CRITERION III - RESEARCH, INNOVATIONS AND EXTENSION

3.3 Research Publications and Awards

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Bangalore-60



Partial purification and characterisation of α -amylases from the digestive tract of the Indian major carp *Labeo rohita* (Hamilton, 1822)

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ABSTRACT

Partial purification of α-amylases from the digestive tract of the Indian major carp *Labeo rohita* (Hamilton, 1822) through acetone fractionation and ion exchange chromatography (DEAE-SephadexA-50) resulted in 8-fold purification with 86% recovery. Characterisation of amylase activity revealed two pH optima at 4.5 and 6.5. Activity was stable over wide pH ranges of 3.5 to 4.5 and 7 to 12. Optimum incubation temperature was 35°C. The enzyme lost 91% activity at 60°C within 15 min and was inhibited by Amylase inhibitor Type-1 (wheat); 1, 10 Phenanthroline; Ethylene diamine tetra-acetate (EDTA) and Phenyl methyl sulphonyl fluoride (PMSF). Heavy metal ions Hg⁺⁺ and Cu⁺⁺ strongly inhibited the enzyme activity, while Zn⁺⁺ and Bi⁺⁺ inhibited to a lesser extent. Native polyacrylamide gel electrophoresis of the purified α-amylase fractions revealed four bands, with corresponding molecular weights of 43.59; 52.36; 55.42 and 54.01 kDa. α-Amylase activity from *L. rohita* exhibited linear hydrolysis of starch upto 7% concentration in 60 min.

Keywords: α-Amylase, Characterisation, Digestive tract, Labeo rohita, Purification

Introduction

The production of freshwater fish in India was 5.29 million t during 2017-18 and about 33% of this production comprised the Indian major carp (IMC) Labeo rohita (Hamilton, 1822) which contributed 1.75 million t next to Catla catla (GOI, 2018). The rohu Labeo rohita (Family Cyprinidae) is the most popular species among the IMCs. In aquaculture operations, feed accounts for 50% of the cost of production and the protein sources for the feed are more expensive than the carbohydrate sources. The protein sparing action of carbohydrate is well known in fishes (Wilson, 1994; Stone, 2003; Krogdohl et al., 2005). Starch, the predominant carbohydrate in fish feed is made available to the fish by the action of α-amylases and therefore understanding the nature of amylases in fish species will pave ways for selection of appropriate carbohydrate source. The information pertaining to the purification of amylases in L. rohita and their characterisation is limited (Moreau et al., 2001; Roychan and Chaudhari, 2001; Kushwaha, et al. 2012). This paper reports on the partial purification and characterisation of α-amylases in L. rohita.

Materials and methods

Enzyme extracts

Specimens of *L. rohita* (average length 45 cm; 995 g) were obtained from the culture ponds of the Regional

Research Centre of ICAR-Central Institute of Freshwater Aquaculture (ICAR-CIFA) at Bangalore, Karnataka, India. The digestive tract (DT) and liver (L) of the specimens were dissected out under ice cold conditions and washed repeatedly with ice-cold distilled water. The tissues were homogenised individually with distilled water (4 ml g⁻¹; 15 g tissue in 60 ml) and centrifuged at 16,000 rpm for 20 min at 4°C. The supernatants (crude enzyme extract) were frozen and stored at -20°C in 20 ml aliquots for use in purification studies.

Enzyme estimation

α-Amylase activity was estimated using 1% starch solution in Tris-HCl buffer (0.1 M, pH 7.0) as the substrate. The assay mixture contained 0.05 ml crude enzyme extract plus 1.0 ml substrate and was incubated at 25°C for 1 h. The resulting reducing sugars were determined by the method of Nelson (1944) and Somogyi (1952) using glucose as the standard. Enzyme activity was expressed as μg glucose liberated per mg protein per hour. Protein in the crude enzyme extract and other enzyme fractions was estimated by the method of Lowry *et al.* (1951) using bovine serum albumin as the standard. All assays were carried out in triplicate.

