Manuscript ID: FR-IFC-029

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Date	:	5 th February 2022
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	Grade					
Evaluation Criteria	A (Excellent)	В	С	D	E (Worst)	
1. Appropriateness of Contents			x			
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3. Manuscript Format			х			
4. Research Methodology				х		
5. Data Analysis				х		
6. Relevance to the Journal		х				

	(REVIEWER'S SECTION) REVIEWER'S COMMENTS/SUGGESTIONS	(AUTHOR'S SECTION) AUTHOR'S ACTION/RESPONSE *NOTE FOR AUTHOR: Please state your response to the reviewer's comments/suggestion below
1.	Title : Ethnic food fermentation from Bengkulu as a source of lactic acid bacteria It should reflect the article: • The title does not very much reflect the contain of the article. • There is not any information and discussions about the ethnic food fermentation from Bengkulu in the results and discussion. • The content of this manuscript is isolation and identification of LAB from fermented bamboo shoot	
2.	Abstract Background, Aim, Methodology and Conclusion: • The background of the research is not clear. It is not stated explicitly and clearly • It is more appropriate if the study aim is to isolate and identified LAB from fermented Betung bamboo shoot, and yellow bamboo shoot • Methodology in the abstract is quite clear • Conclusion: the author wanted to find LAB in fermented bamboo shoots. Bacteria that has been found were gram positive bacteria and a group of lactic acid bacteria is not a conclusion	
3.	Keywords: - Min. 3 and Max. 6	
4.	Introduction Concise with sufficient background O Not enough information about this fermented betung bamboo shoots such as the raw materials and ingredients, the condition and time of fermentation process, and description of the product. O Related research and similar	

 traditional fermented product reported by other researchers are not evaluated. The background is not clear. The purpose of the research is to 	
 The background is not clear. The 	
purpose of the research is to	
investigate LAB strains in fermented	
Betung bamboo shoots, but the MM	
and results are isolation and	
identification of LAB	
5. Research design/Methodology	
Clearly described and reproducible:	
 The research design/methodology is not 	
 described clearly Sample preparation: the quantity of all the 	
materials were not mentioned.	_
• The time of fermentation in the MM is	
different from the diagram in figure 1, and	
also different from the one in the	
introduction	
 Isolation and identification steps need to be written already step by steps 	
written clearly step by step	
6. Data Analysis	
Results well presented and discussed	
 Results are not well presented and 	
discussed	
 The authors do not explain how 	
many isolates are obtained from	
MRSA.	
• There was not any discussion.	
 Only shows the facts, d anvery 	
limited information	
	_
7. Conclusion	
 A clear summary of the study The conclusion written by the authors is not a 	
conclusion since L. plantarum and L.	
fermentum are gram positive bacteria and LAB	
	_
8. References	
References should follow the journal's format	
9. English Proficiency:	
Some grammatical errors	
10 Additional comments/suggestions by the	

reviewer about the article:

- The article should be rewrite from abstract to conclusion for proper articles.
 Results and discussion are very limited. They should be precented.
- limited. They should be presented clearly, every step and discussed in more comprehensive supported by suitable references
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Overall Evaluation

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COMMENT SHEET

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	Grade				
Evaluation Criteria	A (Excellent)	В	С	D	E (Worst)
7. Appropriateness of Contents		v			
8. Originality of Topic		v			
9. Manuscript Format			v		
10. Research Methodology			v		
11. Data Analysis			v		
12. Relevance to the Journal		v			

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	REVIEWER'S COMMENTS/SUGGESTIONS	AUTHOR'S ACTION/RESPONSE			
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		response to the reviewer's comments/suggestion below			
11.	Title	comments/suggestion below			
	The title does not yet describe the method use d. There should be a word isolation of lactic a cid bacteria.				
12.	Abstract It has not given the importance of isolating lactic acid b acteria from the product. Methods need to be summarize d				
13.	Keywords It should be added to the product name.				
14.	Introduction It has not yet described the importance of isolating lactic c acid bacteria from the product.				
15.	Research design/Methodology Method clearly described and reproducible.				
16.	Data Analysis It is necessary to add a discussion about the differences in lactic acid bacteria obtained from differences in bamb oo types that are strengthened by reference.				
17.	Conclusion It should be associated with the source of lactic acid bac teria isolation				

18.	References Ok	
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1

Ethnic food fermentation from Bengkulu as a source of lactic acid bacteria

2 Abstract

3	In order to avoid extinction, strains of lactic acid bacteria must be studied. This study aims to find Lactic
4	Acid Bacteria (LAB) strains in fermented Betung bamboo shoots (Dendrocalamus Asper Schult) and Yellow
5	bamboo shoots (Bambusa Vulgaris Schrad). Due to the ethnic diet of the rejang tribe, this fermented
6	foodstuff is only found in Bengkulu province. Which was made by combining bamboo shoots with river
7	fish and allowing it to stand for a few days until a distinct aroma emerges. The LAB identification of began
8	with homogenizing 10 g of the samples, which then get serially diluted with 1 percent sterile NaCl and
9	spreaded on MRSA media. The isolates were identified molecularly using 16S rRNA gene amplification,
10	which included the procedures of isolating genomic DNA, amplification using DNA, sequencing, and
11	nucleotide sequence analysis on GenBank. Lactobacillus plantarum strain B1 and Lactobacillus plantarum
12	strain B2 were identified on fermented Betung bamboo shoots, while Lactobacillus plantarum S1 and
13	Lactobacillus fermentum S2 on Yellow Bamboo shoots. Lactobacillus plantarum and fermentum isolated
14	from fermented bamboo shoots were gram positive bacteria and a group of lactic acid bacteria.

15 Keywords: Lactic Acid Bacteria, Bamboo shoot, Ethnic Food Fermentation, PCR, 16S rRNA

16 1. Introduction

There is a great need to develop the traditional food which comprises the ethnic diet of a particular region. Moreover, it is also important to prevent the extinction of traditional foods such as fermented foods that contain lactic acid bacteria (Dewi *et al.*, 2014). One of the tribes that has fermented food and needs to be maintained is the Rejang tribe, which is the largest tribe in Bengkulu (Dewi, 2015).

There are a variety of fermented foods in the world especially in Asia. Most of Asian fermented foods
 are non-dairy products featuring various other raw materials such as cereals, soybeans, fruit,
 vegetables and fish and other products (Rhee *et al.*, 2011). Indonesia is rich in fermented foods

24	including Dadih, Bekasam and Lemea. Curd, fermented buffalo milk from Minangkabau, West	
25	Sumatra, various types of LAB isolated from curd (Wirawati et al., 2019). Bekasam, a fermented	
26	Indonesian freshwater fish product that tastes sour and contains lactic acid bacteria (LAB) is popular	
27	in Central Java, South Sumatra and South Kalimantan (Desniar et al., 2013). Lemea is a processed fish	
28	and bamboo shoots originating from Bengkulu, precisely the Rejang tribe, which is fermented for 3-	
29	7 days and generally uses freshwater fish with lactic acid bacteria as the main actor (Xu et al., 2021).	
30	River fish that are often used to make lemea are freshwater fish. One of the freshwater fish that can	
31	be used is betok fish, lemea containing lactic acid bacteria (Xu <i>et al.,</i> 2021). Lactic acid bacteria consist	_
32	of microbial strains that convert carbohydrates into lactic acid (Dinoto et al., 2020), LAB isolated	
33	results were identified based on phenotypic and genotypic characteristics (Lawalata et al., 2011).	
34	Genotypic LAB identification was carried out by PCR technique in the form of amplifying and	
35	sequencing the universal region of the 16S rRNA gene (Dinoto <i>et al.,</i> 2020). Lactic Acid Bacteria (LAB)	
36	strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) has been previously	
37	studied The purpose of this study was to investigate Lactic Acid Bacteria (LAB) strains in fermented	
38	Betung bamboo shoots (Dendrocalamus asper Schult) and Yellow bamboo shoots (Bambusa vulgaris	
39	Schrad).	
40	2. Materials and methods	
41	2.1 Sample Preparation	
42	The process of processing fermented bamboo shoots begins with slicing thin samples and soaking	
43	them for 30 hours, then washing and filtering them. The next step is fermentation for 48 hours at	
44	room temperature by mixing sliced bamboo shoots, betok fish, lemongrass and salt and water	
45	(Figure 1)	

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...

Commented [A1]: Please give the latin name of fish

46 2.2 LAB isolation

47	Isolation of LAB was carried out using a device that was sterilized beforehand and carried out
48	aseptically where 10 g of the lemea sample was homogenized and then serially diluted with 1%
49	NaCl. And each dilution series was spread on MRSA media and then petridish was incubated at
50	37°C for 48 hours. The isolates obtained need to be purified and identified
51	2.3 Identification of LAB Strain Fermented Bamboo Shoot (Lemea)
52	Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA
53	amplification, sequencing and analysis of nucleotide sequences in GenBank (Widodo et al., 2017).
54	DNA isolation was Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit (Geneaid,
55	GBB100). DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red
56	Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA Recovery Kit
57	(Zymo Research, D4001). The PCR results were visualized by electrophoresis as much as 1uL of the
58	PCR product was assessed with 0.8% TBE agarose.

