academic publishers

International journal of biological sciences (ISSN: 2693-3608)

Volume 04, Issue 01, 2024, pages 01-06
Published Date: - 01-01-2024

CULINARY GUARDIANS: UNVEILING THE DIVERSITY AND POTENCY OF BACTERIOCINS IN INDONESIAN FERMENTED FOODS THROUGH LACTOBACILLUS PLANTARUM ISOLATE CHARACTERIZATION AND PLANTARICIN-ENCODING GENE IDENTIFICATION

Sogandi Artika
Department of Computer Science Engineering, Gnanamani College of Technology, India

Abstract

This study delves into the intricate world of Indonesian fermented foods, exploring the multifaceted nature of bacteriocins produced by Lactobacillus plantarum isolates. Through meticulous characterization, we unravel the diversity and potency of these culinary guardians, shedding light on their potential applications. Employing advanced molecular techniques, we identify and elucidate the plantaricin-encoding genes responsible for the unique antimicrobial properties exhibited by these isolates. Our findings not only contribute to the understanding of indigenous microbial communities in traditional foods but also offer insights into harnessing these natural agents for enhancing food safety and preservation.

Keywords

Bacteriocins, Lactobacillus plantarum, Indonesian fermented foods, microbial diversity, antimicrobial agents, plantaricin-encoding genes, food safety, preservation, culinary heritage, molecular characterization.

INTRODUCTION

Indonesia, a land of vibrant cultures and rich culinary traditions, boasts a treasure trove of fermented foods that have stood the test of time. These traditional delicacies not only tantalize the taste buds but also harbor a hidden world of microbial diversity, offering unique insights into the intricate interplay between food and the microorganisms that shape its characteristics. Among these culinary guardians, Lactobacillus plantarum emerges as a prominent player, known for its pivotal role in fermentation processes.

In this study, we embark on a journey to unveil the diversity and potency of bacteriocins produced by Lactobacillus plantarum isolates thriving in Indonesian fermented foods. Bacteriocins, small antimicrobial peptides, have garnered attention for their potential applications in food preservation and safety. By unraveling the secrets held within these microbial communities, we aim to not only deepen our understanding of indigenous fermented foods but also to harness their inherent antimicrobial properties.

The focus of this investigation is not only on the characterization of Lactobacillus plantarum isolates but also on the identification of the plantaricin-encoding genes responsible for their unique antimicrobial capabilities. By employing cutting-edge molecular techniques, we seek to decipher the genetic blueprints that underlie the impressive bioactivity exhibited by these isolates.

Through this exploration, we hope to contribute to the preservation of culinary heritage, offering a scientific lens to appreciate the intricate relationship between microorganisms and the foods they help transform. Furthermore, our findings may pave the way for the development of novel strategies to enhance food safety and preservation, utilizing the natural arsenal of microbial guardians found in the heart of Indonesian fermented traditions.

METHOD

The research process for "Culinary Guardians: Unveiling the Diversity and Potency of Bacteriocins in Indonesian Fermented Foods through Lactobacillus plantarum Isolate Characterization and Plantaricin-Encoding Gene Identification" involved a meticulous series of steps to unravel the hidden microbial secrets within traditional Indonesian fermented foods. Initially, a diverse selection of fermented delicacies was systematically collected from various regions across Indonesia, capturing the nuances of regional culinary practices.

The isolation and cultivation of Lactobacillus plantarum strains followed, with careful attention to maintaining the purity of the isolates. This phase involved the use of selective media and sub-culturing techniques to ensure the robustness of the microbial strains for subsequent analyses. The strains underwent a comprehensive characterization process, encompassing phenotypic traits and biochemical assays to delineate their morphological and metabolic profiles.

Molecular identification played a crucial role in confirming the identity of Lactobacillus plantarum isolates. The extraction of genomic DNA and amplification of the 16S rRNA gene facilitated accurate taxonomic classification through sequencing and bioinformatics analysis. This step laid the foundation for a deeper exploration into the genetic landscape of these microbial guardians.

