

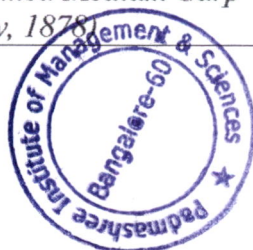
CRITERION III – RESEARCH, INNOVATIONS AND EXTENSION

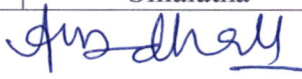
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**RESEARCH ARTICLE****PROBIOTIC NON LACTIC ACID BACTERIA: STUDY OF BACTERIOCIN FOR THE ANTAGONISTIC ACTIVITY.****Rashmi. D and Sharmila. T.**

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Key words:-

Antagonistic activity, Bacteriocins, Non lactic acid bacteria, Kirby-bauer disc diffusion.

Abstract

Bacteriocins are very useful as therapeutic agents. They act as an important and safer components as preservative and hence find their application in a wide range of medicine, agriculture, food and dairy products. Isolation of bacteriocins and its significant application has remained a challenging task. Production of bacteriocins of beneficial grade and their utilization as antibiotics and in food grade products without any harmful side effects also appear to be a tedious work. This work was initiated by isolation of non lactic acid bacteria from various food materials like pulses and cow's milk, morphological identification by colony characteristics and microscopic examination by Gram's staining. Qualitative identification of non lactic acid bacteria by catalase test. Bacteriocins production was detected by antimicrobial activity test against the indicator organisms by Kirby bauer disc diffusion method. Here we are presenting the results of the identification tests of the isolated bacteria and that of the antimicrobial studies. Future prospective includes the optimization of cultural, nutritional parameters and use of inducers to enhance the production, purification and characterization of bacteriocins. Significance of bacteriocins would be exploited in replacing the use of antibiotics and as preservative in food industries.

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Introduction:-

The viable microbial food supplements which beneficially influence the health of humans are known as probiotics. Antibacterial activity is one of the important probiotic properties for a strain to be a functional probiotic. Bacteria are being used as probiotic supplements for use in animal feeds, for human dietary supplements as well as in registered medicines. Their heat stability and ability to survive the gastric barrier makes them attractive as food additives and this use is now being taken forward. *Bacillus* or spore probiotics are being used extensively in humans as dietary supplements, in animals as growth promoters and competitive exclusion agents in aquaculture. Bacteriocins are ribosomally synthesized, proteinaceous compounds that inhibit the growth of closely related bacteria. Even within the subcategory of bacteriocins, the peptides vary significantly in terms of the gene cluster responsible for expression, and chemical and structural composition. In 1925, Gratia demonstrated the inhibitory activity of bacteriocin which was later determined to be colicin V (Cascales et.al; 2007). After, in 1928 nisin activity was reported by Rogers (Lubelski et.al; 2007). Bacteriocin has the ability to target a subgroup of pathogenic bacteria in a complex bacterial community. This has gained a potential application in medicine, agriculture and food where

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FOCUS

Molecular mechanisms involved in biosynthesis and regulation of carotenoids in plants

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ABSTRACT

Carotenoids are coloured compounds beneficial to plants and humans. Some of the major health benefits carotenoids provide include Vitamin A precursors and, antioxidants besides being involved in several physiological functions. Even though several carotenoids are synthesised by plants, only a few like beta/ alpha carotenes and cryptoxanthin serve as Vitamin A precursors. The rest are useful as antioxidants. To draw maximum benefits from carotenoids, we need to incorporate these in crop improvement programmes for enhancing available Vitamin A precursor carotenoids. Therefore, it is essential to study biosynthesis of carotenoids, their genetics and their control. In this review, we focus on factors regulating carotenoid biosynthesis, metabolism and storage in plastids. Transcriptional and genetic control of carotenoid production in plants is discussed in the review using several mutants too. Further, environmental regulation of carotenoid biosynthesis is also highlighted. Carotenoid-rich fruits and vegetables have greater economic value owing to their health-promoting effects. Besides, carotenoids have several industrial applications. Therefore, knowledge of regulation mechanism in carotenoid production in plants can help develop crop varieties or technologies, thus generating carotene-rich fruits and vegetables.

Key words: Carotenoid biosynthesis, regulation, plastid, fruit, transcription factor

INTRODUCTION

Carotenoids are naturally-occurring, lipophilic, C₄₀ isoprenoid compounds of red, yellow and orange coloured pigments. They are usually found in all photosynthetic organisms (bacteria, algae and plants) as well as in some non-photosynthetic bacteria and fungi. Colour is an important factor that makes flowers, fruits and vegetables economically valuable. This, in turn, is directly related to accumulation of carotenoids. Orange colour from β -carotene, and red colour in tomatoes and watermelon from lycopene are some examples. Apart from the appealing colour of carotenoids in fruits such as tomatoes, water-melon and papaya, and in vegetables such as carrot, red-bell-peppers and green leafy vegetables such as spinach, broccoli and lettuce, these are also nutritionally important to humans. Consumption of carotenoid-rich

fruits and vegetables has several health benefits. These are precursors for Vitamin A synthesis - deficiency of which leads to age-related macular degeneration. Carotenoids also act as free-radical scavengers owing to their antioxidant property, and help in prevention of several degenerative diseases, cardiovascular diseases and cancer (Fraser and Bramley, 2004; Fiedor and Burda, 2014). In plants, carotenoids have diverse functions: they serve as components of the light-harvesting apparatus during photosynthesis, they attract pollinators and seed-dispersal agents (Pandurangiah *et al.*, 2016). In view of the importance of carotenoids in plants and humans, focus is now on carotenoid research, particularly, in horticulture crops. There are several review articles on carotenogenesis and its regulation in plants (Fraser and Bramley, 2004; Walter and Strack, 2011; Giuliano, 2014). A major focus of carotenoid research is to find compositional variation



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Original Article

Molecular characterization of gluten hydrolysing *Bacillus* sp. and their efficacy and biotherapeutic potential as probiotics using Caco-2 cell line

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Abstract

Aim

To isolate and characterize indigenous gluten hydrolysing bacteria from wheat sourdough and curd samples and further evaluation of their probiotic potentiality.

Methods and Results

Indigenous gluten hydrolysing isolates GS 33, GS 143, GS 181 and GS 188 were identified as *Bacillus* sp. by molecular-typing methods and studied extensively for their functional and probiotic attributes. All the tested isolates could survive at pH 2 and toxicity of 0.3% bile and also exhibited cell surface hydrophobicity and autoaggregation phenotype. The isolates were adhered strongly to Caco-2 cells and coaggregated with *Escherichia coli* MTCC 433 and *Listeria monocytogenes* MTCC 1143 preventing pathogen invasion into Caco-2 cells *in vitro*. In addition, the minimum inhibitory concentration of selected antibiotics for all the investigated gluten hydrolysing isolates was within the breakpoint values as recommended by the European Food Safety Authority.

Conclusion

The indigenous high intensity gluten hydrolysing bacteria exhibited high resistance to gastric and pancreatic stress and possessed antibacterial, aggregation, adhesion and pathogen exclusion properties, and as a potential probiotics, either alone or in consortium would be useful in the development of gluten-free wheat foods.

Significance and Impact of the Study

Exploring new indigenous gluten hydrolysing bacteria from wheat sourdough and curd samples would be beneficial in developing gluten-free wheat foods using potential indigenous probiotics.



