UNIMAS
UNIVERSITI MALAYSIA SARAWAK

FACULTY OF
RESOURCE SCIENCE &
TECHNOLOGY

BIOTECHNOLOGY

RESEARCH AT FRST, UNIMAS

Research in biotechnology is at the forefront of scientific innovation, combining biology, chemistry, and engineering principles to develop revolutionary solutions that impact various sectors, from healthcare to agriculture and environmental conservation. At Faculty of Resource Science & Technology, UNIMAS, we are dedicated to advancing knowledge and pushing the boundaries of this exciting field.

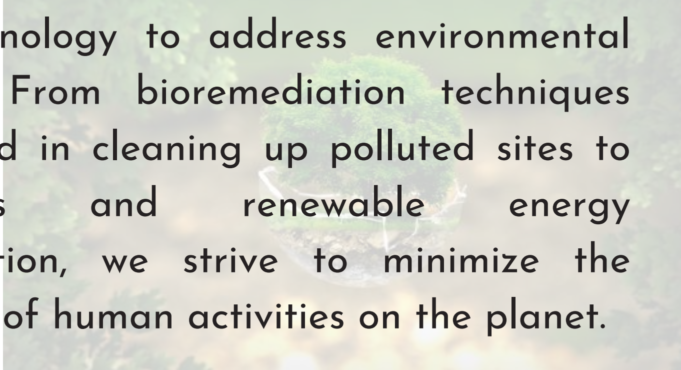
Community-Driven University For a Sustainable World

WHY BIOTECHNOLOGY RESEARCH IS IMPORTANT?

Advancing Healthcare

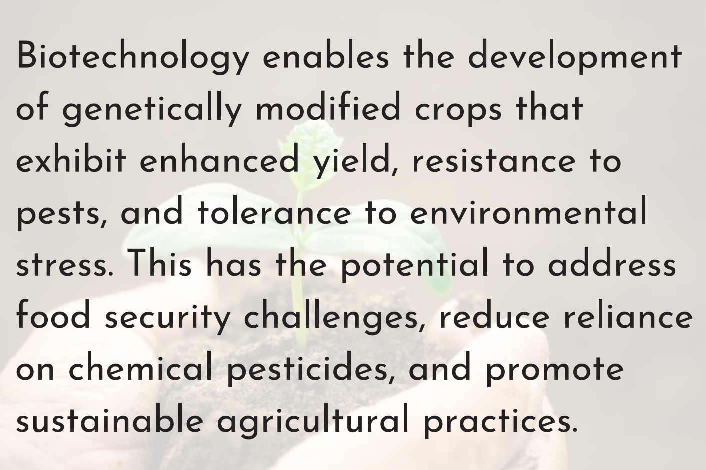
Biotechnology plays a vital role in developing new therapies, diagnostics, and vaccines. Through genetic engineering and biopharmaceutical production, we are paving the way for personalized medicine, targeted treatments, and more effective disease management.

Environmental Conservation



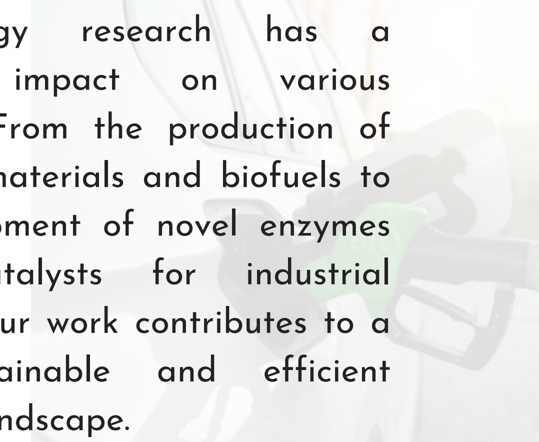
Our research focuses on leveraging biotechnology to address environmental issues. From bioremediation techniques that aid in cleaning up polluted sites to biofuels and renewable energy production, we strive to minimize the impact of human activities on the planet.

Sustainable Agriculture

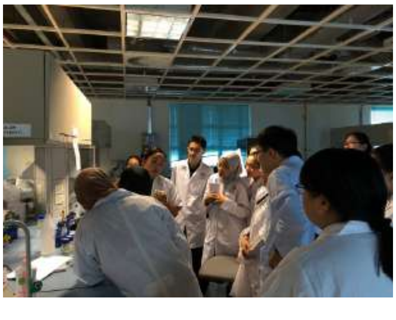


Biotechnology enables the development of genetically modified crops that exhibit enhanced yield, resistance to pests, and tolerance to environmental stress. This has the potential to address food security challenges, reduce reliance on chemical pesticides, and promote sustainable agricultural practices.

Industrial Applications



Biotechnology research has a profound impact on various industries. From the production of bio-based materials and biofuels to the development of novel enzymes and biocatalysts for industrial processes, our work contributes to a more sustainable and efficient industrial landscape.



MEET OUR EXPERTS

MEET OUR EXPERTS

MICROBIOLOGY

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Assoc. Prof. Dr Lesley Maurice Bilung
Assoc. Prof. Dr Elexson Nillian
Ts. Dr Hashimatul Fatma Hashim
Dr Ngieng Ngui Sing
Mdm Fazia Mohd Sinang

ANIMAL BIOTECHNOLOGY

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Assoc. Prof. Dr Chung Hung Hui
Dr Muhammad Redza Mohd Radzi

GENETICS

Prof. Dr Edmund Sim Ui Hang
Prof. Dr Ho Wei Seng
Prof. Dr Hairul Azman Roslan

MOLECULAR BIOLOGY

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Assoc. Prof. Dr Dayang Salwani Awang Adeni
Dr Nurashikin Suhaili
Dr Rosmawati Saat

ENZYMOLOGY

Prof. Dr Awang Ahmad Sallehin Awang Husaini
Dr Ngieng Ngui Sing

IMMUNOLOGY

Dr Muhammad Redza Mohd Radzi

MEET OUR EXPERTS

NICHE: MICROBIOLOGY

Assoc. Prof. Dr Lesley Maurice Bilung

BSc., MSc., PhD (UPM)

blesley@unimas.my

Assoc. Prof. Dr Micky Vincent

BSc.Ed. (Hons.) (UM), MSc. (UPM), PhD (Iowa State, USA)

vmicky@unimas.my

Ts Dr Hashimatul Fatma Hashim

BSc. Hons. (USM), MSc (UNIMAS), PhD (University College London)

hhfatma@unimas.my

Dr Ngieng Ngui Sing

BSc.(UKM), MSc.(UNIMAS), PhD (UNIMAS)

snngui@unimas.my

Assoc. Prof. Dr Elexson Nillian

BSc. (Hons) (UNISEL), MSc., PhD (UPM)

nelexson@unimas.my

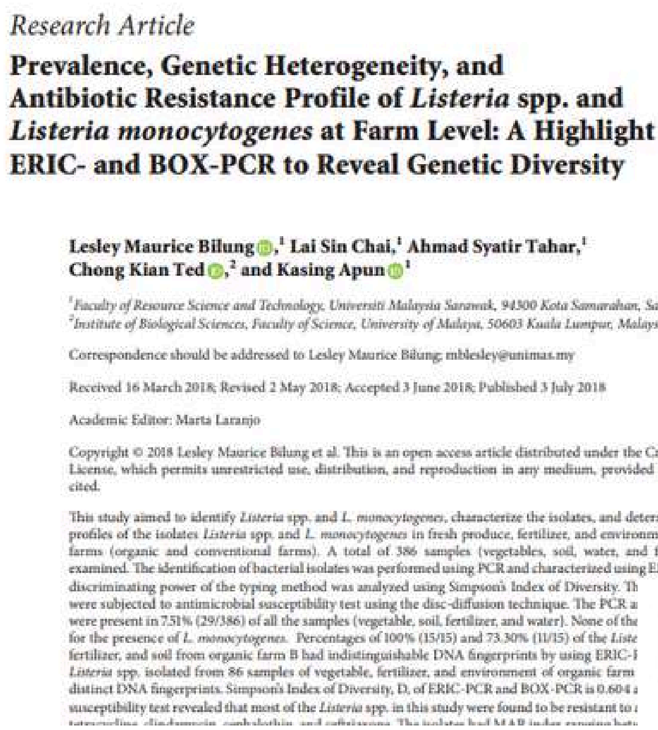
Mdm Fazia Mohd Sinang

BMedSc (UM), MSc. (UPM)

msfazia@unimas.my

NICHE: MICROBIOLOGY

SOME OF OUR RECENT WORKS



Research Article

Prevalence, Genetic Heterogeneity, and Antibiotic Resistance Profile of *Listeria* spp. and *Listeria monocytogenes* at Farm Level: A Highlight of ERIC- and BOX-PCR to Reveal Genetic Diversity

Lesley Maurice Bilung,[1] **Lai Sin Chai**,[1] **Ahmad Syatir Tahar**,[1]
Chong Kian Ted,[2] **and Kasing Apun**[1]

[1]*Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, M*
[2]*Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia*

Correspondence should be addressed to Lesley Maurice Bilung; mblesley@unimas.my

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This study aimed to identify *Listeria* spp. and *L. monocytogenes*, characterize the isolates, and determine the
profiles of the isolates *Listeria* spp. and *L. monocytogenes* in fresh produce, fertilizer, and environmental san
farms (organic and conventional farms). A total of 386 samples (vegetables, soil, water, and fertilizer with manure) were
examined. The identification of bacterial isolates was performed using PCR and characterized using ERIC-PCR and BOX-PCR. The
discriminating power of the typing method was analyzed using Simpson's Index of Diversity. Th
were subjected to antimicrobial susceptibility test using the disc-diffusion technique. The PCR a
were present in 7.51% (29/386) of all the samples (vegetable, soil, fertilizer, and water). None of the
for the presence of *L. monocytogenes*. Percentages of 100% (15/15) and 73.30% (11/15) of the *Liste*
fertilizer, and soil from organic farm B had indistinguishable DNA fingerprints by using ERIC-I
Listeria spp. isolated from 86 samples of vegetable, fertilizer, and environment of organic farm
distinct DNA fingerprints. Simpson's Index of Diversity, D, of ERIC-PCR and BOX-PCR is 0.604 a
susceptibility test revealed that most of the *Listeria* spp. in this study were found to be resistant to a

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Growth Kinetics of Ethidium Bromide Mutagenized *Lipomyces starkeyi* Strains

Open Access

Micky Vincent[1,*], Latifah Suali[1], Afizul Safwan Azahari[1], Patricia Rowena Mark Baran[1], Elexson Nillian[1], Lesley Maurice Bilung[1]

[1] Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

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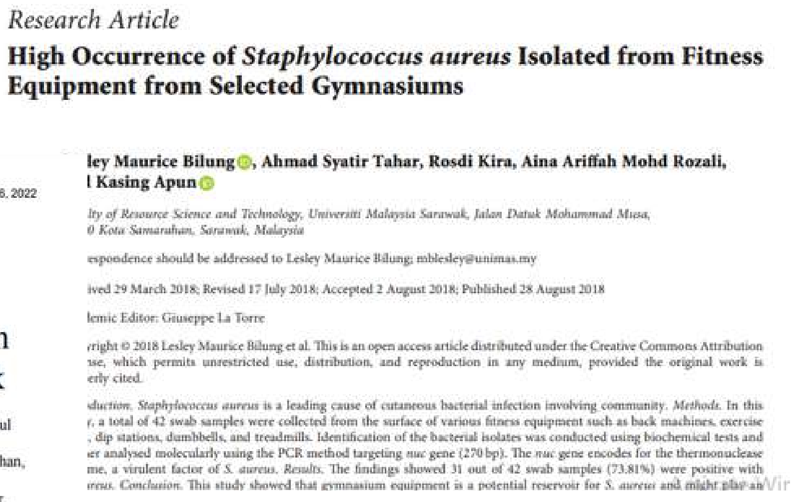
ABSTRACT

Yeast growth and biomass production are greatly influenced by the length of the incubation period during cultivation. Therefore, this study was conducted to investigate the growth kinetics of five *Lipomyces starkeyi* strains as determined by biomass production. The five *L. starkeyi* strains, namely *L. starkeyi* ATCC 12659, *L. starkeyi* MV-1, *L. starkeyi* MV-4, *L. starkeyi* MV-5 and *L. starkeyi* MV-8, were inoculated in sterilized Yeast Malt broth, and, incubated for 192 hr at ambient temperature. Biomass yields were assessed and calculated gravimetrically every 24 hr. Results indicated that the optimal biomass production of *L. starkeyi* ATCC 12659, *L. starkeyi*



Research Article

High Occurrence of *Staphylococcus aureus* Isolated from Fitness Equipment from Selected Gymnasiums

ley Maurice Bilung, **Ahmad Syatir Tahar, Rosdi Kira, Aina Ariffah Mohd Rozali,**
l Kasing Apun

lty of Resource Science and Technology, Universiti Malaysia Sarawak, Jalan Datuk Mohammad Musa,
0 Kota Samarahan, Sarawak, Malaysia

espondence should be addressed to Lesley Maurice Bilung; mblesley@unimas.my

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lemic Editor: Giuseppe La Torre

duction. *Staphylococcus aureus* is a leading cause of cutaneous bacterial infection involving community. *Methods.* In this
, a total of 42 swab samples were collected from the surface of various fitness equipment such as back machines, exercise
, dip stations, dumbbells, and treadmills. Identification of the bacterial isolates was conducted using biochemical tests and
er analysed molecularly using the PCR method targeting *nuc* gene (270 bp). The *nuc* gene encodes for the thermonuclease
me, a virulent factor of *S. aureus*. *Results.* The findings showed 31 out of 42 swab samples (73.81%) were positive with
reus. *Conclusion.* This study showed that gymnasium equipment is a potential reservoir for *S. aureus* and might play an

