prevention, and for preventing recurrent events in patients with established disease as secondary prevention. Risk factors should be conceived as prevention or treatment of the ath-erosclerotic disease process itself. CHD risk factors are modifiable and unmodifiable; the presence of unmodifiable risk factors may necessitate more intense management of modifiable risk factors.<sup>9</sup>

In the last twenty years, considerable advances have been achieved in the determination and improvement of CHD risk factors including diabetes and hypertension. Lipids and lipoproteins have become increasingly important in clinical practice, primarily because of their association with CHD, in case of their abnormalities known as dyslipidemia, and became the major risk factor for the development of this disease, according to epidemiological studies, especially in affluent countries where fat consumption is high.<sup>10</sup>

**MATERIAL AND METHODS**

The present study was conducted in our institution from June 2020 to December 2021. The sample size was calculated by using G-power and was obtained to be 120 subjects. Out of which 90 CHD patients were selected with history of angina or surviving myocardial infarction with or without DM and HTN, admitted and diagnosed in coronary care unit. CHD cases with liver impairment, renal disease or thyroid disease were not included in the study. 90 clinically healthy subjects aged 41 to 70 years who served as population-based controls were chosen.

Blood sample was collected from the cubital vein of the arm of each patient by a 5cc disposable syringe, which was transferred quickly to a heparinized collecting tube and finally preserved into an ice pot. All these tubes were then transferred to a test tube, were allowed to stand



## Review Article

## Vitamin D nemesis of COVID-19

Akshaya Sridhar<sup>1</sup>, Monisha Mohan<sup>2</sup>, Kalai Selvi Rajendiran<sup>3</sup>, Priyanka Sekar<sup>4</sup>, Anand Shanker Singh<sup>5</sup>, Selvaraj Nambiar<sup>6</sup>, Ananda Vayaravel Cassinadane<sup>7,\*</sup><sup>1</sup>Sri Ramachandra Institute of Higher Education and Research, Chennai, Tamil Nadu, India<sup>2</sup>Saveetha Medical College and Hospital, Chennai, Tamil Nadu, India<sup>3</sup>Dept. of Biochemistry, Panimalar Medical College Hospital & Research Institute, Chennai, Tamil Nadu, India<sup>4</sup>Sri Venkateshwaraa Medical College Hospital and Research Centre, Pondicherry, India<sup>5</sup>Chinnaya Degree College, Haridwar, Uttarakhand, India<sup>6</sup>University Hospitals of Leicester, United Kingdom<sup>7</sup>Sri Venkateshwaraa College of Paramedical Sciences, Pondicherry, India

## ARTICLE INFO

## Article history:

Received 20-08-2021

Accepted 07-09-2021

Available online 08-10-2021

## Keywords:

Vitamin D

Covid-19

Cytokine storm

Interleukin-6

Immunomodulation

## ABSTRACT

The surge in the spread of the corona virus disease (COVID-19) pandemic alerted us to opt for the preventive medicine, as prevention is always better than cure. Apart from wearing mask, frequent hand washing and social distancing, strengthening our immune response plays a pivotal role in preventing infections. Vitamin D not only aids in calcium and phosphate homeostasis but also acts as an immunomodulator; the deficiency of which is linked with various respiratory and systemic infections. Hence we took up this review to study the effect of vitamin D in corona illness. Vitamin D exerts the expression of pro-inflammatory cytokines, hinders zinc metabolism, lowers Interleukin 6 levels and thereby inhibits cytokine storm in covid patients. Studies have proved that the covid patients have vitamin D deficiency and its supplementation improves the disease severity as well as the length of hospital stay. To conclude, Vitamin D supplementation can protect as well as halt the progression of corona virus disease. Further trials are needed to set the therapeutic levels in various stages of corona illness.

This is an Open Access (OA) journal, and articles are distributed under the terms of the Creative Commons Attribution-NonCommercial-Share Alike 4.0 License, which allows others to remix, tweak, and build upon the work non-commercially, as long as appropriate credit is given and the new creations are licensed under the identical terms.

For reprints contact: [reprint@ipinnovative.com](mailto:reprint@ipinnovative.com)

## 1. Introduction

Vitamin D, a fat soluble prohormone required for calcium and phosphate metabolism plays a pivotal role in maintaining bone and muscle health.<sup>1</sup> It is also involved in cellular proliferation and differentiation,<sup>2</sup> regulating gene expression and signal transduction. Vitamin D, by binding with its receptor secures against endogenous and exogenous stresses and possess non calcaemic role like immunomodulation in regulating innate immunity and autoimmune response.<sup>3</sup>

\* Corresponding author.

E-mail address: [anvayaravel@gmail.com](mailto:anvayaravel@gmail.com) (A. V. Cassinadane).

The outbreak of COVID-19 has set in a global pandemic - a health crisis situation; thereby making it a mandate requisite to prevent the public from the jaws of corona virus infection and progression. The relationship between vitamin D deficiency and respiratory health was well-established.<sup>4</sup> Vitamin D levels are lowered in acute or critical illness which sets in inflammatory episode. The corona virus enters the host cells through binding with angiotensin converting enzyme (ACE2) receptors in the respiratory tract.<sup>5</sup> The virus can be eliminated at an earlier stage of infection by improving the host immune response. However strategies need to be developed to improve immune responses; one of them is to utilize a potential immunomodulator to improve



Encl-2,

9:22



**IJAR**  
**INDIAN JOURNAL OF APPLIED RESEARCH**  
 PUBLISHED NO 2215 - 505X  
 IF OF LIAR: 6.03 (SJIF)  
 PEER REVIEW, INTERNATIONAL JOURNAL  
 JOURNAL DOI: 10.3010/IJAR

Thursday, Mar 31<sup>st</sup>, 2022  
 9:22:52 PM  
 editor@ijar.in  
 +91 98 86 00 3436  
 Publishes on 1<sup>st</sup> Day Of The Month

HOME ABOUT US EDITORIAL BOARD ADVISORY BOARD EDITORS & ASSOCIATES PRESS RELEASES PUBLICATIONS CONTACT US

**MEDICAL COUNCIL OF INDIA (MCI) VAID PUBLICATION AS PER FEBRUARY 2020 OAZETTE**

**I - Indian  
J - Journal of  
A - Applied  
R - Research**

Upload your Article  
 Author Guidelines  
 Download

JOURNAL PROMOTED BY INDIAN SOCIETY FOR HEALTH

36572  
 9855  
 26.94

BOOK PUBLICATION SPECIAL ISSUE CURRENT ISSUE PAGE SEARCH SUBSCRIPTION FORM PEER REVIEW PROCESS LATEST JOURNALS

**IJAR - Indian Journal of Applied Research**

IJAR - Indian Journal of Applied Research is a double reviewed monthly print journal that accepts research works from scholars, academicians, professors, doctores, lecturers, and experts in their respective expertise of studies. Work after publication will be available on the website facilitated based on issues of the month and its publication date. Moreover, the Journal serves the research world since October, 2011.

The Journal is wide and available for diverse intellectual and educational pursuit from all corners of the society to enrich the learning experience of the group readers.

The Periphery of the Subject areas includes:

Accounting	Business	Education	Healthcare	Information Technology
Law	Management	Marketing	Mathematics	Medical Research
Physics	Psychology	Science	Social Sciences	Sports
Statistics	Teaching	Technology	Travel	Writing

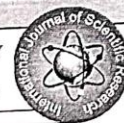
UGC CARE JOURNAL APPROVAL STATUS  
 QUALITY APPROVED JOURNAL - BRAZIL - CETS 1000  
 100% NO PLAGIARISM  
 JOURNAL TEMPLATES  
 LATEST NEWS  
 READ MORE



**ORIGINAL RESEARCH PAPER**

**INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH**

**A STUDY ON ACTIVATION OF THE CARBON CONCENTRATING MECHANISM BY CARBON DI-OXIDE DEPRIVATION OVERLAPS WITH MASSIVE TRANSCRIPTIONAL REARRANGEMENT IN CHLAMYDOMONAS REINHARDTII**



**Biochemistry**

**Dr. Anand Shanker Singh** Associate Professor, Department Of Chemistry, Chinmaya Degree College, Bhel, Haridwar  
**Dr. G. Radhika** MBBS, MD ( Biochemistry ), HOD , Department Of Biochemistry, Sri .venkateshwara Medical College And Hospital, Pondicherry  
**Dr. Ankita Singh\*** DNB, DGO, MBBS \*Corresponding Author  
**Dr. Debarshi Jana** Young Scientist, IPGMER And SSKM Hospital, Kolkata, WB.

**ABSTRACT**

A CO<sub>2</sub>-concentrating mechanism (CCM) is essential for the growth of most eukaryotic algae under ambient (392 ppm) and very low (<100 ppm) CO<sub>2</sub> concentrations. In this study, we used replicated deep mRNA sequencing and regulatory network reconstruction to capture a remarkable scope of changes in gene expression that occurs when *Chlamydomonas reinhardtii* cells are shifted from high to very low levels of CO<sub>2</sub> (≤100 ppm). CCM induction 30 to 180 min post-CO<sub>2</sub> deprivation coincides with statistically significant changes in the expression of an astonishing 38% (5884) of the 15,501 nonoverlapping *C. reinhardtii* genes. Of these genes, 1088 genes were induced and 3828 genes were downregulated by a log<sub>2</sub> factor of 2. The latter indicate a global reduction in photosynthesis, protein synthesis, and energy-related biochemical pathways. The magnitude of transcriptional rearrangement and its major patterns are robust as analyzed by three different statistical methods. De novo DNA motif discovery revealed new putative binding sites for Myeloid oncogene family transcription factors potentially involved in activating low CO<sub>2</sub>-induced genes. The (CA)<sub>n</sub> repeat (9 ≤ n ≤ 25) is present in 29% of upregulated genes but almost absent from promoters of downregulated genes. These discoveries open many avenues for new research.

**KEYWORDS**

Carbon Concentrating Mechanism, *Chlamydomonas reinhardtii*, mRNA.

**INTRODUCTION**

In nature, *Chlamydomonas reinhardtii* and other eukaryotic algae depend on a CO<sub>2</sub>-concentrating mechanism (CCM) to supply sufficient inorganic carbon (Ci; CO<sub>2</sub> or bicarbonate) for photosynthesis-fueled cell growth and proliferation. Mutant cells lacking key components of the CCM molecular machinery or its regulatory system do not grow or grow poorly unless supplied with high concentrations of CO<sub>2</sub> (e.g., >10,000 ppm) that are well above the ambient level of ~392 ppm.<sup>1</sup> Because the diffusion rate of CO<sub>2</sub> in aqueous environments is ~10,000 times slower than in air, most natural populations of microalgae exist in CO<sub>2</sub>-limited conditions. This is especially true for dense algal populations growing under abundant sunlight. Under such conditions, CO<sub>2</sub> concentrations can become very low (<100 ppm) and cells induce the CCM to maximal levels. CO<sub>2</sub> starvation induces the transcription of numerous genes encoding proteins closely associated with the CCM and its activities.<sup>2</sup> Indeed, *C. reinhardtii* and most other eukaryotic algae have developed a finely tuned regulatory system that suppresses expression of CCM-related genes under conditions of replete CO<sub>2</sub> (i.e., >0.1% CO<sub>2</sub>) and activates expression of these genes when CO<sub>2</sub> becomes limiting.<sup>3</sup> Previous studies using RNA gel blot analyses and microarray analyses have revealed a number of CCM-associated genes and other CO<sub>2</sub>-responsive genes whose transcription is tied to the physiological changes that accompany cell acclimation to CO<sub>2</sub> stress conditions.<sup>4</sup>

Here, we report an extensive global analysis of the massive transcriptional changes evoked by the deprivation of Ci in *C. reinhardtii*. We measured these transcriptional events using replicated deep RNA sequencing (RNA-Seq) on the Illumina platform. The highly reproducible RNA-Seq experiments not only confirm earlier observations based on array analyses quoted above but also extend the list of differentially expressed genes from a few hundred to over 4000.

We report the discovery of an extensive system of head-to-head (HTH; also called divergent) gene pairs, many of them sharing bidirectional or convergent promoters. HTH conformation and bidirectional or shared promoters frequently perform the highly accurate coregulation of gene pairs encoding subunits of the same protein complex or two proteins of similar or related functions. Here, we focus on those HTH, similar or related, gene pairs that are most relevant to the CCM. Advanced computational techniques also have allowed an extensive evaluation of potential regulatory elements in promoter regions in CO<sub>2</sub>-responsive genes and the discovery of new elements shared by several of the most highly stimulated CO<sub>2</sub>-responsive genes. We also report a previously unrecognized pattern of expression for many genes that suggests a significant, but transient, decrease in gene transcription immediately after a shift to very low CO<sub>2</sub> conditions (ASVLCO<sub>2</sub>).