Acetone fractionation (AF)

The crude enzyme extract obtained was subjected to solvent fractionation by the addition of chilled acetone



Dr. Anuradha. M Principal

Padmashree Institute of Management & Sciences



Original Research Paper

Carotenoid Content in Cherry Tomatoes Correlated to the Color Space Values L*, a*, b*: A Non-destructive Method of Estimation

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ABSTRACT

Cherry tomatoes are rich sources of carotenoids. The carotenoids are known to be precursors of vitamin A and also act as an antioxidant. It is important to visually judge the tomato surface color for higher β carotene content since this is the major provitamin A carotenoid. Estimation of carotenoids by HPLC (High Performance Liquid Chromatography) and spectrophotometric methods in tomatoes are very expensive and time consuming. Therefore, colorimeters can be used to describe the color and determine the carotenoid content in a relatively easy and inexpensive manner. The objective of this study was to determine, if the carotenoid content within cherry tomatoes measured by conventional method could correlate with colorimetric CIE (Commission International del'Eclairage) L*, a*, b* color space values. Strong correlations were found between color surface value a* and total carotenoids (0.82) and lycopene content (0.87). We also observed positive correlation for the b* color value with β carotene (0.86). The L* value was negatively correlated (-0.78) with an increase in carotenoids. These close associations between color space values L*, a*, b* and carotenoids will help the breeders to quickly screen large germplasm/ breeding lines in their breeding program for improvement in carotenoid content through this time saving, inexpensive and nondestructive method at fully ripe stage.

Keywords: β carotene, Carotenoid, Lycopene, Tomato.

INTRODUCTION

Color is one of the important quality parameters of fruits and vegetables. The color of tomatoes is the most important quality character to determine the ripeness. The color of tomatoes is the initial external factor that makes them appealing to the consumer's decision for purchasing them. The complexity of tomato color is due to the presence of a diverse carotenoid pigment system with appearance conditioned by pigment types and concentrations, and subject to both genetic and environmental regulation (Radzevicius et al., 2014). Color of tomatoes is an important desired character which can be achieved by genetic improvement of breeding lines with varying concentration of carotenoids. The tomatoes are harvested and consumed at the red ripe stage of

ripening, which occurs due to the degradation of chlorophyll at green stage and rapid accumulation of carotenoids particularly lycopene and β carotene. In this study, we have assessed surface color differences among the cherry tomatoes and its relation to their total carotenoid, lycopene and β carotene content. Carotenoid content in fruits can be assessed in laboratory through spectrophotometer measurement of tomato fruit extracts, but this method is time consuming and tedious (Lichtenthaler 1987). Colorimeters can be used to determine the carotenoid content in fruits and vegetables in a quick, easy and in a non-destructive manner. In 1931, the Commission International del'Eclairage (CIE) made possible to express color in exact quantitative and numerical



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Molecular Docking of Phytochemical compounds against Sars-Cov-2 Surface Glycoprotein and Envelope Protein

Subbalakshmi G*, Chaya D, Sushmitha M, Fouzia Bano, Anuradha M and Preenon Bagchi

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Abstract: In December 2019 Wuhan city, the capital of Hubei province in China became the epicenter of an outbreak of pneumonia of unknown cause. Chinese scientists had isolated a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-COV-2): previously known as 2019 (COVID-19). In this work we have taken Covid 19's Surface glycoprotein and Envelope protein. Using homology modeling the 3d structure of the proteins are modeled. Phytochemical compounds from the established medicinal herbs are selected and ADME studies are done. Further virtual screening was done and as per the screening results it is seen that the phyto-compounds Withanolide A and Withaferine A has very good docking score with the viral proteins selected.

Keywords: SARS-COV-2, phytocompounds, modeling, ADME, docking

INTRODUCTION

Immune resoponses induced by COVID-19 infection.

Clinically the immune response induced by SARS-COV-2 infection is two phased [1]. During the incubation and non-seven stages, a specific adaptive immune response is required to eliminate the virus and to preclude disese progression to severe stages [1]. Therefore, strategies to boost immune responses at this stage are certainly important [1].