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Draft Genome Sequence of the Gluten-Hydrolyzing Bacterium *Bacillus subtilis* GS 188, Isolated from Wheat Sourdough

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ABSTRACT The draft genome sequence of *Bacillus subtilis* GS 188, a novel spore-forming probiotic bacterium with gluten-hydrolyzing potential, was isolated from wheat sourdough and provides deep insights into the beneficial features of this strain for its use in the preparation of gluten-reduced wheat foods for humans with celiac disease.

Bacillus spp. are currently of keen interest to the probiotic industries, as they are able to withstand various adverse conditions in the gastrointestinal tract and also in consumer products with indefinite shelf lives (1, 2). Moreover, compared to conventional probiotic lactic acid bacteria, *Bacillus* spp., particularly *B. subtilis*, *B. licheniformis*, *B. clausii*, and *B. coagulans*, have been proven to exhibit potential probiotic attributes (1, 3). Therefore, *Bacillus* sp. probiotics have been proposed as nutritional supplements or novel foods (4). However, data on gluten-hydrolyzing *B. subtilis* probiotics are scarce. Given this, in an earlier study we reported the probiotic potentiality of the gluten-hydrolyzing *B. subtilis* GS 188 (5), and here we report the draft genome sequence of the isolate in order to unravel the genetic blueprint that confers gluten-hydrolyzing potential along with probiotic traits and safe use.

Genomic DNA was isolated as described previously (6), and the paired-end sequencing libraries were prepared using an Illumina TruSeq Nano DNA library preparation kit according to the manufacturer's instructions. The mean fragment size distribution of the constructed libraries was 525 bp. Further, the libraries were sequenced on the Illumina NextSeq500 platform using 2 × 150-bp chemistry at Eurofins Genomics (India). The raw reads were filtered using Trimmomatic version 0.35 (7). The filtered 6,639,770 paired-end reads with an average GC content of 44.81% were mapped to the *B. subtilis* ASM904v1 reference genome using the Burrows-Wheeler aligner. Then, a consensus sequence comprising 4,022,027 bp was obtained using SAMtools mpileup (8). Further, with the help of bedtools, the genes were extracted from the consensus using the gene coordinates obtained from GenBank.

A total of 4,141 genes were identified from *B. subtilis* GS 188 with maximum and minimum lengths of 16,466 and 41 bp, respectively. Of these genes, 2,527 were annotated using Blast2Go, while gene ontology annotations were determined using the UniprotKB database. Annotation predicted the presence of genes encoding proteins for motility, sporulation, antimicrobial activity, and cell-to-cell interaction for biofilm formation. In addition, the presence of genes for peptidases and extracellular proteases, along with the genes encoding cell membrane-associated proteins of the high-affinity amino acid transporter system, indicated the extensive proteolytic potential of the isolate. Further, to identify the potential involvement of the genes of *B. subtilis* GS 188 in biological pathways, genes were mapped to reference canonical pathways in KEGG. The identified 4,141 genes were provided as input to KEGG-KAAS. KEGG pathway analysis classified 1,944 enriched genes in the KEGG database into 24 functional pathways; of these genes, the highest numbers accounted for carbohydrate metabolism (256), amino acid metabolism (201),

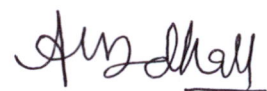
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Mechanism of development of depression and probiotics as adjuvant therapy for its prevention and management ☆

Devaraja Gayathri  , B.S. Rashmi 

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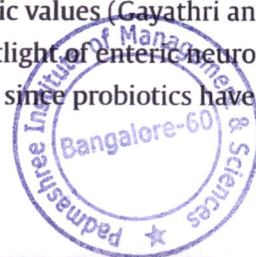
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Abstract

Probiotics are in the spotlight of enteric neuroscience research that influences brain biochemistry, neural development and other behavioural phenomenon. Depression due to mood disorder, pathogenic infections/metabolic disorders, psychiatric illness, stressful life style, alters the function of neurochemicals. Out of various strategies, recent research has shown the mechanism of action of probiotics in alleviating mood disorders. Understanding the causes for depression and anxiety would pave way for the development of therapeutics to surmount the burden of depression and anxiety. Therefore, the present article emphasizes on the causes of generation of depression and possible strategies for their prevention and management through probiotics.

Introduction

A wise man should consider that health is the greatest of human blessings, and learn how by his own thought to derive benefit from his illness; Hippocrates the Father of medicine said: “*let food be thy medicine and medicine be thy food*”. Recent research in clinical nutrition agrees with Hippocrates opinion about food and health. There is a saying- “*We are what we eat*” and it's true that the foods we eat directly influence both our physical as well as mental health and thereby influence our physiology and behavioural aspects (Gomez-Pinilla, 2008). Research has proven that probiotics as conventional and functional food confer both physical and mental health benefits to host (Gareau et al., 2011, Messaoudi et al., 2011). FAO/WHO (2002) defined probiotics as “living bacteria that, which when administered in adequate amounts, confer a health benefit to the host”. Until recently, probiotics were much in discussion on their mode of action in fighting infections, treating several metabolic disorders, improving digestion, enhancing nutrient absorption, modulating immunity, balancing intestinal microbial population, regulating apoptosis- crucial factor in aging and also for their metabolites with therapeutic values (Gayathri and Rashmi, 2014, Asha and Gayathri, 2012, Gill, 1998). Now-a-days, probiotics are in spotlight of enteric neuroscience research- a new discipline that merges neuropsychiatry and gastroenterology, since probiotics have been proven to influence neural



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Evaluation and Optimization of Extracellular Digestive Enzymes from *Bacillus* spp. Isolated from Curds

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Abstract

Objective: The aim of the present study was to evaluate the digestive enzyme activity of the four *Bacillus* spp. and to optimize the physical parameters.

Methods: The enzymes were produced by submerged fermentation supplementing enzyme specific substrates. The fermentation broths were centrifuged and the supernatants were used as source of crude enzyme. Amylase activity was determined by 3, 5-dinitro salicylic acid method using starch as substrate while copper soap method was used to evaluate lipase activity. Further, protease activity was measured by Lowry's method; whereas, phytase activity was assayed using sodium phytate as substrate. All the enzymes were optimized for pH, temperature and substrate concentration. The total protein content per one ml. of the crude enzyme in the supernatant was quantified by Lowry's method.

Results: All the four tested isolates *B. subtilis* GS 1, *B. cereus* GS 3, *B. cereus* GS 199 and *B. subtilis* GS 547 showed high extracellular digestive enzyme activity at pH range 5 to 8 and temperature 20 to 50°C.

Conclusion: The four tested *B. subtilis* GS 1, *B. cereus* GS 3, *B. cereus* GS 199 and *B. subtilis* GS 547 could be promising extracellular digestive enzyme producing isolates. Further, evaluation of *in vivo* efficacy and safety in animal models and clinical trials would be helpful in assisting digestive enzyme deficiencies using these extracellular enzyme preparations or whole cell bacteria.

Keywords: Digestive enzymes; Amylase; Lipase; Protease; Phytase; *Bacillus*

Introduction

Microbial enzymes are being increasingly used as therapeutics that play an important role in alleviating the burden of several digestive and malabsorption disorders. Use of microbial enzymes to substitute pancreatic enzymes has been considered safe with very less side effects and also proven economic [1]. Further, microbial derived digestive enzymes were proven to exert efficient digestive property at very low doses and also can possess a broader pH range of activity than animal and plant based counterparts [2]. Furthermore, GRAS (generally regarded as safe) strains of bacteria and probiotics with extracellular digestive enzyme activity were also extensively studied for their oral administration in order to improve digestion in the host [3].