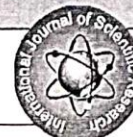
Finally, we employ a vastly expanded pool of transcriptomic data to strengthen earlier observations of metabolic and physiological changes that occur when CO<sub>2</sub> becomes limiting in the environment, including significant decreases in transcripts encoding proteins involved in photosynthesis, cytoplasmic, chloroplast, and mitochondrial protein synthesis, energy use, protein transport, and other Gene Ontology (GO) categories.

**METHODS AND MATERIALS**  
**CI Deprivation**

*Chlamydomonas reinhardtii* wild-type strain CC124 was used for analysis. Briefly, cells were grown in 2 liters of Tris Phosphate medium at 25°C and 3% CO<sub>2</sub> to a density of 1 X 10<sup>6</sup> cells/mL before being transferred to a 3-liter autoclavable glass bioreactor (Applikon Biotechnology) that was connected with EZ control for analysis of temperature, pH, and dissolved oxygen.<sup>5</sup> The bioreactor was illuminated with a light intensity of 200 μmol photons m<sup>-2</sup> s<sup>-1</sup>, and an input gas containing 5% CO<sub>2</sub> was introduced. Algal cells were allowed to equilibrate with the new environment for 1 h. Following a sampling of the culture, the input gas for the bioreactor was shifted to 100 ppm CO<sub>2</sub>, which was monitored in the culture using two CO<sub>2</sub> transmitters (Vaisala; models GMT221 and GMT222). Samples were taken at 15, 30, 60, and 180 min following the shift to 100 ppm CO<sub>2</sub>. During the experiment, pH was maintained at 7.2 using 3 M KOH.

**Preliminary Analysis of RNA Samples**

To confirm induction of the carbon-concentrating mechanism, preliminary analysis of RNA samples was performed using qRT-PCR. RNA samples were prepared for analysis using the Plexor Two-Step qRT-PCR system (Promega). qRT-PCR analysis was performed using a 7500 Real-Time PCR System (Life Technologies). The genes LCIA (AB168092), LCIB (XM\_001698292), and mitochondrial carbonic anhydrase (CAH4, XM\_001695951) were chosen for analysis as they have been observed to increase in expression during carbon deprivation.<sup>19</sup> CAH2 (X54488) was also selected as a control gene reported as displaying a moderate decrease in expression in response to carbon deprivation. CIA5/CCM1 (AF317732) was used as a positive control as it shows constitutive expression during carbon deprivation. Fluorescently labeled primer pairs were designed for each of the aforementioned genes. Quantitative PCR analysis was performed using a 7500 Real-Time PCR System by measuring the threshold cycle (Ct) of each gene. Using the Ct values of CIA5/CCM1 for each RNA sample as a baseline control, the change in Ct for each gene could be used to calculate the fold change response of each gene throughout the time course.



A STUDY ON CLASSIFICATION OF INHIBITORS OF FATTY ACID TRANSPORT PROTEIN-2 IN CELL

Biochemistry

**Dr. Anand Shanker Singh** Associate Professor, Department Of Chemistry, Chinmaya Degree College, Bhel , Haridwar.

**Dr . G . Radhika** MBBS, MD ( Biochemistry ), HOD , Department Of Biochemistry, Sri .venkateshwara Medical College And Hospital , Pondicherry.

**Dr . R . Praveen Kumar\*** MD ( Paediatrics ), MBBS, Assistant Professor, department Of Paediatric, Rajah Muthiah Medical College. \*Corresponding Author

**Dr. Debarshi Jana** Young Scientist, IPGMER And SSKM Hospital, Kolkata, WB.

ABSTRACT

Inhibition of uptake of fatty acids in non-adipose tissues seems an attractive mechanism for treatment of lipotoxicity, dyslipidemia and other elements related to metabolic syndrome and obesity. Fatty acid transport proteins (FATPs) are bifunctional proteins involved in the uptake and activation of fatty acids by esterification with coenzyme A. To date, only inhibitors specific to FATP1 and FATP4 have been identified. Here we characterize a FATP2-specific fatty acid uptake inhibitor, CB5. Identified in a high throughput screening in yeast transformed with human FATP2, CB5 is effective in inhibiting the uptake of fatty acid at low micro-molar ranges in cell lines that are models for intestines, liver, muscle, pancreas and adipose tissue with varying potencies.

Inhibition was also specific for long and very-long chain fatty acids and not for medium chain fatty acids, which are transported by diffusion. Finally, CB5 was effective in protecting the cell lines that are models for liver and pancreas and primary liver cells from lipotoxic effects of saturated fatty acid, palmitic acid. High throughput screening also identified clozapine and chlorpromazine, atypical antipsychotics drugs, as inhibitors of FATP2-mediated fatty acid uptake in yeast system. However, atypical antipsychotics were ineffective in inhibiting the uptake of FA-analog C1-BODIPY-C12 in HepG2 cells. They were also ineffective in protecting HepG2 cells from the lipotoxic effects generated by saturated fatty acid compared to CB5 that exhibited protection to the cells, demonstrating that they are not effective inhibitors of fatty acid transport compared with CB5.

KEYWORDS

Fatty acid transport proteins, Dyslipidemi, Atypical antipsychotics drugs.

INTRODUCTION

Fatty Acid in diseased states

The rising prevalence of obesity and related disorders is an increasing global threat predicting a decrease in the life expectancy of future generations'. According to 2011-2012 data, more than one-third (34.9%) of US adults and 17% of children and adolescents (between 2-19 years) were obese. Since 1980, obesity among children has tripled in United States'. A major part of the risk is the increasing prevalence of the pathogenic events that follow obesity; which includes, but is not restricted to, insulin resistance (IR), metabolic syndrome (MS), type II diabetes mellitus (T2DM), nonalcoholic fatty liver disease (NAFLD) and cardiovascular diseases (CVD). The etiology of these diseases is still poorly understood as they continue to pose burden on the health management sectors in developed countries.

The role of transport proteins as regulators of lipid metabolism is of great interest specially in understanding the pathophysiology of various diseases such as dyslipidemia, lipotoxicity, cardiomyopathy and so on. However, very few studies have targeted the protein-mediated uptake of fatty acids as therapeutic interventions to reduce the disease conditions. FATP1 and FATP4 inhibitors have been reported, however, these inhibitors were screened on the basis of inhibition of long-chain acyl CoA synthetase activity rather than the transport activity and were not effective in animals'. In order to understand the linkage and role of FATPs in the excessive accumulation of fat in various diseased states, Sandoval et al., 2010' utilized a high-throughput screening assay in yeast transformed with human FATP2 to screen library for inhibitors of fatty acid uptake. This led to the identification of 2-benzyl-3-(4-chlorophenyl)-5-(4-nitrophenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one, also known as CB5 or Grassofermata.

CB5 was shown to be capable of inhibiting the uptake of FA-analog C1-BODIPY-C12 using a live cell based assay in yeast as well as mammalian cell lines that are models for liver, small intestines and adipose tissue (HepG2, Caco-2 cells and 3T3-L1 adipocytes, respectively). In another HTS of 2000 compounds', compounds structurally related to phenothiazine group were identified as inhibitors of FA uptake. This included the atypical antipsychotics, chlorpromazine and clozapine as hits. Both compounds at 80µM concentration when tested in yeast cells caused intermediate levels of inhibition of FA-analog C1-BODIPY-C12'. Thus it was predicted that

dyslipidemia caused by these antipsychotics is due the mechanism involving the inhibition of FA uptake using FATPs.

In the current study, we have further characterized CB5 for its activity as an inhibitor in various cell lines that are models for pancreatic islets, muscles and human adipocytes. CB5 inhibition was specific for long and very long chain fatty acid and was protective against lipotoxicity caused by saturated fatty acids. We also compared the inhibition activity of AAP drugs to CB5 and show that their mechanism of action in causing dyslipidemia is different from inhibition of FA uptake and thus do not involve FATPs.

MATERIALS AND METHODS:

Materials:

CB5 (2-benzyl-3-(4-chlorophenyl)-5-(4-nitrophenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one) and its analogs were purchased from ChemBridge Corporation (San Diego, CA, USA). Fluorescent fatty acid analog C1-BODIPY-C12 (4,4-Difluoro-5-Methyl-4-Bora-3a,4a-Diaza-s-Indacene-3-Dodecanoic Acid) (Catalogue no. D-3283), BODIPY-FL-C5 (4,4-Difluoro-5,7-Dimethyl-4-Bora-3a,4a-Diaza-s-Indacene-3-Pentanoic Acid) and BODIPY-FL-C16 (4,4-Difluoro-5,7-Dimethyl-4-Bora-3a,4a-Diaza-s-Indacene-3-Hexadecanoic Acid) were purchased from Molecular Probes/Invitrogen (Eugene, OR, USA). First-generation antipsychotic drug Haloperidol (H1512), second-generation drugs Clozapine (C6305) and Risperidone (R3030); 13C labeled oleic acid (catalog no. 490431) and tyloxapol (catalog no. T0307) were purchased from Sigma Aldrich. Olanzapine (O253750) was purchased from Toronto Research Chemicals (Ontario, Canada) and Quetiapine purchased from Key Organics/BIONET (External ID: KS-1099). Pancreatic lipase inhibitor, Orlistat, was a gift from GlaxoSmithKline (60mg per capsule). Palmitic-acid (PA) (P-0500) was purchased from Sigma and 50mM stock prepared in 100% ethanol. Fatty acid-free and nuclease, protease-free Bovine Serum Albumin (BSA) was purchased from CalBiochem (Cat. No. 126609). Verapamil, 0.1M PBS (pH 7.4), 10mM NADPH (freshly prepared in PBS), acetonitrile, human and mouse (Balb-C) microsomes (as used by Kansas University).

METHODS

For each cell type, fatty acid transport kinetics were evaluated according to the method described in Arias-Barral, et al.'. A range of

## INVESTIGATION OF COSMIC RAY INTENSITY VARIATION DURING HIGHLY DISTURBED GEOMAGNETIC CONDITIONS

Pradosh Kumar Sharma

Department of Physics

Chinmaya PG College, Shivalik Nagar, BHEL, Haridwar, U.K.

Subhash C. Kaushik

Department of Physics

Govt. P. G. Autonomous College, Datia, (M.P.)

### ABSTRACT -

Abstract: Shocks driven by energetic coronal mass ejections (CME's) and other interplanetary (IP) transients are mainly responsible for initiating large and intense geomagnetic storms. Observational results indicate that galactic cosmic rays (CR) coming from deep surface interact with these abnormal solar and IP conditions and suffer modulation effects. The current solar cycle has provided a long list of these highly energetic events influencing the Earth's geomagnetic field up to a great extent. We have selected such intense geo-effective CME's occurred during recent solar cycle and studied their possible influence on cosmic ray intensity as well as on Earth's geomagnetic field using the hourly values of IMF data obtained from the NSSD Center. Solar wind data obtained from various satellites are used in the studies which are available during the selected events period. The super neutron monitor data obtained from Kiel, Oulu and Izmiran stations, well distributed over different latitudes has been used in the present study. Furthermore we have plotted the energy spectra of these events too. It is found that AP and AE indices show rise before the forward turnings of IMF and both the Dst index and cosmic ray intensity show a classic decrease. The analysis further indicates the significant role of the magnitudes of Bz component of IMF substantiating the earlier results. It is further inferred that the magnitude of these responses depends on BZ component of IMF being well correlated with solar maximum and minimum periods. Transient decrease in cosmic ray intensity with slow recovery is observed during the storm phase duration. This study we discuss the behavior of cosmic rays during the phase of highly intense or ultra intense geomagnetic storms, as shocks driven by energetic coronal mass ejections (CME's) and other interplanetary (IP) transients are mainly responsible for initiating large and intense geomagnetic storms. Observational results indicate that galactic cosmic rays (CR) coming from deep surface interact with these abnormal solar and IP conditions and suffer modulation effects. In this paper a systematic study has been performed to analyze the CRI variation during super storms i.e. very intense geomagnetic storms with Dst index  $\geq -100$  nT. The neutron monitor data of three stations Oulu ( $R_c = 0.77$  GV), Climax ( $R_c = 2.97$  GV) and Huancayo ( $R_c = 13.01$  GV) well distributed over different latitudes and hourly values of IMF parameters derived from satellite observations near Earth IP medium from OMNI Data base is used for the period spanning over solar cycle 34. It is found that AP and AE indices show rise before the forward turnings of IMF, while the Dst index shows a classic storm time decrease. The analysis indicates that the magnitude of all the responses depends on BZ component of IMF being well correlated with solar maximum and minimum periods. Transient decrease in CRI with slow recovery is observed during the storm phase duration.