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INTERNATIONAL JOURNAL OF BIOLOGY AND BIOMEDICAL ENGINEERING
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Volume 16, 2022

Contamination of waterborne parasites at water treatment plants and a gravity-feed system: a highlight on water safety for urban and rural communities in Kuching, Sarawak

Ahmad Syatir Tahar[1], Lesley Maurice Bilung[1], Kasing Apun[1], Reena Leeba Richard[1], Hashimatul Fatma Hashim[1], Elexson Nillian[1], Lau Seng[4], Yvonne Ai-Lian Lim[2]
[1]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia
[2]Department of Parasitology, Faculty of Medicine, University of Malaya, 50603, Kuala Lumpur, Malaysia
[3]Department of Science and Technology Studies, Faculty of Science, University of Malaya, 50603, Kuala Lumpur, Malaysia
[4]Institute of Biodiversity and Environmental Conservation, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

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E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d190412

Isolation, identification and diversity of oleaginous yeasts from Kuching, Sarawak, Malaysia

MICKY VINCENT*, HUANG CHAI HUNG, PATRICIA ROWENA MARK BARAN,
AFIZUL SAFWAN AZAHARI, DAYANG SALWANI AWANG ADENI
Resource Biotechnology Program, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia. *email: vmicky@unimas.my

Manuscript received: 25 May 2018. Revision accepted: 6 June 2018.

bstract. *Vincent M, Hung MC, Baran PRM, Azahari AS, Adeni DSA. 2018. Isolation, identification and diversity of oleaginous yeasts rom Kuching, Sarawak, Malaysia. Biodiversitas 19: 1266-1272.* The present study was performed to isolate, identify and determine the
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yeast isolates,
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International Food Research Journal 24(3): 985-989 (June 2017)
Journal homepage: http://www.ifrj.upm.edu.my

Detection of *Bacillus cereus* in formula milk and ultra high temperature (UHT) treated milk products

[1*]Lesley, M. B., [1]Ernie, S.R., [1]Kasing, A. and [2,3]Son, R.

[1]*Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia*
[2]*Department of Food Science, Faculty of Food Science and Technology, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia*
[3]*Food Safety and Food Integrity, Institute of Tropical Agriculture and Food Security, Universiti Putra Malaysia 34300 Serdang, Selangor, Malaysia*

Article history

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Keywords

Bacillus cereus

Abstract

Ultra high temperature (UHT) treated milk products and formula milk are known to be frequently contaminated with *Bacillus cereus*. Presence of *B. cereus* in these milk products is of particular concern considering the majority of consumers are infants and children. Possible sources of contamination are contaminated raw milk, cross-contamination during processing, under-processing and mishandling of milk products. This study was conducted to detect the presence of *B. cereus* in both formula milk (n=12) and UHT milk (n=20) sold in selected retail markets. The approach consisted of enumerating by MPN/g followed by PCR assay aimed at detecting *gyrB* gene in *B. cereus*, that encode for the subunit B protein of DNA gyrase

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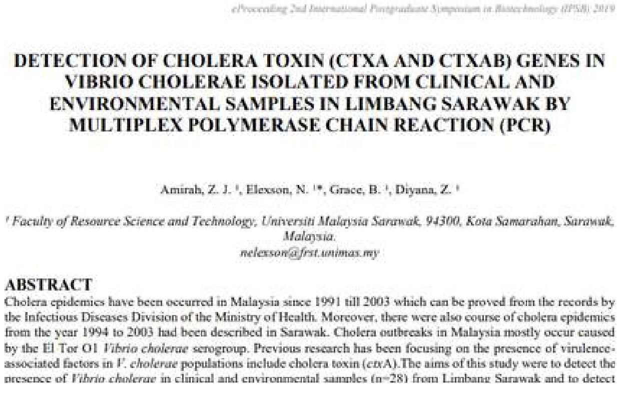

eProceeding 2nd International Postgraduate Symposium in Biotechnology (IPSB) 2019

DETECTION OF CHOLERA TOXIN (CTXA AND CTXAB) GENES IN VIBRIO CHOLERAE ISOLATED FROM CLINICAL AND ENVIRONMENTAL SAMPLES IN LIMBANG SARAWAK BY MULTIPLEX POLYMERASE CHAIN REACTION (PCR)

Amirah, Z. J. [1], Elexson, N. [1*], Grace, B. [1], Diyana, Z. [1]

[1] *Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia.*
nelexson@frst.unimas.my

ABSTRACT

Cholera epidemics have been occurred in Malaysia since 1991 till 2003 which can be proved from the records by the Infectious Diseases Division of the Ministry of Health. Moreover, there were also course of cholera epidemics from the year 1994 to 2003 had been described in Sarawak. Cholera outbreaks in Malaysia mostly occur caused by the El Tor O1 *Vibrio cholerae* serogroup. Previous research has been focusing on the presence of virulence-associated factors in *V. cholerae* populations include cholera toxin (*ctx*A).The aims of this study were to detect the presence of *Vibrio cholerae* in clinical and environmental samples (n=28) from Limbang Sarawak and to detect

MEET OUR EXPERTS

NICHE: FOOD SAFETY & SECURITY

Assoc. Prof. Dr Lesley Maurice Bilung

BSc., MSc., PhD (UPM)

blesley@unimas.my

Assoc. Prof. Dr Elexson Nillian

BSc. (Hons) (UNISEL),
MSc., PhD (UPM)
nelexson@unimas.my

Biotechnology plays a vital role in ensuring food security by increasing crop yields, improving crop quality and nutritional value, enhancing pest and disease resistance, promoting sustainable agriculture practices, and conserving genetic resources. These advancements contribute to a more resilient and productive agricultural system, helping to meet the global demand for safe, nutritious, and affordable food while addressing the challenges posed by population growth, climate change, and limited arable land.

SOME OF OUR RECENT WORKS

International Journal of Current Research and Review
DOI: http://dx.doi.org/10.31782/IJCRR.2021.SP135

Scopus

Original Research

IJCRR
Section: Healthcare
ISI Impact Factor (2019-20): 1.628
IC Value (2019): 90.81
SJIF (2020) = 7.893

Contamination of Intestinal Parasites in Vegetables from Kuching

Ahmad Syatir Tahar[1], Lesley Maurice Bilung[1], Constance Suk Kim Goh[1], Elexson Nillian[1], Yvonne Ai-Lian Lim[2], Reena Leeba Richard[3], Hashimatul Fatma Hashim[1], Kasing Apun[1]

[1]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia; [2]Department of Parasitology, Faculty of Medicine, University of Malaya, 50603, Kuala Lumpur, Malaysia; [3]Department of Science and Technology Studies, Faculty of Science, University of Malaya, 50603, Kuala Lumpur, Malaysia.

ABSTRACT

Background: Contaminated vegetables with intestinal parasites, particularly those eaten raw, represent a proportion humans acquiring foodborne parasitic diseases worldwide. Unfortunately, the risk is often neglected as limited studies reported about the parasitic occurrence from vegetables retailed in Malaysia.

Objective: This study was conducted to determine the occurrence of intestinal parasites in fresh retailed vegetables and Kota Samarahan, Sarawak.

Methods: A total of 108 vegetables (comprising leafy and root-type vegetables) were purchased from three superm three wet markets in Kuching and Kota Samarahan. The samples were processed with 0.95% sodium chloride s underlaid with Sheather's sucrose solution. *Cryptosporidium* and *Giardia* were detected using AquaGlo™ G/C antibo and 4′,6-diamidino-2-phenylindole stain. Other parasites were detected using Lugol's iodine stain.

Results: A total of 24 out of 108 vegetables samples (22.2%) were contaminated with nematode larvae (range: (larvae/g), *Cryptosporidium* oocysts (range: 0.01 – 0.03 oocysts/g), hookworm ova (range: 0.01 – 0.02 ova/g) and ((0.01 cysts/g). There were no significant differences ($p > 0.05$) for means of parasite concentrations in vegetables f markets and wet markets, as well as parasite concentrations from leafy-type and root-type vegetables.

Conclusion: The findings revealed relatively high numbers of intestinal parasites detected from fresh retailed vege nifying potential foodborne transmission of parasitic infections if the vegetables are not prepared hygienically or c Besides, a high proportion of such infection risk may be reduced if farmers also take part in proper sanitation pract vegetable production and transportation.

Key Words: *Cryptosporidium, Giardia*, Helminth, Intestinal parasites, Protozoa, Vegetables

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Pertanika J. Trop. Agric. Sci. 43 (4): 477 - 490 (2020)

PERTANIKA JOURNALS

TROPICAL AGRICULTURAL SCIENCE

Journal homepage: http://www.pertanika.upm.edu.my/

The Feasibility Study of Physicochemical Properties of Sarawak *Liberica* sp. Coffee Pulp

Elexson Nillian*, Nurhuda Syahirah Ismail, Muhamad Eddy Boli, Nick Laurence Buyong, Ngieng Ngui Sng, Dayang Salwani Awang Adeni and Awang Ahmad Sallehin Awang Hussini

Faculty of Resource Science and Technology, University Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia

ABSTRACT

Liberica coffee is a minor species that is planted all around the world. Therefore, there is little study conducted on this coffee species as only one percent is cultivated all around the world. In Malaysia, there is still no research focusing on coffee pulp from Sarawak *liberica* sp. and thus leading to this study. The wastes and by-product such as coffee pulps will become the residues as they were not needed in processing the coffee. This will create environmental pollution. Thus, this research aimed to evaluate the feasibility study on the physicochemical properties of coffee pulp from Sarawak *liberica* sp. including determination by colorimetric assays for phenolic and flavonoid content, antioxidant activity, and reducing sugar analysis. The antibacterial activities of coffee pulp were evaluated against Gram-

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Jurnal Teknologi

Full Pap

EFFICIENCY OF TRADITIONAL DNA EXTRACTION METHOD IN PCR DETECTION OF PORCINE DNA IN MEAT MIXTURES

Zaliha Suadi[a], Lesley Maurice Bilung[a]*, Kasing Apun[a], Aida Azrina Azmi[b]

[a]Department of Molecular Biology, Faculty of Science and Resource Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia
[b]Halal Products Research Institute, Universiti Putra Mala
UPM Serdang, Malaysia

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*Corresponding author
mblesley@unimas.my

Graphical abstract

PCR product sizes of mitochondrial DNA cytochrome b gene for the investigated species.

Abstract

Through the advancement of
effective techniques in specie
stability in harsh conditions co
conducted to determine the e
phenol/chloroform/isoamyl a
commercially available kit by
for amplification of porcine D
and quality of the DNA extrac
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(274-bp), and pork (398-bp), t
DNA extracts. High DNA con
samples extracted using the F
agarose gel was able to dete
minute proportion (1%). The ex
with the presence of a specific
recommended as a cost-effec
extraction kits in detecting pork

Keywords: Meat adulteration
cytochrome b

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Detection of Beneficial Lactic Acid Bacteria (LAB) and Yeast In Sarawak Fermented Food

Elexson Nillian[1,*], Nick Laurence Buyong[1], Dalene Lesen[1], Grace Bebey[1], Azham Zulkharnain[2]

[1] Faculty of Resource Science and Technology, University Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia
[2] Department of Bioscience and Engineering, Shibura Institute of Technology, Japan

ABSTRACT

Sarawak native's fermented food can be a catalyst for boosting the local economy in Sarawak. The Lactic Acid Bacteria (LAB) are generally regarded as safe, have a stability of usage, and originate from natural resources. Lactic acid bacteria and yeast work in synergy to provide a natural way to enhance the nutritive value and flavour of the food. The study aims to investigate the presence of potential probiotic Lactic Acid Bacteria (LAB) and yeast isolated from Sarawak fermented food. Two hundred fifty (n=250) of samples including fifty (n=50) each sample such as fermented shrimps (cencaluk), fermented mustard vegetables (kasam ensabi)