Several studies showed that lipase producing probiotics can be used to reduce cholesterol levels, to overcome malabsorption, aid in the proper digestion of fats in the diet in addition to adjunct therapy in the management and prevention of mental depression [4-8]. Further, probiotics have proven to be useful in the management of colorectal cancer as evaluated in mice system and also possess anticancer properties [10-12]. Interestingly, the treatment of steatorrhea by lipase supplementation therapy has become more successful in the last decade [13]. To consider, in an *in vivo* study, acid resistant lipase from fungi was used to treat steatorrhea in dogs. In the study 4800 U of fungal lipase was used and a significant reduction in stool bulking and fat excretion was observed [14]. Further, microbial proteases are known for efficient proteolytic activity and are extensively used in food processing for gluten intolerance, cow's milk allergy, soy allergy and also in other dietary protein intolerances [15,16]. Addition of microbial beta-galactosidases directly to milk represents a potential enzyme replacement therapy for primary lactase deficiency [17]. In addition, the use of probiotic fermented milk products also found beneficial in improving lactose digestion [18]. Further, biotechnological applications

of phytase in food is gaining importance, since phytate in the diet act as an anti-nutrient [19]. The addition of phytase or fermenting foods with phytase producing strains of GRAS and probiotics can improve nutritional value of plant based foods by improving protein digestion and also mineral bioavailability through phytate hydrolysis [20].

Compared to enzyme preparations, the use of whole microbial cells that secrete extracellular digestive enzyme was found beneficial. Because, enzyme preparations must be supplemented at each meal time to ensure the digestion of ingested diet. In addition, there are several problems associated with the use of enzyme preparations that mainly includes *in vivo* efficacy, efficient delivery against gastric condition in the stomach, formulation and dosage [2,21,22].

Most of the commercially available digestive enzymes are from *Aspergillus* and *Bacillus* spp. *Bacillus* spp. continue to be dominant bacterial workhorses in microbial fermentations due to their stability in wide range of pH and temperature [23]. The GRAS strains of *Bacillus* mainly include *Bacillus subtilis*, *Bacillus cereus*, *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus clausii* and *Bacillus coagulans* [24]. Given this, in the present study, the four isolates namely: *Bacillus subtilis* GS 1, *B. cereus* GS 3, *B. cereus* GS 199 and *B. subtilis* GS 547 isolated

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Ayur-Informatics: Establishing an Ayurvedic Medication for Parkinson's Disorder

Preenon Bagechi, Anuradha M, Ajit Kar

Abstract - Parkinsonism is a degenerative disorder of the Central Nervous System affecting the aged. The receptor proteins identified PARK2 and LRRK2 are modeled by modeller software. The best models selected for each receptor are selected by Ramachandran Plot analysis. Then best model selected are docked with the phyto-compounds. The phyto-compounds having the best docking score are selected as the most suitable ligand and considered for further *in-vitro* receptor ligand binding assay studies.

Keywords--Parkinsonism, Degenerative disorder, Receptor, PARK2, LRRK2, Modelling, Docking

1. INTRODUCTION

Parkinson's disease (PD) is a neuro-degenerative disorder. It occurs as a result of the death of dopamine-generating cells in the substantianigra, a region of the midbrain; the reason of this cell death is unknown [1]. The most obvious symptoms are movement-related; these include shaking, rigidity, slowness of movement and difficulty with walking and gait [2]. Later, thinking and behavioral problems arise, with dementia commonly occurring in the advanced stages of the disorder, whereas depression is the most common psychiatric symptom [3]. Other common symptoms include sensory, sleep with emotional problems. Parkinson's disease is more common in older people at age of 50 [3].

Parkinsonian cases have a genetic origin can cause neuropsychiatric disturbances which can range from mild to severe which includes disorders of speech, cognition, mood, behaviour, and thought [3].

Behavior and mood alterations are more common with or without cognitive impairment usually seen in PD with dementia [3]. Impulsive control behaviors such as medication overuse and craving, binge eating, hypersexuality, or pathological gambling can be seen in PD and have been related to the medications used to manage the disorder [4, 5, 6]. Psychotic symptoms—hallucinations or delusions—occur in 4% of people with PD [3]. It is assumed that the main precipitant of psychotic phenomena in Parkinsonism is dopaminergic excess [3]. Mutations in the SNCA (Alpha-synuclein) receptor, PARK2, LRRK and AMPA (α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid) are noted as causal factors for Parkinsonism.

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The **PARK2** gene, one of the largest human genes, expresses making a protein called parkin [7]. The official name of this gene is "Parkinson protein 2, E3 ubiquitin protein ligase (parkin)" [7]. Parkin's role is seen in the cell machinery that degrades unneeded proteins by tagging damaged and excess proteins [7]. Studies have suggested more than 200 PARK2 gene mutations causing Parkinsonism, a condition characterized by progressive problems with movement and balance [8]. Mutations in this gene are associated with the juvenile form of Parkinson disorder, which appears at very low age, on or before age 20, and some cases of the more common, late-onset form that begins after age 50 [8, 9].

Leucine-rich repeat kinase 2 (**LRRK2**) is an enzyme that in humans is encoded by the PARK8 gene, a member of the leucine-rich repeat kinase family [10]. Variants of this gene are seen associated with Parkinson's disorder [9, 10]. Expressions in LRRK2 mutant genes are implicated in autosomal dominant Parkinson's disease which causes shortening and simplification of the dendritic tree *in vivo* and in cultured neurons [11, 12].

For the present study the following medicinal plants have been selected to study the scope & activity of different compounds on CNS using above mentioned bioinformatic parameter. These are:

<i>Withaniasomnifera</i> compounds present withanolide A and withanone
<i>Rauwolfia serpentina</i> compounds present Rescinnamine & Reserpine
<i>Hydrocotyle asiatica/Centella asiatica</i> compound present Asiaticoside
<i>Aloe vera</i> compound present Kaempferol
<i>Bacopa monnieri</i> compounds present Apigenin & Bacopaside I
<i>Convolvulus pluricaulis</i> compound present beta-sitosterol
<i>Mucuna pruriens</i> compound present levodopa
<i>Ocimum sanctum</i> compound present Eugenol
<i>Tinospora cordifolia</i> compound present Cordifolioside A
<i>Curcuma longa</i> compound present curcumin
<i>Asparagus racemosus</i> compounds present racemosol and rhamnose
<i>Valeriana wallichii</i> compounds present baldrinal and xanthorrhizol
<i>Acorus calamus</i> compound present Calamusenone
<i>Nardostachys jatamansi</i> compound present jatamaninI



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Ayur-Informatics: Establishing an Ayurvedic Medication for Parkinson's Disorder

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The **PARK2 gene**, one of the largest human genes, expresses making a protein called parkin [7]. The official name of this gene is "Parkinson protein 2, E3 ubiquitin protein ligase (parkin)" [7]. Parkin's role is seen in the cell machinery that degrades unneeded proteins by tagging damaged and excess proteins [7]. Studies have suggested more than 200 PARK2 gene mutations causing Parkinsonism, a condition characterized by progressive problems with movement and balance [8]. Mutations in this gene are associated with the juvenile form of Parkinson disorder, which appears at very low age, on or before age 20, and some cases of the more common, late-onset form that begins after age 50 [8, 9].