Keywords: Coronal mass ejection, magnetic cloud, Forbush decrease.

**Introduction** - The kind of interaction between solar wind and terrestrial magnetosphere depends on the structures present in the solar wind. The magnetic cloud is a kind of large scale interplanetary structure resulted as a transient ejection of the solar

plasma in the solar wind. Its characteristics were first time reported in 1981 by a group of scientists [1]. According to their studies performed on the basis of the systematic variation of interplanetary magnetic field component (IMF B) in a flow behind an interplanetary

## SOLAR EJECTA AND GEOPHYSICAL CONDITIONS DURING RECENT SOLAR CYCLES

Pradosh Kumar Sharma

Department of Physics

Chinmaya PG College, Shivalik Nagar, BHEL, Haridwar, U.K.

### ABSTRACT -

The solar outputs in various forms affects the geomagnetic field at short term as well as on long term basis. The ejecta like Coronal Mass Ejection (CME) is a vast structure of plasma and magnetic field orientations which are expelled from the sun into the heliosphere at regular intervals. These CME's when associated with solar flares and ejected towards the earth, becomes more significant, as the plasma structures embedded within them potentially modulates the earth's magnetosphere. This material is detected by remote sensing in-situ spacecraft observations. The effect of solar and interplanetary turbulences on geomagnetic condition has been presented here. These disturbances have been studied for solar cycle 23 and 24. These leads to 230 geomagnetic storms (GMSs), being observe in terms of Disturbance storm time index, Dst. These are categorized on the basis of Dst index and have been investigated using solar geophysical data (SGD) during the period of solar cycle 23 and 24. The results inferred that statistically the maximum number of geomagnetic storms have occurred during the years of solar maximum activity phase. However, it is not necessary that maximum number of disturbed days should occur during the maximum phase only. The results obtained are somehow contradict to the the past results, as observed during the solar minimum activity years, when sunspot numbers (SSNs) have been decreased rapidly; whereas the number of observed geomagnetic disturbances have increased significantly. The correlation coefficient between sunspots and occurrence of geomagnetic storms during the study period is very high, i.e. 0.83 %, which interprets that geophysical condition are strongly correlated with sunspots numbers.

**Keywords:** Coronal mass ejection, solar flare, Interplanetary magnetic field (IMF), Geomagnetic Storm, Disturbance storm time (Dst) and Solar Cycle.

**Introduction -** The Sun being the central part and potential source of energy, provides a series of various activities. These includes a transient solar flare originated from the solar surface, which brings a large amount of solar plasma with it. The other potentially geoeffective bundle of energy is a coronal mass ejection (CME). It is referred to a major solar plasma event and it may be sometime associated with a solar flare. The other solar radiations are disrupting filaments, surges, jets, magnetic clouds etc. The study mainly focus on CME and Solar flares. It is well known that a solar flare is an impulsive transient phenomenon which release a vast amount of solar plasma, matter and energy in a very short interval. Flares also often occurs in association with coronal mass ejection (CMEs) [1]. The coronal mass ejections (CMEs) are described as the large scale ejection of matter from the sun into the

outer corona and sometime even beyond. These CMEs from the sun are now considered to be an important aspect of plasma dynamics of solar corona. The study of these CME's are significant to human being as to enhance our understanding of the heliospheric disturbances and the interaction of solar plasma with planetary bodies. A coronal mass ejection can involve the injection of significant amount of mass and energy into large volume of interplanetary medium [2-4]. CMEs are known as the causes of interplanetary magnetic field fluctuations and many scientists have suggested that the solar cycle dependent modulation of galactic cosmic rays (GCRs) can also be explained by the presence of CMEs related magnetic inhomogeneities in the hemisphere [5-7]. Various investigators have reported the effect of Interplanetary Coronal Mass Ejections on the magnetosphere too.



# Radiation Phenomenon Due to Streamers of Sprites

Meenu Singh<sup>1\*</sup>, Pradosh Kumar Sharma<sup>2</sup>, Parmanand Prakash Pathak<sup>1</sup>

<sup>1</sup>Department of Physics, Gurukula Kangri (Deemed to Be University), Haridwar, India

<sup>2</sup>Chinmaya Degree College, BHEL, Haridwar, India

Email: \*minismeenu7@gmail.com

**How to cite this paper:** Singh, M., Sharma, P.K. and Pathak, P.P. (2022) Radiation Phenomenon Due to Streamers of Sprites. *Journal of Electromagnetic Analysis and Applications*, 14, 31-37.  
<https://doi.org/10.4236/jemaa.2022.143003>

Received: March 1, 2022

Accepted: March 28, 2022

Published: March 31, 2022

Copyright © 2022 by author(s) and Scientific Research Publishing Inc. This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).  
<http://creativecommons.org/licenses/by/4.0/>



## Abstract

An upper atmospheric phenomenon *i.e.*, sprites can be thought to be mainly caused by the propagation of positive corona streamers. This research presents the formulation for the calculation of radiation power received from the propagating corona streamers responsible for the origination of the sprites. The produced magnetic field variation using the calculated electromagnetic radiation power is found to be similar with the previous observation-based research work.

## Keywords

Sprites, Radiation, Electric Field, Magnetic Field, Power, TLEs (Transient Luminous Events)

## 1. Introduction

C.T.R. Wilson, in 1925, firstly produced the theory of existence of thundercloud flashes high above the clouds which Sprites [1]. These sprites are the transient luminous events (TLEs) (Figure 1(a)) which are developed by the electromagnetic coupling between positive CG (cloud to ground) lightning discharges and thunderstorm charges present at stratospheric/mesospheric level. Actually, the sprites phenomenon occurs due the streamers discharges present during the propagation of sprites. They are optical flashes out for few milliseconds only with the speed of  $10^7$  m/s. They may reach at the maximum altitude of 40 to 95 Km and horizontally extend up to ~30 - 40 km. According to Qin *et al.* [2], the variation in their optical shapes and sizes arises for different types of sprites *e.g.*, jelly-fish sprite, column sprite (C-sprite), carrot sprite. These are mostly associated with the positive cloud to ground lightning phenomenon [3].



## Evaluation of ambient air quality in Dehradun city during 2011–2014

AMAR DEEP<sup>1</sup>, CHHAVI P PANDEY<sup>2,\*</sup>, HEMWATI NANDAN<sup>3</sup>, K D PUROHIT<sup>1</sup>, NARENDRA SINGH<sup>4</sup>, JAYDEEP SINGH<sup>4</sup>, A K SRIVASTAVA<sup>5</sup> and NARENDRA OJHA<sup>6</sup>

<sup>1</sup>Department of Physics, H N B Garhwal University, Srinagar, Garhwal 246 174, India.

<sup>2</sup>Wadia Institute of Himalayan Geology, Dehradun 248 001, India.

<sup>3</sup>Department of Physics, Gurukula Kangri Vishwavidyalaya, Haridwar 249 404, India.

<sup>4</sup>Aryabhatta Research Institute of Observational Sciences, Manora Peak, Nainital 263 129, India.

<sup>5</sup>Indian Institute of Tropical Meteorology, Prof Ramnath Vij Marg, New Delhi 110 060, India.

<sup>6</sup>Department of Physics, Graphic Era University, Dehradun 248 002, India.

\*Corresponding author. e-mail: [chhavi@wihg.res.in](mailto:chhavi@wihg.res.in)

MS received 1 September 2017; revised 25 June 2018; accepted 3 July 2018; published online 2 April 2019

The variations in the ambient concentrations of particulate matter (SPM and PM<sub>10</sub>) and gaseous pollutants (SO<sub>2</sub> and NO<sub>2</sub>) at Clock tower (CT), Rajpur road (RR) and Inter State Bus Terminal (ISBT) station in Dehradun city, Uttarakhand, India are analysed for the period of 2011–2014. Mean concentrations are observed to be higher during pre-monsoon season as compared to the winter and monsoon. PM<sub>10</sub> and SPM concentrations with maximum values of  $203 \pm 23$  and  $429 \pm 49 \mu\text{g m}^{-3}$ , respectively, during winter, are found to exceed the national standards by factors of 2 and 3. Winter-time elevated pollution in Dehradun is attributed to the lower ventilation coefficient (derived from Era interim model fields) and minimal precipitation. Nevertheless, the SO<sub>2</sub> and NO<sub>2</sub> levels are observed to be within the criteria notified by the Central Pollution Control Board (CPCB), India. Correlation analysis shows profound impacts of the meteorology and local dynamics on the observed variations in observed trace species. Additionally, the stronger inter-species correlation variations ( $r = 0.79$  for SO<sub>2</sub> with NO<sub>2</sub>, and  $r = 0.89$  for PM<sub>10</sub> with SPM), which may suggest their origin from common sources. Analysis of 'Air Quality Index (AQI)' variations indicates unhealthy atmospheric conditions near the major city centers and bus station. More observations in the region are highly desirable to understand the dispersion of the enhanced pollution in the Dehradun valley.

**Keywords.** Air pollutants; statistical analysis; meteorological parameters; air quality index.

### 1. Introduction

Deleterious changes in atmospheric composition due to the introduction of contaminants are referred as the air pollution. The concentration of air pollutants depends not only on the quantities that are emitted from different emission sources but also on the subsequent chemical and dynamical

processes in the atmosphere. In fact, a thick blanket of pollution traps heat around the earth and therefore, plays a significant role in global warming and climate change (Ramanathan and Feng 2009). Presently, air pollution is deteriorating rapidly over much of the globe during past few decades (e.g., Akimoto 2003). Change in the regional vegetation cover, land use and many



ResearchGate

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/341185767>

## A statistical study on daily solar radiation and meteorological parameters

Conference Paper in AIP Conference Proceedings · May 2020  
DOI: 10.1063/1.5196193

CITATIONS  
0

READS  
74

4 authors, including:



Shubra Kala  
Hemwati Nandan Bahuguna Garhwal University  
23 PUBLICATIONS 147 CITATIONS

[SEE PROFILE](#)



Amar Deep  
Hemwati Nandan Bahuguna Garhwal University  
4 PUBLICATIONS 7 CITATIONS

[SEE PROFILE](#)



Kedar Parshat  
H.N. Bahuguna Garhwal University, Srinagar (Garhwal) Uttarakhand, India  
23 PUBLICATIONS 103 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Hydrogen sensor View project



Study of Fields Associated with Tachyons View project

All content following this page was uploaded by Amar Deep on 02 February 2021.

The user has requested enhancement of the downloaded file.



## Aerosols optical depth and Ångström exponent over different regions in Garhwal Himalaya, India

Amar Deep · Chhavi Pant Pandey · Hemwati Nandan · Narendra Singh · Garima Yadav · P. C. Joshi · K. D. Purohit · S. C. Bhatt

Received: 2 August 2020 / Accepted: 4 April 2021 / Published online: 4 May 2021  
© The Author(s), under exclusive licence to Springer Nature Switzerland AG 2021

**Abstract** Aerosol optical depth (AOD) and Ångström exponent (AE) are observed to be important parameters in understanding the status of ambient aerosol concentration over a particular location and depend not only upon the local but also on the large-scale dynamics of the atmosphere. The present article analyses the AOD and AE parameters retrieved with Moderate Resolution Imaging Spectrometer (MODIS) and Multi-angle Imaging Spectro-Radiometer (MISR) instruments onboard satellites, for the upper (Chamoli) and foothill (Dehradun) regions of Garhwal Himalaya in Uttarakhand, India, from 2006 to 2015. Aerosol properties are investigated at monthly, seasonal, and annual scales. The monthly mean values of

MODIS-derived AOD and AE were observed to be  $0.18 (\pm 0.14)$  and  $1.05 (\pm 0.43)$  respectively over the Dehradun region. The seasonal maximums in AOD with MODIS and MISR were observed as  $0.23 \pm 0.06$  and  $0.29 \pm 0.07$  respectively in the pre-monsoon season, and the minimum values ( $0.099 \pm 0.02$ ) were observed in the post-monsoon season, over the Dehradun region. In contrast, in the Chamoli region, the maximum AOD (MODIS) was  $0.21 \pm 0.06$  observed in the monsoon season and the minimum was  $0.036 \pm 0.007$  in the post-monsoon season. Over a decade, the AE for Chamoli and Dehradun was found to vary from 0.07 to 0.17 and from 0.14 to 0.20 respectively. The median AE for Chamoli and Dehradun was found to be 1.49 and 1.47 respectively, marking the dominance of fine mode particles of anthropogenic origin. Observations show the presence of dust and polluted dust resulting from the long-range transport from the west. The comparison of AOD values from the two sensors shows a significant correlation (0.73) with slightly higher values from MISR over the year. The results obtained are important in understanding the climatic implications due to the atmospheric aerosols over the abovementioned Himalayan region of Uttarakhand, India.