MEET OUR EXPERTS

NICHE: PLANT BIOTECHNOLOGY

Prof. Dr Ho Wei Seng

SmSn, PhD (UKM)

wsho@unimas.my

Prof. Dr Hairul Azman Roslan

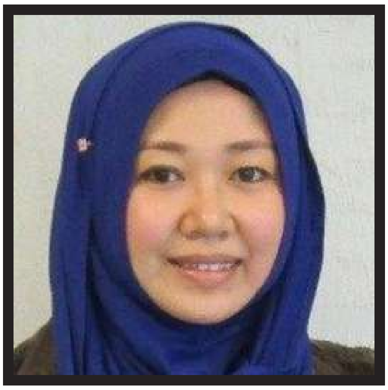
BSc. Hons (UM), MSc., PhD (Liverpool, UK)

rhairul@unimas.my

Prof. Dr Mohd Hasnain Md Hussain

B.Appl, Sc.Hons (USM), MSc. (Newcastle-upon Tyne, UK), PhD (East Anglia, UK)

hhasnain@unimas.my



Mdm Safarina Ahmad

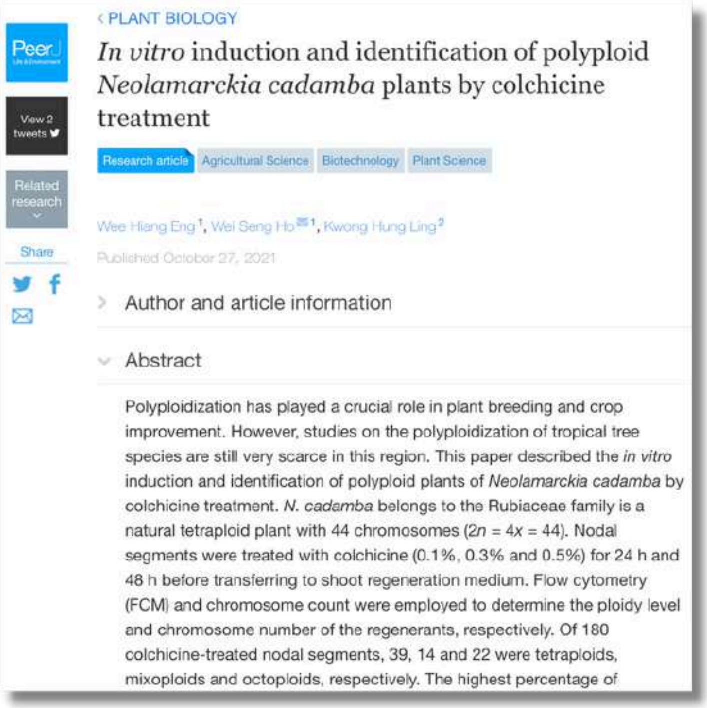
Sc. Hons. (UNIMAS), SSc. (UKM)

asafarina@unimas.my

Plant biotechnology is essential for sustainable agriculture, improved crop productivity, enhanced nutrition, environmental conservation, and adaptation to a changing climate. It offers innovative solutions to address global food security challenges, reduce environmental impacts, and promote the sustainable use of plant resources for the benefit of both human welfare and the planet.

NICHE: PLANT BIOTECHNOLOGY

SOME OF OUR RECENT WORKS



‹ PLANT BIOLOGY

In vitro induction and identification of polyploid *Neolamarckia cadamba* plants by colchicine treatment

Research article | Agricultural Science | Biotechnology | Plant Science

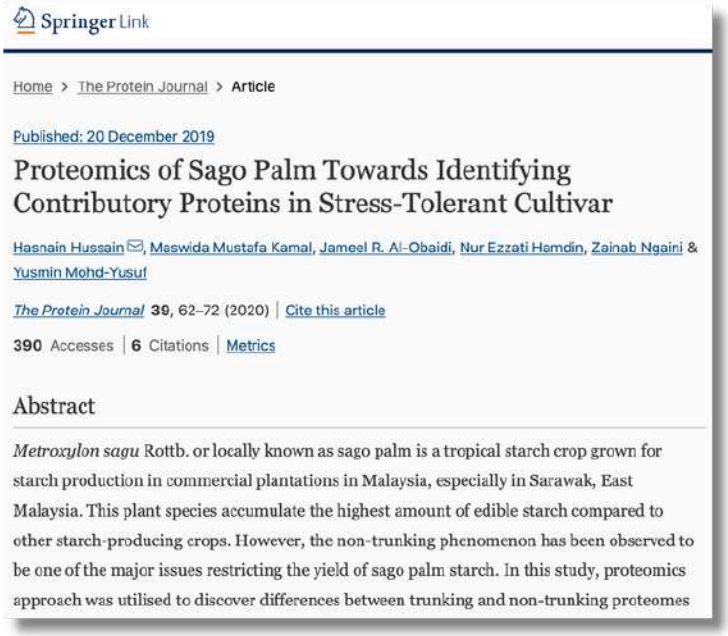
Wee Hiang Eng[1], Wei Seng Ho[1], Kwong Hung Ling[2]

Published October 27, 2021

› Author and article information

⌄ Abstract

Polyploidization has played a crucial role in plant breeding and crop improvement. However, studies on the polyploidization of tropical tree species are still very scarce in this region. This paper described the *in vitro* induction and identification of polyploid plants of *Neolamarckia cadamba* by colchicine treatment. *N. cadamba* belongs to the Rubiaceae family is a natural tetraploid plant with 44 chromosomes ($2n = 4x = 44$). Nodal segments were treated with colchicine (0.1%, 0.3% and 0.5%) for 24 h and 48 h before transferring to shoot regeneration medium. Flow cytometry (FCM) and chromosome count were employed to determine the ploidy level and chromosome number of the regenerants, respectively. Of 180 colchicine-treated nodal segments, 39, 14 and 22 were tetraploids, mixoploids and octoploids, respectively. The highest percentage of



Home › The Protein Journal › Article

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Proteomics of Sago Palm Towards Identifying Contributory Proteins in Stress-Tolerant Cultivar

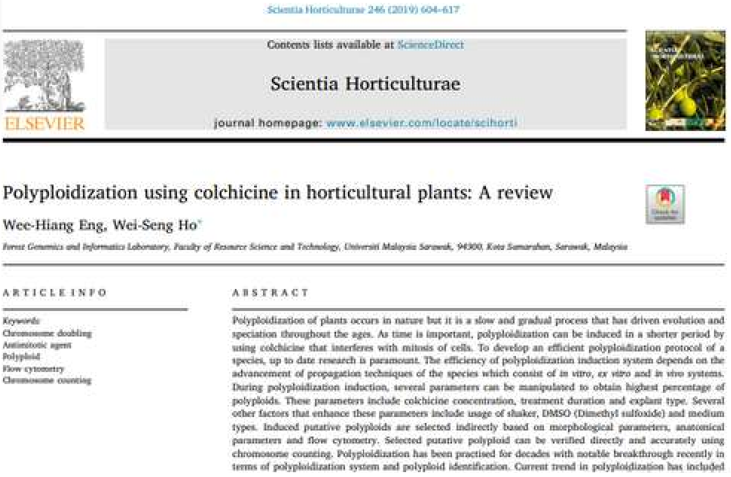
Hasnain Hussain, Maswida Mustafa Kamal, Jameel R. Al-Obaidi, Nur Ezzati Hamdin, Zainab Ngaini & Yusmin Mohd-Yusuf

The Protein Journal **39**, 62–72 (2020) | Cite this article

390 Accesses | **6** Citations | Metrics

Abstract

Metroxylon sagu Rottb. or locally known as sago palm is a tropical starch crop grown for starch production in commercial plantations in Malaysia, especially in Sarawak, East Malaysia. This plant species accumulate the highest amount of edible starch compared to other starch-producing crops. However, the non-trunking phenomenon has been observed to be one of the major issues restricting the yield of sago palm starch. In this study, proteomics approach was utilised to discover differences between trunking and non-trunking proteomes



Scientia Horticulturae 246 (2019) 604–617

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Scientia Horticulturae

journal homepage: www.elsevier.com/locate/scihorti

Polyploidization using colchicine in horticultural plants: A review

Wee-Hiang Eng, Wei-Seng Ho*

Forest Genomics and Informatics Laboratory, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia

ARTICLE INFO

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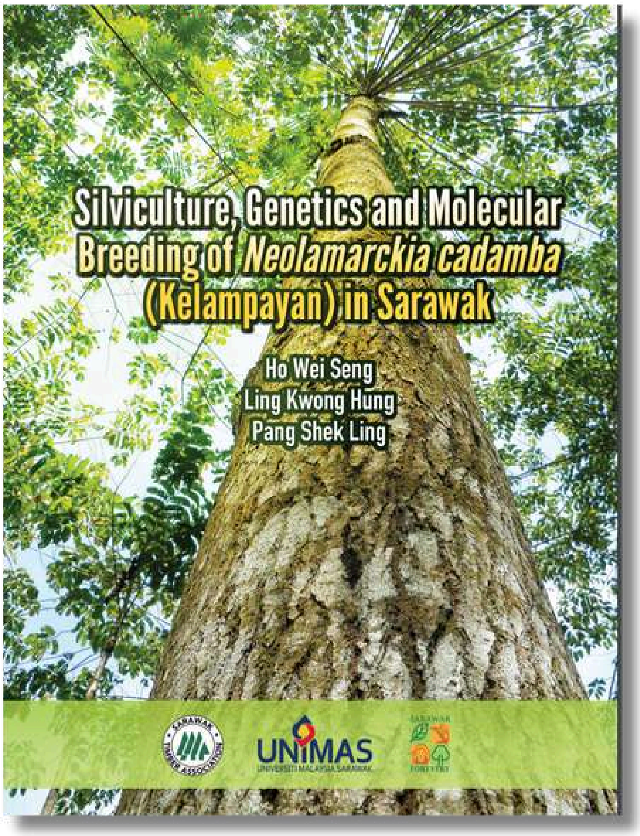
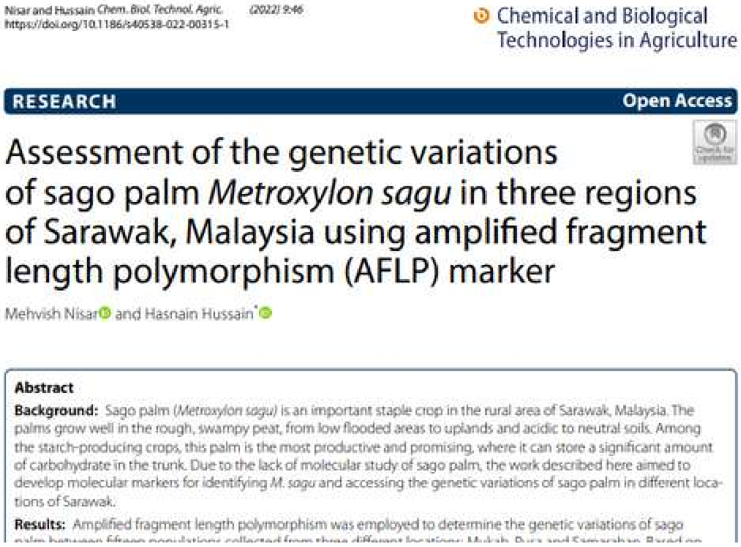
Chromosome doubling
Antimitotic agent
Polyploid
Flow cytometry
Chromosome counting

ABSTRACT

Polyploidization of plants occurs in nature but it is a slow and gradual process that has driven evolution and speciation throughout the ages. As time is important, polyploidization can be induced in a shorter period by using colchicine that interferes with mitosis of cells. To develop an efficient polyploidization protocol of a species, up to date research is paramount. The efficiency of polyploidization induction system depends on the advancement of propagation techniques of the species which consist of *in vitro*, *ex vitro* and *in vivo* systems. During polyploidization induction, several parameters can be manipulated to obtain highest percentage of polyploids. These parameters include colchicine concentration, treatment duration and explant type. Several other factors that enhance these parameters include usage of shaker, DMSO (Dimethyl sulfoxide) and medium types. Induced putative polyploids are selected indirectly based on morphological parameters, anatomical parameters and flow cytometry. Selected putative polyploid can be verified directly and accurately using chromosome counting. Polyploidization has been practised for decades with notable breakthrough recently in terms of polyploidization system and polyploid identification. Current trend in polyploidization has included




Nisar and Hussain *Chem. Biol. Technol. Agric.* (2022) 9:46
https://doi.org/10.1186/s40538-022-00315-1

Chemical and Biological Technologies in Agriculture

RESEARCH **Open Access**

Assessment of the genetic variations of sago palm *Metroxylon sagu* in three regions of Sarawak, Malaysia using amplified fragment length polymorphism (AFLP) marker

Mehvish Nisar and Hasnain Hussain*

Abstract

Background: Sago palm (*Metroxylon sagu*) is an important staple crop in the rural area of Sarawak, Malaysia. The palms grow well in the rough, swampy peat, from low flooded areas to uplands and acidic to neutral soils. Among the starch-producing crops, this palm is the most productive and promising, where it can store a significant amount of carbohydrate in the trunk. Due to the lack of molecular study of sago palm, the work described here aimed to develop molecular markers for identifying *M. sagu* and accessing the genetic variations of sago palm in different locations of Sarawak.

Results: Amplified fragment length polymorphism was employed to determine the genetic variations of sago palm between fifteen populations collected from three different locations: Mukah, Pusa and Samarahan. Based on

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NICHE: ANIMAL BIOTECHNOLOGY

Dr Lee Kui Soon

BSc. Hons. (UNIMAS), MSc., PhD (Bath,UK)

kslee@unimas.my

Associate Prof. Dr Chung Hung Hui

BSc. (UMS), PhD (USM)

hhchung@unimas.my

Dr Muhammad Redza Mohd Radzi

BSc., PhD. (UTM),

mrmredza@unimas.my

Biotechnology offers novel resources to enhance the well-being of humans and animals, as well as to boost livestock productivity. It contributes to the improvement of our food sources, such as meat, milk, and eggs. Additionally, biotechnology can positively influence an animal's environmental footprint. Moreover, it enhances our capacity to identify, treat, and prevent diseases.