59 3. Results and discussion/Results

Bacterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid 60 61 bacteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and 62 S1 are closely related to Lactobacillus plantarum, this type of bacteria is known as lactic acid bacteria 63 which has the potential as biopreservative because it can inhibit the growth of pathogens and 64 destructive with greater inhibition than other lactic acid bacteria. (Azizah et al., 2019). L. plantarum 65 is amylolytic which converts starch to lactic acid (Noor et al., 2018). S2 is closely related to 66 Lactobacillus fermentum, this type of bacteria is known as lactic acid bacteria which belongs to 67 heterofermentative species and can be found in the human intestinal tract where these bacteria can 68 live at the pH of the digestive tract (Manin, 2010). B1 and B2 are isolate codes derived from 69 fermented bamboo shoots. S1 and S2 codes for isolate fermented yellow bamboo shoots. (Table 1). 70 Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration

71		using the Kappa Universal ladder (Figure 2a and 2b). Visualization of 16 S rRNA gene amplification of			
72		isolates B1 , B2, S1 and S 2 at 0.8% TBE agarose concentration using the Kappa Universal ladder			
73		(Figures 3a and 3b). hylogenetic analysis using MEGA 7.0 with Neighbor-joining (unrooted tree) by			
74		NCBI tree method showed that B1, B2 and S1 were closely related to Lactobacillus plantarum (Figures			
75		4a, 4b and 4c). S2 is closely related to Lactobacillus fermentum (Figure 4d). Betung bamboo shoots			
76		contain lactic acid bacteria in the form of Lactobacillus plantarum while yellow bamboo shoots			
77		contain more lactic acid bacteria in the form of Lactobacillus fermentum.			
78	4.	Conclusion			
79		Lactobacillus plantarum and fermentum isolated from fermented bamboo shoots were found to be			
80		gram positive bacteria and belong to a group of lactic acid bacteria.			
81					
82	Cor	flict of interest - Disclose potential conflicts of interest appropriately.			
83	The	authors declare no conflict of interest.			
84	Acknowledgments				
85	Thi	s research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020			

87 References

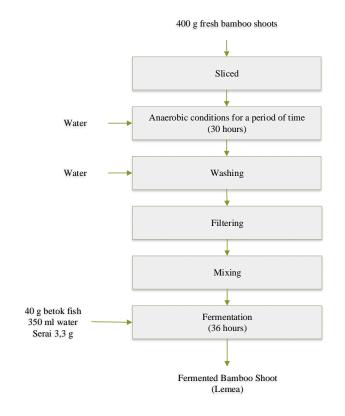
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Types	of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo		Code		Access Number	
Shoots					
Bamboo		B1	Lactobacillus plantarum	M N37236.01	99
Betung					
		B2	Lactobacillus plantarum	MN972325.1	99
Yellow		S1	Lactobacillus plantarum	KM350169.1	99
Bamboo					
		S2	Lactobacillus fermentum	MT538927.1	99

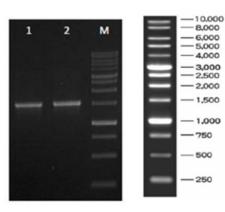
141 Table 1. Comparison of Homology Levels the 16S rRNA gene of BAL isolat with several sequences

144 Figure 1. Fermented Bamboo shoot making process



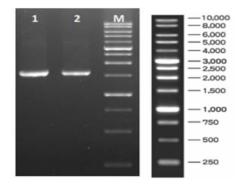
146 Figure 2a. Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose

147 concentration using the Kappa Universal ladder



150 Figure 2b. Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose

151 concentration using the Kappa Universal ladder



157 Figure 3a. Sequence assembly result – PCR product Isolate Code B1

Sequence Assembly 1434 bp

1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITIGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGGGG	TGTGTACAAG	GCCCGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GTGTAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GTCACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATICAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CITCGGITGA	GCCGAAGGCT	TICACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	IGCCAIGGIG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCIGITICC
1321	AGGIGITATC	CCCCGCTICI	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTICGTICG	ACTT

158 159

160 Figure 3b. Sequence assembly result – PCR product Isolate Code B2

1	AGGCGGCTGG	TICCTARARG	GTTACCCCAC	CGACITIGGG	TGTTACAAAC	TCTCATGGTG	
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT	
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT	
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT	
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT	
301	GICACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC	
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC	
421	CIGIATCCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC	
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC	
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG	
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT	
661	ATGGACTACC	AGGGTATCTA	ATCCIGTTIG	CTACCCATAC	TITCGAGCCT	CAGCGTCAGT	
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG	
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT	
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG	
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT	
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT	
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GTTGCTCCAT	
1081	CAGACITICG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT	
1141	GICICAGICC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG	
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG	
1261	CCATCTTTCA	AACTCGGACC	ATGCGGTCCA	AGTIGTIATG	CGGTATTAGC	ATCIGITICC	
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA	
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT		

163 Figure 3c. Sequence assembly result – PCR product Isolate Code S1

Sequence Result Reverse Primer 882bp

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGGGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTC
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACC
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGC
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

164 165

166 Figure 3d. Sequence assembly result – PCR product Isolate Code S2

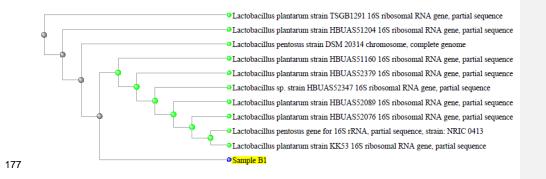
Sequence Result Reverse Primer 849bp

1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGC
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTC
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

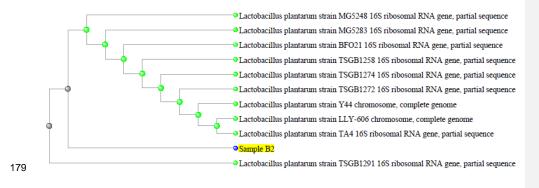
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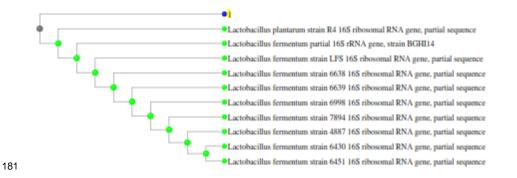
176 Figure 4a. Phylogenetic tree Isolate Code B1



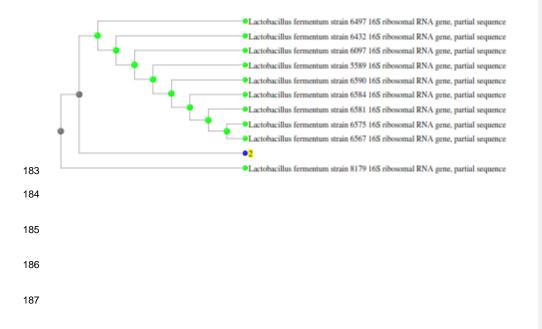
178 Figure 4b. Phylogenetic tree Isolate Code B2



180 Figure 4c. Phylogenetic tree Isolate Code S1



182 Figure 4d. Phylogenetic tree Isolate Code S2



188

Ethnic food fermentation from Bengkulu as a source of lactic acid bacteria

189 Abstract

190	In order to avoid extinction, strains of lactic acid bacteria must be studied. This study aims to find Lactic	
191	Acid Bacteria (LAB) strains in fermented Betung bamboo shoots (Dendrocalamus Asper Schult) and Yellow	
192	bamboo shoots (Bambusa Vulgaris Schrad). Due to the ethnic diet of the rejang tribe, this fermented	
193	foodstuff is only found in Bengkulu province. Which was made by combining bamboo shoots with river	
194	fish and allowing it to stand for a few days until a distinct aroma emerges. The LAB identification of began	
195	with homogenizing 10 g of the samples, which then get serially diluted with 1 percent sterile NaCl and	
196	spreaded on MRSA media. The isolates were identified molecularly using 16S rRNA gene amplification,	
197	which included the procedures of isolating genomic DNA, amplification using DNA, sequencing, and	/
198	nucleotide sequence analysis on GenBank. Lactobacillus plantarum strain B1 and Lactobacillus plantarum	
199	strain B2 were identified on fermented Betung bamboo shoots, while Lactobacillus plantarum S1 and	
200	Lactobacillus fermentum S2 on Yellow Bamboo shoots. Lactobacillus plantarum and fermentum isolated	
201	from fermented bamboo shoots were gram positive bacteria and a group of lactic acid bacteria.	_
202	Keywords: Lactic Acid Bacteria, Bamboo shoot, Ethnic Food Fermentation, PCR, 16S rRNA	

203 5. Introduction

204	There is a great need to develop the traditional food which comprises the ethnic diet of a particular
205	region. Moreover, it is also important to prevent the extinction of traditional foods such as fermented
206	foods that contain lactic acid bacteria (Dewi et al., 2014). One of the tribes that has fermented food
207	and needs to be maintained is the Rejang tribe, which is the largest tribe in Bengkulu (Dewi, 2015).
208	There are a variety of fermented foods in the world especially in Asia. Most of Asian fermented foods
209	are non-dairy products featuring various other raw materials such as cereals, soybeans, fruit,
210	vegetables and fish and other products (Rhee et al., 2011). Indonesia is rich in fermented foods

Commented [MOU2]: How many ethnic food fermentation in Bengkulu; If there are many ethnic fermented food and the authors only focus on the one type of fermented food better say so

Commented [MOU3]: Can we just study LAB to avoid extinction of these bacteria?

Commented [MOU4R3]:

Commented [MOU5]: To find or to isolate and identify?

Commented [MOU6]: Do you mean isolation

Commented [MOU7]: How many isolates were obtained from the samples?	ı
Commented [MOU8R7]:	
Commented [MOU9R7]:	

Commented [MOU10]: L. plantarum and L. fermentum are already known as gram positive bacteria and belong to LAB group.