Protiens

Coronaviruses are a recently characterized group of enveloped viruses which contain large single – stranded RNA genomes of messenger polarity [2]. In corona virus it has spikes protein on its surface, these spike proteins are glycoproteins which are responsible for initial binding of previous SARS corona viruses to lung cells and their activation of the spike protein by a proteolytic cleavage [3, 4].

The spike glycoprotein (spike protein) is the familiar spike that studs the surface of the corona viruses, giving it the appearance of a crown to electron microscopy, hence "corona" (latin: crown) [4].

Spike Protien (S Protein)

The corona virus spike protein is a class-1 fusion protein [5]. The formation of an alpha helical coiled-coil structure is characteristic of this class of fusion protein, which contain in their C-terminal part regions predict to have an alpha helical secondary structure and to form coiled coils [5, 6]. The S2 subunits are the most conserved region of the protein, where as S1 subunit diverge in sequence even among species of a single corona virus [4]. S1 contains two subdomains, a N-terminal domain (NTD) and a C-terminal domain (CTD) [7, 8]. Both are able to function as receptor binding domain (RBDs). And bind variety of proteins and sugars [8].

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FULL TEXT LINKS



Bull Environ Contam Toxicol. 2020 Oct;105(4):645-649. doi: 10.1007/s00128-020-02979-7. Epub 2020 Sep 1.

Absorption and Reduction of Chromium by Fungi

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Affiliations

PMID: 32870333 DOI: 10.1007/s00128-020-02979-7

Abstract

Biosorption has gained increased attention as a reliable and proven technology for the remediation of industrial effluents rich in chromium. The present study was planned to isolate potential fungi from effluents contaminated sites and assess their efficiency for the absorption and reduction of chromium. Two species of Aspergillus and a species of Trichoderma which were isolated from contaminated sites and exhibited resistance to 10 mM of chromium on agar were chosen for the study. A biosorbent was designed by growing these fungal isolates on luffa sponge under shaken condition. The absorption and reduction of chromium, by the designed biosorbent was determined by Atomic Absorption Spectrophotometry and UV Visible Spectrophotometer. Actively growing fungi on luffa sponge showed better absorption (21%-25%) and reduction (28%-35%) capacity when compared to heat killed biosorbent in all fungi tested within 24 h of incubation. Interestingly, there was a liner increase in the absorption and reduction (85%-100%) of chromium by the biosorbent designed by using A. niger.

Keywords: Absorption and reduction; Biosorbent; Chromium; Fungi; Luffa sponge.

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COMPARATIVE STUDY OF METABOLONOMIC PROFILE CHANGES IN POLY CYSTIC OVARIAN SYNDROME AND NORMAL SOUTH INDIAN WOMEN

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Abstract: Polycystic ovarian syndrome (PCOS), is one of the most widely prevailing disorder of infertility affecting reproductive age of females, with a prevalence of 8-13% that depends on the population basis. The most common symptoms observed are irregular cycle of Menstruation, appearance of polycystic ovaries, hypertrichosis, obesity, fertility issues and metabolic abnormalities. The aim of this study was to establish and compare the metabolonomic changes in PCOS women and Normal women from South India. A total of 60 subjects with PCOS and normal control women were studied. The samples of subjects were analysed using Biochemical, endocrinological and metabolomics assays. Our demographical parameters results showed that age is also one of the elements that prompt overweight in women. Biochemical and hormonal assays shows significancant difference between PCOS and control groups. Metabolomics assay outcome shows, there is a significant increase in the level of alanine, serine and tryptophan, with decreasing level of proline and isoleucine in PCOS compared to the control group. Based on this outcome it speculates that, carbohydrate, lipid and amino acid metabolic activities were altered in PCOS.

Key Words: Polycystic ovarian syndrome, Endocrine disorder, Amino acid metabolism.