NICHE: ANIMAL BIOTECHNOLOGY

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ARTICLE IN PRESS

Aquaculture and Fisheries xxx (xxxx) xxx

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Original research article

The first draft genome assembly and data analysis of the Malaysian mahseer (*Tor tambroides*)

Melinda Mei Lin Lau [a], Leonard Whye Kit Lim [a], Hung Hui Chung [a,*], Han Ming Gan [b,c]

[a] Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, 94300, Malaysia
[b] GeneSEQ Sdn Bhd, Bandar Bukit Beruntung, Rawang, Selangor, 48300, Malaysia
[c] Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, Geelong, Victoria, VIC3220, Australia

ARTICLE INFO

Keywords:
Genome
Gene annotation
Tor tambroides
Phylogenetic
Functional annotation

ABSTRACT

The Malaysian mahseer (*Tor tambroides*), one of the most valuable freshwater fish in the world, is mainly targeted for human consumption. The mitogenomic data of this species is available to date, but the genomic information is still lacking. For the first time, we sequenced the whole genome of an adult fish on both Illumina and Nanopore platforms. The hybrid genome assembly had resulted in a sum of 1.23 Gb genomic sequence from the 44,726 contigs found with 44 kb N50 length and BUSCO genome completeness of 87.6%. Four types of SSRs had been detected and identified within the genome with a greater AT abundance than that of GC. Predicted protein sequences had been functionally annotated to public databases, namely GO, KEGG and COG. A maximum likelihood phylogenomic tree containing 52 Actinopterygii species and one Sarcopterygii species as outgroup was constructed, providing first insights into the genome-based evolutionary relationship of *T. tambroides* with other ray-finned fish. These data are crucial in facilitating the study of population genomics, species identification, morphological variations, and evolutionary biology, which are helpful in the conservation of this species.

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biotechnologistsatunimas Congratulations to our biotechnologists, Dr Chung Hung Hui, Melinda, Leonard & their team on their latest publication.

The work records the first draft genome assembly and data analysis of the Malaysian mahseer (Tor tambroides) or locally known as Empurau. The link to the full paper is in our bio.

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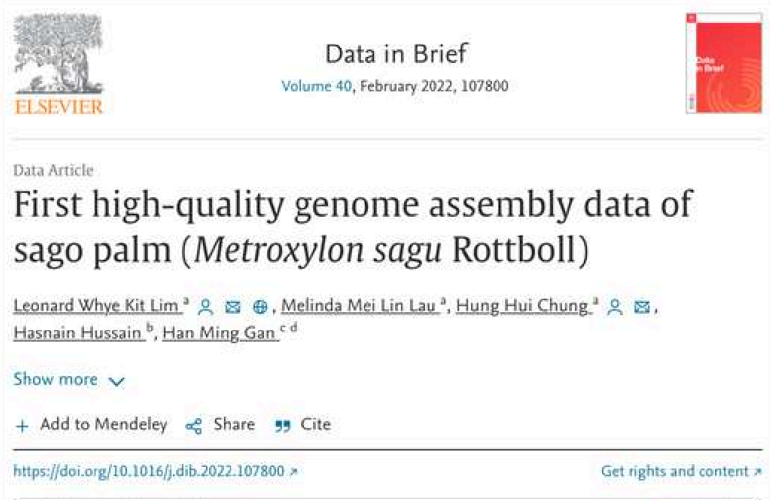
Review Article | Published: 05 May 2021

A Review on the Emerging Asian Aquaculture Fish, the Malaysian Mahseer (*Tor tambroides*): Current Status and the Way Forward

Melinda Mei Lin Lau, Leonard Whye Kit Lim, Sairatul Dahlianis Ishak, Ambok Bolong Abol-Munafi & Hung Hui Chung

Proceedings of the Zoological Society 74, 227–237 (2021) | Cite this article

670 Accesses | 9 Citations | Metrics



ELSEVIER

Data in Brief
Volume 40, February 2022, 107800

Data Article

First high-quality genome assembly data of sago palm (*Metroxylon sagu* Rottboll)

Leonard Whye Kit Lim [a], Melinda Mei Lin Lau [a], Hung Hui Chung [a], Hasnain Hussain [b], Han Ming Gan [c d]

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https://doi.org/10.1016/j.dib.2022.107800

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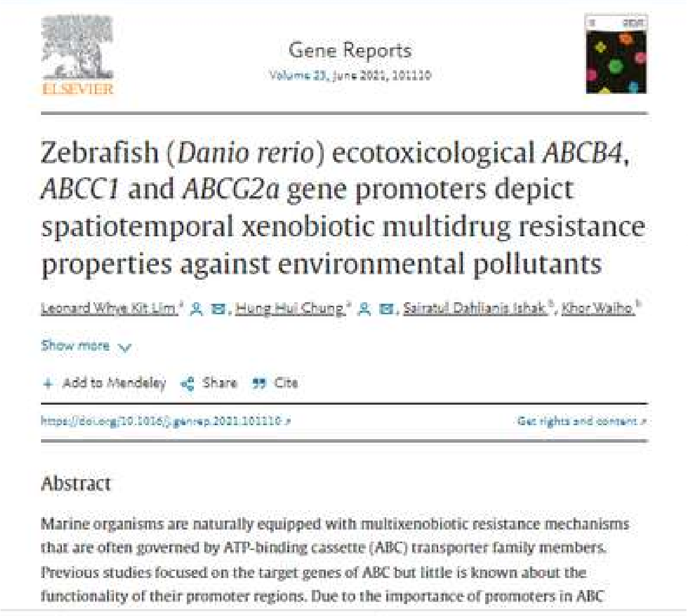

ELSEVIER

Gene Reports
Volume 23, June 2021, 101110

Zebrafish (*Danio rerio*) ecotoxicological *ABCB4*, *ABCC1* and *ABCG2a* gene promoters depict spatiotemporal xenobiotic multidrug resistance properties against environmental pollutants

Leonard Whye Kit Lim [a], Hung Hui Chung [a], Sairatul Dahlianis Ishak [b], Khor Waiho [b]

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https://doi.org/10.1016/j.genrep.2021.101110

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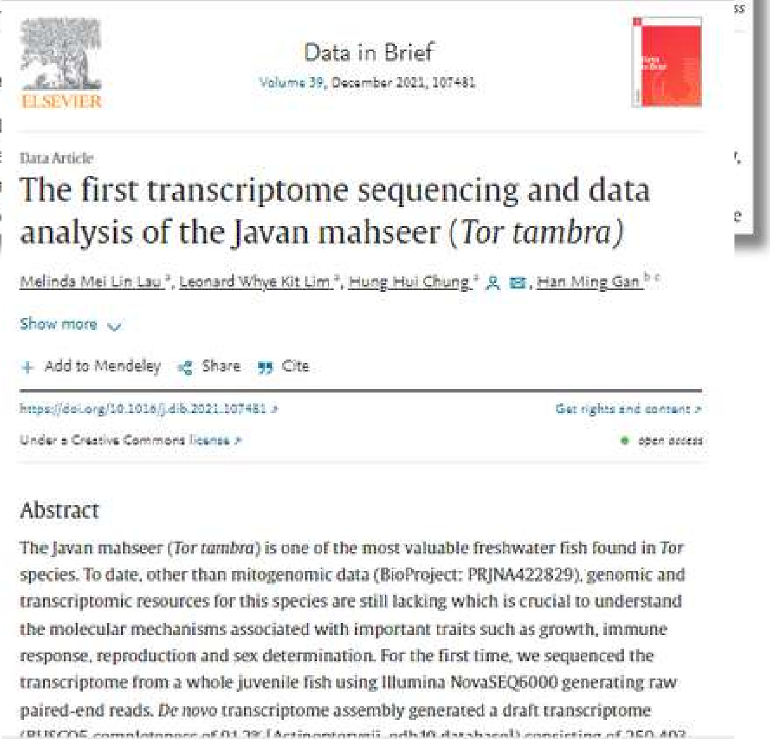
Abstract

Marine organisms are naturally equipped with multixenobiotic resistance mechanisms that are often governed by ATP-binding cassette (ABC) transporter family members. Previous studies focused on the target genes of ABC but little is known about the functionality of their promoter regions. Due to the importance of promoters in ABC



ELSEVIER

Data in Brief
Volume 39, December 2021, 107481

Data Article

The first transcriptome sequencing and data analysis of the Javan mahseer (*Tor tambra*)

Melinda Mei Lin Lau [a], Leonard Whye Kit Lim [a], Hung Hui Chung [a], Han Ming Gan [b c]

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https://doi.org/10.1016/j.dib.2021.107481

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Abstract

The Javan mahseer (*Tor tambra*) is one of the most valuable freshwater fish found in *Tor* species. To date, other than mitogenomic data (BioProject: PRJNA422829), genomic and transcriptomic resources for this species are still lacking which is crucial to understand the molecular mechanisms associated with important traits such as growth, immune response, reproduction and sex determination. For the first time, we sequenced the transcriptome from a whole juvenile fish using Illumina NovaSEQ6000 generating raw paired-end reads. *De novo* transcriptome assembly generated a draft transcriptome

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NICHE: BIOPROCESS TECHNOLOGY

Prof. Dr Awang Ahmad Sallehin Awang Husaini

BSc., MSc. (UPM),
PhD (UMIST)

haahmad@unimas.my

Assoc. Prof. Dr Micky Vincent

BSc.Ed. (Hons.) (UM), MSc.
(UPM), PhD (Iowa State, USA)

vmicky@unimas.my

Assoc. Prof. Dr Dayang Salwani Awang Adeni

B.Eng. Hons. (UTM), MSc.
(UNIMAS), PhD (UPM)

adsalwa@unimas.my

Dr Nurashikin Suhaili

B.Eng. (Hons.) (IIU), MSc.
(UPM), PhD (University
College London, UK)

snurashikin@unimas.my

Dr Rosmawati Saat

BSc. Hons.(UM), MSc.
(Otago, NZ), PhD (UNIMAS)

srosma@unimas.my

NICHE: BIOPROCESS TECHNOLOGY

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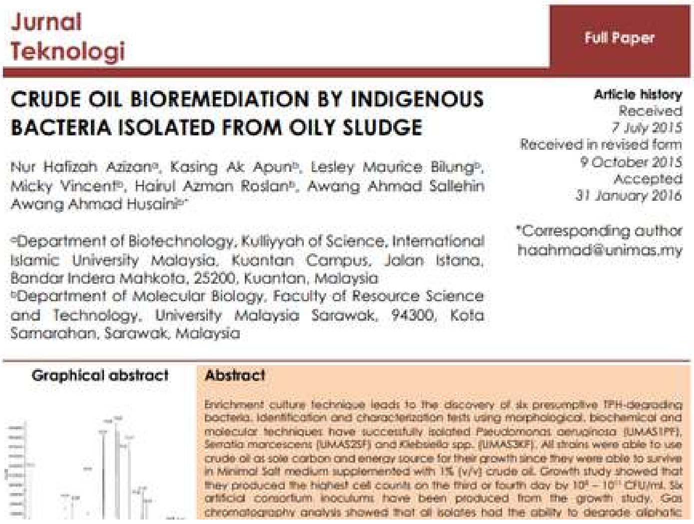

Jurnal Teknologi

Full Paper

CRUDE OIL BIOREMEDIATION BY INDIGENOUS BACTERIA ISOLATED FROM OILY SLUDGE

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Nur Hafizah Azizan[a], Kasing Ak Apun[b], Lesley Maurice Bilung[b], Micky Vincent[b], Hairul Azman Roslan[b], Awang Ahmad Sallehin Awang Ahmad Husaini[b*]

[a]Department of Biotechnology, Kulliyyah of Science, International Islamic University Malaysia, Kuantan Campus, Jalan Istana, Bandar Indera Mahkota, 25200, Kuantan, Malaysia
[b]Department of Molecular Biology, Faculty of Resource Science and Technology, University Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia

*Corresponding author
haahmad@unimas.my

Graphical abstract

Abstract

Enrichment culture technique leads to the discovery of six presumptive TPH-degrading bacteria. Identification and characterization tests using morphological, biochemical and molecular techniques have successfully isolated *Pseudomonas aeruginosa* (UMAS1PF), *Serratia marcescens* (UMAS2SF) and *Klebsiella* spp. (UMAS3KF). All strains were able to use crude oil as sole carbon and energy source for their growth since they were able to survive in Minimal Salt medium supplemented with 1% (v/v) crude oil. Growth study showed that they produced the highest cell counts on the third or fourth day by $10^8 - 10^{11}$ CFU/ml. Six artificial consortium inoculums have been produced from the growth study. Gas chromatography analysis showed that all isolates had the ability to degrade aliphatic

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earch Journal of Biotechnology

Vol. **17 (7)** July **(2022)**
Res. J. Biotech

Autolysis of spent baker's yeast generated from sago bioethanol fermentation: a preliminary study

Mahmod Nik Nur Aziati, Suhaili Nurashikin*, Awang Husaini Awang Ahmad Sallehin and Awang Adeni Dayang Salwani
Faculty of Resource Science and Technology, UNIMAS, 94300 Kota Samarahan, Sarawak, MALAYSIA
*snurashikin@unimas.my

tract
nt Baker's yeast (Saccharomyces cerevisiae) is
ained as a by-product of ethanol fermentation
ustry and is mainly discarded as waste. The spent
st can be potentially converted to yeast extract
ugh autolysis process in which the yeast cells are
d under certain conditions to release valuable and
ictive substances. To date, there are still limited
lies on the autolysis of spent S. cerevisiae generated
owing the production of sago bioethanol. This
arch aims to investigate the feasibility of autolysis
pent Baker's yeast generated from sago bioethanol
nentation by focusing on two important parameters
nely initial pH and incubation time. The spent
er's yeast was autolysed at different initial pH
ies (3, 5 a

Keywords: Autolysis, Bioethanol fermentation, *Saccharomyces cerevisiae*, Spent Baker's yeast, Yeast extract.