Leucine-rich repeat kinase 2 (**LRRK2**) is an enzyme that in humans is encoded by the PARK8 gene, a member of the leucine-rich repeat kinase family [10]. Variants of this gene are seen associated with Parkinson's disorder [9, 10]. Expressions in LRRK2 mutant genes are implicated in autosomal dominant Parkinson's disease which causes shortening and simplification of the dendritic tree *in vivo* and in cultured neurons [11, 12].

For the present study the following medicinal plants have been selected to study the scope & activity of different compounds on CNS using above mentioned bioinformatic parameter. These are:

<i>Withaniasomnifera</i> compounds present withanolide A and withanone
<i>Rauwolfia serpentine</i> compounds present Rescinnamine & Reserpine
<i>Hydrocotyle asiatica/Centella asiatica</i> compound present Asiaticoside
<i>Aloe vera</i> compound present Kaempferol
<i>Bacopa monnieri</i> compounds present Apigenin & Bacopaside I
<i>Convolvulus pluricaulis</i> compound present beta-sitosterol
<i>Mucuna pruriens</i> compound present levodopa
<i>Ocimum sanctum</i> compound present Eugenol
<i>Tinospora cordifolia</i> compound present Cordifolioside A
<i>Curcuma longa</i> compound present curcumin
<i>Asparagus racemosus</i> compounds present racemosol and rhamnose
<i>Valeriana wallichii</i> compounds present baldrinal and xanthorrhizol
<i>Acorus calamus</i> compound present Calamusenone
<i>Nardostachys jatamansi</i> compound present jatamaninl



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Pharmaco-Informatics: Harnessing The Power Of Bioinformatics In Cancer Research & Management: A Review

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Abstract: - One of the greatest challenges faced by the cancer researchers is that the disease varies so much from individual to individual. Even the same type of cancer – blood, brain, kidney, pancreas, and so on – can be different subtly. This concludes that a therapy working excellent in one patient may have absolutely no effect in another. Cancer Research worldwide has set up several centers and started collecting 9,000 tumor cells' samples from a wide range of cancer patients and created a DNA database of cancerous cells. Researchers extract DNA from these tumors and scan them for a series of key genes involved in tumor development and compares & cross-checked against a range of cancer treatments, cancerous genes, to create a map of which treatments in particular works best for cancers associated with which particular genes. This is based on the concept of pharmacogenomics & pharmacoinformatics: certain genes predispose individual to respond to certain molecules in certain ways. Doctors can already test a cancer patient for a single known gene, knowing how tumors with that gene respond to a particular molecule. However currently they don't have a way of testing with a broad panel or set of genes. And to compensate the problem, they don't have a way of quicker and more accurate way of sharing information in-between research labs in the same city, across the country or internationally. With the proposed cancer DNA database, a doctor might analyze a patient's cancerous tumor sample and prescribe a detailed tailored treatment plan within a very short period of time. Bioinformatics research is increasing steadily at an exponential rate. DNA sequences are available to researchers with just an Internet connection – along with free bioinformatics tools to explore any sequence data, predict the presence of genes/mutated genes, and compare features shared between various organisms.

Index Terms: Cancer, bioinformatics, metabolomics, epigenomics, genome, bio-software

I. INTRODUCTION

The greatest challenges faced by the cancer researchers is that the disease varies so much from individual to individual that even the same type of cancer – blood, brain, kidney, pancreas, and so on – can be different subtly [1]. This concludes that a therapy working excellent in one patient may have absolutely no effect in another [2]. Cancer Research worldwide has set up several centers and started collecting 9,000 tumor cells' samples from a wide range of cancer patients and created a DNA database of cancerous cells [3]. Researchers extract DNA from these tumors and scan them for a series of key genes involved in tumor development and compares & cross-checked against a range of cancer treatments, cancerous genes, to create a map of which treatments in particular works best for cancers associated with which particular genes [4]. This is based on the concept of pharmacogenomics & pharmacoinformatics: certain genes predispose individual to respond to certain molecules in certain ways [1]. Doctors can already test a cancer patient for a single known gene, knowing how tumors with that gene respond to a particular molecule. However currently

they don't have a way of testing with a broad panel or set of genes [2, 3]. And to compensate the problem, they don't have a way of quicker and more accurate way of sharing information in-between research labs in the same city, across the country or internationally [1, 4]. Why Bioinformatics - Enter the healer - bioinformatics. With the proposed cancer DNA database, a doctor might analyze a patient's cancerous tumor sample and prescribe a detailed tailored treatment plan within a very short period of time [2, 3, 4]. As Professor Matthew Seymour, director of the National Cancer Research Network (NCRN) in the UK, recently stated, "We have to get clever about how to target drugs. Medications for cancer have to be personalized because no two cancers are identical." So global researchers brought in a big gun – the bioinformatics.

Bioinformatics research is increasing steadily at an exponential rate. DNA sequences are available to researchers with just an Internet connection – along with free bioinformatics tools to explore any sequence data, predict the presence of genes/mutated genes, and compare features shared between various organisms [5, 6]. Cancer - Cancer is

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Influence of Commonly used Manures on the Growth and Nutrient Composition of Periphyton

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Abstract

A 90 day experiment was conducted in out-door, soil-based (10 cm), cement tanks to evaluate the effect of three manures viz. cattle dung, poultry manure and press mud provided at iso-nitrogenous levels, on the growth and nutrient composition of periphyton grown on sugarcane bagasse. Water quality analysis revealed that tanks applied with cattle dung recorded lower ($P>0.05$) pH and those with poultry manure showed higher ($P>0.05$) phosphate content. Total pigment content and biomass of periphyton (dry matter) and plankton (dry weight) showed higher values in poultry manure treatment. Press mud treatment recorded lower plankton dry matter. Crude protein and fat contents were higher ($P<0.05$) in periphyton from poultry manure treatment. Other proximate composition parameters showed no difference ($P>0.05$) among periphyton from different treatments. The proximate composition of plankton also showed higher crude protein, fibre and ash values in poultry manure. The study revealed that poultry manure is superior to cattle dung and press mud, considering the total pigment content, biomass and crude protein content of periphyton and plankton biomass.

Keywords

Periphyton; Plankton; Cattle dung; Poultry manure; Press mud

Plankton perform other important functions in pond aquaculture - a net producer of dissolved oxygen, which is indispensable for fish growth [4] and the most important sink of ammonia-nitrogen, which is excreted by fish [5, 6]. Jhingran [7] observed that natural food also supplies certain digestive enzymes that improve the utilization of artificial diets.

The FAO/AADCP Regional Expert Consultation has emphasized the need for a greater understanding of the role of natural food organisms in semi-intensive farming based on systems that optimize pond fertilization [8]. Judicious organic fertilization of fish ponds can eliminate the need for supplementary feeding [9]. The use of manures such as poultry manure, dung from cow, sheep, goat or pig is well established [10-16]. In India, cattle manure is frequently used in commercial ponds due to its low cost and easy availability [17, 18]; it plays an important role in the enhancement of fish production by providing major nutrients for the augmentation of phytoplankton- zooplankton food chain. Among the organic manures, poultry manure is considered to be the best since it contains more N and P, which play a vital role in plankton production [19]. Poultry manure is now widely used in commercial freshwater aquaculture. Press mud, a sugar factory waste, is a good source of organic matter. It is rich in potash and phosphorus and is used as manure in agriculture [20]. With a conservative yield of 2% and a total production of 1700 million t of sugarcane in 2009 [21], the world output of press mud can be estimated to be about 30 million t.

