

Bharati Vidyapeeth's Dr. Patangrao Kadam Mahavidyalaya,
Sangli
and
Jaysingpur College, Jaysingpur

Action Taken Report
Under
MoU
For Academic Year 2021-22

Estd. - June 1964

Anekant Education Society's

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JAYSINGPUR COLLEGE, JAYSINGPUR

of Arts, Commerce, Science & Computer Science

Jaysingpur - 416 101 Dist. Kolhapur, Maharashtra State, India

AFFILIATED TO SHIVAJI UNIVERSITY, KOLHAPUR

ACCREDITED AT THE 'A' LEVEL BY NAAC - UGC

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e-mail - jspcollegejsp@gmail.com

Ref. No. AES/JCJ/

Date: - 03/12/2021.

To,
Dr. A. R. Supale,
Department of Chemistry
Dr. Patangrao Kadam Mahavidyalaya,
Sangli wadi

Dear Sir,

You have worked as **Invited lecturer** for M.Sc. -II, (Analytical chemistry) on the topic **Thermodynamics** in our college during the year 2021-22. We are very much thankful to you for sharing your academic excellence with our students. We expect the same kind of co-operation from you in future.

Thanking you in anticipation



Yours,

(Signature)
03/12/2021

Co-ordinator

M.Sc. (Analytical chemistry)

Co-ordinator

M.Sc. Chemistry

Jaysingpur College, Jaysingpur

Estd. - June 1964

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Ref. No. AES/JCJ/

Date: - 10 /12 /2021.

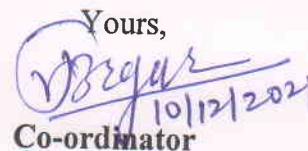
To,
Dr. A. R. Supale,
Department of Chemistry
Dr. Patangrao Kadam Mahavidyalaya,
Sangli wadi

Dear Sir,

You have worked as **Invited lecturer** for M.Sc. -II, (Analytical chemistry) on the topic **Cyclic Voltametry** in our college during the year 2021-22. We are very much thankful to you for sharing your academic excellence with our students. We expect the same kind of co-operation from you in future.

Thanking you in anticipation

Yours,


10/12/2021
Co-ordinator



M.Sc. (Analytical chemistry)

Co-ordinator

M.Sc. Chemistry

Jaysingpur College, Jaysingpur



'Social Transformation Through Dynamic Education'

Bharati Vidyapeeth's

Dr. Patangrao Kadam Mahavidyalaya, Sangli

(Arts, Science & Commerce College)

Affiliated to Shivaji University, Kolhapur.

Accredited with 'B⁺⁺' Grade by NAAC, Bengaluru (CGPA 2.96)

DST-FIST Funded College (Level-0)

Founder

Dr. Patangrao Kadam

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Principal

Dr. D. G. Kanase

M. Sc., Ph. D.

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No.: B.V.D.P.K.M.S./

/2021-2022

Date: 31/05/2022

To,
Dr. S. R. Sabale
Department of Chemistry,
Jaysinpur College,
Jaysinpur.

Dear Sir,

We are very much thankful to you for working as Resource person to deliver guest lectures for M.Sc. I and II year class on topics 'Chromatographic Methods and Advanced Gas Chromatographic Techniques' respectively, during academic year, 2021-22..

Expecting the same co-operation in future.

Thanking you in anticipation.

Best Regards,

(Dr. A. R. Supale)

Co-ordinator,
M.Sc. (Analytical Chemistry),
Dr. Patangrao Kadam Mahavidyalaya,
Sangli.



Anekant Education Societys
Jaysingpur College Jaysingpur



Bharati Vidyapeeth's
Dr. Patangrao Kadam Mahavidyalaya, Sangli

One Day Seminar on
Research Methodology

Organized by
Research & Development Cell

Wednesday, 18th May 2022@ 8.30 am

Guest Speaker

Dr. Suraj D. Umdale
Assistant Professor
Department of Botany,
Jaysingpur College, Jaysingpur.