A. Deep · G. Yadav · K. D. Purohit · S. C. Bhatt  
Department of Physics, H N B University, Garhwal (A Central University), 246174 Srinagar, Uttarakhand, India

C. P. Pandey (✉)  
Wadia Institute of Himalaya Geology, 33 GMS Road,  
Dehradun, 248001 Uttarakhand, India  
e-mail: chhavi@wihg.res.in

H. Nandan · P. C. Joshi  
Department of Physics and, Dept. of Environmental  
Sciences, Gurukula Kangri (Deemed to be University),  
Haridwar, 249404 Uttarakhand, India

N. Singh  
Aryabhata Research Institute of Observational Sciences,  
Manora Peak, Nainital, 263001 Uttarakhand, India

**Keywords** AOD · AE · CALIPSO · MODIS and MISR



ResearchGate

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/355187642>

## ASSESSMENT OF AMBIENT AIR QUALITY AND ITS SOURCES AROUND HYDROPOWER PROJECTS USING HYSPLIT MODEL AND AIR QUALITY INDEX IN ALAKNANDA BASIN, GARHWAL HIMALAYA, INDIA

Article in *Pollution Research* · September 2021

CITATIONS  
0

READS  
13

7 authors, including:



**Bhim Chand**  
GB Pant Institute of Himalayan Environment and Development  
7 PUBLICATIONS 9 CITATIONS

[SEE PROFILE](#)



**Jagdish Chandra Kuntiyal**  
GB Pant National Institute of Himalayan Environment and Sustainable Development  
158 PUBLICATIONS 1,438 CITATIONS

[SEE PROFILE](#)



**Pawan Kumar Thakur**  
Himalayan Forest Research Institute (HFRI) Shimla  
5 PUBLICATIONS 4 CITATIONS

[SEE PROFILE](#)



**Manish Kumar**  
Kalindi College, University of Delhi  
21 PUBLICATIONS 913 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



his current areas of research have mainly been 'ambient air quality', 'aerosol over glaciers and its ion chemistry', 'aerosols climatology' and 'climate change and glacier melting' [View project](#)



EcoLodge - Efficient Production of Butyl-Butyrate from Lignocellulose derived Sugars [View project](#)

All content following this page was uploaded by Bhim Chand on 12 October 2021.  
The user has requested enhancement of the downloaded file.

Short Paper

## Using PCR-PIRA based genotyping for identifying complex vertebral malformation allele in Frieswal young bulls in India

Alyethodi, R. R.<sup>1</sup>; Kumar, S.<sup>1</sup>; Deb, R.<sup>1</sup>; Alex, R.<sup>1</sup>; Singh, U.<sup>1</sup>; Sharma, S.<sup>2</sup>; Ashish,<sup>2</sup>; Choudhary, J.<sup>2</sup>; Sengar, G.<sup>2</sup>; Singh, R.<sup>2</sup>; Tyagi, S.<sup>3</sup> and Birham, P.<sup>1</sup>

<sup>1</sup>Animal Genetics and Breeding Section, ICAR-Central Institute for Research on Cattle, Meerut Cantt, Meerut, 250001, Uttar Pradesh, India; <sup>2</sup>AIIS, Animal Genetics and Breeding Section, ICAR-Central Institute for Research on Cattle, Meerut Cantt, Meerut, 250001, Uttar Pradesh, India; <sup>3</sup>Animal Physiology Section, ICAR-Central Institute for Research on Cattle, Meerut Cantt, Meerut, 250001, Uttar Pradesh, India

Correspondence: R. R. Alyethodi, Animal Genetics and Breeding Section, ICAR-Central Institute for Research on Cattle, Meerut Cantt, Meerut, 250001, Uttar Pradesh, India. E-mail: rfg\_rubman@yahoo.co.in

(Received 18 Mar 2017; revised version 6 Jul 2017; accepted 23 Jul 2017)

### Summary

Complex vertebral malformation (CVM) has considerable economic impact on dairy cattle breeding due to extensive use of artificial insemination (AI). Identifying the carrier is an important factor to reduce the incidence of the genetic disorder. The study was conducted to identify the carriers of CVM in Frieswal cattle by polymerase chain reaction-primer-introduced restriction analysis (PCR-PIRA) method, which was further confirmed by sequencing. Carrier prevalence of 1% was observed in the Frieswal cattle. The results of the study clearly demonstrated the existence of carriers of CVM among Frieswal bull calves. Due to the widespread use of AI it is recommended to screen young bulls at early stages for this defective allele in order to avoid its rapid spread within the population.

**Key words:** CVM, Frieswal, PCR-PIRA

### Introduction

Complex vertebral malformation (CVM) is a lethal syndrome in Holstein population leading to malformed calves that are either spontaneously aborted or die shortly after birth (Kanae *et al.*, 2005). At the molecular level, it is due to a point mutation of the bovine solute carrier family 35 member 3 (SLC35A3) gene that results in the substitution of Valine by Phenylalanine (V180F) which impairs the function of transporter membrane protein [uridine diphosphate (UDP)-N-acetylglucosamine] (Thomsen *et al.*, 2006; Ageholm 2017). This mutation is been reported associated with milk traits, persistency of lactation and somatic cells score (Chen *et al.*, 2010). Since the single point mutation in SLC35A3 gene does not create or abolish any restriction site, it cannot be identified by restriction fragment length polymorphism (RFLP) method. Alternative molecular detection approaches including allele specific-polymerase chain reaction (AS-PCR) (International Patent WO 02/40709 A2, 2002), high resolution melting analysis (Gabor *et al.*, 2012), PCR single stranded conformation polymorphism (Rusc and Kaminski, 2007) and real time based genotyping (Zhang *et al.*, 2012) have been proposed.

Frieswal cattle is a synthetic breed of Holstein-Friesian (HF) (5/8) and Sahiwal (3/8) developed by ICAR-Central Institute for Research on Cattle (ICAR-

CIRC), Meerut, India in collaboration with Ministry of Defence. As imported HF semen has been used for the development of the breed, it is vulnerable to the genetic disorders reported in HF. Hence, the present study was carried out to identify the carriers for CVM in Frieswal bull calves in order to eliminate them from the population.

### Materials and Methods

Frieswal bull calves received from 37 military farms throughout India, reared at Bull Rearing Unit, ICAR-CIRC were used in the study. Genomic DNA was extracted by conventional phenol-chloroform method as described by Sambrook *et al.* (1989) with minor modifications. Genotyping of CVM was done using PCR-primer-introduced restriction analysis (PCR-PIRA) method (Kanae *et al.*, 2005). In brief, PCR-PIRA method employs two sets of primers with a common reverse primer, the generated amplicon sizes for both primer sets are 287 bp. Forward primers of each set create a specific restriction site depending on the nucleotide at the single nucleotide polymorphism (SNP) location. Both forward primers were complementary to sequence from nucleotides 537 to 554 of the bovine SLC35A3 gene, but 2 nucleotides at the fourth and fifth positions from the ends of the primers were different. Three nucleotides the 3' ends of both primers were similar to nucleotides



Copyright ©2018, Choudhary and Dubey  
This is an Open Access article distributed under the terms of the Creative Commons  
Attribution License (<http://creativecommons.org/licenses/by/7.0/>), which permits  
unrestricted use, distribution, and reproduction in any medium, provided the original work  
is properly cited.

ORIGINAL RESEARCH

# Relative probiotic potential of milk bacteria from *Desi* and cross-breed cows and its compatibility with prebiotics

Jyoti CHOUDHARY\*, Ramesh Chand DUBEY\*

Department of Botany and Microbiology, Gurukul Kangri Vishwavidyalaya, Haridwar – 249404, India  
\*Corresponding Authors email: [prfcdubey@gmail.com](mailto:prfcdubey@gmail.com), [jyotichoudharyibt@gmail.com](mailto:jyotichoudharyibt@gmail.com)

Received: 03 January 2018 • Revised: 12 February 2018 • Accepted: 28 February 2018 • Published: 03 March 2018 •

ABSTRACT

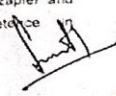
Fifty two lactic acid bacteria (LAB) were isolated from milk of *Desi* and cross-breed cows of India and its functional characteristics were investigated on the basis of morphological and biochemical properties. Among them four bacterial isolates were screened on the basis of *in vitro* probiotic attributes. Isolate CP-12<sup>8</sup> and CP-8<sup>8</sup> which were isolated from *Desi* Indian cows showed high tolerance to low pH, bile, NaCl and certain antibiotics. These isolates exhibited the highest adhesion to hydrocarbons xylene, n-octane and n-hexane. Isolate CP-8<sup>8</sup> exhibited the highest auto-aggregation rate (62%). It was the most resistant isolate against different antibiotics. All the four isolates inhibited the enteric pathogens viz., *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae* and *Salmonella typhi* but the isolate CP-12<sup>8</sup> and CP-8<sup>8</sup> exhibited high antagonistic activity against all pathogens. These two bacterial isolates exhibited good probiotic properties and also grew well in presence of inulin as compared to honey.

KEY WORDS: Lactic acid bacteria, Probiotics, Antibacterial activity, Prebiotics

INTRODUCTION

Probiotics are the live microbial food supplements which beneficially affect the host by improving its intestinal microbial balance. There are many benefits of probiotics including improved nutrition, growth and prevention of various gastrointestinal (GI) disorders. Traditionally, physicians used various antibiotics for treating gastrointestinal disorders. However, the incidence of antibiotic-associated diarrhea (AAD) and resistance of the pathogens to antibiotics require alternative strategies for treatment. AAD results from disruption of the normal microflora of the gut by antibiotics (Wistrom *et al.*, 2001). Lactic acid bacteria (LAB) are widely used in food and pharmaceutical industry, especially for the fermentation of milks and as medicine to improve the gastrointestinal health (Battcock and Azam-Al, 1998). Some LAB strains can be

used as probiotics for human and animals (Chou and Weimer, 1999). In general, LAB used as probiotic should be resistance to host gastrointestinal conditions, adhesion to host intestinal epithelium, and the prevention of growth or invasion of pathogenic bacteria, such as *Salmonella* spp. and *Escherichia coli* in the animal intestine (Chou and Weimer, 1999, Jin *et al.*, 1996). Furthermore, certain LAB strains have been reported earlier for other health benefits, such as stimulation of the immune system of the human hosts (Schiffrin *et al.* 1997). Bacterial strains to be considered as probiotic should contain some essential properties, such as origin of strain, safety, acid, bile resistance, survivability during processing, and storage with beneficial effects (Saarela *et al.*, 2000, Holzapel and Schillinger, 2002). The growing competence




REVIEW

Open Access

# Insights of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2) pandemic: a current review



Jyoti Choudhary<sup>1,2</sup>, Shrivardhan Dheeman<sup>3\*</sup>, Vipin Sharma<sup>4\*</sup>, Prashant Katiyar<sup>2</sup>, Santosh Kumar Kam<sup>5\*</sup> , Manoj Kumar Sarangi<sup>6</sup>, Ankit Kumar Chauhan<sup>7</sup>, Gaurav Verma<sup>8</sup> and Nitin Baliyan<sup>7</sup>

Abstract

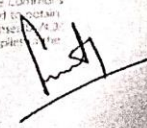
COVID-19, a pandemic of the 21st century caused by novel coronavirus SARS-CoV-2 was originated from China and shattered world economy and human resource. The medical cures via herbal treatments, antiviral drugs, and vaccines still in progress, and studying rigorously. SARS-CoV-2 is more virulent than its ancestors due to evolution in the spike protein(s) mediates viral attachment to the host's membranes. The SARS-CoV-2 receptor-binding spike domain associates itself with human angiotensin-converting enzyme 2 (ACE-2) receptors. It causes respiratory ailments with irregularities in the hepatic, nervous, and gastrointestinal systems, as reported in humans suffering from COVID-19 and reviewed in the present article. There are several approaches, have been put forward by many countries under the world health organization (WHO) recommendations and some trial drugs were introduced for possible treatment of COVID-19, such as Lopinavir or Ritonavir, Arbidol, Chloroquine (CQ), Hydroxychloroquine (HCQ) and most important Remdesivir including other like Tocilizumab, Oritavancin, Chlorpromazine, Azithromycin, Baricitinib, etc. RT-PCR is the only and early detection test available besides the rapid test kit (serodiagnosis) used by a few countries due to unreasonable causes. Development of vaccine by several leader of pharmaceutical groups still under trial or waiting for approval for mass inoculation. Management strategies have been evolved by the recommendations of WHO, specifically important to control COVID-19 situations, in the pandemic era. This review will provide a comprehensive collection of studies to support future research and enhancement in our wisdom to combat COVID-19 pandemic and to serve humanity.