Commented [MOU11]: Could you please give the meaning or definition of traditional food and ethnic food

211		including Dadih, Bekasam and Lemea. Curd, fermented buffalo milk from Minangkabau, West		
212		Sumatra, various types of LAB isolated from curd (Wirawati et al., 2019). Bekasam, a fermented		
213		Indonesian freshwater fish product that tastes sour and contains lactic acid bacteria (LAB) is popular		
214		in Central Java, South Sumatra and South Kalimantan (Desniar et al., 2013). Lemea is a processed fish		Commente other related
215		and bamboo shoots originating from Bengkulu, precisely the Rejang tribe, which is fermented for 3-		
216		7 days and generally uses freshwater fish with lactic acid bacteria as the main actor (Xu et al., 2021).		
217		River fish that are often used to make lemea are freshwater fish. One of the freshwater fish that can		
218		be used is betok fish, lemea containing lactic acid bacteria (Xu <i>et al.</i> , 2021), Lactic acid bacteria consist		Commente lemea/ferme
219		of microbial strains that convert carbohydrates into lactic acid (Dinoto et al., 2020), LAB isolated		Why did the fermented ba Is there any r
220		results were identified based on phenotypic and genotypic characteristics (Lawalata et al., 2011).		bamboo sho
221		Genotypic LAB identification was carried out by PCR technique in the form of amplifying and		
222		sequencing the universal region of the 16S rRNA gene (Dinoto et al., 2020). Lactic Acid Bacteria (LAB)		
223		strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) has been previously		
224		studied The purpose of this study was to investigate Lactic Acid Bacteria (LAB) strains in fermented		Commenter finding? sucl
225		Betung bamboo shoots (Dendrocalamus asper Schult) and Yellow bamboo shoots (Bambusa vulgaris	\backslash	bamboo sho You can use t
226		Schrad).		Commente
				Commenter betung bamb
227	6.	Materials and methods		
228		2.1 Sample Preparation		Commente guantity of e
229		The process of processing fermented bamboo shoots begins with slicing thin samples and soaking		<u>(</u>
230		them for 30 hours, then washing and filtering them. The next step is fermentation for 48 hours at		Commente form the one
231		room temperature by mixing sliced bamboo shoots, betok fish, lemongrass and salt and water		
232		(Figure 1)		
233		2.2 LAB isolation		

Commented [MOU12]: Please explain more about Lemea, and other related subjects

Commented [MOU13]: Is there any reference about emea/fermented bamboo shoots? Why did the authors want to isolated and identified LAB from ermented bamboo shoots? s there any reference about isolation of LAB from fermented pamboo shoots?

Commented [MOU14]: Explain more about this. What is the finding? such species, strain of LAB that were isolated from Tabah bamboo shoots. You can use these findings for your discussion

Commented [MOU15]: Investigation or isolation?

Commented [MOU16]: Why did the authors choose fermented betung bamboo shoots and yellow bamboo shoots?

Commented [MOU17]: Please describe more detail, such the quantity of each material, and the fermentation condition and time.

Commented [MOU18]: The time of fermentation is different form the one in figure 1

234		Isolation of LAB was carried out using a device that was sterilized beforehand and carried out		Commented [MOU19]: Please describe in more detail
235		aseptically where 10 g of the lemea sample was homogenized and then serially diluted with 1%		
236		NaCl. And each dilution series was spread on MRSA media and then petridish was incubated at		
237		37°C for 48 hours. The isolates obtained need to be purified and identified	(Commented [MOU20]: Explain how to do purify the isokates
238	<i>2</i> .3	Identification of LAB Strain Fermented Bamboo Shoot (Lemea)		
239		Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA		
240		amplification, sequencing and analysis of nucleotide sequences in GenBank (Widodo <i>et al.</i> , 2017).		
241		DNA isolation was Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit (Geneaid,		
242		GBB100). DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red		
243		Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA Recovery Kit		
244		(Zymo Research, D4001). The PCR results were visualized by electrophoresis as much as 1uL of the		
245		PCR product was assessed with 0.8% TBE agarose.		
246	7. Res	sults and discussion/Results		Commented [MOU21]: Please show the results (which
246 247		sults and discussion/Results cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid		Commented [MOU21]: Please show the results (which figure/table and then discuss in more comprehensive with support from references /findings from other researchers
	Bac			figure/table and then discuss in more comprehensive with support
247	Bac	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid		figure/table and then discuss in more comprehensive with support
247 248	Bac bac S1 a	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and		figure/table and then discuss in more comprehensive with support
247 248 249	Bac bac S1 a wh	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria		figure/table and then discuss in more comprehensive with support
247 248 249 250	Bad bad S1 i wh des	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain? Commented [MOU23]: Which lactic acid bacteria or L.
247 248 249 250 251	Bac bac S1 i wh des is i	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and structive with greater inhibition than other lactic acid bacteria. (Azizah <i>et al.</i> , 2019). <i>L. plantarum</i>		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain?
247 248 249 250 251 252	Bac bac S1 i wh des is <i>i</i> <i>Lac</i>	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and structive with greater inhibition than other lactic acid bacteria. (Azizah <i>et al.</i> , 2019). <i>L. plantarum</i> amylolytic which converts starch to lactic acid (Noor <i>et al.</i> , 2018). S2 is closely related to		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain? Commented [MOU23]: Which lactic acid bacteria or L.
247 248 249 250 251 252 253	Bad bad S1 i wh des is <i>i</i> <i>Lac</i> het	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and structive with greater inhibition than other lactic acid bacteria. (Azizah <i>et al.</i> , 2019). <i>L. plantarum</i> amylolytic which converts starch to lactic acid (Noor <i>et al.</i> , 2018). S2 is closely related to <i>ctobacillus fermentum</i> , this type of bacteria is known as lactic acid bacteria which belongs to		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain? Commented [MOU23]: Which lactic acid bacteria or L.
247 248 249 250 251 252 253 254	Bad bad S1 : wh des is <i>Lac</i> het	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and structive with greater inhibition than other lactic acid bacteria. (Azizah <i>et al.</i> , 2019). <i>L. plantarum</i> amylolytic which converts starch to lactic acid (Noor <i>et al.</i> , 2018). S2 is closely related to <i>ctobacillus fermentum</i> , this type of bacteria is known as lactic acid bacteria which belongs to terofermentative species and can be found in the human intestinal tract where these bacteria can		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain? Commented [MOU23]: Which lactic acid bacteria or L.
247 248 249 250 251 252 253 254 255	Bad bad S1 i wh des is <i>Lac</i> het live	cterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid cteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and are closely related to <i>Lactobacillus plantarum</i> , this type of bacteria is known as lactic acid bacteria hich has the potential as biopreservative because it can inhibit the growth of pathogens and structive with greater inhibition than other lactic acid bacteria. (Azizah <i>et al.</i> , 2019). <i>L. plantarum</i> amylolytic which converts starch to lactic acid (Noor <i>et al.</i> , 2018). S2 is closely related to <i>ctobacillus fermentum</i> , this type of bacteria is known as lactic acid bacteria which belongs to terofermentative species and can be found in the human intestinal tract where these bacteria can e at the pH of the digestive tract (Manin, 2010). B1 and B2 are isolate codes derived from		figure/table and then discuss in more comprehensive with support from references /findings from other researchers Commented [MOU22]: Other species or strain? Commented [MOU23]: Which lactic acid bacteria or L.

258		using the Kappa Universal ladder (Figure 2a and 2b). Visualization of 16 S rRNA gene amplification of		
259		isolates B 1, B2, S1 and S 2 at 0.8% TBE agarose concentration using the Kappa Universal ladder		
260		(Figures 3a and 3b). hylogenetic analysis using MEGA 7.0 with Neighbor-joining (unrooted tree) by		
261		NCBI tree method showed that B1, B2 and S1 were closely related to Lactobacillus plantarum (Figures		
262		4a, 4b and 4c). S2 is closely related to Lactobacillus fermentum (Figure 4d). Betung bamboo shoots		
263		contain lactic acid bacteria in the form of Lactobacillus plantarum while yellow bamboo shoots		
264		contain more lactic acid bacteria in the form of <i>Lactobacillus fermentum</i> .	_	Commented [MOU24]: What do you mean with yellow bamboo shoots contain more lactic acid bacteria in the form of L. fermentum.
265	8.	Conclusion		
266		Lactobacillus plantarum and fermentum isolated from fermented bamboo shoots were found to be		
267		gram positive bacteria and belong to a group of lactic acid bacteria.		Commented [MOU25]: This is not a conclusion. L. planatrum dan L. fermentum are gram positive bacteria and lactic and lactic
268				acid bacteria
269	Cor	nflict of interest - Disclose potential conflicts of interest appropriately.		
270	The	e authors declare no conflict of interest.		

Acknowledgments

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274 References

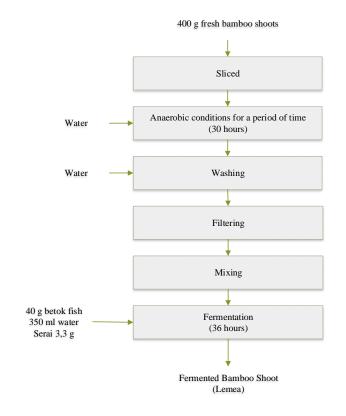
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Types	of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo		Code		Access Number	
Shoots					
Bamboo		B1	Lactobacillus plantarum	M N37236.01	99
Betung					
		B2	Lactobacillus plantarum	MN972325.1	99
Yellow		S1	Lactobacillus plantarum	KM350169.1	99
Bamboo					
		S2	Lactobacillus fermentum	MT538927.1	99

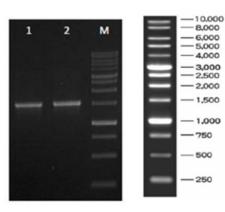
328 Table 1. Comparison of Homology Levels the 16S rRNA gene of BAL isolat with several sequences

331 Figure 1. Fermented Bamboo shoot making process



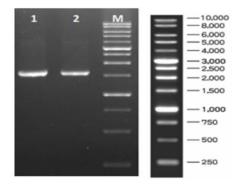
333 Figure 2a. Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose

334 concentration using the Kappa Universal ladder



337 Figure 2b. Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose

338 concentration using the Kappa Universal ladder



344 Figure 3a. Sequence assembly result – PCR product Isolate Code B1

Sequence Assembly 1434 bp

order	stree riceeting.	1				
1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTTTGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GTCACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATICAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CITCGGITGA	GCCGAAGGCT	TICACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	IGCCAIGGIG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCIGITICC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CICAAAIGIA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGITCGTTCG	ACTT

345 346

347 Figure 3b. Sequence assembly result – PCR product Isolate Code B2

1	AGGCGGCTGG	TICCTARARG	GTTACCCCAC	CGACITIGGG	TGTTACAAAC	TCTCATGGTG	
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT	
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT	
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT	
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT	
301	GICACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC	
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC	
421	CIGIATCCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC	
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC	
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG	
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT	
661	ATGGACTACC	AGGGTATCTA	ATCCIGTTIG	CTACCCATAC	TITCGAGCCT	CAGCGTCAGT	
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG	
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT	
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG	
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT	
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT	
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GTTGCTCCAT	
1081	CAGACITICG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT	
1141	GICICAGICC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG	
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG	
1261	CCATCTTTCA	AACTCGGACC	ATGCGGTCCA	AGITGTTATG	CGGTATTAGC	ATCIGITICC	
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA	
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT		