Facilitating the growth of periphyton by installing substrates in ponds adds a new dimension to natural food production. Periphyton is readily consumed by browsers such as rohu and fimbriatus and is also helpful in improving water quality by producing oxygen, trapping suspended solids and taking up ammonia and nitrate. Studies have demonstrated comparative growth of carps in periphyton-based systems and feed-driven systems [22-24].

Although some investigations have been performed on the effect of fertilizers on plankton production [25, 26], comparative studies on the effect of poultry manure, cattle dung and press mud on the growth of periphyton are lacking. Therefore, the present study was undertaken with the aim of determining the

Introduction

Pond fertilization is a common practice in aquaculture aimed at increasing the production of natural food for farmed fishes. Inorganic fertilizers are expensive and their use by smallholder farmers may be limited [1]. Animal wastes are widely used in many countries to sustain pond productivity at a low cost [2, 3]. Organic fertilizers decompose and release nitrogen, phosphorous and potassium which are used by phytoplankton for growth and reproduction. In addition, they provide attachment sites for bacteria and other microscopic organisms.



Digestibility and digestive enzyme activity in *Labeo fimbriatus* (Bloch, 1795) fed periphyton grown on sugarcane bagasse

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ABSTRACT

An experiment of 60 days duration was carried out to compare dry matter and protein digestibility of periphyton grown on sugarcane bagasse bundles and a pelleted feed in *Labeo fimbriatus* (Bloch, 1795). Advanced fingerlings maintained in glass aquaria were allowed to feed on fresh periphyton or pelleted feed (20% crude protein) daily morning, the fecal matter collected following standard procedure and analysed for proximate composition. Acid insoluble ash was used as the reference marker for digestibility estimation. Activity of total protease, trypsin, chymotrypsin, carboxypeptidase - A and B, amylase, lipase and cellulase in the gut of fish was estimated at the end of the feeding trial. Periphyton and pelleted feed showed similar ($p>0.05$) protein digestibility (92.29 and 89.21% respectively), while total dry matter digestibility was higher ($p<0.05$) with peiphyton (85.44 and 75.16% respectively). Among the proteases estimated, activity of total protease and carboxypeptidase B was higher ($p<0.05$) in fish fed periphyton, whereas activity of others showed no difference between those receiving periphyton and pelleted feed ($p>0.05$). Activity of carbohydrases and lipase was higher in fish fed pelleted feed. Results of the study clearly indicated that *L. fimbriatus* can efficiently utilise periphyton.

Keywords: Digestibility, Digestive enzymes, Fringe-lipped carp, *Labeo fimbriatus*, Periphyton, Pelleted feed, Sugarcane bagasse

Introduction

Increase in production of several herbivorous fish species has been reported in periphyton-based aquaculture (Wahab *et al.*, 1999; Azim *et al.*, 2005; Keshavanath *et al.*, 2001b, 2002, 2004; Gangadhar and Keshavanath, 2012). *Labeo fimbriatus* (Bloch, 1795) is considered as a suitable candidate for species diversification in culture. Though slow-growing, this medium sized carp is in good demand due high market value, excellent flavour and meat quality especially in peninsular India (Basavaraju *et al.*, 1995). Published work on *L. fimbriatus* is limited (Mridula *et al.*, 2003; Saravanan *et al.*, 2011; Rao 2011; Swain *et al.*, 2013). *L. fimbriatus* is basically a benthic fish which graze on algae, protozoa, rotifers and diatoms that grow on submerged rocks and twigs (Bhatnagar and Karamachandani, 1970; Talwar and Jhingran, 1991; Das, 2011). In a grow-out study, Jena *et al.* (2011) demonstrated the compatibility of this species in polyculture with major carps. Keshavanath *et al.* (2002) and Mridula *et al.* (2003) have reported *L. fimbriatus* as a good periphyton grazer.

Digestibility is the relative measure of the extent to which ingested food and its nutrient components are

digested and absorbed by the animal and is considered as one of the important factors in diet evaluation. The ability of *L. fimbriatus* to digest periphyton and absorb nutrients has not been quantified yet. Hence, the present study was undertaken using sugarcane bagasse, which has been already reported to be a good periphyton substrate (Keshavanath *et al.*, 2001a; Mridula *et al.*, 2003; Gangadhara and Keshavanath, 2008) that enhances fish growth (Ramesh *et al.*, 1999; Keshavanath *et al.*, 2001b; Gangadhara and Keshavanath, 2012). Activity of major digestive enzymes *viz.*, total protease, trypsin, chymotrypsin, carboxypeptidase A and B, amylase, lipase and cellulase in the gut of fish fed periphyton in comparison with fish fed pelleted feed was estimated to validate the results.

Materials and methods

Growing periphyton

Outdoor cement tanks (6 x 4 x 1.2 m) with 5 cm soil base were used for growing periphyton. Sugarcane bagasse was used as the substrate for growing periphyton. Fresh bagasse procured from local sugarcane juice vending



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Digestibility of Dry Matter and Nutrients from *Azolla pinnata* by *Labeo calbasu* (Hamilton, 1822) with a Note on Digestive Enzyme Activity

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Abstract

Digestibility of feed ingredients in the compounded diet is an important factor affecting the growth of fish. A study was conducted in indoor plastic tubs to estimate the *in vivo* digestibility of dry matter and nutrients by a minor carp *Labeo calbasu* for a non-conventional feed ingredient – azolla, incorporated at levels ranging from 0-40% using crude fibre as the marker. The activities of major digestive enzymes were also estimated in the gut of fish fed varied levels of azolla. The digestibility values were the highest ($p < 0.05$) at 10% azolla inclusion level. While the total dry matter digestibility and fat digestibility values of control diet were comparable with that of azolla diets up to 30% incorporation, with a decline thereafter; protein and NFE digestibilities were comparable up to 40% incorporation. Activities of majority of digestive enzymes were the highest ($p < 0.05$) at 10% azolla incorporation level showing a decreasing trend at still higher levels. The study reveals the usefulness of azolla for inclusion in calbasu diets. Azolla can be used up to 30% without affecting the digestibility.

Keywords: Digestibility, *Labeo calbasu*, azolla, digestive enzyme, non-conventional ingredients

Introduction

Feed constitutes the major expenditure in any fish culture operation (Mukhopadhyay & Jena, 1999) which contributes to cost increase per unit production (New & Csavas, 1993). Farmers and feed

manufacturers alike are attempting to reduce feed cost and secure ingredients to produce cost-effective diets. Several studies have been done to make supplementary feeding cost-effective, using less expensive plant protein sources (Jackson et al., 1982; De Silva & Gunasekera, 1989; Shamna et al., 2015; Asadujjaman & Hossain, 2016). Azolla (*Azolla pinnata*), an aquatic weed, is rich in protein; total protein ranging from 25 to 30%. Other constituents in Azolla are minerals, chlorophyll, carotenoids, amino acids, and vitamins. *A. pinnata* is consumed by some macrophytophagous fish (Cassani, 1981). It is easy to cultivate and has higher productivity and nutritive value. The use of azolla as a fish feed ingredient is well documented (Dutta, 2011, Gangadhar et al., 2014; 2015). Digestibility of individual ingredients in the compounded diet is considered as one of the important factors affecting the growth of fish (De Silva et al., 1990) and hence this study was undertaken to evaluate the digestibility of ingredients before and after its incorporation in diet.