**Keywords:** COVID-19, Coronavirus, ACE-2 receptor, Drug repurposing

\* Correspondence: saranshivemajumdar@gmail.com; dvhheeman@gmail.com; [shrivardhan@icmr.gov.in](mailto:shrivardhan@icmr.gov.in)  
Department of Microbiology, School of Life Sciences, Sardar Bhagwan Singh University, Dehradun, Uttarakhand 248161, India  
Department of Pharmaceutical Sciences, Faculty of Ayurvedic and Medicinal Sciences, Suraskula Kazni Deemed to be University, Haridwar, Uttarakhand 247404, India  
Department of Biotechnology and Biochemistry, School of Life Sciences, Sardar Bhagwan Singh University, Dehradun, Uttarakhand 248161, India  
Full list of author information is available at the end of the article



© The Author(s) 2021 **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.







## Genome-wide analysis of the heat stress response in Zebu (Sahiwal) cattle

Kusum Mehla <sup>a,b,\*</sup>, Ankit Magotra <sup>b</sup>, Jyoti Choudhary <sup>d</sup>, A.K. Singh <sup>d</sup>, A.K. Mohanty <sup>c</sup>, R.C. Upadhyay <sup>a</sup>, Surendran Srinivasan <sup>a</sup>, Pankaj Gupta <sup>a</sup>, Neelam Choudhary <sup>a</sup>, Bristo Antony <sup>a</sup>, Farheen Khan <sup>a</sup>

<sup>a</sup> Dairy Cattle Physiology Division, National Dairy Research Institute, Karnal 132001 (Haryana), India  
<sup>b</sup> Dairy Cattle Breeding Division, National Dairy Research Institute, Karnal 132001 (Haryana), India  
<sup>c</sup> Animal Biotechnology Centre, National Dairy Research Institute, Karnal 132001 (Haryana), India

### ARTICLE INFO

Article history:  
 Accepted 12 September 2013  
 Available online 27 September 2013

Keywords:  
 Heat stress  
 Sahiwal  
 cDNA microarray  
 HSPs  
 Regulation

### ABSTRACT

Environmental-induced hyperthermia compromises animal production with drastic economic consequences to global animal agriculture and jeopardizes animal welfare. Heat stress is a major stressor that occurs as a result of an imbalance between heat production within the body and its dissipation and it affects animals at cellular, molecular and ecological levels. The molecular mechanism underlying the physiology of heat stress in the cattle remains undefined. The present study sought to evaluate miRNA expression profiles in the cattle blood in response to heat stress. In this study we report the genes that were differentially expressed in response to heat stress using global scale genome expression technology (Microarray). Four Sahiwal heifers were exposed to 42 °C with 90% humidity for 4 h followed by normothermia. Gene expression changes include activation of heat shock transcription factor 1 (HSF1), increased expression of heat shock proteins (HSP) and decreased expression and synthesis of other proteins, immune system activation via extracellular secretion of HSP. A cDNA microarray analysis found 140 transcripts to be up-regulated and 77 down-regulated in the cattle blood after heat treatment ( $P < 0.05$ ). But still a comprehensive explanation for the direction of fold change and the specific genes involved in response to acute heat stress still remains to be explored. These findings may provide insights into the underlying mechanism of physiology of heat stress in cattle. Understanding the biology and mechanisms of heat stress is critical to developing approaches to ameliorate current production issues for improving animal performance and agriculture economics.

© 2013 Elsevier B.V. All rights reserved.

### 1. Introduction

Cattle, like other homeotherms, modulate internal body temperature by coupling the amount of heat produced through metabolism with the heat flow from the animal to its surrounding environment. Heat stress occurs as a result of an imbalance between heat production within the body and its dissipation (Kumar et al., 2011). Heat stressed cattle experience reduction in food intake, growth, immunity, milk yield and reproduction efficiency (Hahn, 1999). Environmental-induced hyperthermia jeopardizes animal welfare. The welfare of dairy cows can be evaluated on the basis of the temperature humidity index (THI) values. This index is usually used for evaluating the degree of stress on dairy cattle caused by weather conditions (Hartn and Mader, 1997), as it comprises the effects of both ambient temperature and relative humidity in an index. In the critical range of THI of 70–72, performance of dairy cattle declines and cooling becomes

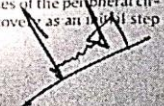
desirable. At THI of 72–78, milk production is seriously affected. In the dangerous category at THI of 78–82, the performance is severely affected and cooling becomes essential (Huber, 1996).

The detrimental effects of heat stress on animal welfare will likely become more of an issue if earth's climate continues to warm as predicted (IPCC, 2007). According to the IPCC fourth assessment report, a warming of up to 2 °C above 1990–2000 levels would have significant impacts on many unique and vulnerable systems. Changes in extreme temperature will accompany continued global warming. Thus raising the question how organisms adapt to extreme temperature events.

In the present investigation we sought to evaluate the changes occurring in genome-scale gene expression profile of the Indian zebu cattle (Sahiwal) during hyperthermia followed by normothermia. We used microarray-based global gene expression profiling as a high-resolution assay to understand the unique traits in cattle which make them resilient to climate change. Microarray technology is a powerful tool for seeking insights into gene regulation and its significance for biological function. However, our understanding of such relationships during environmental stress remains fragmentary.


The rationale behind the current study was to build a high confidence dataset of the differentially expressed genes of the peripheral circulation during the stage of heat stress and recovery as an initial step

Abbreviations: miRNA, messenger RNA; HSF1, heat shock transcription factor 1; HSPs, heat shock proteins; cDNA, complementary DNA; THI, temperature humidity index; IPCC, Intergovernmental Panel on Climate Change; CR, climate-controlled room; RT, rectal temperature; RR, respiration rates; IVT, in vitro transcription; aRNA, amplified RNA; ANOVA, analysis of variance; MAS3, Molecular Annotation System 3; GO, gene ontology.  
 \* Corresponding author. Tel.: +91 9012124960.  
 E-mail address: [mehlakusum@gmail.com](mailto:mehlakusum@gmail.com) (K. Mehla).





## Evaluation of Probiotic Potential and Safety Assessment of *Lactobacillus pentosus* MMP4 Isolated From Mare's Lactation

Jyoti Choudhary<sup>1</sup>  · R. C. Dubey<sup>1</sup> · Gyanendra Sengar<sup>2</sup> · Shrivardhan Dheeman<sup>1</sup>

© Springer Science+Business Media LLC part of Springer Nature 2018

### Abstract

Lactic acid bacteria isolated from indigenous milk of different animals were investigated for their efficacy, safety, and probiotic potential. The most potential isolate MMP4 was screened from mare's milk, which was further identified as *Lactobacillus pentosus* by using 16S rRNA gene sequencing and phylogeny. The probiotic potential of strain MMP4 was assessed by its ability to survive under acidic environment and in presence of bile salts along with the ability to inhibit food-borne as well as clinical pathogenic microorganisms such as *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Salmonella typhi*. The phenol tolerance with cogent hydrophobicity to different hydrocarbons was demonstrated. Bile salt hydrolase activity of *L. pentosus* MMP4 was confirmed by detecting the *Bsh* gene by using colony PCR. The presence of *Mub*, *Map*, and *EF-Tu* genes involved in adhesion conferred the behavior of passage and adherence to gastrointestinal tract. Scanning electron microscopy of intestinal autopsy from albino mice revealed the attachment of bacterial cells on the mucus-lined intestinal walls against pathogens and further proved *in vivo* adhesion ability. The presence of intrinsic antibiotic resistance and lack of DNase, gelatinase, and hemolytic activity in MMP4 support its safety as probiotic traits. Thus, MMP4 bears an excellent and pragmatic properties for being used as probiotic and may be exploited in dairy industry.

**Keywords** Probiotics · Lactic acid bacteria · Polymerase chain reaction (PCR) · Antimicrobials · *Lactobacillus*

### Introduction

Probiotics are "live microorganisms" which when administered in adequate amounts confer a health benefits on the host [1]. Milk and milk-based products are the main ingredients of food in India. In Indian subcontinent, during 7500 BC, the Aryans used to eat "ghee" (cow's milk-based product) prior and later butter-milk (cow's milk-based product) during Mahabharata epoch [2]. Furthermore, peoples started to consume milk and

milk products of other animals such as goat, sheep, and mare, which are the possible sources of probiotic bacteria. The viable microorganisms with probiotic profile play an important role in maintaining the integrity for immunological, digestive, and respiratory functions. Exploration of effective probiotic bacteria bears high score of immunomodulation and safety appraisal being carried out to develop safer food products [19].

Probiotic microorganisms must possess the desired properties, such as survival in the gastrointestinal (GI) tract, persistence in host, and safety assurance for consumer [3]. They favorably maintain the balance of intestinal microflora, promote intestinal integrity and mobility, inhibit the growth of harmful bacteria, and increase resistance against infections [4]. The survival ability contributed by adherence in GI tract influenced with gastric and bile ambience further competitive advantage and become beneficial to maintain microbial homeostasis. These traits have been proven beneficial in competitive exclusion of pathogenic bacteria due to niche occupation by lactic acid bacteria (LAB) [5, 6]. Milk and milk-based products bear huge diversity of probiotic microorganisms, in which these can easily utilize lactose as an energy sources for their growth and proliferation. The mode of action of probiotics is intertwined with

<sup>✉</sup> Jyoti Choudhary  
 jyotichoudhary1987@gmail.com

<sup>✉</sup> R. C. Dubey  
 profrcdubey@gmail.com

<sup>✉</sup> Shrivardhan Dheeman  
 vshdheeman@gmail.com

<sup>1</sup> Department of Botany and Microbiology, Gurukul Kangri Vishwavidyalaya, Haridwar 249404, India

<sup>2</sup> Division of Animal Genetics and Breeding, Central Institute for Research on Cattle, Meerut 250001, India



IMG-20230717-WA0002.jpg

10:58 AM

### Submission Summary

Conference Name	2023 International Conference on New Frontiers in Communication, Automation, Management and Security (ICCAMS)
Paper ID	192
Paper Title	Monitor and Control Electricity for Home Appliances
Abstract	Electricity is a vital part of modern life, therefore, it is crucial to learn how to utilize it safely. Over time, current systems for domestic power regulation have been analyzed with an eye toward improvement. However, existing Power Monitoring and Switching (PMAS) methods have a greater error rate and cannot be remotely monitored. As a result, this research suggests a SMACS for monitoring and controlling domestic appliances. The relevance of the application is in its ability to monitor the power consumption of home appliances via the use of hardware and IoT techniques. An Arduino UNO, a liquid-crystal display (LCD), an ACS312 current sensor module, some relays, and some AC sources all go into making the prototype of the suggested system. The software library is mined for parts, and identical simulation and prototype results are identified. Due to its absence from the system, the ESP0266 WiFi module has been included in the design. Thing speak is used to record the information in the cloud. Data is accessed using a mobile app (Virtuoso), so it may be visualized numerically and graphically. Through the use of mobile apps, this research offers consumers a simple mechanism for keeping tabs on and adjusting the power usage of standard home equipment. The results demonstrate that the present Power Monitoring and Switching (PMAS) system produces 8.8% of current errors for the hairdryer appliance, whereas the suggested system gives just 1.6% of existing faults.
Created on	7/17/2023, 12:51:06 AM
Last Modified	7/17/2023, 12:51:06 AM
Authors	<p><b>Rajaseenthosh Tulele</b> ( MSH Academy ) &lt; trsk_mech@gmail.com &gt;</p> <p>Dr Pradosh Kumar Sharma ( Chinmaya Degree College ) &lt; dipksharma25@gmail.com &gt;</p> <p>B. Lakshmi ( Velagapudi Ramakrishna Siddhartha Engineering College (Autonomous) ) &lt; itslakshmi h@gmail.com &gt;</p> <p>Dr.A. Prakash ( FET Campus, Jain Deemed To Be University ) &lt; prakash_a@jainuniversity.ac.in &gt;</p> <p>Dr. Manish Kumar Verma ( Lovely Professional University ) &lt; manish.23900@pu.co.in &gt;</p> <p>Dr.V.V.S Sasank ( Koneru Lakshmaiah Education Foundation ) &lt; sasank64@gmail.com &gt;</p> <p>AshokKumar Nagarajan ( Mohan Babu University ) &lt; ashoknoc@gmail.com &gt;</p>
Primary Subject Area	TECHNOLOGY TRENDS
Submission Files	IEEE Monitor and Control Electricity for home Appliances.doc (233.5 Kb, 7/17/2023, 12:50:59 AM)

[Edit Submission](#)   [Back to Author Console](#)



## JOURNAL OF CRITICAL REVIEWS

ISSN- 2394-5125 VOL 10, ISSUE 03, 2023

### Function of Molecular Biology in Cancer Treatment

<sup>1</sup>Dr Manisha

Associate Professor and Head of Botany Department,  
Chinmaya Degree College, BHEL, Haridwar  
College is affiliated to Hemwati Nandan Bahuguna Garhwal University, Srinagar, Garhwal

[manisha26solunki@gmail.com](mailto:manisha26solunki@gmail.com)

<sup>2</sup>Dr J Nelson Samuel Jebastin

Assistant Professor in Bioinformatics, Department of Zoology, Annamalai University,  
Annamalainagar, Chidambaram, Cuddalore Dt., TN. 608 002.