350 Figure 3c. Sequence assembly result – PCR product Isolate Code S1

Sequence Result Reverse Primer 882bp

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGGGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTC
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACC
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGC
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

351 352

353 Figure 3d. Sequence assembly result – PCR product Isolate Code S2

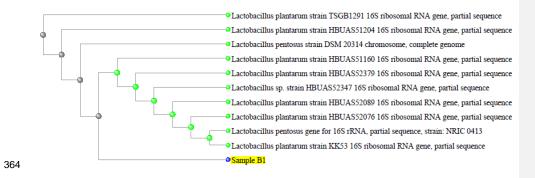
Sequence Result Reverse Primer 849bp

1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGC
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTC
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

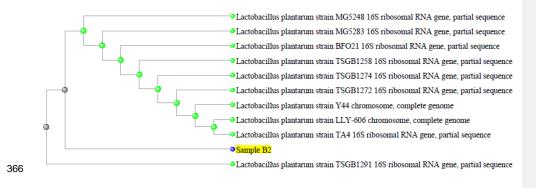
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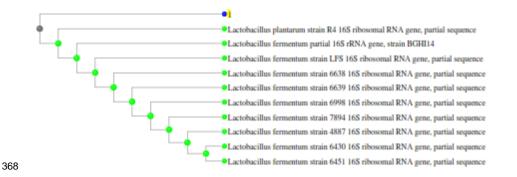
363 Figure 4a. Phylogenetic tree Isolate Code B1



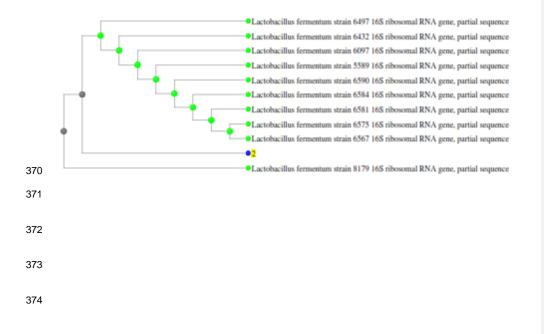
365 Figure 4b. Phylogenetic tree Isolate Code B2



367 Figure 4c. Phylogenetic tree Isolate Code S1



369 Figure 4d. Phylogenetic tree Isolate Code S2



MANUSCRIPT EVALUATION FORM

Date	:	5 th February 2022
Manuscript ID	:	FR-IFC-029
Please return by	:	5 th March 2022
Title of Manuscript	:	Ethnic food fermentation from Bengkulu as a source of lactic acid bacteria

- 1. IF YOU CANNOT REVIEW THIS MANUSCRIPT OR MEET THE DEADLINE, PLEASE INFORM US WITHOUT DELAY.
- 2. Your review should consider the article's scholarly merit including originality of the research issue and/or methodology, adequacy and rigor of the research methodology and techniques used, quality and rigor of data analysis, comprehensiveness of literature review, and the readability and presentation of the article. Please provide detailed and specific comments to all items. Also, where appropriate please provide suggestions for revision.

COMMENT SHEET

Using item 2 in page 1 as a guideline, please indicate the reasons for your recommendations. Most author(s) will appreciate frankness, combined with a modicum of tact. Even if you recommend that the manuscript be accepted for publication, please provide some general comments to the author(s).

Evaluation Criteria		Grade					
		A (Excellent)	В	С	D	E (Worst)	
13.	Appropriateness of			x			
Contents				~			
14.	Originality of Topic		х				
15.	Manuscript Format			х			
16.	Research Methodology				х		
17.	Data Analysis				х		
18.	Relevance to the		v				
Journal			х				

	(REVIEWER'S SECTION)	(AUTHOR'S SECTION)			
	REVIEWER'S COMMENTS/SUGGESTIONS	*NOTE FOR AUTHOR: Please state your response to the reviewer's comments/suggestion below			
21.	 Bengkulu as a source of lactic acid bacteria It should reflect the article: The title does not very much reflect the contain of the article. There is not any information and discussions about the ethnic food fermentation from Bengkulu in the results and discussion. The content of this manuscript is isolation and identification of LAB from fermented bamboo shoot 	The title has been corrected to: Identification of lactid acid bacteria isolated from ethnic fermented bamboo shoot " <i>Lemea</i> " in Bengkulu, Indonesia			
22.	 Abstract Background, Aim, Methodology and Conclusion: The background of the research is not clear. It is not stated explicitly and clearly It is more appropriate if the study aim is to isolate and identified LAB from fermented Betung bamboo shoot, and yellow bamboo shoot Methodology in the abstract is quite clear Conclusion: the author wanted to find LAB in fermented bamboo shoots. Bacteria that has been found were gram positive bacteria and a group of lactic acid bacteria is not a conclusion 	 The abstract has been remade, focusing on the process of isolation and identification of lactic acid bacteria from lemea products. This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of <i>Lemea</i>. The methodology in the abstract has been c larified: betung shoots (<i>Dendrocalamus aspe r Schult</i>) and yellow bamboo (<i>Bambusa vulg aris Schrad</i>) have been used. Furthermore, it was remotely analyzed on M RSA media and four LAB isolates were obtain ed. Molecular identification using the 16S rR NA method. 			
23.	Keywords: - Min. 3 and Max. 6	Keywords: <i>Lemea</i> , bamboo shoot, 16S rRNA, LA B			
24.	Introduction Concise with sufficient background O Not enough information about this fermented betung bamboo shoots such as the raw materials and ingredients, the condition and time of fermentation process, and description of the product. O Related research and similar	 Information about the raw materials used has been added to the composition in 2.1 sample preparation Bosparch on a similar traditional formented 			
	traditional fermented product	• Research on a similar traditional fermented			

	 reported by other researchers are not evaluated. The background is not clear. The purpose of the research is to investigate LAB strains in fermented Betung bamboo shoots, but the MM and results are isolation and identification of LAB 	 product has been reported, namely eksam and has been evaluated in the introduction The title, objectives, background and conclusion have been adjusted according to the method
25.	 Research design/Methodology Clearly described and reproducible: The research design/methodology is not described clearly Sample preparation: the quantity of all the materials were not mentioned. The time of fermentation in the MM is different from the diagram in figure 1, and also different from the one in the introduction Isolation and identification steps need to be written clearly step by step 	 The method has been described in more detail with Fig1 and 2 The number of ingredients has been added The fermentation time has been synchronized which is 48 hours in the sample preparation and Fig 1 Isolation and identification steps have been added
26.	 Data Analysis Results well presented and discussed Results are not well presented and discussed The authors do not explain how many isolates are obtained from MRSA. There was not any discussion. Only shows the facts, d anvery limited information 	 Results have been presented. Each Table and Figure has been explained in more detail The resulting isolates were 4 isolates and supported by the image of the isolate in Fig 3 Each result explanation has been added a discussion Non-factual information has been added discussion/Results
27.	Conclusion A clear summary of the study • The conclusion written by the authors is not a conclusion since L. plantarum and L. fermentum are gram positive bacteria and LAB	The conclusion has been corrected according to the reviewer's suggestion Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 16S rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad) while Lactobacillus plantarum was found in yellow

28.		nces res should follow the journal's format	bamboo shoots (<i>Bambusa vulgaris Schrad</i>) and betung (<i>Dendrocalamus asper Schult</i>). Reference has followed the format
29.	•	Proficiency: grammatical errors	The grammar has been corrected.
30.		bonal comments/suggestions by the er about the article: The article should be rewrite from abstract to conclusion for proper articles. Results and discussion are very limited. They should be presented clearly, every step and discussed in more comprehensive supported by suitable references There should be clear correlation among back ground, aim, MM, results and conclusion	 The article has been rewritten. The results have been made clearer and supported with the latest references. It has been correlated with the title, objectives, methods, results, and discussion.

Overall Evaluation

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MANUSCRIPT EVALUATION FORM

Respon penuis terhadap evaluasi riviewer 2

FOOD RESEARC		
Date	: 5 th February 2022	
Manuscript ID	: FR-IFC-029	
Please return by	: 5 th March 2022	
Title of Manuscript	: Ethnic food fermentation from Bengkulu as a source of lactic a bacteria	icid

- 1. IF YOU CANNOT REVIEW THIS MANUSCRIPT OR MEET THE DEADLINE, PLEASE INFORM US WITHOUT DELAY.
- 2. Your review should consider the article's scholarly merit including originality of the research issue and/or methodology, adequacy and rigor of the research methodology and techniques used, quality and rigor of data analysis, comprehensiveness of literature review, and the readability and presentation of the article. Please provide detailed and specific comments to all items. Also, where appropriate please provide suggestions for revision.

COMMENT SHEET

Using item 2 in page 1 as a guideline, please indicate the reasons for your recommendations. Most author(s) will appreciate frankness, combined with a modicum of tact. Even if you recommend that the manuscript be accepted for publication, please provide some general comments to the author(s).