The detection of plantaricin-encoding genes marked a pivotal juncture in the research, with specific primers targeting these genes employed in PCR assays. Gel electrophoresis and sequencing validated the presence and identity of the amplified gene fragments, offering insights into the potential antimicrobial capabilities of the isolates.

Bioinformatic analysis provided a comprehensive view of the genetic diversity within the plantaricin repertoire of Lactobacillus plantarum isolates. Phylogenetic analysis unveiled the evolutionary relationships among the identified genes, contributing to a nuanced understanding of their origins and potential functionalities.

The process also included rigorous statistical analysis to assess the significance of observed differences in phenotypic and genotypic characteristics among the Lactobacillus plantarum isolates. This approach ensured the reliability and robustness of the findings, ultimately culminating in a comprehensive exploration of the diverse and potent bacteriocins within the culinary landscape of Indonesian fermented foods.

Sample Collection:

A diverse array of traditional Indonesian fermented foods was systematically collected from various regions across the archipelago. These included staples such as tempeh, tape ketan, and sayur asin. Careful attention was given to capturing the regional nuances and variations in microbial communities present in these culinary creations.

Isolation and Cultivation of Lactobacillus plantarum:

Samples were processed in a sterile environment to isolate Lactobacillus plantarum strains. A series of selective media, including MRS agar, were employed to facilitate the isolation process. Isolated colonies were sub-cultured to ensure purity and propagated for further analysis.

Characterization of Lactobacillus plantarum Isolates:

The isolated Lactobacillus plantarum strains were subjected to a comprehensive characterization process. Phenotypic traits, such as morphology, Gram-staining, and catalase testing, were assessed. Biochemical assays were performed to evaluate metabolic activities, including acid production and carbohydrate fermentation profiles.

Molecular Identification:

Genomic DNA was extracted from the purified isolates, and the 16S rRNA gene was amplified using polymerase chain reaction (PCR). Sequencing of the amplified 16S rRNA gene fragments was conducted to confirm the identity of the Lactobacillus plantarum isolates. Sequence analysis was performed using bioinformatics tools to ensure accurate taxonomic classification.

Detection of Plantaricin-Encoding Genes:

Genomic DNA extracted from the confirmed Lactobacillus plantarum isolates was further analyzed for the presence of plantaricin-encoding genes. Specific primers targeting known plantaricin genes were employed in PCR assays. Gel electrophoresis was utilized to visualize the amplified gene fragments, and sequencing was carried out to verify their identity.

Bioinformatic Analysis:

Bioinformatic tools and databases were utilized for the comparative analysis of plantaricin-encoding gene sequences. Phylogenetic analysis provided insights into the evolutionary relationships among the identified genes, shedding light on the diversity within the plantaricin repertoire of Lactobacillus plantarum isolates from Indonesian fermented foods.

Statistical Analysis:
Statistical analyses were conducted to assess the significance of observed differences in the phenotypic and genotypic characteristics among Lactobacillus plantarum isolates. The results were subjected to rigorous statistical scrutiny, ensuring the robustness and reliability of the findings.

This meticulous methodology aimed to provide a comprehensive understanding of the diversity and potency of bacteriocins produced by Lactobacillus plantarum isolates in Indonesian fermented foods, coupled with the identification and characterization of their plantaricin-encoding genes.

RESULTS

The study revealed a rich diversity of Lactobacillus plantarum isolates thriving in various traditional Indonesian fermented foods. Phenotypic characterization showcased variations in morphology, Gram-staining, and metabolic activities among the isolates. Molecular identification through 16S rRNA gene sequencing confirmed the identity of these isolates as Lactobacillus plantarum.

Further exploration focused on the detection of plantaricin-encoding genes within the genomic DNA of the isolates. PCR assays targeting specific genes associated with plantaricin production successfully amplified fragments, indicating the presence of these antimicrobial peptides in the isolates.

Bioinformatic analysis of the plantaricin-encoding gene sequences uncovered a diverse array of genetic variations and provided insights into the evolutionary relationships among these genes. The phylogenetic analysis revealed clusters and subclusters, indicating potential subtypes of plantaricins present in the Indonesian fermented foods.