Dr. S. R. Sabale
Coordinator

Dr. A. R. Supale
Coordinator

Prof. Dr. M. V. Kale
Ag. Principal

Prof. Dr. D. G. Kanase
Principal

Jaysingpur College, Jaysingpur

Dr. Patangrao Kadam Mahavidyalaya

Registration link- <https://forms.gle/EAiUK4XWJPYeUfGq7>

Joining link- <https://bit.ly/rmw2022> (On Microsoft Team Platform)

All students & Research Scholars are cordially invited for the Lecture

Monitoring and Assessment of Water Quality using Multivariate Statistics of Physico-chemical Parameters to establish Baseline Level around proposed Jaitapur Nuclear Power Plant (JNPP), India

Shinde R.D.¹, Burungale S.H.², Supale A.R.³, Chikode P.P.¹ and Sabale S.R.^{1*}

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Abstract

This study illustrates the usefulness of multivariate statistical techniques to provide straightforward data interpretation as well as valuable insights of datasets to get better information about the water quality and helps to design monitoring networks for effective management of available water resources. In this study, Multivariate statistical analysis, Cluster analysis, Principal Component Analysis, Factor Analysis, Water Quality Index and Piper diagram are used to analyze the water data and to prepare the baseline of water parameters around the proposed JNPP. Piper diagram indicates that the primary salinity ("non-carbonate alkali") exceeds 50 % which means that the chemical properties of water are dominated by alkalis and strong acids. Water quality indices indicate that water is non-polluted and fully fit for drinking purposes.

Principal component analysis and factor analysis applied for water parameters point towards the common source of minerals and high level of dissolved organic matter. Trace metal analysis shows significant but little participation of zinc, copper, nickel, iron and barium in water quality. The baseline developed and the data obtained will be useful for the water quality analysis after post-plant operation in this region.

Keywords: Water, JNPP Region, Physico-chemical parameters, Multivariate Statistics, Baseline.

Introduction

Safe water is a basic human right and pre-condition for health and development, yet it is still denied to millions of people of the developing world. Poor sanitation and hygiene coupled with insufficient safe water cause water-related diseases leading to 3.4 million deaths per year and most of them are children^{21,23}. India in 1974 enacted 'The Water Act' for prevention and control of water pollution to maintain and restore purity of water in the country. The act was further amended in 1992 and 2003. Currently, India's environment has become fragile and is of concern because of increasing industrialization, urbanization and growth in population⁹. Water quality expresses the suitability of water to sustain

various uses and processes. Every use or process requires certain physical, chemical and biological characteristics of water. Physical and chemical parameters of water are easily defined and hence, criteria set for water quality are largely based on physical and chemical conditions of the water. Biological methods of analyzing water quality are based on a diversity index derived from information theory. These indices express the relative importance of species, also they are dimensionless and independent of the sample size collected.

Once the water gets contaminated, it is difficult to restore its quality. Consequently, directly or indirectly everyone gets affected. Heavy metal contamination is a major problem in several communities and agricultural areas. Commercial agrochemicals, sewage water and industrial wastewater are the measured sources of heavy metal contamination^{15,16,25}. The contamination in an aquatic community is of major concern because of its toxicity, abundance and persistence in the environment. This may contaminate the aquatic ecosystem or public health^{4,22}. Thus the analysis of water quality is important to preserve the environmental system.

The application of basic and multivariate statistical methods including Cluster analysis (CA), Principal Component Analysis (PCA), Factor Analysis (FA) and Water Quality Index (WQI) for the investigation of water quality data are widely found in literature^{2,3,8,24,26}. Government has responded to the water findings by implementing required appropriate action plans at diverse locations⁶. Hence it is important to provide the detailed composition of water parameters to help the local environmental policymakers.

Study area

Jaitapur is a small village situated in the Rajapur Tehsil of Ratnagiri District, Maharashtra. It lies on the Arabian Sea coast. Nuclear Power Corporation of India Limited (NPCIL) proposed a Nuclear Power Plant with a 9900 MW capacity near Jaitapur. This project is located at 16.55° N; 73.35° E, a part of Konkan in the Western Ghats of Maharashtra. The issue was highlighted by different non-governmental organizations because of the adverse effects of radiation and different types of pollution. Also, many other industries like thermal power, mining of aluminium etc. are being constructed in this Konkan region. This Konkan region is famous for mango production and export especially