Orange fin labeo, *Labeo calbasu* is an herbivorous fish belonging to *Cyprinidae*, found commonly in rivers and freshwater lakes in and around South Asia and South-East Asia and at several places is referred to as the "Black Rohu". It thrives better in tanks and lakes than in running waters and can also tolerate slightly brackish water. It is a bottom dweller and can tolerate high turbid water during dry season. It is a commercially important species often cultured in South Western China, India, Pakistan, Bangladesh and Thailand. It is a popular food fish next to three Indian major carps *Labeo rohita*, *Catla catla* and *Cirrhinus mrigala* (Gupta & Banerjee, 2015). The fish is in great demand in the market. Ghosh et al. (1933) stated that its liver oil contains vitamin A. The present study was conducted to estimate the

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Carcass Characteristics of Farmed Medium Carp *Hypselobarbus pulchellus* (Day, 1878)

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Abstract

The carcass quality traits of an endemic carp, *Hypselobarbus pulchellus*, were assessed to determine its flesh yield and quality. Fish were stocked at 5000 no. ha⁻¹ in 0.1 ha earthen composite aquaculture ponds with a mean temperature of 24.6°C and given supplementary feed once daily. Fish weighing between 1.8-2.5 kg were assessed for carcass and offal yields as well as carcass cutability, organoleptic evaluation and proximate composition. Dressed fish (n=10) were cut at three median places to yield head, first, second and third body sections. The fish had a length of 48.2±6.4 cm and weight of 2.1±0.71 kg with a condition factor (K) of 3.5±0.7. The second body section (BS) of the fish had the maximum girth, area and weight followed by first and third body sections. The girth, area and weight of the three BS were linearly proportional to the weight of the fish but not to its length. The variations in the characteristics were also higher in the bigger sections. The three body sections constituted 64% of the weight of fish, while the offal and head comprised 26 and 10% respectively. Mean yield on dressing of fish was 70% with a meat: bone ratio of 3.27. There were no differences between the first, second and third body sections in their proximate composition. Brine cooked sections evaluated by a panel were not significantly different in taste. The fish had a proximate composition of 73.2±0.7% moisture, 23±0.6% protein, 5.3±1.6% fat and 1.4±0.2% ash.

Keywords: Carcass, characteristics, analysis, *Hypselobarbus pulchellus*, composition

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Introduction

Hypselobarbus pulchellus (Day 1870) locally known as 'Haragimeenu' is an important endemic fish of the Krishna River basin that is highly sought after for its tasty flesh and efforts are being made to raise the fish through aquaculture. Due to its herbivore and grass diet, it has been touted as an indigenous alternative to grass carp in aquaculture (David & Rahman, 1975). However, the acceptance of a fish by the aquaculture farmer depends not only on its quick growth but also on its flesh yield and quality, the latter being denoted by the carcass quality characters. Carcass quality characteristics have been used for diverse purposes in aquaculture such as assessing the effects of starvation in common carp (Assareh et al., 2013); for predicting the processing yields in rainbow trout selective breeding programs (Haffray et al., 2013), to assess the influence of dietary protein/energy ratio in Eurasian perch (Mathis et al., 2003), to evaluate performance of pike perch reared in recirculatory systems at suboptimal temperatures (Zakes et al., 2013) and to differentiate between populations of coho salmon (Neira et al., 2004). Flesh quality traits have been extensively used in salmonid breeding for quality improvement (Gjedrem, 1997), but such efforts have been few in other fish (Nguyen et al., 2010 a;b). Differences have been observed in carcass quality of common carp grown on different feeds (Oberle et al., 1997). Carcass quality of farmed mrigal and silver carp have been compared (Sahu et al., 2014a), while carcass characteristics of catla, rohu and hilsa have been studied as a function of their size (Sahu et al., 2013a;b; 2014b). But there have been no reports on the carcass characteristics and meat quality of either wild or aquaculture produced *H. pulchellus*. This paper attempts to address the gap and describe the carcass quality characteristics and proximate composition of farmed *H. pulchellus* (Day 1870).



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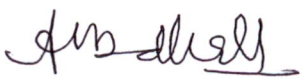
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Occurrence of endogenous Piper yellow mottle virus in black pepper

[K. P. Deeshma](#) & [A. I. Bhat](#) [VirusDisease](#) **28**, 213–217 (2017)**217** Accesses | **4** Citations | [Metrics](#)

Abstract

Some badnaviruses are known to occur as endogenous viruses integrated into their host genome. In the present study, Piper yellow mottle virus (PYMoV), a badnavirus infecting black pepper was shown to occur as endogenous virus based on the PCR, reverse transcription (RT)-PCR, ELISA and Southern hybridization tests. Black pepper plants that tested positive in PCR for PYMoV gave negative reaction in RT-PCR indicating that they harbour endogenous PYMoV (ePYMoV) sequences. The RT-PCR (–ve) plants tested negative in ELISA and also in PCR using outward primers to amplify the full circular genome. Further, the presence of ePYMoV sequences in the black pepper genome was confirmed by Southern hybridization analysis using cloned PYMoV genomic fragments as probes. Among different open reading frames (ORFs) of the virus, ORF 3 was more frequently integrated. This



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Short communication

Detection and quantification of phytic acid in black pepper variety Panniyur-1 using Polyacrylamide Gel Electrophoresis

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Abstract

Inositol hexakisphosphate (InsP6), commonly called phytic acid is a major phosphorus store in plants. It has important functions in germination and growth of seedlings and also help in plant defence against various biotic as well as abiotic stresses. The quantity of InsP6 is estimated commonly by tedious procedures like HPLC, NMR spectroscopy, TLC etc. Some of these methods also involve the use of harmful radioactive elements. Polyacrylamide gel electrophoresis (PAGE) is a rather easier and simpler method for the estimation of phytate in plant sample. PAGE was used to detect and quantify InsP6 in leaf tissues of black pepper variety Panniyur1. Crude extract of Panniyur1 leaf tissue and different concentrations of the commercially available phytate standards were prepared and analysed using PAGE. Standard curve was plotted using the band intensities (volume) (y-axis) and concentrations of phytate standard (x-axis). The estimated quantity of phytate in the sample based on standard curve was 620 nmoleg⁻¹ fresh weight of leaf tissue.

Keywords: Black pepper, Inositol hexakisphosphate (InsP6), Phytic acid, Polyacrylamide gel electrophoresis

Black pepper (*Piper nigrum*), belonging to the Piperaceae family is one of the major spice crops of Kerala. It is renowned as the “king of spices” owing to its enormous medicinal and other uses, and “black gold” as it fetches the highest return from international trade. Apart from the use as a spice, black pepper has many other uses like dietary, medicinal, perfumery and preservative. The crop has an antioxidant potential, anti-inflammatory potential, anti-microbial property, anti-cancerous property and neuro protectant activity.

Myo-inositol hexakisphosphate (InsP6), also called phytic acid, is an important phosphorus storage compound found in eukaryotic cells. It is commonly seen in plant parts including storage organs like seeds, roots and tubers. It also helps in germination and growth of seedlings. Studies have shown that

InsP6 performs a key role in plant defence mechanism, as plants defective in InsP6 are found more susceptible to diseases including viral, bacterial and fungal pathogens (Murphy et al., 2008). In guard cells, InsP6 acts as a key signalling molecule produced in response to drought stress hormone abscisic acid and triggers the release of endomembrane stored calcium ions (Lemtiri-Chlien et al., 2003). Phytic acid also plays a role as a co-factor in auxin mediated gene expression of the auxin receptor, Transport Inhibitor Response 1 (TIR1) (Tan et al., 2007). In eukaryotic cells, it is found to help mRNA export and repair of DNA double strand breaks.