Introduction

Baker's yeast (*Saccharomyces cerevisiae*) is commonly utilised in the fermentation industry and the production generates large quantities of spent yeast as their by-products[9,24]. About 400 000 tons of spent Baker's yeast are produced as a by-product by the brewing industry annually. The waste, in general, is still underused and is normally discarded into the environment[5]. The spent yeast is a rich source of proteins, essential amino acids, RNA, vitamins B and minerals which essentially serve as a raw material in the production of yeast extract[23]. The extracts from the spent yeast can serve as promising sources of valuable ingredients

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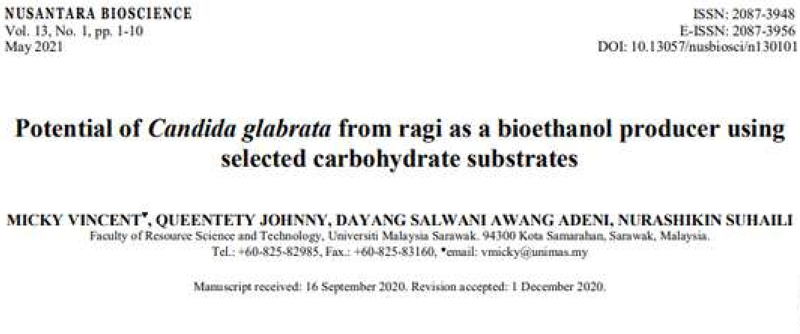

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E-ISSN: 2087-3956
DOI: 10.13057/nusbiosci/n130101

Potential of *Candida glabrata* from ragi as a bioethanol producer using selected carbohydrate substrates

MICKY VINCENT*, QUEENTETY JOHNNY, DAYANG SALWANI AWANG ADENI, NURASHIKIN SUHAILI
Faculty of Resource Science and Technology, Universiti Malaysia Sarawak. 94300 Kota Samarahan, Sarawak, Malaysia.
Tel.: +60-825-82985, Fax.: +60-825-83160, *email: vmicky@unimas.my

Manuscript received: 16 September 2020. Revision accepted: 1 December 2020.

Abstract. *Vincent M, Johnny Q, Adeni DSA, Suhaili N. 2021. Potential of* Candida glabrata *from ragi as a bioethanol producer using selected carbohydrate substrates. Nusantara Bioscience 13: 1-10.* The flexibility and efficiency of fermenting microorganisms to convert substrates to ethanol are important factors in achieving high bioethanol yields during ethanolic fermentation. In this study, *Candida*
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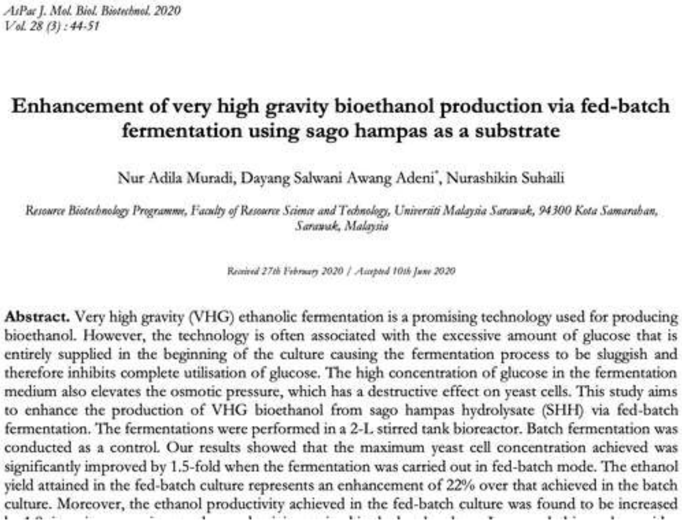
amylases resulted in



AsPac J. Mol. Biol. Biotechnol. 2020
Vol. 28 (3) : 44-51

Enhancement of very high gravity bioethanol production via fed-batch fermentation using sago hampas as a substrate

Nur Adila Muradi, Dayang Salwani Awang Adeni*, Nurashikin Suhaili

Resource Biotechnology Programme, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

Received 27th February 2020 / Accepted 10th June 2020

Abstract. Very high gravity (VHG) ethanolic fermentation is a promising technology used for producing bioethanol. However, the technology is often associated with the excessive amount of glucose that is entirely supplied in the beginning of the culture causing the fermentation process to be sluggish and therefore inhibits complete utilisation of glucose. The high concentration of glucose in the fermentation medium also elevates the osmotic pressure, which has a destructive effect on yeast cells. This study aims to enhance the production of VHG bioethanol from sago hampas hydrolysate (SHH) via fed-batch fermentation. The fermentations were performed in a 2-L stirred tank bioreactor. Batch fermentation was conducted as a control. Our results showed that the maximum yeast cell concentration achieved was significantly improved by 1.5-fold when the fermentation was carried out in fed-batch mode. The ethanol yield attained in the fed-batch culture represents an enhancement of 22% over that achieved in the batch culture. Moreover, the ethanol productivity achieved in the fed-batch culture was found to be increased

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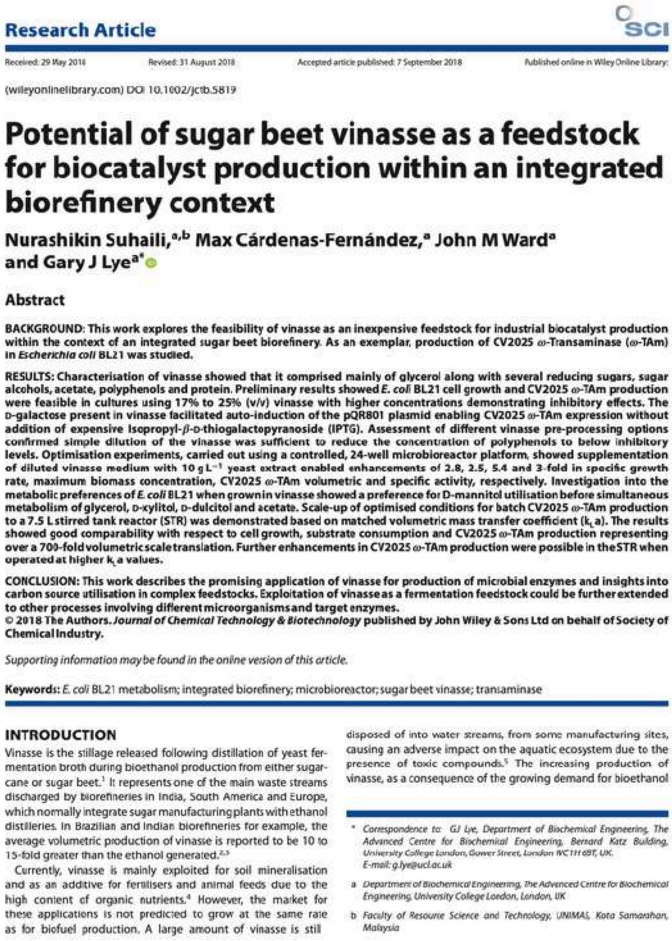

Research Article

SCI

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(wileyonlinelibrary.com) DOI 10.1002/jctb.5819

Potential of sugar beet vinasse as a feedstock for biocatalyst production within an integrated biorefinery context

Nurashikin Suhaili,[a,b] Max Cárdenas-Fernández,[a] John M Ward[a] and Gary J Lye[a*]

Abstract

BACKGROUND: This work explores the feasibility of vinasse as an inexpensive feedstock for industrial biocatalyst production within the context of an integrated sugar beet biorefinery. As an exemplar, production of CV2025 ω-Transaminase (ω-TAm) in *Escherichia coli* BL21 was studied.

RESULTS: Characterisation of vinasse showed that it comprised mainly of glycerol along with several reducing sugars, sugar alcohols, acetate, polyphenols and protein. Preliminary results showed *E. coli* BL21 cell growth and CV2025 ω-TAm production were feasible in cultures using 17% to 25% (v/v) vinasse with higher concentrations demonstrating inhibitory effects. The D-galactose present in vinasse facilitated auto-induction of the pQR801 plasmid enabling CV2025 ω-TAm expression without addition of expensive Isopropyl-β-D-thiogalactopyranoside (IPTG). Assessment of different vinasse pre-processing options confirmed simple dilution of the vinasse was sufficient to reduce the concentration of polyphenols to below inhibitory levels. Optimisation experiments, carried out using a controlled, 24-well microbioreactor platform, showed supplementation of diluted vinasse medium with 10 g L^{-1} yeast extract enabled enhancements of 2.8, 2.5, 5.4 and 3-fold in specific growth rate, maximum biomass concentration, CV2025 ω-TAm volumetric and specific activity, respectively. Investigation into the metabolic preferences of *E. coli* BL21 when grown in vinasse showed a preference for D-mannitol utilisation before simultaneous metabolism of glycerol, D-xylitol, D-dulcitol and acetate. Scale-up of optimised conditions for batch CV2025 ω-TAm production to a 7.5 L stirred tank reactor (STR) was demonstrated based on matched volumetric mass transfer coefficient (k_La). The results showed good comparability with respect to cell growth, substrate consumption and CV2025 ω-TAm production representing over a 700-fold volumetric scale translation. Further enhancements in CV2025 ω-TAm production were possible in the STR when operated at higher k_La values.

CONCLUSION: This work describes the promising application of vinasse for production of microbial enzymes and insights into carbon source utilisation in complex feedstocks. Exploitation of vinasse as a fermentation feedstock could be further extended to other processes involving different microorganisms and target enzymes.

Supporting information may be found in the online version of this article.

Keywords: *E. coli* BL21 metabolism; integrated biorefinery; microbioreactor; sugar beet vinasse; transaminase

INTRODUCTION

Vinasse is the stillage released following distillation of yeast fermentation broth during bioethanol production from either sugarcane or sugar beet.[1] It represents one of the main waste streams discharged by biorefineries in India, South America and Europe, which normally integrate sugar manufacturing plants with ethanol distilleries. In Brazilian and Indian biorefineries for example, the average volumetric production of vinasse is reported to be 10 to 15-fold greater than the ethanol generated.[2,3]

Currently, vinasse is mainly exploited for soil mineralisation and as an additive for fertilisers and animal feeds due to the high content of organic nutrients.[4] However, the market for these applications is not predicted to grow at the same rate as for biofuel production. A large amount of vinasse is still disposed of into water streams, from some manufacturing sites, causing an adverse impact on the aquatic ecosystem due to the presence of toxic compounds.[5] The increasing production of vinasse, as a consequence of the growing demand for bioethanol

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* *Correspondence to: GJ Lye, Department of Biochemical Engineering, The Advanced Centre for Biochemical Engineering, Bernard Katz Building, University College London, Gower Street, London WC1H 6BT, UK. E-mail: g.lye@ucl.ac.uk*

a *Department of Biochemical Engineering, The Advanced Centre for Biochemical Engineering, University College London, London, UK*

b *Faculty of Resource Science and Technology, UNIMAS, Kota Samarahan, Malaysia*

Malaysian Journal Of Science 40(3): 43-53 (October 2021)

THE CHARACTERISTICS OF SAGO FROND SAP FROM TWO SELECTED GROWTH STAGES; *ANGKAT PUNGGUNG* AND *UPONG MUDA* PALMS

Nurazureen Matnin[1a], Dayang Salwani Awang Adeni[2a*], Muhammad Norhelmi Ahmad[3a] and Nurashikin Suhaili[4a]

[a]Resource Biotechnology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, MALAYSIA. E-mail: nurazureen.matnin@gmail.com[1]; adsalwa@unimas.my[2]; nrwhelmi92@gmail.com[3]; snurashikin@unimas.my[4]
*Corresponding Author: adsalwa@unimas.my

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ABSTRACT Sago frond is produced in abundance upon harvesting of the sago palms for starch extraction, hence need to be utilized and developed into beneficial products. In this study, the sap which contains sugars and starch is obtained by roller crushing the skinned frond for use as fermentation medium. Fronds from two selected growth stages (namely *Angkat punggung* and *Upong muda*) and two different positions within the rosette (inner and outer circle) of the sago palm were studied. Based on the results, the outer circle frond of *Upong muda* palm gave the highest volume of sap at 290mL/kg which equivalent to 1600 mL/frond. On top of that, sago frond sap has an acidic pH, with glucose as major sugar component and contained various kinds of minerals like calcium, potassium and manganese. All fronds from two selected growth stages contain glucose between 28-68 g/L and xylose 21-29 g/L, respectively. After 21 days of storage, it can be concluded that the amount of reducing sugars and starch in most samples obtained from two selected growth stages decreased slightly from the original. Subsequently after this study, both fresh and stored sago frond sap can be used as a fermentation substrate without any pre-treatment or modification.

Keywords: *Angkat punggung*, fermentation, starch, sugar, *Upong muda*.