Green synthesis of magnetite nanoparticles (Fe_3O_4 NPs) using *Acacia concinna* fruit extract and their antibacterial activity

Shubhangi Mane-Gavade, Arihant Malgave, Gurunath Nikam, Amruta Koli, Amit Supale, and Sandip Sabale*

This paper describes green, simple, and efficient method for the synthesis of magnetite nanoparticles (Fe_3O_4 NPs) using *Acacia concinna* fruit extract for the first time. *A. concinna* fruit extract is used as reducing and stabilizing agent. Reduction of Fe^{3+} ions by *A. concinna* fruit extract is examined by UV-visible absorption spectra (UV-Vis-NIR). To recognize the functional group responsible for Fe_3O_4 , the NPs are characterized by Fourier transform infra-red spectroscopy (FTIR). The structural analysis of Fe_3O_4 NPs is done by X-ray diffraction (XRD) which confirms cubic spinel structure and the average crystallite size of obtained NPs is found to be 28 nm. The morphological studies of Fe_3O_4 NPs are done by scanning electron microscope (SEM) which depicts the quasi-spherical morphology. The green synthesized Fe_3O_4 NPs shows distinctive antibacterial activities against gram-negative *E. coli* and *Pseudomonas aeruginosa* microorganism which confirms its potential in biomedical applications.

These potential applications of Fe_3O_4 NPs have inspired the fast development of various synthetic techniques such as coprecipitation, hydrothermal treatment, spray pyrolysis, ultrasound irradiation, microwave-assisted method, and solvothermal method.^[4,5] While, most of these methods rely on the use of toxic reducing agents and special equipment which make them less eco-friendly and costly. Hence, there is urgent need to develop environmentally benign methods, where, natural products could be used that are biocompatible, low cost, and easily available and one such method is the green synthesis.^[6] It makes use of plant extracts that acts as an efficient reducing and capping agent in Fe_3O_4 NPs synthesis. It is economic and valuable alternative with toxic free approach.^[7]

Many researchers reported the synthesis of Fe_3O_4 NPs using *Artemisia annua*,^[8] leaf extract of *Perrilla frutescens*,^[9] *Tridax procumbens*,^[10] and *Caricaya papaya*,^[11] peel extract of *plantain*,^[12] and also seed extract of grape *proanthocyanidin*.^[13] However, no literature reports are available for the synthesis of Fe_3O_4 NPs using aqueous fruit extract of *Acacia concinna*.

In the present work, we report simple green route for the synthesis of magnetite NPs using *A. concinna* fruit extract. The phytochemicals present in *A. concinna* fruit extract are not only responsible for the formation of Fe_3O_4 NPs but also act as capping agent for Fe_3O_4 NPs. *A. concinna* is relatively large genus of plants belonging to *fabaceae* family^[14]. The synthesized Fe_3O_4 NPs were characterized using different characterization techniques and tested against pathogenic microorganisms.

1. Introduction

Magnetic nanoparticles (MNPs) have been attracting much attention because of their probable applications either as photocatalysis, ferro fluid technology, drug delivery, pigment, magnetic storage, magnetic ink printing, microwave absorption, biosensors, bio-separation, and in vivo drug delivery.^[1,2] Particularly, magnetite nanoparticles (Fe_3O_4 NPs) have attracted enormous interest, due to their unique magnetic properties, high electrical resistivity, and high chemical stability. It is often known that the activity of Fe_3O_4 NPs strongly depends on their size, shape, and crystal phase.^[3] Generally, the shape has a huge impact on the resulting properties of Fe_3O_4 NPs and their potential applications.

2. Result and Discussion

2.1. Morphological and Structural Properties of Fe_3O_4 NPs

Scanning electron microscope (SEM) was used to examine the surface morphology and structure obtained Fe_3O_4 NPs. **Figure 1A** shows representative SEM images of Fe_3O_4 NPs produced by *A. concinna* fruit extracts during the biosynthesis reaction. The morphology observed was quasi-spherical and several agglomerates can be appreciated. Various studies describe this agglomeration as a steric effect caused by the interaction of the active sites of the