The compound InsP6, although it has got important roles in vital physiological functions of plant and animal systems, has an anti-nutritional effect as it

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Novel EST-SSR marker development and validation in black pepper cultivars and varieties

Sherin Jose, R. Sujatha, K. P. Deeshma · Published 4 April 2018 · Biology · Journal of Tropical Agriculture

Expressed Sequence Tags-Simple Sequence Repeat (EST-SSR) markers are more preferred because it is more efficient, fast and low cost. The main objective of the study was to develop new EST-SSR markers in black pepper. Sixty eight unigene sequences containing 70 SSRs were detected from 1048 unigenes using MicroSatellite (MISA) identification tool. Sixty two mononucleotides, two dinucleotides and six trinucleotides were the repeat motifs obtained. Nine primer pairs were designed for eight unigene... [Expand](#)

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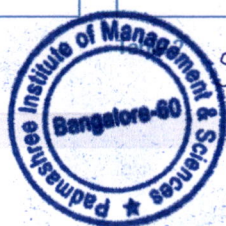
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Name	FS	Primer	Length (bp)	% GC	Tm (°C)	SNP sites (bp)	Sequence details
PS01	F1	TATTTGATGCTGTTGAGGCTGCG	21	46	61.2	111	(TGA) ₁
	R1	GAGTTTCAAGAGCAAAACATD9	22	47	60.1		
PS02	F1	CGAGCAAGGTCAGGCGAAGC	29	48	62.9	208	(TCA) ₁
	R2	CGAGCTCAACTTATTTCTTCT	22	45	58.4		
PS03	F3	GATTAAGAAGGATGATGATG	21	48	59.1	201	(AGG) ₁
	R3	GATCAGGCTTTCACAGGG	21	48	59.1		
PS04	F4	GGGACGCTGCTCAGAGGGA	18	47	59.8	146	(GCT) ₁
	R4	GGGACGCTCAGGAGGCTTC	20	46	58.4		
PS05	R4b	CAGAGCAGTATTCAGAACT	20	47	58.4	282	
PS06	F5	TGGGAGCAGTACATACAA	20	46	58.1	188	(CA) ₁
	R5	CAGCTTCAAGGAGATGAGG	21	52	61.2		
PS06	F6	OLGCAAGGAGGAGAAACAAEA	22	45	58.4	228	(T) ₁ (TCT) ₁
	R6	CAAGAGCTGATGATGAGGGA	21	45	57.1	145	
PS07	F7	ATGCTTCAGGCGAAGCTTCA	22	45	58.1	182	(TA) ₁
	R7	GTGAAAGGCTCAGGAGGCTC	22	45	58.4		
PS08	F8	AAGTAACTGCTACAGACTTCT	22	50	62.1	201	(CT) ₁
	R8	TCAGTCTTATGATATGCAAC	21	48	59.1		

Type of SSR	Repeat motif	Number of unigenes	Total	Grand total	Frequency (%)
Mononucleotide	(A) _n	51	28	72	59.1
	(G) _n	9			
	(C) _n	1			
	(T) _n	5	7		
	(CA) _n	4			
	(TA) _n	1	1		
Dinucleotide	(TA) _n	1	1	2	2.8
	(CA) _n	1	1		
	(CT) _n	0	0		
Trinucleotide	(TGA) _n	1	1	6	8.6
	(GAT) _n	1	1		
	(TCA) _n	1	1		
	(GAG) _n	1	1		
	(GCA) _n	1	1		
	(GCT) _n	1	1		

Table 1



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Note

Effect of dietary protein levels on the growth of Carnatic carp *Barbodes carnaticus* (Jerdon, 1849) fingerlings

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ABSTRACT

Fingerlings of *Barbodes carnaticus* (Jerdon 1849) (6.40±0.267 cm, 2.46±0.39 g) were reared in aerated plastic tubs (40 l) with five iso-energetic diets formulated to contain crude protein levels ranging from 25 to 45% using pure ingredients. Initially, the diet was fed at @5% of the biomass and gradually adjusted based on daily feed consumption. The fish were allowed to feed for 6 h and thereafter the unconsumed feeds were siphoned out. The following day, faecal matter was collected from each tank by filtering the water with a fine meshed nylon cloth (15 µm), dried, pooled and stored for proximate analysis. Water from each tub was replaced with 50% freshwater every day after faecal matter collection. The feeding trial was conducted for a period of 60 days. Proximate composition of feed and faecal matter was analysed. Acid insoluble ash was used as the reference marker for dry matter, protein and fat digestibility determination. The growth parameters and protein efficiency ratio (PER) were higher (p<0.05) in fish fed 35% protein diet compared to other diets. The feed conversion ratio (FCR) was lower (p<0.05) in 35, 40 and 45% protein diets compared to the lower protein diets. The carcass proximate composition revealed the lowest moisture (p<0.05) and highest protein (p>0.05) and fat content (p<0.05) in fish fed 35% protein diet compared to other diets. The digestibility of dry matter and nutrients was higher (p<0.05) with 35% protein diet. The study revealed crude protein requirement of 35% by the fingerlings of *B. carnaticus*.

Keywords: *Barbodes carnaticus*, Dietary protein, Fingerlings

Indian major carps contribute the lion's share to freshwater aquaculture production in India, around 80% by volume. India is regarded as a 'carp country' due to the rich diversity of carps in its freshwater ecosystems. The country is blessed with 15-20 varieties of minor carps that have a huge potential for freshwater aquaculture, yet to be exploited. A need for diversification of farmed fish species has been emphasised (NACA/FAO, 2000). These carp species, some of which belong to the minor carps, can be considered as alternatives to the major carp species for diversification in freshwater aquaculture. *Barbodes carnaticus* (Jerdon 1849), commonly known as Carnatic carp, is one such species endemic to the Western Ghats of India. The breeding technology of the species has already been standardised at the Regional Research Centre of ICAR-Central Institute of Freshwater Aquaculture, Bangalore. *B. carnaticus* is characterised by an elongated and stocky body. Compared to other members of the genus, this species attains larger size; the maximum weight recorded being 12 kg and length 90 cm (Talwar and Jhingran, 1991). The higher growth rate of *B. carnaticus* in the first year of its life span along with other favourable characteristics makes this species an excellent

candidate for freshwater aquaculture (Manojkumar and Kurup, 2010).