<sup>3</sup>Dr.K.Kalalarasi

Assistant professor, PG and Research Department of Biotechnology,  
Padmavani arts and science college for women, Salem II.

<sup>4</sup>Rajaram Das

Associate Professor,, Roland Institute of Pharmaceutical Sciences, Odisha.

#### Abstract

RNAi, zinc finger nucleases, and CRISPR's ability to eliminate cancer is positive. These are promising research fields. However, cancer is a complicated and diverse illness, thus curing or eliminating it is difficult. RNA interference (RNAi) may selectively mute or downregulate gene expression. It targets oncogenes and inhibits cancer cell growth in lab tests. RNAi-based medicines must overcome delivery issues and off-target consequences before being extensively employed in clinical settings. ZFNs and CRISPR enable exact DNA sequence changes. They may disrupt oncogenes and target cancer-related genetic alterations. These methods worked in preclinical and early clinical trials, but further study is required to guarantee their safety, efficiency, and long-term effects. These molecular biology tools may improve cancer research and therapy, but a multifaceted approach to cancer control and management is needed. Early diagnosis, prevention, personalised treatment, targeted medicines, immunotherapies, and a better understanding of cancers complicated molecular underpinnings. In conclusion, RNAi, zinc finger nucleases, and CRISPR are potential cancer-fighting weapons, but further study and integration with other methods are needed to attain a cancer-free society. Molecular biology advances help us understand and cure cancer.

**Keywords:** Cancer, Oncogenes, Proto-oncogenes, Mutagenesis, Viral infection, Tumour, CRISPR

## Recent Advances in Research Concerning the Synthetic Biology of Biological Pesticides Derived from Plants

**<sup>1</sup>Dr Sangeeta Bhimrao Dongre**

Assistant Professor

Department of Zoology, Government College Of Arts and Science Aurangabad, Maharashtra  
India, 431004

[sangeetadongre24@gmail.com](mailto:sangeetadongre24@gmail.com)

**<sup>2</sup>Aadya Jha**

Research Scholar, Department of Botany, University of Kalyani, West Bengal, India.

[jhaaadya5@gmail.com](mailto:jhaaadya5@gmail.com)

**<sup>3</sup>Dr Manisha**

Associate Professor and Head of Botany Department,

Chimaya Degree College, BHEL, Haridwar

College is affiliated to Hemwati Nandan Bahuguna Garhwal University, Srinagar, Garhwal  
[manisha26solanki@gmail.com](mailto:manisha26solanki@gmail.com)

**<sup>4</sup>Dr. Khushal N. Pathade**

Assistant Professor and Head

P.G. Department of Botany, Dr. R. G. Bhojar Arts, Commerce and Science College,  
Seloo Dist. Wardha, Maharashtra

Email- [pathade.khushal@gmail.com](mailto:pathade.khushal@gmail.com)

### Abstract

The use of chemical pesticides in agriculture has raised concerns regarding their detrimental effects on human health and the environment. As a result, there has been growing interest in developing alternative pest control methods, including the use of biological pesticides derived from plants. Synthetic biology has emerged as a powerful tool to engineer and optimize the production of these bio pesticides. This review aims to summarize the recent advances in synthetic biology research concerning the development and production of plant-derived biological pesticides. We discuss various strategies employed to enhance pesticide activity, increase production yields, and improve formulation and delivery systems. Furthermore, we highlight the role of genetic engineering, metabolic engineering, and genome editing techniques in the design and modification of plants for enhanced bio pesticide production. The potential benefits and challenges associated with synthetic biology approaches are also examined, along with the current regulatory landscape surrounding genetically modified organisms (GMOs) used for bio pesticide production. Overall, this review provides a comprehensive overview of the recent progress made in synthetic biology research pertaining to plant-derived biological pesticides, offering insights into the future directions and opportunities in this rapidly evolving field.



## JOURNAL OF CRITICAL REVIEWS

ISSN- 2394-5125 VOL 10, ISSUE 03, 2023

### Intervention in Molecular Biology to Increase Enzyme Activity and Produce Commercial Enzymes

<sup>1</sup>Dr Manisha

Associate Professor and Head of Botany Department,  
Chinmaya Degree College, BHEL, Haridwar  
College is affiliated to Hemwati Nandan Bahuguna Garhwal University, Srinagar, Garhwal  
manisha26solanki@gmail.com

<sup>2</sup>Dr. Khushal N. Pathade

Assistant Professor and Head, P.G. Department of Botany  
Dr. R. G. Bhojar Arts, Commerce and Science College, Seloo Dist. Wardha, Maharashtra  
pathade.khushal@gmail.com

<sup>3</sup>M.Krishnaveni

Assistant Professor in Biochemistry, Nadar Saraswathi College of Arts & Science, Theni, Tamilnadu,  
India. venibio87@gmail.com

<sup>4</sup>Dr. Brahman Pasumarthi

Associate professor, Biology, Dept of Humanities and sciences,  
PACE Institute of Technology and Sciences, Ongole, Prakasam District,  
Andhra Pradesh, India.  
brahmampp147@gmail.com

#### Abstract

Metagenomics and directed evolution have changed how we look for new enzymes in harsh settings and how we change current enzymes to make them do what we want. Researchers can make enzymes with more activity, stability, and substrate selectivity using next-generation sequencing, site-directed mutagenesis, fusion protein, surface display, and other molecular biology techniques. These enzymes are used in industry. Many large-scale industrial enzyme processes still need to get around the limits of catalytic process activity. This piece talks about how enzymes are used in industry and how metabolic engineering is being used to make enzymes work better and produce more.

**Keywords:** Enzyme; Molecular biology; Metagenomics;

#### Introduction

The change in the chemistry business is making it harder to make chemicals with microbes and enzymes. To switch from petrochemicals to green chemistry, we must avoid getting stuck when we look for new enzymes, make biocatalysts, and design fake enzymes. Non-natural chemical processes can be sped up by enzymes for each natural molecule. These enzymes change in vivo to digest new manmade chemicals [1]. Enzymes are used in many businesses,



## Importance of Medicinal plants having anticarcinogenic and antioxidant activities used in Ayurvedic Medicinal System

Dr. A. Vijayalakshmi,<sup>1</sup> Dr. M. Malinidevi,<sup>2</sup> Dr. Manisha,<sup>3</sup> Dr. M. Krishnaveni,<sup>4</sup>  
Dr. Tata Prasanna Kumari<sup>5</sup>

<sup>1</sup> Associate Professor, Chemistry, R. M. K. Engineering College, Thiruvallur, Chennai, Tamil Nadu

<sup>2</sup> Assistant Professor, M.Sc., M.A. (Hospital Administration), Divine Mother College, Korkadu, Villianur, Pondicherry

<sup>3</sup> Associate Professor and Head of Botany Department, Chinmaya Degree College, BHEL, Haridwar, Uttarakhand

<sup>4</sup> Assistant Professor in Biochemistry, Nadar Saraswathi College of Arts & Science, Theni, Tamilnadu, India.

<sup>5</sup> Assistant Professor, department of Pharmaceutical analysis, KL College of Pharmacy, Koneru Lakshmaiah Education Foundation deemed to be University, Green fields, Vaddeswaram, Guntur District, Andhra Pradesh, India

### ABSTRACT

Internationally malignant growth is a sickness which seriously impacts the human populace. New treatments to treat and prevent this deadly disease are always in high demand. Natural compounds are getting more attention from scientists and researchers because they are thought to have fewer harmful side effects than current treatments like chemotherapy. The Plant Realm delivers normally happening auxiliary metabolites which are being explored for their anticancer exercises prompting the improvement of new clinical medications. New technologies are emerging to further develop the field as a result of these compounds' success as standard cancer treatments. Nanoparticles for nanomedicines are one example of a new technology that aims to control the release of plant-derived drugs and investigate novel administration strategies to enhance their anticancer properties. The demand for medicinal plant-derived naturally-derived compounds and the properties that make them potential targets for anticancer treatments are the subject of this review.

**Key words:** anticancer, secondary metabolites, polyphenols, cytotoxicity, epigenetics

Received 14.12.2022

Revised 30.01.2023

Accepted 24.02.2023

### INTRODUCTION

There has been a lot of progress made in cancer treatment and prevention over the years. The disease is characterized by uncontrollable and unstoppable cell proliferation throughout the body. Thusly, shaping cancers of threatening cells with the possibility to be metastatic. Chemotherapy, radiation therapy, and drugs derived from chemicals are some of the current treatments. Chemotherapy, for example, can put patients under a lot of stress and make their health worse. As a result, alternative cancer treatments and therapies are prioritized. In developing nations, herbal medicines have been and continue to be the primary source of medical treatment for many years. Because of their natural antiseptic properties, plants have been used in medicine. As a result, research has focused on the potential properties and applications of extracts from terrestrial plants for the preparation of nanomaterial-based drugs for diseases like cancer. Numerous plant species are already being used to treat or stop cancer from growing. Plant species with anticancer properties have been identified by a number of researchers, with an emphasis on those that have been utilized in herbal medicine in developing nations. The ability of certain compounds, which are specific to the plant kingdom and are necessary for the survival of plants as well as the "housekeeping" of the organism, to stop cancerous



## Sugarcane bagasse: an important lignocellulosic substrate for production of enzymes and biofuels

Pratiksha Yadav<sup>1</sup> · Anu<sup>2</sup> · Santosh Kumar Tiwari<sup>3</sup> · Vinod Kumar<sup>4</sup> · Davender Singh<sup>5</sup> · Sandeep Kumar<sup>6</sup> · Manisha<sup>7</sup> · Vinay Malik<sup>8</sup> · Bijender Singh<sup>1,2</sup>

Received: 23 February 2022 / Revised: 25 April 2022 / Accepted: 6 May 2022  
 © The Author(s), under exclusive licence to Springer-Verlag GmbH Germany, part of Springer Nature 2022

### Abstract

Sugarcane bagasse (SCB), a by-product of sugarcane industry, is a rich source of cellulose (45%), hemicellulose (32%), and lignin (17%) with low ash content. Being produced in large quantities by sugar industries, it is a great challenge for environment because it is mostly burnt in-open or either disposed improperly causing environmental pollution. Due to rich source of fermentable sugars, it is used as a substrate for producing microbial enzymes and biofuels. Secondly, high fuel prices, limited fossil fuel reserves, and environment pollution due to burning of fossil fuels have also highlighted the need for renewable and sustainable sources of energy such as biofuels. Sugarcane bagasse is a renewable, easily available, and cost-effective alternative for synthesis of biofuels and various microbial enzymes in submerged (SmF) as well as solid-state fermentations (SSF). However, for biofuel production, the main hindrance in utilizing bagasse is the requirement of large amount of enzymes for conversion of lignocellulosic biomass into fermentable sugars. Therefore, there is an utmost need for the production of enzymes using cost-effective and easily accessible substrates such as sugarcane bagasse followed by utilizing these enzymes for saccharification of carbohydrate polymers into fermentable sugars for biofuels. However, the presence of lignin hampers the saccharification of cellulose and hemicellulose into easily fermentable sugars. Therefore, pretreatment reduces lignin content of sugarcane bagasse and makes cellulose and hemicellulose easily accessible for enzymatic hydrolysis. Enzymatic hydrolysate can be further fermented to biofuels using aerobic and anaerobic microorganisms.