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EDITORIAL

Role of Nutrition in COVID-19: Present Knowledge and Future Guidelines

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COVID-19 pandemic has become a serious threat to human beings, which is badly affecting the lives of mankind. The causative agent of COVID-19 is a novel coronavirus (SARS-CoV-2) that causes severe acute respiratory syndrome. The COVID-19 infection has been transmitted from animals to humans, and now it has spread astoundingly worldwide. In a severe case of COVID-19 disease, atypical pneumonia leads to the death of a diseased person. Some risk factors associated with COVID-19 include older age, smoking, cardiovascular disease (CD), obesity, respiratory diseases (RD), and a higher Sequential Organ Failure Assessment score. Due to the unavailability of effective drugs against COVID-19, people have been forced to implement strict regulations, including social distancing and lockdown. These restrictions have affected human populations in various aspects, viz., psychological, social, economic, etc. Although few vaccines have been developed, such as covishield, Sputnik, and covaxin, etc., still the question remains about their efficacy and how to prevent re-infection among fully vaccinated people.

However, several reports suggested that fully vaccinated individuals also get infected by mutated strains of SARS-CoV-2, and developing disease with less severity [1]. Few drugs like chloroquine, hydroxychloroquine, remdesivir, nirmesirvir, nafamostat mesylate, remdesivir, etc., were used for COVID-19 treatment, but still, these drugs could not be the final solution against COVID-19 [2].

Structural bioinformatics studies would play an essential role in understanding the basic mechanism behind using few specific drug in COVID-19 [3]. However, we are still unaware about the exact role of nutrition and its modulation on the epidemiology of COVID-19 disease. Hence, in the present context, the evaluation of the relation between nutrition and the COVID-19 pandemic has been done. While searching the solution to COVID-19, it has been suggested that the nutritional status of an individual may alter the immune system positively or negatively; hence it has a big role to play in the modulation of SARS-CoV-2 infection [4].

Due to the lockdown during COVID-19, the eating habits of people have changed, which has led to the weakening of the immune system, and because of that, people may suffer from chronic disease in the future [5]. A balanced diet can boost the immune system, which will help to fight against many types of infections, including SARS-CoV-2, and live a healthy life. Another major aspect that is being ignored during this COVID-19 pandemic is that due to strict regulations, people have been quarantined to protect themselves from SARS-CoV-2 infection. This has changed the eating habits and daily routine of people, which could result in increased energy intake by consuming large amounts of fats, carbohydrates, and proteins. This high energy intake could have serious effects on some disease conditions like diabetes, heart disease, kidney disease, as well as COVID-19. Hence, there is an urge to shift our focus towards food intake that will play a significant role in keeping us healthy and functioning normally [6]. It has been strongly proposed that reduced obesity could be very helpful to minimize the chances of type 2 diabetes as well as severe COVID-19 disease [7]. Vitamin C is one of the best nutrients which can help to improve the immune system of an individual [8]. The change in nutrient supplements and their effects on the immune system in different age groups must be well understood during and after COVID-19 [9]. Importantly, it has been directed that minerals, vitamins C, A, D, and zinc play crucial roles in boosting the immune system during COVID-19. In viral, bacterial, fungal, and parasitic infections, the host's immune system is important for the protection and fight against these pathogens. The quick action of the immune system against foreign enemies can increase the metabolic rate; hence there is a requirement of good energy sources for the biosynthesis of regulatory molecules. In such circumstances, vitamins such as folate, A, B6, B12, C, D, and E, as well as trace minerals such as copper, iron, selenium, and zinc, have been found to play important roles in supporting the immune system and reducing infection risks. All these nutrients could play important role in supporting the antiviral and antibacterial defence system. Similarly, the gut microbiota could also be critical for regulating the host immune system [9, 10].