Grade						
	Evaluation Criteria	A (Excellent)	В	С	D	E (Worst)
10	A	(Excellent)				(worst)
19.	Appropriateness of		v			
Con	itents		•			
20.	Originality of Topic		v			
21.	Manuscript Format			v		
22.	Research Methodology			v		
23.	Data Analysis			v		
24.	Relevance to the					
Journal			V			

	(REVIEWER'S SECTION)	(AUTHOR'S SECTION)		
	REVIEWER'S COMMENTS/SUGGESTIONS	AUTHOR'S ACTION/RESPONSE		
		*NOTE FOR AUTHOR: Please state your response to the reviewer's comments/suggestion below		
31.	Title The title does not yet describe the method use d. There should be a word isolation of lactic a cid bacteria.	The title has been corrected to : Identification of lactid acid bacteria isolated from ethnic fermented bamboo shoot " <i>Lemea</i> " in Bengkulu, Indonesia		
32.	Abstract It has not given the importance of isolating lactic acid b acteria from the product. Methods need to be summarize d	The abstract has been remade, focusing on the process of isolation and identification of lactic acid bacteria from lemea products.		
33.	Keywords <i>It should be added to the product name.</i>	Product name has been added Keywords: Lemea, bamboo shoot, 16S rRNA, LAB		
34.	Introduction It has not yet described the importance of isolating lactic c acid bacteria from the product.	Introduction The reason for isolation has been added to the introduction, namely looking for LAB strains from traditional foods		
35.	Research design/Methodology Method clearly described and reproducible.	The methods of sample preparation, isolation and identification have been described in the isolation and sample preparation stages		
36.	Data Analysis It is necessary to add a discussion about the differences in lactic acid bacteria obtained from differences in bamb oo types that are strengthened by reference.	The discussion on the differences in lactic acid bacteria obtained from different types of bamboo has been strengthened by adding the appropriate literature as a reference.		
37.	Conclusion It should be associated with the source of lactic acid bac teria isolation	The conclusion has been corrected according to the reviewer's suggestion Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus plantarum and Lactobacillus fermentum were		

		isolates which were identified molecularly by 16S rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad) while Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).
38.	References _{Ok}	-
39.	English Proficiency Need to be checked again	English Proficiency has been checked according to the suggestion
40.	Additional comments/suggestions by the reviewer about the article	-

Overall Evaluation

|--|

Accept		Major Revision	
Minor Revision	v	Reject	

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Commented [H26]: The article has been rewritten. The results have been made clearer and supported with the latest references. It has been correlated with the title, objectives, methods, results, and discussion.

1			
2	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea"		
3	in Bengkulu, Indonesia		Commented [H27]: The title has been corrected. The title describes the method used. The word "lactic acid bacteria
4			isolation" has been added.
5	Abstract		Commented [H28]: The abstract has been remade, focusing on the process of isolation and identification of lactic acid bacteria from
6	Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The		lemea products.
7	Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product		
8	known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid		
9	bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of <i>Lemea</i> .	_	Commented [H29]: This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of <i>Lemea</i> .
10	The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 hours. Different types of		
11	bamboo shoots are expected to provide different types of LAB. Betung shoots (Dendrocalamus asper		
12	Schult) and yellow bamboo (Bambusa vulgaris Schrad) have been used. The isolation stage begins with 10		Commented [H30]: The methodology in the abstract has been clarified: betung shoots (Dendrocalamus asper Schult) and yellow ba
13	grams of homogenized <i>Lemea</i> sample, then 1 ml is taken and 9 ml of sterile 1% NaCl is added. Then serial		mboo (Bambusa vulgaris Schrad) have been used.
14	dilutions were carried out starting from 10 $^{-1}$ to 10 $^{-7}$ and spread on MRSA media for each dilution series.		
15	Incubate at 37 °C for 48 hours to obtain isolates. The isolates were identified molecularly using the 16S	_	Commented [H31]: The abstract has been remade, focusing on the process of isolation and identification of lactic acid bacteria from
16	rRNA method. The results of the study found 4 isolates from 2 types of Lemea. After identification, it was		lemea products.
17	known that the four isolates were bacteria of the genus Lactobacillus. Lactobacillus fermentum was only		Commented [H32]: Identification
18	found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while		
19	Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung		
20	(Dendrocalamus asper Schult).	_	Commented [H33]: Furthermore, it was remotely analyzed o n MRSA media and four LAB isolates were obtained. Molecular ident
21	Keywords: Lemea, bamboo shoot, 16S rRNA, LAB		ification using the 16S rRNA method.
21			Commented [H34]: Product name has been added
22	9. Introduction		
23	The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North		

Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the

Rejang people live. *Lemea* is an ethnic food from the Rejang tribe. Ethnic foods are meals that have their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are fermented into *Lemea* by the Rejang people (Dewi *et al.*, 2014). Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by the Rejang to produce *Lemea*. Betok, kepala timah, and mujahir fish are the most common fish used. The odor and flavour are unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 2011). Indigenous fermented foods have been extensively researched.

32 There are various fermented foods in the world, especially in Asia. Fermented foods made from 33 bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially Lactobacillus 34 (Tomar, 2016). Meakri, from Meghalaya Indian fermented bamboo shoots as a source of Lactobacillus, has characteristics suitable for probiotics (Das et al., 2020). Lactobacillus is a group of 35 LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 36 pathogenic microbes (Yang et al., 2021). LAB isolated from fermented bamboo shoots are potential 37 probiotic candidates that are beneficial for health (Mohamad et al., 2020). LAB strains are selected 38 39 for their decreased content of cholesterol, antioxidant activity, and anti bacterial activity (Jitpakdee 40 et al., 2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende et al., 2022). 41

Bekasam is an Indonesian fermented food that is similar to Lemea. Bekasam is a traditional fermented food popular in Sumatera and Kalimantan (Desniar et al., 2013). The sour taste in Bekasam is almost the same as in Lemea. The difference between these two products is the carbohydrate source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play a role in the fermentation process. The source of carbohydrates used for rice in Lemea is bamboo shoots. Fermentation time for Lemea is 2-3 days, while Bekasam takes 10 days. **Commented [H35]:** The reason for isolation has been added to the introduction, namely looking for LAB strains from traditional foods

48	Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates
49	were found, and 3 of them had potential as probiotics (Wasis et al., 2019). A total of 180 LAB isolates
50	have been isolated from Indonesian fermented foods (Sukmarini et al., 2014). Research on the effect
51	of different types of bamboo shoots on strains of LAB produced during Lemea processing has not
52	been carried out.
53	Therefore, this research is very important to be carried out at this time because there is still a scarcity
54	of information. Studies on the molecular identification of <i>Lemea</i> isolates are still needed. This study
55	aims to identify and isolate LAB strains in fermented betung bamboo shoots (Dendrocalamus Asper
56	Schult) and yellow bamboo shoots (Bambusa Vulgaris Schrad).

57 10. Materials and methods

58 2.1 Sample Preparation

59 Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are 60 thinly sliced and soaked for 30 hours. Then they were washed, filtered, and weighed as much as 61 400 grams, and they added 40 g of betok fish, 350 ml of water, and 3.3 g of lemongrass, and 62 fermented for 48 hours (Figure 1).

63 2.2 LAB isolation

64	Isolation LAB was carried out using a device that was sterilized before hand and carried out
65	aseptically where 10 g of the Lemea sample was homogenized and then serially diluted with 1
66	percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was
67	incubated at 37°C for 48 hours. The isolates obtained need to be purified and identified.
68	Purification was carried out by the plate scratch method, which was repeated so that pure isolates
69	were found. The purification process is perfect and will produce separate colonies between
70	strokes. The selected colonies are then identified to determine the strain of the colonies obtained.

Commented [H36]: The methods of sample preparation, isolation and identification have been described in the isolation and sample preparation stages

Commented [H37]: The number of ingredients has been added

Commented [H38]: The fermentation time has been synchronized which is 48 hours in the sample preparation and Fig 1

Commented [H39]: The method has been described in more detail with Fig1 and 2

Commented [H40]: Isolation and identification steps have been added

71	(Figu	ıre 2).		
72	a. Iden	tification of LAB		
73	Mole	ecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA		
74	amp	lification, sequencing and analysis of nucleotide sequences in GenBank (Veljovic <i>et al.,</i> 2007)	Co	mmented [H41]: identification steps have been added
75	i.	DNA Isolation		
76		DNA isolation was Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit		
77		(Geneaid, GBB100). Stages of isolation based on the procedure kit.		
78	ii.	DNA amplification		
79		DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red		
80		Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA		
81		Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis		
82		as much as 1uL of the PCR product was assessed with 0.8% TBE agarose.		
83	iii.	DNA sequenching and phylogenetic analysis		
84		Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping		
85		arrangement performed by comparing obtained (inquiry) with those already in the Gene		
86		Bank, with the information base hunted on the NCBI webpage		
87		(http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size		
88		of the PCR amplification fragment was determined by comparing the position of the DNA		
89		marker size (Marker) with the sample fragment size.		
90	11. Results	and discussion/Results		
91	3.1 Isol	ation of lactic acid bacteria from Lemea		
92	Iso	lation found 4 bacterial isolates from 2 types of <i>Lemea</i> samples. <i>Lemea</i> made from betung		mmented [H42]: The resulting isolates were 4 isolates and oported by the image of the isolate in Fig 3
93		mboo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found		
94	we	re coded B1, B2, S1 and S2 (Figure 3). The bacterial isolates found were lactic acid bacteria		mmented [H43]: Results have been presented. Each Table d Figure has been explained in more detail

95	because they were able to grow on MRSA specific media with cocci characteristics, a milky white
96	color with a convex surface and smooth edges. The number of isolates obtained was less than
97	that of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang
98	et al., 2008). The morphological characteristics of the isolates found in this study were almost
99	the same as the previous findings isolated from Lemea produced by a cottage industry in
100	Kepahyang Regency, Bengkulu (Kurnia <i>et al.</i> , 2020).
101	3.2 Identification of Lemea isolates
102	The results of genomic DNA amplification of the 4 isolates can be seen in Figures 4a and 4b.
103	Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size.
104	Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434
105	bp for isolate B1 (Fig. 5a), 1424 bp for B2 (Fig. 5b). The nucleotide sequence S1 isolate was 882
106	bp (Figure 5c) and 849 bp for the S2 isolate (Figure 5d). The results of the analysis using the
107	BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to
108	Lactobacillus plantarum while isolates S2 had Lactobacillus fermentum.
109	The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% similar to the
110	partial sequences of the comparison isolates (Table 1). The bacteria were found to be a strain
111	of Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree,
112	isolate B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure
113	6a), solate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA
114	(Figure 6b). S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal
115	RNA (Figure 6c), solate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567
116	16S ribosomal RNA. The type of isolate that was identified from Bekasam was lactobacillus
117	plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus Lactobacillus.
118	Bacillus subtilis, Lactobacillus brevis, and Lactobacillus plantarum were found in dominating

Commented [H44]: Each result explanation has been added a discussion

Commented [H45]: Results have been presented. Each Table and Figure has been explained in more detail