**Keywords** Lignocellulosic biomass · Cellulolytic enzymes · Pretreatment · Fermentation · Value-added products

✉ Bijender Singh  
 ohlanbs@gmail.com; ohlanbs@cuh.ac.in

<sup>1</sup> Department of Biotechnology, Central University of Haryana, Jant-Pali, Mahendergarh, Haryana 123031, India

<sup>2</sup> Laboratory of Bioprocess Technology, Department of Microbiology, Maharshi Dayanand University, Rohtak 124001, Haryana, India

<sup>3</sup> Department of Genetics, Maharshi Dayanand University, 124001, Rohtak, Haryana, India

<sup>4</sup> Department of Chemistry, Central University of Haryana, Jant-Pali, Mahendergarh 123031, Haryana, India

<sup>5</sup> Department of Physics, RPS Degree College, Mahendergarh 123031, Haryana, India

<sup>6</sup> Department of Biotechnology, Shobhit Institute of Engineering and Technology (Deemed to Be University), Modipuram, Meerut 250110, UP, India

<sup>7</sup> Department of Botany, Chimaya Degree College, Haridwar 249403, Uttarakhand, India

<sup>8</sup> Department of Zoology, Maharshi Dayanand University, Rohtak 124001, Haryana, India

### Abbreviations

SCB	Sugarcane bagasse
SSF	Solid-state fermentation
ABE	Acetone-butanol-ethanol
U/ml	Unit per ml
U/g	Unit per gram
SmF	Submerged fermentation
STB	Stirred tank bioreactor
RSM	Response surface methodology

### 1 Introduction

Sugarcane is one of the major cultivated crops in tropical and sub-tropical parts of the world. India is the 2nd largest producer of sugarcane after Brazil with an estimated sugarcane production of 306 million tons per year [1]. Sugarcane bagasse (SCB) is the main by-product of sugar industry, which is produced in huge amount, i.e., 100 million tons per year in India. About 50% of SB is utilized in the generation



## Enhanced production and immobilization of phytase from *Aspergillus oryzae*: a safe and ideal food supplement for improving nutrition

Pragya<sup>1</sup>, Krishna Kant Sharma<sup>2</sup>, Sandeep Kumar<sup>3</sup>, Manisha<sup>4</sup>, Davender Singh<sup>5</sup>, Vijay Kumar<sup>6</sup>, Bijender Singh<sup>1,7,\*</sup>

<sup>1</sup>Laboratory of Bioprocess Technology, Department of Microbiology, Maharshi Dayanand University, Rohtak 124001, India

<sup>2</sup>Laboratory of Enzymology and Recombinant DNA Technology, Department of Microbiology, Maharshi Dayanand University, Rohtak 124001, India

<sup>3</sup>Department of Biotechnology, Shobhit Institute of Engineering and Technology (Deemed to be University), Modipuram, Meerut 250110, India

<sup>4</sup>Department of Botany, Chimaya Degree College, Haridwar 249403, India

<sup>5</sup>Department of Physics, RPS Degree College, Mahendergarh 123023, India

<sup>6</sup>Department of Botany, Shivaji College, University of Delhi, New Delhi 110027, India

<sup>7</sup>Department of Biotechnology, Central University of Haryana, Jant-Pali, Mahendergarh 123031, India

\*Corresponding author. Laboratory of Bioprocess Technology, Department of Microbiology, Maharshi Dayanand University, Rohtak-124001, Haryana, India. Department of Biotechnology, Central University of Haryana, Jant-Pali, Mahendergarh-123031, Haryana, India. E-mail: ohanbs@gmail.com

### Abstract

Microbial phytases are potentially excellent candidates for eliminating anti-nutrient i.e. phytic acid, due to hydrolysis of phospho-monoester linkages present in the phytic acid. An average 2.29-fold increase in phytase production was obtained after statistical optimization in solid-state fermentation. *Aspergillus oryzae* SB550 phytase was immobilized on a Ca-alginate matrix with an effectiveness of 53%. Immobilized phytase retained > 50% activity after recycling for five cycles and also displayed more stability in the presence of organic solvents, metal ions, and detergents as compared to free enzyme. Values of  $K_m$  and  $V_{max}$  of immobilized phytase were recorded as 0.66 mM and 666.6  $\mu\text{mol}/\text{L}\cdot\text{min}$  respectively. Immobilized phytase efficiently hydrolyzed the phytate contents in wheat and pearl millet flours, exhibiting > 70% catalytic activity even after three cycles. Phytase supplementation resulted in the improved nutritional quality of these flours. Furthermore, the safety assessment of the treated and untreated samples reveals the absence of any aflatoxin in the phytase produced by the mould. The results revealed the improved stability of phytase after immobilization and as a safe and significant additive for application in the food industry.

### Significance and impact of study

The present study demonstrates the effectiveness of statistical tools in enhancing *A. oryzae* SB550 phytase production followed by entrapment in Ca-alginate beads. Immobilized phytase hydrolyzed phytic acid present in wheat and pearl millet flours. The dephytization ability as well as the reusability of the immobilized phytase, makes it an extremely interesting food and feed additive for the industry. Based on the safety assessment, and the fact that the *A. oryzae* is considered a safe lineage, there will be no safety issues using this phytase as a food additive.

**Keywords:** phytase, optimization, immobilization, stability, safety assessment, nutrition

### Introduction

Microbial phytases are potentially excellent candidates for eliminating anti-nutrients from plant-based diets due to their natural activity of breaking the phospho-monoester linkages present in the phytates (Singh et al. 2020, Kumari and Bansal 2021). The sector for food enzymes is increasing at a speed of 5%–9% every year, but the global requirement for phytase is not supplied due to higher production and operational costs (Kumari et al. 2016, Sapna and Singh 2017). The expense for the production of an enzyme is generally supposed by the key components that were employed throughout the formulation of the enzyme. In this respect, the use of statistical approach in various bioprocessing practices has attracted substantial attentiveness to optimize the production of phytases (Kumari et al. 2016, Sapna and Singh 2017, Singh et al. 2020, Kumari and Bansal 2021). In statistical analysis, the model of experiments has been recognized as an effective setup that permits

to examine the reciprocal relatedness amid distinct variables throughout an extent of values, while keeping the number of lab experiments to a minimum (Buddhiwant et al. 2016, Kumari and Bansal 2021). Previous studies have shown that statistical technique has improved phytase production in solid-state fermentation (SSF) significantly as compared to classical approaches (Singh and Satyanarayana 2008, Bhavsar et al. 2013, Sapna and Singh 2014, Kumari et al. 2016).

In the food industry, the usage of phytase promotes nutritional advantages by liberating inorganic phosphorus and other macro- and micro-nutrients (particularly trace minerals and vitamins) complexed with phytic acid. Daily phytate intake is expected to be 2000–2600 mg/day for vegetarian meals and diets (Lopes et al. 2021). Its usage in the unbound form is constrained by the decrease of activity under the unfavorable circumstances of digestion, low stability, and high commercial cost (Lopes et al. 2021).

Received: September 26, 2022. Revised: November 16, 2022. Accepted: December 23, 2022  
© The Author(s) 2022. Published by Oxford University Press on behalf of Applied Microbiology International. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com



## Biochemical Activities of Saracaasoca: An Endangered Plant

Dr.K.Rajalakshmi,<sup>1</sup> Dr Manisha,<sup>2</sup> Dr.S.Bhavya,<sup>3</sup> Dr. Priyanka Shankarishan,<sup>4</sup>  
Dr. Bilman Kumar Sarma<sup>5</sup>

<sup>1</sup>Assistant professor in Chemistry, Shrimati Indira Gandhi College (affiliated to Bharathidasan University), Tiruchirapalli 620002

<sup>2</sup>Associate Professor and Head of Botany Department, Chinmaya Degree College, BHEL, Haridwar

<sup>3</sup>Assistant Professor Department of Biochemistry, Mahalashmi Women's College of Arts and Science (Affiliated to University of Madras), Chennai - 71

<sup>4</sup>Assistant Professor, Department of Applied Biology, University of Science and Technology Meghalaya (USTM), India

<sup>5</sup>Assistant Professor, Department of Zoology, Rangapara College

### Abstract

The phytochemical relationship between the antibacterial and antioxidant properties of various *Saracaasoca* (Roxb.) explant extracts is discussed in this report. *Wilde de* Alkaloids, flavonoids, glycosides, saponins, phenols, steroids, tannins, and triterpenoids were found in the various extracts (bark, flower, and leaves) that were the subject of the preliminary phytochemical analysis that was carried out in the current investigation. Methanolic, ethanolic, and aqueous extracts were used to estimate phenols and flavonoids quantitatively. The disk diffusion method was used to test the antibacterial activity of various *S. asoca* explant extracts against gram positive and gram negative bacteria. The compounds' antibacterial activities were compared to those of a standard strain, and the evaluated and presented antibacterial properties of the imine base and its solvent extract indicate that the compounds play an active role. At 200 g/L-1, methanol bark extract had the highest DPPH, or radical scavenging activity—a measure of antioxidant property—following the order Ascorbic acid > Bark extract of *S. asoca*, while at higher concentrations, the same order followed by Bark extract changed positions. The current study confirms the photochemical, antibacterial, and antioxidant properties of every *S. asoca* plant extract.

DOI Number: 10.48047/NQ.2022.20.11.NQ66963

NeuroQuantology 2022; 20(11):9672-9677

9672

### Introduction

Plants are without a doubt an excellent source of natural products with biological activity. It is essential to have access to straightforward biological tests when researching bioactive natural compounds in order to identify required activities (Sener et al., 1994). The IUCN has designated this species as "globally vulnerable" in 2013. [www.iucnredlist.org/apps/redlist/details/34623/0](http://www.iucnredlist.org/apps/redlist/details/34623/0). *Saracaasoca* is a restoratively significant and universally weak plant species

tracked down in the evergreen backwoods of India (Thakur et al., 1989). India is often referred to as the world's medicinal garden, and *Saracaasoca* is widely regarded as one of the most widely used plants from antiquity to the present day. *Roxb. saracaasoca* The small evergreen tree known as *De Wilde* is a member of the family *Caesalpiniaceae*. It is also known as *Asoka*, *Sita Asoka*, and *Haempushpam*. With a height of 9 meters, it is an evergreen tree. The flowers are arranged in dense corymbs and





## A Review of Therapeutic Herbs

**Dr Manisha<sup>1</sup>**

Associate Professor and Head of Botany Department  
Chinmaya Degree College, BHEL, Haridwar, Uttarakhand  
[manisha26solanki@gmail.com](mailto:manisha26solanki@gmail.com)

**Dr T. Natarajan<sup>2</sup>**

Associate Professor / Reader, Department of Maruthuvam  
Nandha Siddha Medical College and Hospital , Erode , Tamilnadu- 638052  
[drnataraj88@gmail.com](mailto:drnataraj88@gmail.com)

**Prof. Dr. Jayesh Gujarathi<sup>3</sup>**

Professor in Chemistry, Pratap College Amalner Autonomous  
[jayeshgujarathi496@gmail.com](mailto:jayeshgujarathi496@gmail.com)

**Dr Arti Gupta<sup>4</sup>**

Prof of Chemistry, Affiliation Jiwaji University, Gwalior  
[artiguptachemistry@gmail.com](mailto:artiguptachemistry@gmail.com)

### ABSTRACT

Prehistoric people employed medicinal herbs. In emerging nations, medical plant and herbal product preservation, purity, and efficacy are becoming major concerns. Vedas, Quran, and Bible reference herbal treatments and healthcare products extensively. For centuries, medicinal herbs have been used to flavor and preserve food, cure illness, and prevent epidemics. Almost all cultures have prioritized medicinal herbs. Many of the medicines we use today come from plants. Good-for-you herbs have been used for millennia to cure ailments, flavor food, and prevent sickness. The way plants work on a biological level is determined by their secondary metabolites. Plant products regulate microbial development. People have known for a long time that they can help with health problems. Plants have been a great source of natural compounds that are good for human health, especially in the last ten years when natural medicines have been studied in more depth. Herbal treatments for cancer are safe and work well. Chemicals made by a plant's secondary metabolism give it biological abilities that are used all over the world to treat infectious diseases.