The plant-based food materials have been found to enhance the immunity against COVID-19 in all age groups [11]. Several plant-based food items have been shown to boost intestinal beneficial bacteria, which contributes to an immune system that is

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Structural significance of Nephrylsin from *Streptococcus suis* GZ1 in the degradation of A β peptides, a causative agent in Alzheimer's disease

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A β plaque degradation
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Molecular docking
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ABSTRACT

Alzheimer's disease (AD) is a progressive brain disorder. The accumulation of amyloid beta (A β) peptides in the human brain leads to AD. The cleavage of A β peptides by several enzymes is being considered as an essential aspect in the treatment of AD. Nephrylsin (NEP) is an important enzyme that clears the A β plaques in the human brain. The human NEP activity has been found reduced due to mutations in NEP and the presence of inhibitors. However, the role of NEP in the degradation of A β peptides in detail at the molecular level is not yet clear. Hence, in the present study, we have investigated the structural significance of NEP from the bacterial source *Streptococcus suis* GZ1 using various bioinformatics approaches. The homology modelling technique was used to predict the three-dimensional structure of NEP. Further, molecular dynamic (MD) simulated model of NEP was docked with A β peptide. Analysis of MD simulated docked complex showed that the wild-type NEP-A β -peptide complex is more stable as compared to mutant complex. Hydrogen bonding interactions between NEP with Zn²⁺ and A β peptide confirm the degradation of the A β peptide. The molecular docking and MD simulation results revealed that the active site residue Glu-538 of bacterial NEP along with Zn²⁺ interact with His-13 of A β peptide. This stable interaction confirms the involvement of NEP with Glu-538 in the degradation of the A β peptide. The other residues such as Glu203, Ser537, Gly140, Val587, and Val536 could also play an important role in the cleavage of A β peptide in between Asp1-Ala2, Arg5-His6, Val18-Phe19, Gly9-Tyr10, and Arg5-His6. Hence, the predicted model of the NEP enzyme of *Streptococcus suis* GZ1 could be useful to understand the A β peptide degradation in detail at the molecular level. The information obtained from this study would be helpful in designing new lead molecules for the effective treatment of AD.

1. Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder that causes an irreversible and gradual decline of memory, language skills, perception of time and space, and the ability to care for oneself. Amyloid plaque formation is a pathological hallmark in AD [1,2]. The A β ₁₋₄₀ and A β ₁₋₄₂ peptides are the main constituents of amyloid plaques in AD [3–5]. The familial autosomal dominant (FAD) mutations and improper proteolytic degradation increases A β ₁₋₄₂ and A β ₁₋₄₀ peptides deposition in the brain [6]. In the human brain, the formation of A β peptide is a continuous process, and it is estimated to have a physiological production rate of 7.6% per hour [7]. The enzymes such as Insulin Degrading Enzyme (IDE), Human Endothelin Converting Enzymes (hECE), Angiotensin Converting Enzyme (ACE), Cathepsin B, Cathepsin

D, and Nephrylsin (NEP) present in the human brain are known to play an important role in A β peptide clearance [8–12]. Similarly, in a recent review role of amyloid beta peptide-degrading microbial enzymes and their implication in drug designing has been discussed [13].

The NEP is also known as neutral endopeptidase-24.11 (E.C.3.4.24.11), Enkephalinase, neutrophil cluster-differentiation antigen 10, or common acute lymphoblastic leukemia antigen [14]. The NEP is a 90–110 kDa plasma membrane glycoprotein of the neutral zinc metalloendopeptidase family [15]. In the human brain, NEP is expressed at pre- and post-synaptic membranes and is involved in the regulation of neuropeptide signalling. It is also expressed in the tunica media and endothelium of cortical and leptomeningeal blood vessels, where it is involved in the regulation of vascular tone. *In-vivo* assay with radio labelled A β peptide reported the involvement of NEP enzyme in the

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Exploring bioactive peptides as potential therapeutic and biotechnology treasures: A contemporary perspective

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ABSTRACT

In preceding years, bioactive peptides (BAPs) have piqued escalating attention owing to their multitudinous biological features. To date, many potential BAPs exhibiting anti-cancer activities have been documented; yet, obstacles such as their safety profiles and consumer acceptance continue to exist. Moreover, BAPs have been discovered to facilitate the suppression of Coronavirus Disease 2019 (CoVID-19) and maybe ideal for treating the CoVID-19 infection, as stated by published experimental findings, but their widespread knowledge is scarce. Likewise, there is a cornucopia of BAPs possessing neuroprotective effects that mend neurodegenerative diseases (NDs) by regulating gut microbiota, but they remain a subject of research interest. Additionally, a plethora of researchers have attempted next-generation approaches based on BAPs, but they need scientific attention. The