Proteins are the structural components and energy source in diets of fish and play a key role as they are very essential for body maintenance and growth. Generally, fish requires higher levels of protein in diets and this nutrient is the costliest dietary constituent. A significant reduction in feed cost can be achieved if diets with low protein could be fed to fish without compromising growth and health (Webster *et al.*, 2000). However, inadequate protein in the diet results in reduction of growth. On the other hand, if too much protein is supplied in the diet, only part of it will be used to make new proteins and the remainder will be converted to energy (Wilson, 2002). Hence determination of optimum protein requirement for fish is the first step to the development of low-cost feeds. Earlier studies have given an estimate of the protein requirement of Indian cultivable carps using purified diets (Sen *et al.*, 1978; Singh and Sinha, 1981; Rao, 1987; Singh *et al.*, 1987; Singh and Bhanot, 1988; Swamy and Mohanty, 1988; Swamy *et al.*, 1988; Mohanty *et al.*, 1990). Jena *et al.* (2012) reported the protein requirement of the minor carp *Labeo fimbriatus*, to be 30.14% based on



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Digestibility of dry matter and nutrients from three ingredients by the carps, *Labeo fimbriatus* (Bloch, 1795) and *Cyprinus carpio* Linnaeus, 1758 with a note on digestive enzyme activity

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ABSTRACT

This study was conducted in indoor, aerated plastic tubs to estimate the digestibility of dry matter and nutrients by the carps, *Labeo fimbriatus* (Bloch, 1795) and *Cyprinus carpio* Linnaeus, 1758, from three feed ingredients viz., azolla, soybean meal and silkworm pupa incorporated at levels ranging from 0-40% in a diet comprising equal amounts of rice bran and groundnut oil cake using crude fibre as the marker. Activity of the major digestive enzymes was also estimated in the gut of fish at the end of the experimental trial. Utilisation of azolla protein was comparable with that of control diet up to 20% incorporation in both *L. fimbriatus* and common carp. Major nutrients from soybean were better utilised up to 40% incorporation by the two species. Protein digestibility from silkworm pupae increased at 20% incorporation and decreased at 40% in *L. fimbriatus*, while fat and nitrogen-free extract digestibility was higher at 20-40% incorporation. In common carp, higher digestibility of protein and fat was recorded at 10-30% inclusion levels of silkworm pupa.

Keywords: Azolla, *Cyprinus carpio*, Digestibility, *Labeo fimbriatus*, Silkworm pupa, Soybean

Introduction

Digestibility which is the quantification of the digestive processes provides a relative measure of the extent to which ingested food and its nutrient components are digested and absorbed by the animal. Apparent digestibility coefficients (ADCs) vary between fish species and feedstuffs. Determining the digestibility of nutrients in a feedstuff is important not only to enable formulation of diets that maximise the growth of cultured fish by providing appropriate amounts of available nutrients, but also to limit the wastes produced by the fish. Digestibility of individual ingredients in the compounded diet is considered as one of the important factors affecting the growth of fish (De Silva *et al.*, 1990); therefore, digestibility evaluation of each ingredient is desirable before incorporation in the diet.

Azolla has been recognised as one of the potential ingredients for use in aquaculture (Gangadhar *et al.*, 2014; 2015). It is easy to cultivate and has high productivity and nutritive value. *Azolla pinnata* is a species of aquatic fern found in quiet and slow-moving water bodies round the year (Lumpkin and Puckett, 1982). Use of azolla as a fish feed ingredient is well documented (Dutta, 2011).

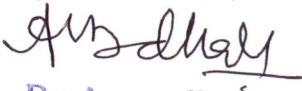
Soybean, *Glycine* sp. is another most promising plant protein ingredient because of its high protein content and

excellent amino acid profile, easy availability, reasonable price and lower faecal nutrient output (Castro *et al.*, 2011). Soybean meal is used in the diets of various carp and catfish species. Fish meal substitution in feeds at quantities of up to 50-60% by soybean meal has been practiced in recent years (Dawood *et al.*, 2015; Priyadarshini *et al.*, 2015).

Silkworm pupae are wastes from the silkworm industry, often discarded in the open environment or used as fertiliser. Due to high protein content, silkworm pupa meal has been found to be a suitable livestock feed, notably for monogastric species like poultry, pigs and fish (Trivedy *et al.*, 2008). Silkworm pupa is more suitable than mustard oil cake and rice bran as a feed ingredient in carps (Chakrabarthy *et al.*, 1973). Studies have shown that it could be included up to 30-50% in the diets of carps (Jayaram and Shetty, 1980; Nandeesh *et al.*, 2000) and mahseer (Shyama, 1993).

Labeo fimbriatus (Bloch, 1795), commonly called 'fringe-lipped carp' has been considered as a candidate for species diversification in carp polyculture. Though slow-growing, this medium sized carp is in good demand due to high market value, excellent flavour and meat quality (Basavaraju *et al.*, 1995). *Cyprinus carpio* Linnaeus, 1758, the common carp, accounts for the world's second highest farmed fish production in Asia (Milstein, 1992).




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Existing & Novel Methods of Water Harvesting

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Abstract: - Through ground water utilization has substantially enhanced domestic utility and crop productivity – due to widespread over exploitation, underground water level is going down day by day at an alarming rate in most parts of India especially in Karnataka & Tamil Nadu. Further, the two main sources of irrigation in India are canals and groundwater – both sources are also facing extreme downward trend. To combat such alarming situation, the urgent need is to explore novel methods of water harvesting especially through rain water harvesting which has been highlighted in the present study.

Index Terms: groundwater, rainwater, Runoff, harvesting, Rooftop catchments

I. INTRODUCTION

Due to deforestation and increasing population, land pressure rises and as land pressure rises, more and more marginal and semi-marginal areas in the world are being used for cultivation. Noteworthy that much of this land is located in the arid or semi-arid belts where rain is less falls irregularly and as a result much of the precious water is soon lost as surface runoff. Recent droughts in India have highlighted the risks to human beings and livestock, which occur when rains falter or fail. Irrigation is the most obvious response to drought and there is now increasing interest in a low cost alternative - generally referred to as "water harvesting". Water harvesting is the collection of runoff for productive purposes usually in irrigation. Instead of runoff being left to cause erosion, it can be harvested and utilized. In the semi-arid drought-prone areas, water harvesting is a directly productive form of soil and water conservation and yields and reliability of production can be significantly improved with this method. Water harvesting can be considered as a rudimentary form of irrigation; the difference is that with water harvesting the farmer (or more usually, the agropastoralist) has not much control over timing. Runoff can be harvested only when it rains [1]. Rainwater harvesting is the accumulation and deposition of rainwater for reuse on-site instead of than allowing it to Run-off (Runoff is generated by rainstorms and its occurrence and quantity are dependent on the characteristics of the rainfall event, i.e. intensity, duration and distribution). Hence, it means capturing rain, the run-off in one's own village or town and taking measures for keep that water clean by not allowing polluting activities to take place in the catchment. Rainwater can be collected from

rivers or roofs is redirected to a deep pit (well, shaft, or borehole), a reservoir with percolation. Its uses include water for gardens, livestock and irrigation including domestic use with proper treatment, etc. The harvested water can also be used as drinking water, longer-term storage and for other purposes such as groundwater restoring & recharge [1] (Fig. 1).

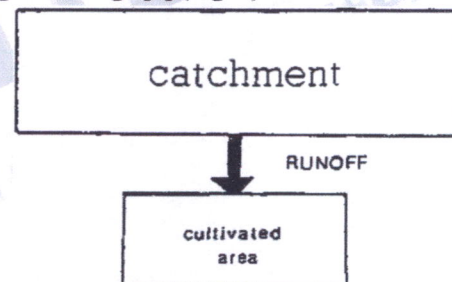


Fig. 1: The principle of Rain water harvesting [1]

Water harvesting techniques which harvest runoff falls under the following terminologies:

Rainwater Harvesting: while all systems which collect discharges from watercourses are grouped under the term [1, 2]:

Floodwater Harvesting: A wide variety of water harvesting techniques for many different applications are known. Productive uses include provision of domestic and stock water, concentration of runoff for crops, fodder and tree production and less frequently water supply for fish and duck ponds. Therefore, water harvesting is undertaken through the following ways

- * Capturing runoff from rooftops
- * Capturing runoff from local catchments