MEET OUR EXPERTS

NICHE: GENETICS

Prof. Dr Edmund Sim Ui Hang

BSc. (UM), PhD (Queensland, AUS)

uhsim@unimas.my

Prof. Dr Ho Wei Seng

SmSn, PhD (UKM)

wsho@unimas.my

Prof. Dr Hairul Azman Roslan

BSc. Hons (UM), MSc., PhD (Liverpool, UK)

rhairul@unimas.my

Biotechnology has revolutionized genetics study by providing powerful tools for genome analysis, genetic engineering, functional genomics, personalized medicine, evolutionary genetics, and conservation biology. These advancements have deepened our understanding of genes, their functions, and their impact on health, disease, and biodiversity, leading to breakthroughs in various scientific fields and potential applications in healthcare, agriculture, and environmental conservation.

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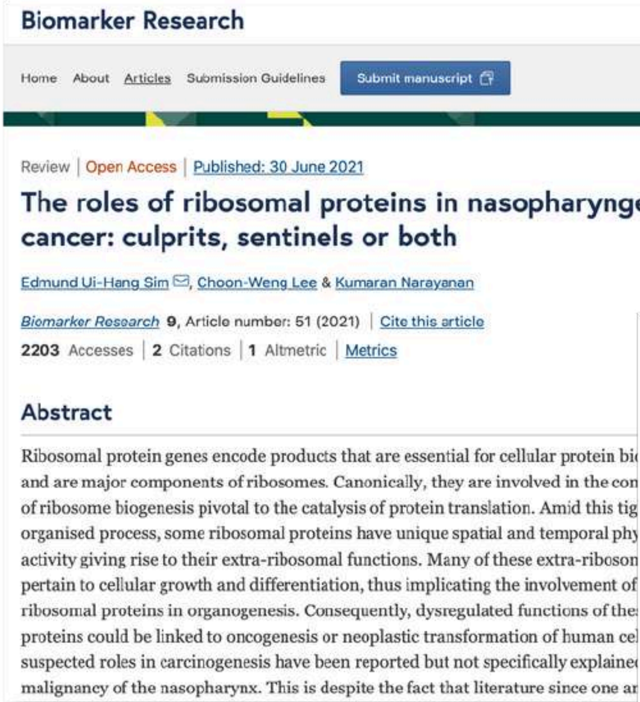

Review | Open Access | Published: 30 June 2021

The roles of ribosomal proteins in nasopharyngeal cancer: culprits, sentinels or both

Edmund Ui-Hang Sim, Choon-Weng Lee & Kumaran Narayanan

Biomarker Research **9**, Article number: 51 (2021) | Cite this article

2203 Accesses | **2** Citations | **1** Altmetric | Metrics

Abstract

Ribosomal protein genes encode products that are essential for cellular protein bi
and are major components of ribosomes. Canonically, they are involved in the con
of ribosome biogenesis pivotal to the catalysis of protein translation. Amid this tig
organised process, some ribosomal proteins have unique spatial and temporal phy
activity giving rise to their extra-ribosomal functions. Many of these extra-ribosom
pertain to cellular growth and differentiation, thus implicating the involvement of
ribosomal proteins in organogenesis. Consequently, dysregulated functions of the
proteins could be linked to oncogenesis or neoplastic transformation of human ce
suspected roles in carcinogenesis have been reported but not specifically explaine
malignancy of the nasopharynx. This is despite the fact that literature since one a

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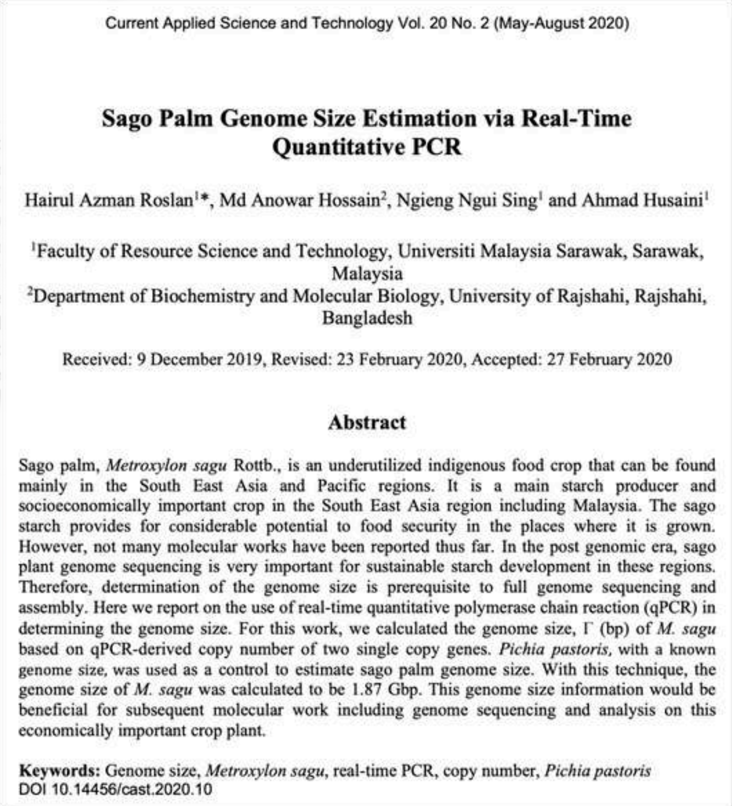


Current Applied Science and Technology Vol. 20 No. 2 (May-August 2020)

Sago Palm Genome Size Estimation via Real-Time Quantitative PCR

Hairul Azman Roslan[1]*, Md Anowar Hossain[2], Ngieng Ngui Sing[1] and Ahmad Husaini[1]

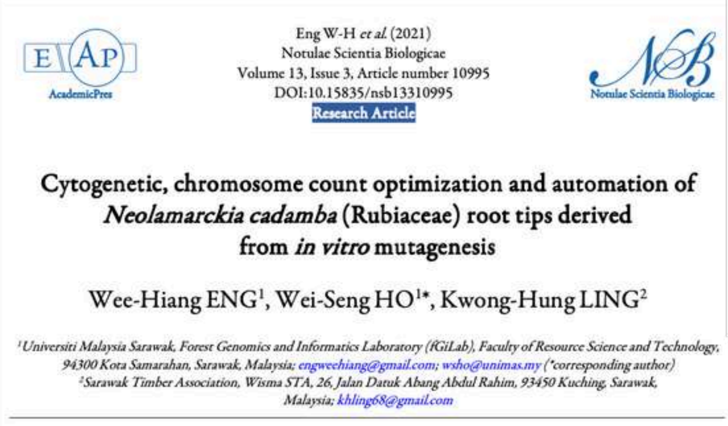
[1]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Sarawak, Malaysia
[2]Department of Biochemistry and Molecular Biology, University of Rajshahi, Rajshahi, Bangladesh

Received: 9 December 2019, Revised: 23 February 2020, Accepted: 27 February 2020

Abstract

Sago palm, *Metroxylon sagu* Rottb., is an underutilized indigenous food crop that can be found mainly in the South East Asia and Pacific regions. It is a main starch producer and socioeconomically important crop in the South East Asia region including Malaysia. The sago starch provides for considerable potential to food security in the places where it is grown. However, not many molecular works have been reported thus far. In the post genomic era, sago plant genome sequencing is very important for sustainable starch development in these regions. Therefore, determination of the genome size is prerequisite to full genome sequencing and assembly. Here we report on the use of real-time quantitative polymerase chain reaction (qPCR) in determining the genome size. For this work, we calculated the genome size, Γ (bp) of *M. sagu* based on qPCR-derived copy number of two single copy genes. *Pichia pastoris*, with a known genome size, was used as a control to estimate sago palm genome size. With this technique, the genome size of *M. sagu* was calculated to be 1.87 Gbp. This genome size information would be beneficial for subsequent molecular work including genome sequencing and analysis on this economically important crop plant.

Keywords: Genome size, *Metroxylon sagu*, real-time PCR, copy number, *Pichia pastoris*
DOI 10.14456/cast.2020.10



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Notulae Scientia Biologicae
Volume 13, Issue 3, Article number 10995
DOI:10.15835/nsb13310995
Research Article

Cytogenetic, chromosome count optimization and automation of *Neolamarckia cadamba* (Rubiaceae) root tips derived from *in vitro* mutagenesis

Wee-Hiang ENG[1], Wei-Seng HO[1]*, Kwong-Hung LING[2]

*[1]Universiti Malaysia Sarawak, Forest Genomics and Informatics Laboratory (fGiLab), Faculty of Resource Science and Technology, 94300 Kota Samarahan, Sarawak, Malaysia; engweehiang@gmail.com; wsho@unimas.my (*corresponding author)*
[2]Sarawak Timber Association, Wisma STA, 26, Jalan Datuk Abang Abdul Rahim, 93450 Kuching, Sarawak, Malaysia; khling68@gmail.com

Abstract

Chromosome count is the only direct way to determine the number o
study is often considered trivial that seldom described and discussed in detai
the chromosome count protocol should be revised and revisited before it be
study, we encountered challenges in obtaining a clear micrograph for the chr
cells of *Neolamarckia cadamba* (Roxb.) Bosser (Rubiaceae) root tips. Sev
through micrograph observation, such as existing unwanted particles in cells,
chromosome clumping. To overcome these, root tip types, staining method

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Chiang Mai J. Sci. 2017; 44(4) : 1304-1310
http://epg.science.cmu.ac.th/ejournal/
Contributed Paper

Sequence Characterized Amplified Region Markers for Species-specific Identification of Three Threatened *Aquilaria* Species

Hairul Azman Roslan* [a], Md. Anowar Hossain [a,c], Nur Qistina Othman [a,b], Cheksum Supiah Tawan [b] and Isa Ipor [b]

[a] Genetic Engineering Laboratory, Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia.
[b] Department of Plant Science and Environmental Ecology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia.
[c] Department of Biochemistry and Molecular Biology, University of Rajshahi, Rajshahi-6205, Bangladesh.
*Author for correspondence; e-mail: hairulroslan@hotmail.com

Received: 26 January 2016
Accepted: 13 June 2016

MEET OUR EXPERTS

NICHE: MOLECULAR BIOLOGY

Prof. Dr Awang Ahmad Sallehin Awang Husaini

BSc., MSc. (UPM), PhD (UMIST)

haahmad@unimas.my

Prof. Dr Mohd Hasnain Md Hussain

B.Appl, Sc.Hons (USM), MSc. (Newcastle-upon Tyne, UK), PhD (East Anglia, UK)

hhasnain@unimas.my

Prof. Dr Edmund Sim Ui Hang

BSc. (UM), PhD (Queensland, AUS)

uhsim@unimas.my

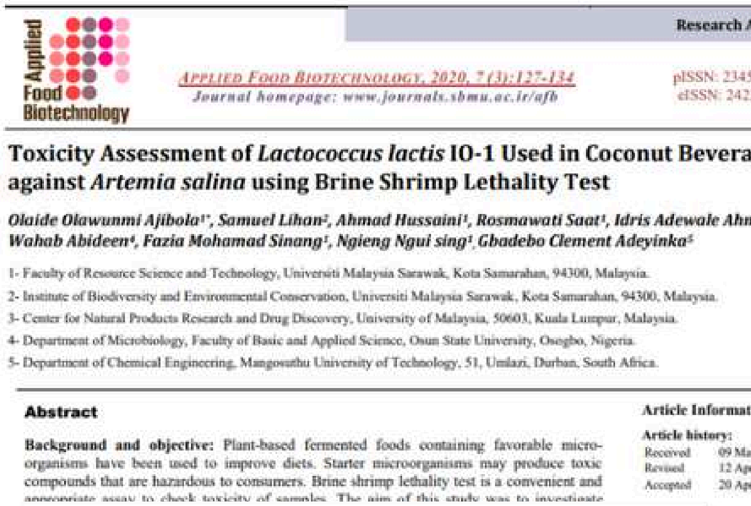
Prof. Dr Hairul Azman Roslan

BSc. Hons (UM), MSc., PhD (Liverpool, UK)

rhairul@unimas.my

NICHE: MOLECULAR BIOLOGY

SOME OF OUR RECENT WORKS



Research Article

Applied Food Biotechnology

APPLIED FOOD BIOTECHNOLOGY, 2020, 7 (3):127-134
Journal homepage: www.journals.sbmu.ac.ir/afb

pISSN: 2345-5357
eISSN: 2423-4214

Toxicity Assessment of *Lactococcus lactis* IO-1 Used in Coconut Beverages against *Artemia salina* using Brine Shrimp Lethality Test

***Olaide Olawunmi Ajibola*[1*]*, Samuel Lihan*[2]*, Ahmad Hussaini*[1]*, Rosmawati Saat*[1]*, Idris Adewale Ahn Wahab Abideen*[4]*, Fazia Mohamad Sinang*[1]*, Ngieng Ngui sing*[1]*, Gbadebo Clement Adeyinka*[5]**

1- Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, 94300, Malaysia.
2- Institute of Biodiversity and Environmental Conservation, Universiti Malaysia Sarawak, Kota Samarahan, 94300, Malaysia.
3- Center for Natural Products Research and Drug Discovery, University of Malaysia, 50603, Kuala Lumpur, Malaysia.
4- Department of Microbiology, Faculty of Basic and Applied Science, Osun State University, Osogbo, Nigeria.
5- Department of Chemical Engineering, Mangosuthu University of Technology, 51, Umlazi, Durban, South Africa.