**Keywords:** Medicinal plants, Phytochemistry, Herbal medicine, Secondary metabolites

## Studies on effects of nitrogen and phosphorus on wheat crop growth and production

Dr. Korla Swapnavahini<sup>1</sup>, Dr. Manisha<sup>2</sup>, Dr. N. Baratha Jyothi<sup>3</sup>, Dr Manisha Atul Bora<sup>4</sup>, Dr. T. Ramesh<sup>5</sup>

<sup>1</sup>Assistant Professor, Department of Biotechnology, Dr B.R. Ambedkar University, Srikalakulam, Etcherla - 532410  
<sup>2</sup>Associate Professor and Head of Botany Department, Chinmaya Degree College, BHBL, Haridwar, College is affiliated to Hemwati Nandan Bahuguna Garhwal University, Srinagar, Garhwal  
<sup>3</sup>Assistant Professor In Zoology, Maris Stella College (A) Vijayawada, NTR district, Andhra Pradesh, India  
<sup>4</sup>Associate Professor in Chemistry, B.J.S.'S Arts, Science & Commerce College, Wagholi Pune, Maharashtra India 412207, Affiliated to S. P. Pune University  
<sup>5</sup>Scientist, G.S. Gill Research Institute, a Unit of Guru Nanak Educational Society, Affiliated to University of Madras, Guru Nanak Salai, Velachery - 42

### Abstract

Nitrogen (N) and phosphorus (P) are the main supplements for crop creation. In a plant cell, the N helps make the structural, genetic, and metabolic compounds. N is primarily a necessary component of chlorophyll, the plant compound that is responsible for photosynthesis. The plant can get the nitrogen it needs from the soil by mineralizing organic materials. Bacteria can fix nitrogen, and the plant can release nitrogen as residue decays. Minerals in the soil don't release enough nitrogen to support plants; consequently, high production necessitates fertilization. Phosphorus plays a role in the complex structure of plants' nucleic acids. Regulation of protein synthesis requires the nucleic acid; along these lines, P is significant in cell division and improvement of new plant tissue. P is one of the 17 fundamental supplements for plant development and connected with complex energy changes in the plant. High-dose application of N and P fertilizers was once a major factor in crop production and productivity growth. Nitrogen (N) and additionally phosphorus (P) accessibility can restrict development of essential makers across the majority of the world's amphibian and earthly environments. These limitations are ordinarily beaten in agribusiness by applying manures to further develop yields. However, excessive anthropogenic N and P inputs have a negative impact on natural environments and have far-reaching ecological and evolutionary repercussions for entire ecosystems as well as individual species. A global fertilization experiment with significant redistribution of nutrients across various ecosystems can be viewed as the extent to which global N and P cycles have been disrupted over the past century. In this study, we investigate how the availability of N and P influences organisms' stoichiometry and genomic characteristics, which in turn can influence: i) abundances of plants and animals; ii) population dynamics and interactions among trophics; and (iii) the productivity of agricultural crops and the dynamics of the ecosystem. In order to gain a deeper comprehension of how bioavailable N and P travel through the environment and ultimately affect biodiversity and ecosystem services, our research priorities are outlined. However, adding chemical fertilizers to crops for an extended period of time has negative consequences, such as diminishing returns and no increase in crop productivity. In terms of nitrous oxide gas, one of the greenhouse gases, and eutrophication caused by P pollution in water streams, high doses of chemical fertilizers are a major contributor to climate change. This chapter discusses the importance of N and P to plants and the environment, as well as how efficiently they are used.

**Keywords:** nitrogen use efficiency, phosphorus, yield, phosphorus and agriculture.

### INTRODUCTION

Crop nitrogen use efficiency (NUE) in world wheat creation has been assessed to be wasteful with just a normal of 33% of prepared N being recuperated during creation. The most common causes of N loss in soil are denitrification from excessive rainfall and nitrate leaching. In the Indian Wheat Belt, ongoing fertilizer management procedures have resulted in the loss of nitrogen to ground and surface water. One of the primary reasons for the low NUE of ongoing fertilizer management processes has been cited as excessive application of nitrogen prior to planting as an example of insufficient coordination between N applications and the requirements of the crops. As indicated by the USDA, for the last twenty years, near 150 kg ha<sup>-1</sup> has been the standard N application sum in the Wheat Belt locale of the INDIA, and around 75% of N applications, including the past fall, was applied prior to planting. The standard utilization pace of mineral N in the dirt for Wheat for the initial 3 weeks subsequent to rising up out of the ground is under 0.5 kg ha<sup>-1</sup> every day. After the first three weeks, the Wheat plant consumes approximately 3.7 kg ha<sup>-1</sup> per day of nitrogen until it reaches the tasselling stage. The highest rate ever recorded was a consumption of 6 kg ha<sup>-1</sup> per day (J.S. Scheepers, personal communication). Before the plant reaches its peak N uptake phase, early season leaching of preplant nitrogen applications to areas below the crop-rooting zone is dependent on the current soil and weather conditions. The plant can begin denitrification several weeks before it enters its active uptake phase, so introducing a large amount of available N into the soil profile is risky because it runs the risk of being lost to leaching. As the pace of N manure applied in a solitary pre-plant N application increments, the effectiveness of the N application will diminish. NUE, on the other hand, has been observed to rise when applied during the growing season as opposed to prior to planting. To increase NUE, it has been suggested that N should be applied when crops require it.

## Survey of critically endangered flora of Western Ghats of India

Dr Manisha<sup>1</sup>, Dr. N. Baratha Jyothi<sup>2</sup>, Dr Bir Abhimanyu Kumar<sup>3</sup>, Dr. I. Jayashree<sup>4</sup>, Dr. DH. Geetha<sup>5</sup>

<sup>1</sup>Associate Professor and Head of Botany Department, Chinmaya Degree College, BHEL, Haridwar, College is affiliated to Hemwati Nandan Bahuguna Garhwal University, Srinagar, Garhwal

<sup>2</sup>Assistant Professor In Zoology, Maris Stella College (Autonomous) Vijayawada

<sup>3</sup>Deputy Director, Student Registration Division, IGNOU New Delhi

<sup>4</sup>Assistant Professor, Department of Botany, Vellalar College for Women (Autonomous) Erode- 638 012

<sup>5</sup>Assistant Professor, Department of Botany, Vellalar College for Women (Autonomous) Erode- 638 012

### Abstract

The Mountains of the Western Ghats are the second most significant haven on the planet for compromised species. The ongoing paper is an endeavor to concentrate on the protection evaluation of intriguing, jeopardized furthermore, compromised species (RET) of the southern Western Ghats. When a species is in danger of extinction, it is considered endangered. Since before recorded history, innumerable species have become terminated from normal cycles. The current review was directed to recognize the uncommon, imperiled and undermined endangered plants in Western Ghats of Tamil Nadu, India. Concerns about the growing number of threatened species worldwide have increased. Formative tasks, and expanded reliance on woodlands both for food and job have delivered numerous species compromised. More than 150 species in India are in danger of extinction and require immediate intervention to maintain their populations. Various plant species are horrendously removed exclusively from the woods. Aside from anthropogenic dangers, a few animal varieties are undermined due to obtrusive species and environmental change. The only viable option for saving many species from extinction is species recovery in light of growing and ongoing threats. Here, we audit the current recuperation programs in the nation and propose a complete move toward in the protection and recuperation of large numbers of the fundamentally imperiled species. We feature issues that should be tended to and talk about techniques for recuperating the fundamentally imperiled species in the country. Between 2021 and 2022, the Western Ghats RET-listed climbing species were collected and identified. The assortment and distinguished RET plant species from the review were chosen from various slopes (woodland) of Western Ghats. During the work they chose concentrate on locales were visited, plant examples were gathered and methodically squeezed, put away for recognizable proof.

**Keywords:** Endangered plants, ecological interactions, genetic enrichment, niche modelling, species recovery, western ghats

### INTRODUCTION

Concerns about the growing number of threatened species worldwide have increased. Many species are in danger due to development projects and an increasing reliance on forests for food and income. More than 150 species in India are in danger of extinction and require immediate intervention to maintain their populations. Several plant species are only harvested destructively from forests. Invasive species and climate change also pose a threat to a number of species, in addition to those caused by human activity. In the radiance of expanding and proceeded with dangers, species recuperation is the main feasible choice for reestablishing a significant number of them from elimination. Here, we survey the current recuperation programs in the nation and propose a thorough methodology in the preservation and recuperation of a considerable lot of the fundamentally imperiled species. We feature gives that should be tended to and examine methodologies for recuperating the fundamentally imperiled species in the country.

### Background

India is regarded as one of the world's mega-diversities due to its abundance of flowering plants. One-third of the 18,000 flowering plant species discovered in India are thought to be endemic to the Western Ghats. Among the 5,000 species that were reported, there were nearly 1600 endemic species of trees, shrubs, climbers, and herbs. The Western Ghats are home to 54 monotypic genera. In terms of the concentration of endemic taxa and floristic composition, the southern Western Ghats are by far the richest region. Rain forests frequently contain climbers. There are more species in climbing plant taxa than in non-climbing taxa. It is believed that highly diversified clades should exhibit greater genetic differentiation between populations. There are more species in climbing plant taxa than in non-climbing taxa. The majority of lianas can only be found in tropical forests, where they can make up to 45 percent of the woody stems and 35 percent of the total number of woody plant species. Climbing plants can be found in any forest and anywhere else on earth. Endemic species are more helpless against annihilation than additional inescapable species on account of their restricted geographic reaches and consequently have become one of the best proxies for distinguishing preservation needs. Priority areas or hotspots where biodiversity is most in danger must be identified when conservation resources are limited. An important insight into the biogeography of a country or geographical region can be gained from the endemism of its flora, as well as from its diversity centers and centers of adaptive evolution.



## 16. EFFECTS OF TWO CONCENTRATIONS OF SULPHUR DIOXIDE FUMIGATION ON PHASEOLUSAUREUS

Madhu Sharma\*, Manisha<sup>1</sup>, Jyoti S. Parashar<sup>2</sup>

1-Department of Botany, Chinmaya Degree College, Haridwar, Uttarakhand (India)

2-M.P. Bhoj (Open) University, Bhopal. (India)

### ABSTRACT

The effect of SO<sub>2</sub> on growth, Chlorophyll, protein and total free amino acids of *Phaseolus aureus* (Green Gram or moong) was investigated by exposing to 0.5 ppm and 1 ppm of SO<sub>2</sub>. The experiments were performed at Central Institute of Agriculture, Engineering, Nabi Bagh, Bhopal (M.P.). 0.5 ppm and 1 ppm of SO<sub>2</sub> was given to 20 days old plants for thirty days. Results were noted for 30, 45, 60, 75, 90, days old plants. Total free amino acids and Chlorophyll were quantified. Exposure of plants, developed visible injury symptoms & suffered growth reductions. Amount of chlorophyll decreased in the leaves due to SO<sub>2</sub> fumigations. There was an increase in total free amino acid in the leaves of total free amino acid in the leaves of fumigated plants over control, respectively.

- Keywords : Chlorophyll, Amino acid, SO<sub>2</sub> Pollution.

### Introduction

India today is one of the first ten industrial countries of the world. She has reached to a stage of development where transformation is taking place from an agricultural base towards an industrial core associated with good industrial infrastructure there is also increase in the number of effluents and emissions particularly poisonous gases in the atmosphere primary offenders include SO<sub>2</sub>, fluoride, ozone and oxides of nitrogen along with particulate matter like cement, soot, kiln and lead particles. SO<sub>2</sub> is the major air pollutant and its concentration in the atmosphere of some industrial cities is relatively high. The phyto-toxicity of SO<sub>2</sub> is due to its acidic nature and formation of sulphides. Green plants serve as a natural sink for air pollutants by providing enormous surface of expanded leaves for the absorption and setting of gases and particulate matter. They are silent sufferers in a polluted atmosphere and they express their sufferings in the form of foliar injury and reduction in growth and yield. The present study has been undertaken to study the effects of SO<sub>2</sub> on *Phaseolus aureus* Roxb. Syn. *Vignaradiata* L. wilczek (greengram) variety. K-851 belongs to family Leguminosae.

### Materials and Method

The leaves of test plant *Phaseolus aureus* Roxb. was collected from both control and fumigated plant for morphological study and biochemical analysis. The following parameter like chlorophyll were determined using spectrophotometer (Duxbury and Yentsch, 1956; McLachlan and Zalik, 1983). Total free amino acids were determined with use of ninhydrin (Lee and Sashi, 1966). Nitrogen contents were estimated from the oven dried leaf samples. The samples