Abbreviations: AAs, Amino acids; A β , Amyloid β ; ACBPs, Anticancer bioactive peptides; AChE, Acetylcholinesterase; AD, Alzheimer's disease; ADNF, Activity-dependent neurotrophic factor; AEGIS-SELEX, Artificially expanded genetic information system-SELEX; AFM-SELEX, Atomic force microscopy-SELEX; Aib, α -Amino-isobutyric acid; AIDS, ACE-2-interacting Domain of SARS-CoV-2; ALS, Amyotrophic lateral sclerosis; AP-1, Activator protein 1; AQ, Aquashine; BAPs, Bioactive peptides; BACE1, Beta-site amyloid precursor protein (APP) cleaving enzyme-1; Bax, B-cell lymphoma protein 2-associated X; BBB, Blood-brain barrier; BChE, Butyrylcholinesterase; Bcl-2, B-cell lymphoma 2; BCM-7, Betacasomorphin-7; BMP-2, Bone morphogenic protein-2; BR, Brightening; CAS, Catalytic anionic site; Cdk5, Cyclin-dependent kinase 5; CE-SELEX, Capillary electrophoresis-SELEX; CIP, Cdk5 inhibitory peptide; CNT-PLLA, Carbon nanotube-poly-L-lactic acid; CoVID-19, Coronavirus disease 2019; CRF, Corticotrophin-releasing factor; CuAAC, Copper(I)-catalyzed alkyne-azide cycloaddition; OGLcNAc, O-linked N-acetyl-D-glucosamine; cyO8, Cycloviolacin O8; E-PB, Electrochemical peptide-based; EX-4, Exendin-4; FDM, Fused deposition modelling; GAPDH, Glyceraldehyde-3-phosphate dehydrogenase; GLP-1R, Glucagon-like peptide 1 receptor; hACE2, Human angiotensin-converting enzyme 2; HAH, Hyaluronate-alginate hybrid; hCMCs, Human circulating multipotent cells; HD, Huntington's disease; HDMP, Human defensin-6 mimic peptide; hMSCs, Human mesenchymal stem cells; HTT, Huntingtin; IFN- α , Interferon-alpha; IL-6, Interleukin 6; IP-SELEX, Immunoprecipitation-coupled-SELEX; KTN, Keratin; LDH, Lactate dehydrogenase; LTM, Long-term memory; LTP, Long-term potentiation; MB, Methylene blue; MC, Methylcellulose; Mcl-1, Myeloid cell leukemia-1; MERS-CoV, Middle East respiratory syndrome coronavirus; mHTT, Mutant huntingtin; MPP⁺, 1-methyl-4-phenylpyridinium; MPTP, 1-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine; MTT, 3-(4,5-dimethyl thiazolyl)-2,5-diphenyl-tetrazolium bromide; ND, Neurodegenerative disease; NF- κ B, Nuclear factor kappa B; NK, Nattokinase; OBP, Odorant-binding protein; OGP, Osteogenic growth peptide; PA, Peptide amphiphile; PAC1, Pituitary adenylate cyclase-activating polypeptide type 1 receptor; PARP, Poly (ADP-ribose) polymerase; PCNA, Proliferating cell nuclear antigen; PD, Parkinson's disease; PEG, Polyethylene glycol; PEGDA, Polyethylene glycol diacrylate; PEU, Poly(ester urea); pI, Isoelectric point; PLLD, Polylysine dendrimers; PLN, Phospholamban; PEOGMA-PHPMA, Poly(oligo(ethylene glycol) methyl ether methacrylate)-Poly(2-hydroxypropyl methacrylate); PSA, Prostate-specific antigen; PSC, Peptide sesame cake; PTMs, Post-translational modifications; RAFT, Reversible addition-fragmentation chain transfer; RBD, Receptor-binding domain; RBM, Receptor-binding motif; ROS, Reactive oxygen species; SARS-CoV-2, Severe acute respiratory syndrome coronavirus 2; SELEX, Systematic evolution of ligands by the exponential enrichment; SF, Silk fibroin; SHR, Spontaneously hypertensive rat; SIRT6, Sirtuin 6; TAT, Cell penetrating peptide; TNF α , Tumor necrosis factor α ; TP, Tyrosine phosphatase; TPE, Tetraphenylethene; TUNEL, Terminal deoxynucleotidyl transferase dUTP nick end labelling; VEGF, Vascular endothelial growth factor; VIP, Vasoactive intestinal peptide; 3D, Three-dimensional.