Abstract

Background and objective: Plant-based fermented foods containing favorable micro-organisms have been used to improve diets. Starter microorganisms may produce toxic compounds that are hazardous to consumers. Brine shrimp lethality test is a convenient and appropriate assay to check toxicity of samples. The aim of this study was to investigate

Article Informat

Article history:
Received 09 Ma
Revised 12 Ap
Accepted 20 Ap

Springer Link

Home > Advances in Traditional Medicine > Article

Short Communication | Published: 30 September 2020

Anticancer and antimicrobial peptides from medicinal plants of Borneo island in Sarawak

Hasnain Hussain ✉, Nurhazlina Hamdan & Edmund Ui-Hang Sim

Advances in Traditional Medicine **21**, 189–197 (2021) | Cite this article

290 Accesses | **4** Citations | Metrics

Abstract

The interest in drug discovery from plants-based metabolites has been of interests to researchers, especially for health well-being and for therapeutic reasons. The work described here was to explore the in vitro anticancer and antimicrobial peptides from six traditional medicinal plants commonly used in Sarawak, Malaysian Borneo. Proteins were extracted from plants with a common protein extraction buffer. Evaluation for in vitro anticancer activity was done against normal and carcinomas nasopharyngeal cell line; NP69 and HK-1 respectively by using established MTT microtiter plate assays. Antimicrobial activity was tested against *Staphylococcus aureus* and *Escherichia coli*, a Gram-positive and Gram-negative respectively,

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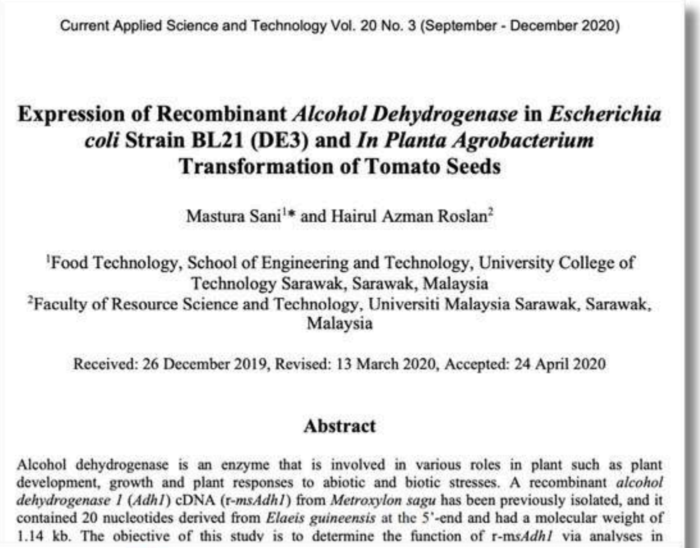

Current Applied Science and Technology Vol. 20 No. 3 (September - December 2020)

Expression of Recombinant *Alcohol Dehydrogenase* in *Escherichia coli* Strain BL21 (DE3) and *In Planta Agrobacterium* Transformation of Tomato Seeds

Mastura Sani[1]* and Hairul Azman Roslan[2]

[1]Food Technology, School of Engineering and Technology, University College of Technology Sarawak, Sarawak, Malaysia
[2]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Sarawak, Malaysia

Received: 26 December 2019, Revised: 13 March 2020, Accepted: 24 April 2020

Abstract

Alcohol dehydrogenase is an enzyme that is involved in various roles in plant such as plant development, growth and plant responses to abiotic and biotic stresses. A recombinant *alcohol dehydrogenase 1* (*Adh1*) cDNA (r-*msAdh1*) from *Metroxylon sagu* has been previously isolated, and it contained 20 nucleotides derived from *Elaeis guineensis* at the 5'-end and had a molecular weight of 1.14 kb. The objective of this study is to determine the function of r-ms*Adh1* via analyses in

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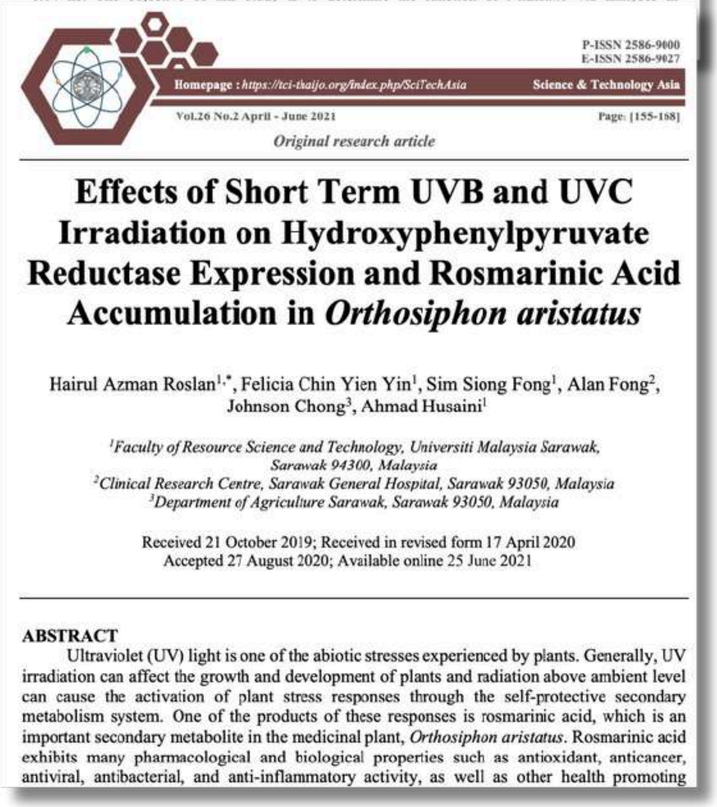

P-ISSN 2586-9000
E-ISSN 2586-9027

Homepage : *https://tci-thaijo.org/index.php/SciTechAsia* Science & Technology Asia

Vol.26 No.2 April - June 2021 Page: [155-168]

Original research article

Effects of Short Term UVB and UVC Irradiation on Hydroxyphenylpyruvate Reductase Expression and Rosmarinic Acid Accumulation in *Orthosiphon aristatus*

Hairul Azman Roslan[1,*], Felicia Chin Yien Yin[1], Sim Siong Fong[1], Alan Fong[2], Johnson Chong[3], Ahmad Husaini[1]

[1]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Sarawak 94300, Malaysia
[2]Clinical Research Centre, Sarawak General Hospital, Sarawak 93050, Malaysia
[3]Department of Agriculture Sarawak, Sarawak 93050, Malaysia

Received 21 October 2019; Received in revised form 17 April 2020
Accepted 27 August 2020; Available online 25 June 2021

ABSTRACT

Ultraviolet (UV) light is one of the abiotic stresses experienced by plants. Generally, UV irradiation can affect the growth and development of plants and radiation above ambient level can cause the activation of plant stress responses through the self-protective secondary metabolism system. One of the products of these responses is rosmarinic acid, which is an important secondary metabolite in the medicinal plant, *Orthosiphon aristatus*. Rosmarinic acid exhibits many pharmacological and biological properties such as antioxidant, anticancer, antiviral, antibacterial, and anti-inflammatory activity, as well as other health promoting

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Penyelidik UKM dan UNIMAS Hasilkan Sistem Penskoran Madu Kelulut UKSF

13/09/2022 / Admin

Post Views: 638

Oleh Siti Aishah Mohd Yusof

Foto Ikhwan Hashim

BANGI 12 September 2022 – Sekumpulan penyelidik dari Universiti Kebangsaan Malaysia (UKM) dan Universiti Malaysia Sarawak (UNIMAS) berjaya menghasilkan satu inovasi hakcipta sistem penskoran bagi produk madu kelulut iaitu Unique Kelulut SuperFood Factor (UKSF).

Sistem penskoran madu kelulut UKSF itu dapat membantu meningkatkan lagi kualiti madu kelulut Malaysia ke peringkat antarabangsa.

Timbalan Naib Canselor Hal Ehwal Penyelidikan dan Inovasi, Prof. Dato' Dr. Wan Kamal Mujani berkata sistem penskoran yang dihasilkan itu juga boleh diguna pakai bagi semua produk madu kelulut yang dihasilkan kerana tidak terhad kepada Malaysia sahaja, malah kepada Indonesia, Brazil dan beberapa negara pengeluar lain di dunia.

MEET OUR EXPERTS

NICHE: ENZYMOLOGY

Prof. Dr Awang Ahmad Sallehin Awang Husaini

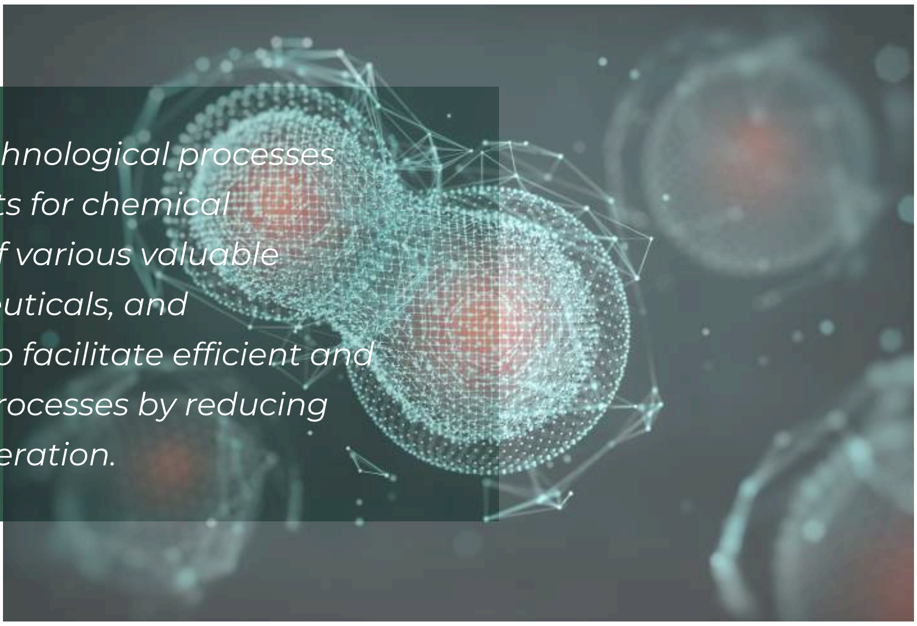
BSc., MSc. (UPM),
PhD (UMIST)

haahmad@unimas.my

Dr Ngieng Ngui Sing

BSc.(UKM), MSc.(UNIMAS),
PhD (UNIMAS)

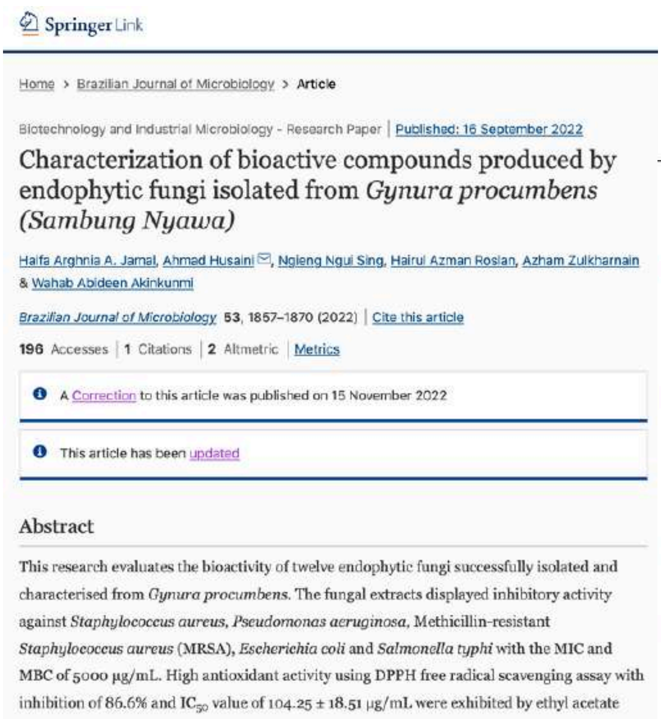
snngui@unimas.my



Enzymes are widely utilized in biotechnological processes and industries. They serve as catalysts for chemical reactions, enabling the production of various valuable products such as biofuels, pharmaceuticals, and biodegradable plastics. Enzymes also facilitate efficient and environmentally friendly industrial processes by reducing energy consumption and waste generation.