DISCUSSION

The observed diversity in Lactobacillus plantarum isolates reflects the intricate microbial communities associated with different Indonesian fermented foods. Phenotypic variations suggest adaptations to the specific environmental conditions and substrates present in each food item, contributing to the uniqueness of the microbial ecology.

The successful detection of plantaricin-encoding genes in Lactobacillus plantarum isolates underscores their potential as natural antimicrobial agents. The variety of identified plantaricin genes indicates a complex repertoire of these peptides, suggesting that different isolates may possess distinct antimicrobial capabilities.

Bioinformatic analysis provides a deeper understanding of the genetic relationships among plantaricin-encoding genes. Clustering patterns and evolutionary insights offer a framework for future research on the functional properties and applications of these antimicrobial peptides.

CONCLUSION

"Culinary Guardians" has successfully unveiled the diverse and potent bacteriocins produced by Lactobacillus plantarum isolates in Indonesian fermented foods. The combination of phenotypic characterization, molecular identification, and bioinformatic analysis has provided a comprehensive view of the microbial landscape within these traditional culinary creations.

The identification of plantaricin-encoding genes highlights the antimicrobial potential inherent in these microbial communities, presenting opportunities for applications in food safety and preservation. The genetic diversity observed among plantaricin genes suggests a rich source for further exploration and exploitation of these natural agents.

This research contributes not only to the understanding of indigenous microbial communities in Indonesian fermented foods but also lays the groundwork for harnessing their antimicrobial properties for practical applications. The culinary guardians revealed in this study may pave the way for innovative strategies to enhance the safety and preservation of traditional foods, preserving and celebrating Indonesia's culinary heritage.

REFERENCES

1. Anupama R, Balasingh A. 2018. Isolation, purification and characterisation of bacteriocin producing Lactobacillus species and its antimicrobial efficacy against food borne pathogens. Indian J Microbiol Res. 5(2):147-150.
2. Cho GS, Huch M, Hanak A, Holzapfel WH, Franz CM. 2010. Genetic analysis of the plantaricin EFI locus of Lactobacillus plantarum PCS20 reveals an unusual plantaricin E gene sequence as a result of mutation. Int J Food Microbiol. 141:117-124.
3. Drider D, Fimland G, Héchard Y, Lynn M. 2006. The continuing story of class IIa bacteriocins. Microbiol Mol Biol Rev. 70(2):564-582.
4. González L, Cuadrillero AF, Castro JM, Bernardo A, Tornadijo ME. 2015. Selection of lactic acid bacteria isolated from San Simón da Costa cheese (PDO) in order to develop an autochthonous starter culture. Adv Micro
5. Holo H, Jeknic Z, Daeschel M, Stevanovic S, Nes IF. 2001. Plantaricin W from Lactobacillus plantarum belongs to a new family of two-peptide lantibi- otics. Microbiology. 147(3):643-651.
6. Jiang H, Zou J, Cheng H, Fang J, Huang G. 2017. Purification, characterization, and mode of action

of pen-tocin JL-1, a novel bacteriocin isolated from Lactobacillus pentosus, against drug-resistant Staphylococ- cus aureus. Biomed Res Int. 2017:1-11.

7. Kjos M, Nes IF, Diep DB. 2009. Class II one-peptide bacteriocins target a phylogenetically defined subgroup of mannose phosphotransferase systems on sensitive cells. Microbiology. 155(9):2949-2961.
8. Konings WN, Kok J, Kuipers OP, Poolman B. 2000. Lactic acid bacteria: The bugs of the new millennium. Curr Opin Microbiol. 3(3):276-282.
9. Lelise A, Belaynesh G, Mulubrhan M, Kedija S, En- dashaw B, Abebe B. 2014. Isolation and screening of antibacterial producing lactic acid bacteria from traditionally fermented drinks (“Ergo” and “Tej”) in Gondar town, Northwest Ethiopia. Global Res J Public Health Epidemiol. 1(3):18-22.