I. INTRODUCTION:

Globally, polycystic ovarian syndrome (PCOS) is one of the most conspicuous endocrine deformities in the reproductive stage of females. Recent investigations show that the level of incident of PCOS is in the middle of 3-10% [1]. Critical metabolic aggravations like Hyperandrogenism, oligomenorrhea, anovulation, and hyperinsulinemia are normal symptoms of PCOS [2]. Likewise, they have a higher chance of developing type 2 diabetes mellitus (DM2) and cardiovascular disease (CVD) [3]. Despite the fact that it is considered as a polygenic attribute that has come about because of the connection of vulnerable genomic variations and ecological elements [6], the exact pathogenesis of PCOS is as yet difficult to understand.

Increasingly contrasts in the predominance, seriousness, metabolic unsettling influences and their relationship are observed across different ethnic population, which is progressively common among women at child bearing age. Some investigation appears, creating anomalous glucose tolerance, which is uncommon in Southern and Eastern Europeans contrasted with Southern Asia and Hispanics [8].

The indications of PCOS are defenseless to change concerning Geographic area, ethnic starting point, and social practices. Routine clinical practices can distinguish these, and this emphasizes the need to comprehend the metabolic dysfunction in PCOS for prevention of long term complications through appropriate screening, diagnosis or mediation in south Indian women. r. Anuradha. M

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Management & Sciences

COMPARATIVE STUDY OF METABOLONOMIC PROFILE CHANGES IN POLY CYSTIC OVARIAN SYNDROME AND NORMAL SOUTH INDIAN WOMEN

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INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

COMPARATIVE STUDY ON GENOMIC SEQUENCE OF SARS-COV2, SARS-COV1, H1N1 AND H3N2 VIRUSES

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Abstract: Viruses cause various diseases and syndrome in humans. Some have even evolved with time to show infection in humans. Human Beta coronaviruses of SARS-CoV-2, SARS-CoV, and influenza virus are very common pandemic caused viruses. Even the symptoms, transmission and the severity of the disease also very close to each other. But, current pandemic caused SARS-CoV-2 infection and mortality rate was too high. At present, there are no specific, effective drugs or vaccines for SARS-CoV-2.But, there are some drugs, vaccines, treatment and prevention of influenza virus are available. Based on this information, this study highlighted to compare the genomic sequence and GC content of SARS-CoV-2, SARS-CoV-1 and influenza viruses. From this study we conclude SARS-CoV-2 sequence has high genomic variety of due to this reason it's get consecutive transmutation.

Keywords: SARS-CoV-2, COVID 19, SARS-CoV-1, influenza viruses, H1N1, H3N2

I. INTRODUCTION:

The novel coronavirus 2019 (SARS-CoV-2), Severe acute respiratory syndrome coronavirus (SARS-CoV), and influenza A viruses are major pathogens that primarily target the human respiratory system. Diseases associated with their infections vary from mild respiratory illness to acute pneumonia, respiratory failure and even death.

The current pandemic was caused by new betacoronavirus (SARS-CoV-2). It was identified in china at December 2019, WHO was announced a pandemic in March 2020 (WHO, 2020). These cases were characterized by acute pneumonia-associated symptoms, such as fever, dry cough, chills, shortness of breath, and muscle pain (Lu et al., 2020). It spreads mainly through droplets of salivation or release from the nose henceforth requested to cover nose and mouth while coughing or sneezing and to maintain social distance in common places (Dharmendra Kumar et al., 2020) for this reason this outbreak is rapidly spread worldwide. As per WHO's report on 25th December, 7,81,94,947 individuals are infected and death rate is more than 17,36,752 occur in world. In India total number of infected cases are 1,01,46,845 and death rate was 1,47,097. (https://worldhealthorg.shinyapps.io/covid/).

Severe acute respiratory syndrome (SARS) is a viral respiratory disease caused by a SARS-associated coronavirus. This outbreak was identified in china at 2003 and spread to 4 other countries, most of the cases had animal exposure before developing the disease Some investigations disclosed that SARS-CoV strains were transmitted to palm civets from other animals (Guan et al., 2003; Wang et al., 2004). Hu etal., suggest

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