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119	strains of Soidon fermented bamboo shoot food without salt from Indian Manipur (Jeyaram et	
120	al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz)	
121	have been previously studied and isolated as 2 species, namely Lactobacillus plantarum and	
122	Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from Indonesian	
123	fermented foods are dominated by Lactobacillus plantarum (Rahayu, 2003). This research is	
124	expected to provide information on which LAB strains have been isolated from different types	
125	of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the	
126	bacterial community by increasing the abundance of Firmicutes, Actinobacteria and	
127	Proteobacteria (Li et al., 2021).	Comment and explaine
128	Lactobacillus fermentum was only found in lemea made from yellow bamboo shoots (Bambusa	
129	vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa	
130	vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in	
131	foodstuffs that trigger the growth of Lactobacillus (Macfarlane & Cummings, 1999).	
132	Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in	
133	the gut. Bamboo shoots are a good source of fiber (Felisberto et al., 2017). At 100 g of fresh	
134	weight, bamboo shoots of B. vulgaris contain 6.51 g of carbohydrates, 4.24 g of fiber, 4.90 g of	
135	D. Asper, and 3.54 g of fiber (Chongtham et al., 2011). Different bamboo species contain	
136	different macronutrients (Adebola et al., 2014). Differences in the content of bamboo shoots	
137	affect the types of bacteria found in Lemea products.	Comment
138 12.	Conclusion	
139	Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus	
140	plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 165	

141 rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots

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Commented [H55]: Each result explanation has been added a discussion

- (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots 142
- (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult). 143
- Conflict of interest Disclose potential conflicts of interest appropriately. 144
- The authors declare no conflict of interest. 145
- Acknowledgments 146
- This research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020 147
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Commented [H56]: The conclusion has been corrected according to the reviewer's suggestion Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus.

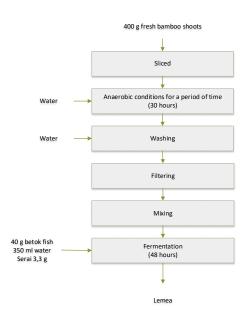
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Figure 1. Fermented Bamboo shoot making process





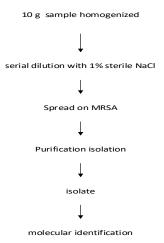
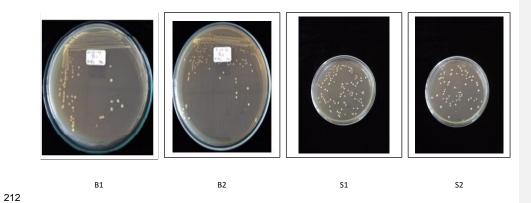
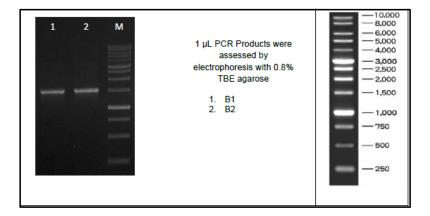


Figure 3. Isolate B1, B2,S1 dan S2



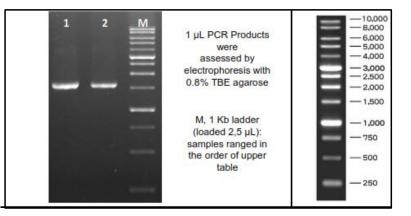
213 Figure 4a. Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose

214 concentration using the Kappa Universal ladder



216 Figure 4b. Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose

217 concentration using the Kappa Universal ladder



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Figure 5a. Sequence assembly result – PCR product Isolate Code B1

1	AGGCGGCTGG	TTCCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGITCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GTCACCGGCA	GICTCACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CTTCGGTTGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTICI	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT

Figure 5b. Sequence assembly result – PCR product Isolate Code B2

Seque	ence Assembly	y 1424 bp				
1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGI
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GICACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGO
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIATCCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAG
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CICCACCGCI	TGTGCGGGGCG
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATO
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGI
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGI
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGITCITCCA	TATATCTACG	CATTTCACCO
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTITC	CGATGCACTI
841	CTTCGGTTGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACO
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTI
961	AGCCGIGGCI	TICIGGITAA	ATACCGTCAA	TACCIGAACA	GITACICICA	GATATGTTCT
1021	TCTTTAACAA	CAGAGITITA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GITGCICCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTO
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCTITCA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TEGECACTER
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

223 224 Г

Figure 5c. Sequence assembly result – PCR product Isolate Code S1

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGGGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTO
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTO
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACO
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGO
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

Figure 5d. Sequence assembly result – PCR product Isolate Code S2

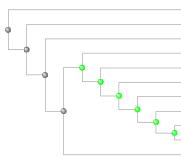
1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
51	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCO
21	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
81	CGGTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
41	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
101	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGO
61	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
21	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTO
81	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
41	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
01	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
61	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCO
21	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTO
/81	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATO
841	CACTTCTCC					

Types c	f Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung	g B1	Lactobacillus plantarum	M N37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

231 Table 1. Comparison of Homology Levels the 16S rRNA gene of BAL isolat with several sequences

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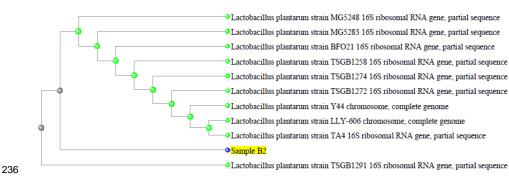
233 Figure 6a. Phylogenetic tree Isolate Code B1



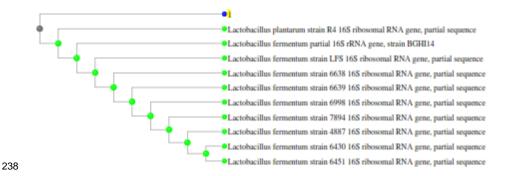
Lactobacillus plantarum strain TSGB1291 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS51204 16S ribosomal RNA gene, partial sequence
 Lactobacillus pentosus strain DSM 20314 chromosome, complete genome
 Lactobacillus plantarum strain HBUAS51160 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS52379 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS52379 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS52089 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS52076 16S ribosomal RNA gene, partial sequence
 Lactobacillus plantarum strain HBUAS52179 16S ribosomal RNA gene, partial sequence
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 Lactobacillus plantarum strain HBUAS52179 16S ribosomal RNA gene, partial sequence



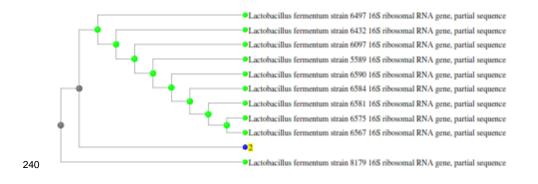
235 Figure 6b. Phylogenetic tree Isolate Code B2



237 Figure 6c. Phylogenetic tree Isolate Code S1



239 Figure 6d. Phylogenetic tree Isolate Code S2





Manuscript ID: FR-IFC-029-June 5, 2022

10 pesan

Yenni Okfrianti <yenni79okfrianti@gmail.com> Kepada: foodresearch.my@outlook.com 5 Juni 2022 pukul 20.11

Dear Son Radu, PhD Chief Editor

The manuscript has been revised according to the attached comments Thank you. I hope this manuscript can be accepted.

Best regards, Yenni Okfrianti

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Food Research <foodresearch.my@outlook.com> Kepada: Yenni Okfrianti <yenni79okfrianti@gmail.com> 6 Juni 2022 pukul 16.38

Dear Yenni Okfrianti

There were formatting errors in regards to the citations, coding appeared next to citations. Please also ensure to make changes Only on the manuscript provided previously because the Editor had already made minor editing on it and also the comments were given on that document. Your cooperation is much appreciated.

Best regards, Son Radu, PhD Chief Editor

From: Yenni Okfrianti <yenni79okfrianti@gmail.com> Sent: Sunday, 5 June, 2022 9:11 PM To: foodresearch.my@outlook.com <foodresearch.my@outlook.com> Subject: Manuscript ID: FR-IFC-029-June 5, 2022

[Kutipan teks disembunyikan]

Yenni Okfrianti <yenni79okfrianti@gmail.com> Kepada: Food Research <foodresearch.my@outlook.com> 8 Juni 2022 pukul 02.16

Dear Son of Radu, PhD,

Chief editor

Formatting errors with respect to citations have been revised and the revised section is highlighted in yellow and listed in the reference section.

Changes made to the manuscript are those that were previously rendered. Thank you

Best Regard Yenni Okfrianti [Kutipan teks disembunyikan] FR-IFC-029_Revisi 07062022.docx 3844K

Food Research <foodresearch.my@outlook.com> Kepada: Yenni Okfrianti <yenni79okfrianti@gmail.com> 10 Juni 2022 pukul 01.31

Dear Yenni Okfrianti

Figure 2 was not cited in the manuscript. If it is not needed please remove and revise figure labels.

Best regards, Son Radu, PhD Chief Editor

From: Yenni Okfrianti <<u>yenni79okfrianti@gmail.com</u>> Sent: Wednesday, 8 June, 2022 3:16 AM To: Food Research <<u>foodresearch.my@outlook.com</u>> Subject: Re: Manuscript ID: FR-IFC-029-June 5, 2022

[Kutipan teks disembunyikan]

Yenni Okfrianti <yenni79okfrianti@gmail.com> Kepada: Food Research <foodresearch.my@outlook.com>

Dear Son Radu, PhD Chief Editor

Figure 2 which could not be cited in the manuscript has been removed. All image labels are customized.

Best regards, Yenni Okfrianti [Kutipan teks disembunyikan]

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Food Research <foodresearch.my@outlook.com> Kepada: Yenni Okfrianti <yenni79okfrianti@gmail.com>

Dear Yenni Okfrianti,

Please provide us with a clean copy of the manuscript.