NICHE: ENZYMOLOGY

SOME OF OUR RECENT WORKS



Home > Brazilian Journal of Microbiology > Article

Biotechnology and Industrial Microbiology - Research Paper | Published: 16 September 2022

Characterization of bioactive compounds produced by endophytic fungi isolated from *Gynura procumbens (Sambung Nyawa)*

Haifa Arghnia A. Jamal, Ahmad Husaini, Ngieng Ngui Sing, Hairul Azman Roslan, Azham Zulkharnain & Wahab Abideen Akinkunmi

Brazilian Journal of Microbiology **53**, 1857–1870 (2022) | Cite this article

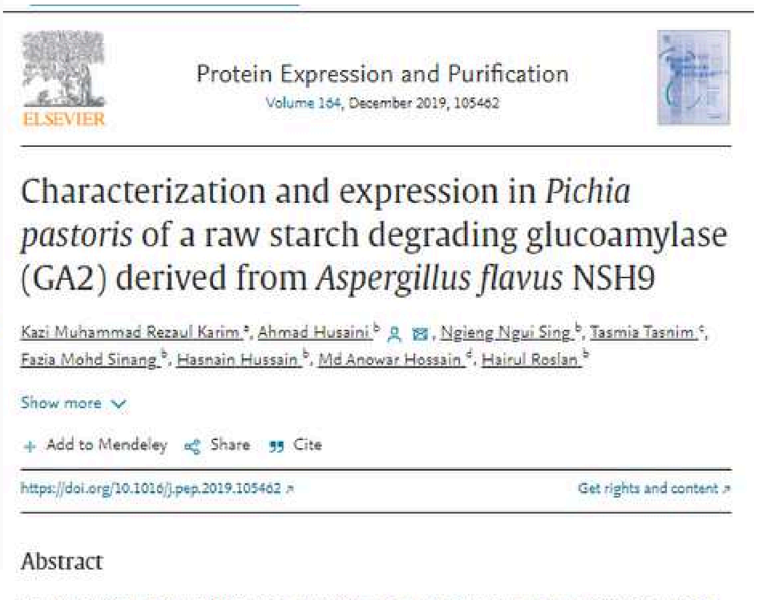
196 Accesses | **1** Citations | **2** Altmetric | Metrics

A Correction to this article was published on 15 November 2022

This article has been updated

Abstract

This research evaluates the bioactivity of twelve endophytic fungi successfully isolated and characterised from *Gynura procumbens*. The fungal extracts displayed inhibitory activity against *Staphylococcus aureus, Pseudomonas aeruginosa*, Methicillin-resistant *Staphylococcus aureus* (MRSA), *Escherichia coli* and *Salmonella typhi* with the MIC and MBC of 5000 µg/mL. High antioxidant activity using DPPH free radical scavenging assay with inhibition of 86.6% and IC_{50} value of 104.25 ± 18.51 µg/mL were exhibited by ethyl acetate



Protein Expression and Purification
Volume 164, December 2019, 105462

Characterization and expression in *Pichia pastoris* of a raw starch degrading glucoamylase (GA2) derived from *Aspergillus flavus* NSH9

Kazi Muhammad Rezaul Karim [a], Ahmad Husaini [b], Ngieng Ngui Sing [b], Tasmia Tasnim [c], Fazia Mohd Sinang [b], Hasnain Hussain [b], Md Anowar Hossain [d], Hairul Roslan [b]

Show more

https://doi.org/10.1016/j.pep.2019.105462

Abstract

ng a pH and thermostable glucoamylase with a
ed in Pichia pastoris to produce recombinant
oamylase gene (2039 bp), and cDNA (1839 bp)
ilar to glucoamylase from Aspergillus oryzae
ed to be a signal peptide for secretion, and the


Research Article

Decolourisation Capabilities of Ligninolytic Enzymes Produced by *Marasmius cladophyllus* UMAS MS8 on Remazol Brilliant Blue R and Other Azo Dyes

Ngieng Ngui Sing, Ahmad Husaini, Azham Zulkharnain, and Hairul Azman Roslan

Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

Correspondence should be addressed to Ahmad Husaini; haahmad@unimas.my

Received 27 July 2016; Accepted 20 December 2016; Pu

Academic Editor: Dong-sheng Shen

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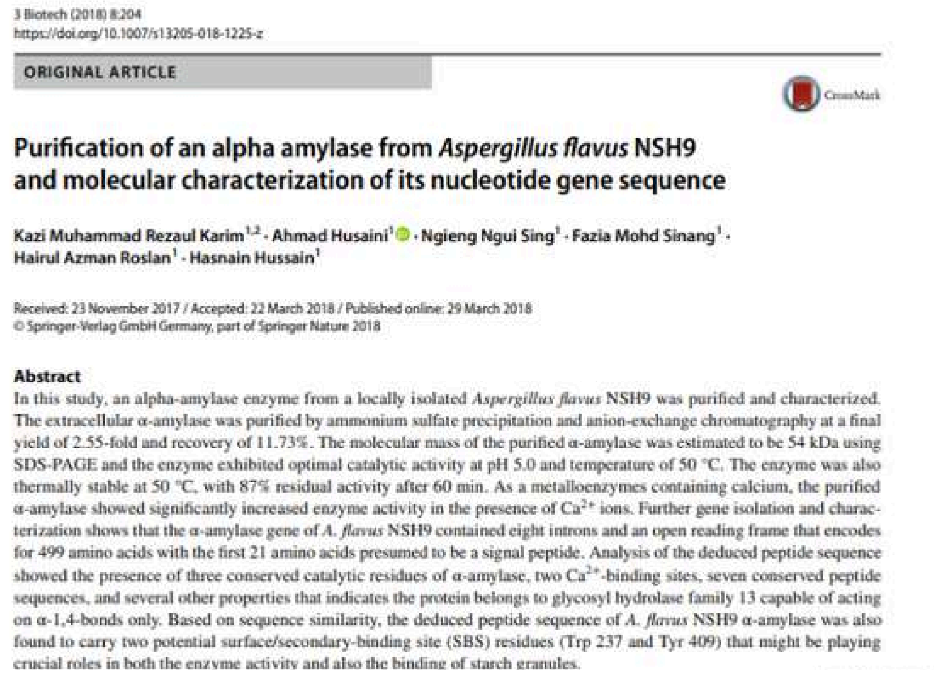
cited.

Marasmius cladophyllus was examined for its ability t
(RBBR) and screened for the production of ligninolyti
decrease in absorbance ratio of A_{592}/A_{500} shows that
Marasmius cladophyllus produces laccase and lignin pe
activities were increased, with laccase activity recorded
dye decolourisation using the culture medium shows th


3 Biotech (2018) 8:204
https://doi.org/10.1007/s13205-018-1225-z

ORIGINAL ARTICLE

Purification of an alpha amylase from *Aspergillus flavus* NSH9 and molecular characterization of its nucleotide gene sequence

Kazi Muhammad Rezaul Karim[1,2] · Ahmad Husaini[1] · Ngieng Ngui Sing[1] · Fazia Mohd Sinang[1] · Hairul Azman Roslan[1] · Hasnain Hussain[1]

Received: 23 November 2017 / Accepted: 22 March 2018 / Published online: 29 March 2018
© Springer-Verlag GmbH Germany, part of Springer Nature 2018

Abstract

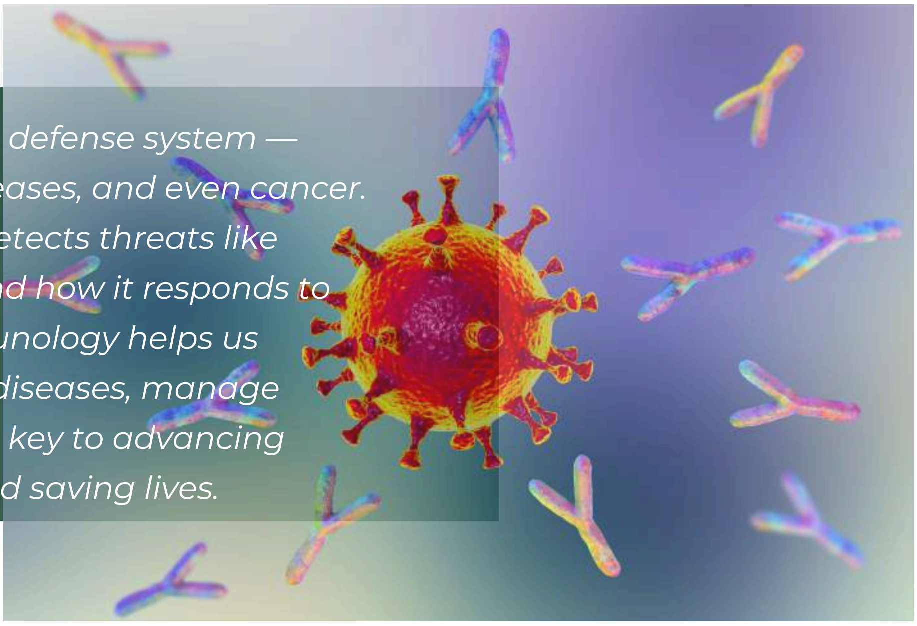
In this study, an alpha-amylase enzyme from a locally isolated *Aspergillus flavus* NSH9 was purified and characterized. The extracellular α-amylase was purified by ammonium sulfate precipitation and anion-exchange chromatography at a final yield of 2.55-fold and recovery of 11.73%. The molecular mass of the purified α-amylase was estimated to be 54 kDa using SDS-PAGE and the enzyme exhibited optimal catalytic activity at pH 5.0 and temperature of 50 °C. The enzyme was also thermally stable at 50 °C, with 87% residual activity after 60 min. As a metalloenzymes containing calcium, the purified α-amylase showed significantly increased enzyme activity in the presence of Ca^{2+} ions. Further gene isolation and characterization shows that the α-amylase gene of *A. flavus* NSH9 contained eight introns and an open reading frame that encodes for 499 amino acids with the first 21 amino acids presumed to be a signal peptide. Analysis of the deduced peptide sequence showed the presence of three conserved catalytic residues of α-amylase, two Ca^{2+}-binding sites, seven conserved peptide sequences, and several other properties that indicates the protein belongs to glycosyl hydrolase family 13 capable of acting on α-1,4-bonds only. Based on sequence similarity, the deduced peptide sequence of *A. flavus* NSH9 α-amylase was also found to carry two potential surface/secondary-binding site (SBS) residues (Trp 237 and Tyr 409) that might be playing crucial roles in both the enzyme activity and also the binding of starch granules.

MEET OUR EXPERTS

NICHE: IMMUNOLOGY

Dr Muhammad Redza Mohd Radzi

BSc., PhD. (UTM),
mrmredza@unimas.my



Immunology is the study of the body's defense system — how it protects us from infections, diseases, and even cancer. It explores how our immune system detects threats like bacteria, viruses, and harmful cells, and how it responds to keep us healthy. Understanding immunology helps us develop vaccines, treat autoimmune diseases, manage allergies, and fight pandemics. It's the key to advancing medicine, improving public health, and saving lives.

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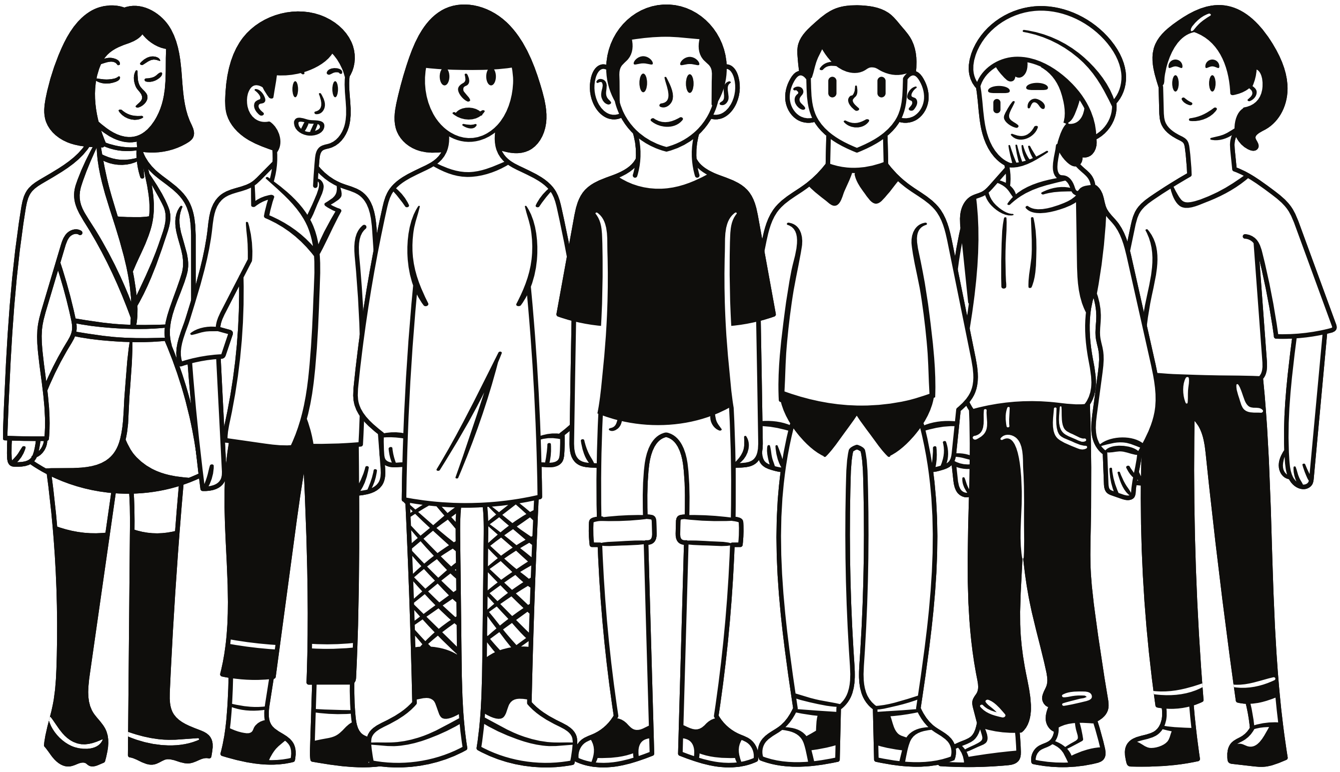

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