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Article

Modifying Thermostability and Reusability of Hyperthermophilic Mannanase by Immobilization on Glutaraldehyde Cross-Linked Chitosan Beads

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Abstract: In the current study, the purified β -mannanase (Man/Cel5B) from *Thermotoga maritima* was immobilized on glutaraldehyde cross-linked chitosan beads. The immobilization of Man/Cel5B on chitosan beads was confirmed by Fourier-transform infrared spectroscopy (FTIR) and X-ray diffraction (XRD) analysis. After immobilization, the protein loading efficiency and immobilization yield were found to be 73.3% and 71.8%, respectively. The optimum pH for both free and immobilized enzymes was found to be pH 5.5. However, the optimum temperature of immobilized Man/Cel5B increased by 10 °C, from 85 °C (free Man/Cel5B) to 95 °C (immobilized). The half-life of free and immobilized enzymes was found to be 7 h and 9 h, respectively, at 85 °C owing to the higher thermostability of immobilized Man/Cel5B. The increase in thermostability was also demonstrated by an increase in the energy of deactivation (209 kJmol⁻¹) for immobilized enzyme compared to its native form (92 kJmol⁻¹), at 85 °C. Furthermore, the immobilized Man/Cel5B displayed good operational stability as it retained 54% of its original activity after 15 repeated catalytic reactions concerning its free form.

Keywords: β -mannanase; docking; hyperthermostable; kinetics

1. Introduction

Mannans are an integral part of hemicellulose and are predominantly found in the soft woods, plant endosperms, seeds, and vacuoles of a wide variety of plants [1–3]. Mannans are also present as glycoproteins in the cell walls of some yeasts, fungi, and bacteria [4]. β -1,4-mannanase (mannan mannohydrolase, EC 3.2.1.78) is an endo-acting hydrolase that randomly cleaves the β -1,4-mannosidic linkages in the main chain of mannans (linear mannan, galactomannan, glucomannan, and galactoglucomannan), therefore producing manno-oligosaccharides (MOS) of various lengths [5]. β -mannanase has wide industrial applications as it is used for the production of partially hydrolyzed guar gum, MOS, fruit juice clarification, paper/pulp bio-bleaching, synthesis of detergents, amelioration of animal or poultry feed, and saccharification of biomass [6,7].

Despite the versatility of β -mannanase, the use of these enzymes in soluble form at the industrial scale has some limitations including low stability, unmanageable recovery and reuse, short shelf life, difficulty in handling, and loss of activity at prolonged operational



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Date : 27 / 06 /2022.

To,
The Principal,
Anekant Education Society's,
Jaysingpur College, Jaysingpur.

Subject: Regarding student exchange program under MoU

Respected Sir/Madam,

Pursuant to the MoU signed between Anekant Education Society's Jaysingpur College Jaysingpur and Bharati Vidyapeeth's Patangrao Kadam Mahavidyalaya, Sangli. The Ph. D. student Burud Mahesh Dileep (NET-JRF) working under the guidance of Dr. A. R. Supale, Assistant professor P.G. Department of Chemistry Bharati Vidyapeeth's Patangrao Kadam Mahavidyalaya, Sangli. Interested in joining the student exchange program at DST-FIST Laboratory, Jaysingpur College Jaysingpur for research work under the guidance of Co-ordinator DST-FIST laboratory Dr. S. R. Sabale, Assistant Professor, Department of Chemistry Jaysingpur College Jaysingpur.

So, kindly request to you do needful.

Thanking you,

Yours faithfully,

A. R. Supale

(Dr. A. R. Supale)

Asst. Professor in Chemistry

Forwarded Through:

Dr. Patangrao Kadam
Principal

Bharati Vidyapeeth's

Dr. Patangrao Kadam Mahavidyalaya, Sangli

Approval
Sabale
27.6.2022

PRINCIPAL

Jaysingpur College, Jaysingpur

To,
The Principal,
for permission

Sabale