Best regards, Son Radu, PhD Chief Editor

From: Yenni Okfrianti <<u>yenni79okfrianti@gmail.com</u>> Sent: Monday, 13 June, 2022 6:33 PM

[Kutipan teks disembunyikan]

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13 Juni 2022 pukul 17.33

14 Juni 2022 pukul 01.59

1	RDO-43	Commented [H1]: Code of abstract
2		
3	Ethnic Food Fermentation From Bengkulu as a Source of Lactic Acid Bacteria	
4	^{1,2} *Okfrianti, Y, ² Herison C, ² Fahrurrozi, ² Budiyanto	
5 6	¹ Department of Nutrition, Poltekkes Kemenkes Bengkulu Indragiri No 3 Padang Harapan, Bengkulu ² Department of Agriculture, Universitas Bengkulu WR. Supratman, Kandang Limun, Bengkulu	Commented [H2]: Authors and affiliations address clear
7 8	*Corresponding author: yeni@poltekkesbengkulu.ac.id	
9	Author No.1: ORCID 0000-0001-7998-3633	
10	Author No.2: ORCID 0000-0002-8326-5105	
11	Author No.3: ORCID 0000-0002-3254-3013	
12	Author No.4: ORCID 0000-0002-2508-2351	Commented [H3]: Authors ORCID have been clarified
13	Abstract	
14	In order to avoid extinction, strains of lactic acid bacteria must be studied. This study aims to find Lactic	
15	Acid Bacteria (LAB) strains in fermented Betung bamboo shoots (Dendrocalamus Asper Schult) and Yellow	
16	bamboo shoots (Bambusa Vulgaris Schrad). Due to the ethnic diet of the rejang tribe, this fermented	
17	foodstuff is only found in Bengkulu province. Which was made by combining bamboo shoots with river	
18	fish and allowing it to stand for a few days until a distinct aroma emerges. The LAB identification of began	
19	with homogenizing 10 g of the samples, which then get serially diluted with 1 percent sterile NaCl and	
20	spreaded on MRSA media. The isolates were identified molecularly using 16S rRNA gene amplification,	
21	which included the procedures of isolating genomic DNA, amplification using DNA, sequencing, and	
22	nucleotide sequence analysis on GenBank. Lactobacillus plantarum strain B1 and Lactobacillus plantarum	
23	strain B2 were identified on fermented Betung bamboo shoots, while Lactobacillus plantarum S1 and	
24	Lactobacillus fermentum S2 on Yellow Bamboo shoots. Lactobacillus plantarum and fermentum isolated	Commented [H4]: The species name has been corrected
25	from fermented bamboo shoots were gram positive bacteria and a group of lactic acid bacteria.	

26 Keywords: Lactic Acid Bacteria, Bamboo shoot, Ethnic Food Fermentation, PCR, 16S rRNA

27	1.	Introduction	Commented [L5]: Heading bold
27	1.		Commented [L5]: Heading bold
28		There is a great need to develop the traditional food which comprises the ethnic diet of a particular	
29		region. Moreover, it is also important to prevent the extinction of traditional foods such as fermented	
30		foods that contain lactic acid bacteria (Dewi et al., 2014). One of the tribes that has fermented food	Commented [L6]: "et al" in italic style for citations
31		and needs to be maintained is the Rejang tribe, which is the largest tribe in Bengkulu (Dewi, 2015).	
32		There are a variety of fermented foods in the world especially in Asia. Most of Asian fermented foods	
33		are non-dairy products featuring various other raw materials such as cereals, soybeans, fruit,	
34		vegetables and fish and other products (Rhee et al., 2011). Indonesia is rich in fermented foods	
35		including Dadih, Bekasam and Lemea. Curd, fermented buffalo milk from Minangkabau, West	
36		Sumatra, various types of LAB isolated from curd (Wirawati et al., 2019). Bekasam, a fermented	
37		Indonesian freshwater fish product that tastes sour and contains lactic acid bacteria (LAB) is popular	
38		in Central Java, South Sumatra and South Kalimantan (Desniar et al., 2013). Lemea is a processed fish	
39		and bamboo shoots originating from Bengkulu, precisely the Rejang tribe, which is fermented for 3-	
40		7 days and generally uses freshwater fish with lactic acid bacteria as the main actor (Xu et al., 2021).	
41		River fish that are often used to make lemea are freshwater fish. One of the freshwater fish that can	
42		be used is betok fish, lemea containing lactic acid bacteria (Xu et al., 2021). Lactic acid bacteria consist	
43		of microbial strains that convert carbohydrates into lactic acid (Dinoto et al., 2020), LAB isolated	
44		results were identified based on phenotypic and genotypic characteristics (Lawalata et al., 2011).	
45		Genotypic LAB identification was carried out by PCR technique in the form of amplifying and	
46		sequencing the universal region of the 16S rRNA gene (Dinoto <i>et al.,</i> 2020). Lactic Acid Bacteria (LAB)	 Commented [H7]: "et al" in italic style for citations
47		strains in fermented Tabah bamboo shoots (<i>Gigantochloa nigrociliata</i> buse-kurz) has been previously	
48		studied The purpose of this study was to investigate Lactic Acid Bacteria (LAB) strains in fermented	
49		Betung bamboo shoots (Dendrocalamus asper Schult) and Yellow bamboo shoots (Bambusa vulgaris	
50		Schrad).	Commented [L8]: The research objectives have been cla

search objectives have been clarified

51 2. Materials and methods

52	2.1 Sample Preparation	Commented [L9]: Subheadings are written in normal style
53	The process of processing fermented bamboo shoots begins with slicing thin samples and soaking	
54	them for 30 hours, then washing and filtering them. The next step is fermentation for 48 hours at	
55	room temperature by mixing sliced bamboo shoots, betok fish, lemongrass and salt and water	
56	(Figure 1)	
57	2.2 LAB isolation	
58	Isolation of LAB was carried out using a device that was sterilized beforehand and carried out	
59	aseptically where 10 g of the lemea sample was homogenized and then serially diluted with 1%	
60	NaCl. And each dilution series was spread on MRSA media and then petridish was incubated at	
61	37° C for 48 hours. The isolates obtained need to be purified and identified	
62	2.3 Identification of LAB Strain Fermented Bamboo Shoot (Lemea)	
63	Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA	
64	amplification, sequencing and analysis of nucleotide sequences in GenBank (Widodo <i>et al.</i> , 2017).	Commented [H10]: All references are cited in the body
65	DNA isolation was Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit (Geneaid,	
66	GBB100). DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red	
67	Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA Recovery Kit	
68	(Zymo Research, D4001). The PCR results were visualized by electrophoresis as much as 1uL of the	
69	PCR product was assessed with 0.8% TBE agarose.	
70	3. Results and discussion/Results	
71	Bacterial sequence homology based on 16S rRNA gene sequencing analysis. The types of lactic acid	
72	bacteria species on bamboo shoots of betung and yellow bamboo have 99% similarity. B1, B2, and	
73	S1 are closely related to Lactobacillus plantarum, this type of bacteria is known as lactic acid bacteria	
74	which has the potential as biopreservative because it can inhibit the growth of pathogens and	

75	destructive with greater inhibition than other lactic acid bacteria. (Azizah et al., 2019). L. plantarum	
76	is amylolytic which converts starch to lactic acid (Noor et al., 2018). S2 is closely related to	
77	Lactobacillus fermentum, this type of bacteria is known as lactic acid bacteria which belongs to	
78	heterofermentative species and can be found in the human intestinal tract where these bacteria can	
79	live at the pH of the digestive tract (Manin, 2010). B1 and B2 are isolate codes derived from	_
80	fermented bamboo shoots. S1 and S2 codes for isolate fermented yellow bamboo shoots. (Table 1).	
81	Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration	
82	using the Kappa Universal ladder (Figure 2a and 2b). Visualization of 16 S rRNA gene amplification of	
83	isolates B 1, B2, S1 and S 2 at 0.8% TBE agarose concentration using the Kappa Universal ladder	
84	(Figures 3a and 3b). hylogenetic analysis using MEGA 7.0 with Neighbor-joining (unrooted tree) by	
85	NCBI tree method showed that B1, B2 and S1 were closely related to Lactobacillus plantarum (Figures	
86	4a, 4b and 4c). S2 is closely related to Lactobacillus fermentum (Figure 4d). Betung bamboo shoots	
87	contain lactic acid bacteria in the form of Lactobacillus plantarum while yellow bamboo shoots	
88	contain more lactic acid bacteria in the form of Lactobacillus fermentum.	
89 4 .	Conclusion	

90 Lactobacillus plantarum and fermentum isolated from fermented bamboo shoots were found to be

- 91 gram positive bacteria and belong to a group of lactic acid bacteria.
- 92

93 Conflict of interest - Disclose potential conflicts of interest appropriately.

- 94 The authors declare no conflict of interest.
- 95 Acknowledgments
- 96 This research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020

Commented [H11]: Citations according to the guidelines provided

Commented	H12]: All References are cited in the body	/
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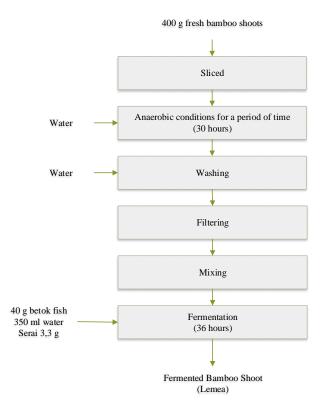
151 Table 1. Comparison of Homology Levels the 16S rRNA gene of BAL isolat with several sequences

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Commented [H14]: Species name has been correctly writen

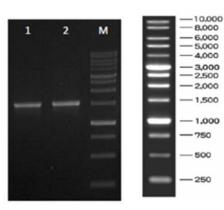
Types of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung	B1	<mark>Lactobacillus plantarum</mark>	M N37236.01	99
	B2	<mark>Lactobacillus plantarum</mark>	MN972325.1	99
Yellow Bamboo	S1	<mark>Lactobacillus plantarum</mark>	KM350169.1	99
	S2	<mark>Lactobacillus</mark> fermentum	MT538927.1	99

152 Figure 1. Fermented Bamboo shoot making process



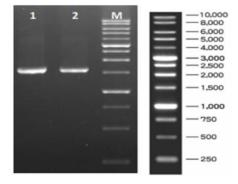
154 Figure 2a. Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose

155 concentration using the Kappa Universal ladder



156

- 157 Figure 2b. Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose
- 158 concentration using the Kappa Universal ladder



159 160

161

-

162

164 Figure 3a. Sequence assembly result – PCR product Isolate Code B1

Sequence Assembly 1434 bp

ooqui	chee Hooennoi	1 1 10 1 00					
1	AGGCGGCTGG	TTCCTAAAAG	GTTACCCCAC	CGACTITIGGG	TGTTACAAAC	TCTCATGGTG	
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATT	
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT	
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT	
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT	
301	GTCACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC	
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC	
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC	
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC	
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG	
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT	
661	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT	
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG	
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT	
841	CITCGGTIGA	GCCGAAGGCT	TICACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG	
901	CCCAATAAAT	CCGGACAACG	CITECCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT	
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT	
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT	
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT	
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	IGCCAIGGIG	
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG	
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC	
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA	
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT	

165 166

168

167 Figure 3b. Sequence assembly result – PCR product Isolate Code B2

1	AGGCGGCTGG	TICCTARARG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG	
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT	
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT	
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT	
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTI	CCTCCGGTTT	
301	GTCACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC	
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC	
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TITGCATAGT	ATGTCAAGAC	
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CICCACCGCI	IGIGCGGGGCC	
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG	
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CICCAACACI	TAGCATTCAT	CGTTTACGGT	
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TITCGAGCCT	CAGCGTCAGT	
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG	
781	CTACACATGG	AGTICCACIG	TCCTCTTCIG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT	
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG	
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGIT	
961	AGCCGIGGCT	TICIGGITAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT	
1021	TCTTTAACAA	CAGAGITITA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GITGCICCAT	
1081	CAGACITICG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT	
1141	GICICAGICC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	IGCCATGGIG	
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG	
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGITGTTATG	CGGTATTAGC	ATCTGTTTCC	
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA	
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT		

Commented [H15]: Show gene sequencing result

169 Figure 3c. Sequence assembly result – PCR product Isolate Code S1

Sequence Result Reverse Primer 882bp

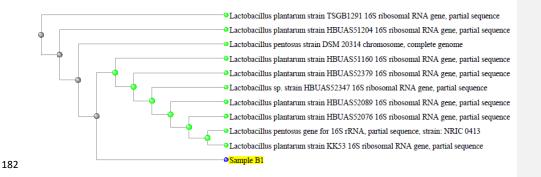
1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGGGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTC
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACC
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGC
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

171 Figure 3d. Sequence assembly result – PCR product Isolate Code S2

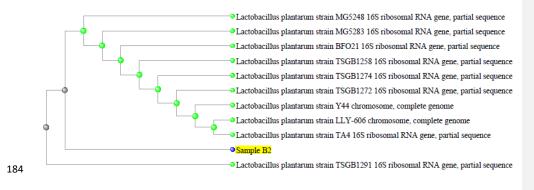
Sequence Result Reverse Primer 849bp

1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGC
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTC
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

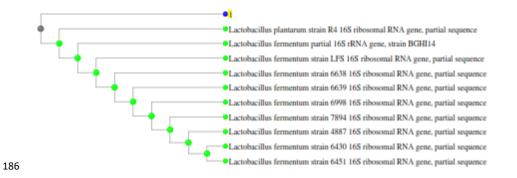
181 Figure 4a. Phylogenetic tree Isolate Code B1



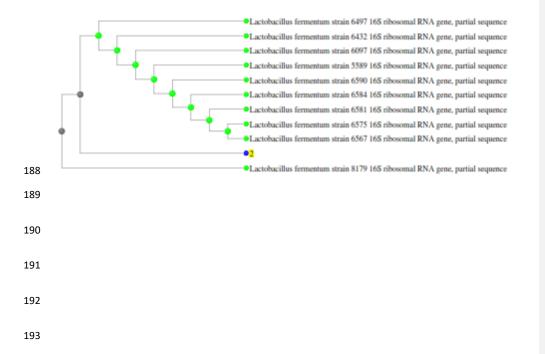
183 Figure 4b. Phylogenetic tree Isolate Code B2



185 Figure 4c. Phylogenetic tree Isolate Code S1



187 Figure 4d. Phylogenetic tree Isolate Code S2



1	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea"	
2	in Bengkulu, Indonesia	
3	^{1,2} *Okfrianti, Y., ² Herison, C., ² Fahrurrozi and ² Budiyanto	
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12		
13	Abstract	
14	Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The	
15	Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product	
16	known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid	
17	bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of Lemea.	
18	The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 h. Different types of	
19	bamboo shoots are expected to provide different types of LAB. Betung shoots (Dendrocalamus asper	
20	Schult) and yellow bamboo (Bambusa vulgaris Schrad) have been used. The isolation stage begins with 10	
21	g_of homogenized Lemea sample, then 1 mL is taken and 9 mL of sterile 1% NaCl is added. Then serial	
22	dilutions were carried out starting from 10 $^{-1}$ to 10 $^{-7}$ and spread on MRSA media for each dilution series.	
23	Incubate at 37 °C for 48 h to obtain isolates. The isolates were identified molecularly using the 16S rRNA	
24	method. The results of the study found 4 isolates from 2 types of Lemea. After identification, it was known	
25	that the four isolates were bacteria of the genus Lactobacillus. Lactobacillus fermentum was only found	_
26	in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus	

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27 plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus

28 asper Schult).

29 Keywords: Lemea, Bamboo shoot, 16S rRNA, LAB

30 1. Introduction

The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North 31 Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the 32 33 Rejang people live. Lemea is an ethnic food from the Rejang tribe. Ethnic foods are meals that have their origins in an ethnic group's history and culture (Kwon, 2015). (Kwon, 2015). Bamboo shoots and 34 35 river fish are fermented into Lemea by the Rejang people- (Dewi et al., 2014). (Dewi et al., 2014). 36 Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by 37 the Rejang to produce Lemea . Betok, kepala timah, and mujahir fish are the most common fish used. 38 The odour and flavour are unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 2011). (Fox, 2011). Indigenous fermented foods have been extensively 39 40 researched.

41 There are various fermented foods in the world, especially in Asia. Fermented foods made from 42 bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially Lactobacillus (Kiran 43 et al., 2016). (Tomar, 2016). Meakri, from Meghalaya Indian fermented bamboo shoots as a source 44 of Lactobacillus, has characteristics suitable for probiotics (Das et al., 2020)_(Das et al., 2020). 45 Lactobacillus is a group of LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of pathogenic microbes (Yang et al., 2021). (Yang et al., 2021). LAB isolated from 46 47 fermented bamboo shoots are potential probiotic candidates that are beneficial for health 48 (Mohamad et al., 2020) (Mohamad et al., 2020). LAB strains are selected for their decreased content 49 of cholesterol, antioxidant activity, and anti-bacterial activity (Jitpakdee et al., 2022)(Jitpakdee et al.,

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50	2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende et

52 Bekasam is an Indonesian fermented food that is similar to Lemea. Bekasam is a traditional 53 fermented food popular in Sumatera and Kalimantan (Desniar et al., 2013). (Desniar et al., 2013). 54 The sour taste in Bekasam is almost the same as in Lemea. The difference between these two 55 products is the carbohydrate source and fermentation time. Carbohydrate sources are a source of 56 nutrition for bacteria that play a role in the fermentation process. The source of carbohydrates used 57 for rice in Lemea is bamboo shoots. Fermentation time for Lemea is 2-3 days, while Bekasam takes 58 10 days.

- 59 Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates 60 were found, and 3 of them had potential as probiotics (Wasis et al., 2019). (Wasis et al., 2019). A total 61 of 180 LAB isolates have been isolated from Indonesian fermented foods_(Sukmarini et al., 2014). 62 (Sukmarini et al., 2014). Research on the effect of different types of bamboo shoots on strains of LAB 63 produced during *Lemea* processing has not been carried out. 64 Therefore, this research is very important to be carried out at this time because there is still a scarcity
- 65 of information. Studies on the molecular identification of Lemea isolates are still needed. This study 66 aims to identify and isolate LAB strains in fermented betung bamboo shoots (Dendrocalamus Asper 67 Schult) and yellow bamboo shoots (Bambusa Vulgaris Schrad).

68 2. Materials and methods

- 69 2.1 Sample preparation
- 70 Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are 71 thinly sliced and soaked for 30 h. Then they were washed, filtered, and weighed as much as 400 g

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al., 2022) (Mende et al., 2022) 51

72	and th	ey added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for
73	48 h (F	igure 1).
74		
75		
76	2.2 LAB is	plation
77	Isolatio	on LAB was carried out using a device that was sterilized before hand and carried out
78	asepti	cally where 10 g of the Lemea sample was homogenized and then serially diluted with 1
79	percer	nt sterile NaCl. And each dilution series was spread on MRSA media and then petridish was
80	incuba	ted at 37°C for 48 h. The isolates obtained need to be purified and identified. Purification
81	was ca	rried out by the plate scratch method, which was repeated so that pure isolates were found.
82	The p	urification process is perfect and will produce separate colonies between strokes. The
83	selecte	ed colonies are then identified to determine the strain of the colonies obtained.
84	2.2 Identij	fication of LAB
85	Molec	ular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA
86	amplif	ication, sequencing and analysis of nucleotide sequences in GenBank (Veljovic <i>et al.</i> , 2007). Formatted: Font: Italic
87	(Veljo v	vic et al., 2007)
88	2.2.1	DNA Isolation
89		DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA
90		Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.
91	2.2.2	DNA amplification
92		DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red
93		Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA

94			Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis	
95			as much as 1 uL of the PCR product was assessed with 0.8% TBE agarose.	
96		2.2.3	DNA sequenching and phylogenetic analysis	
97			Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping	
98			arrangement performed by comparing obtained (inquiry) with those already in the Gene	
99			Bank, with the information base hunted on the NCBI webpage	
100			(http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size	
101			of the PCR amplification fragment was determined by comparing the position of the DNA	
102			marker size (Marker) with the sample fragment size.	
103	3.	Posults a	nd discussion	
105	э.	Results a		
104		3.1 Isolat	ion of lactic acid bacteria from Lemea	
105		Isola	tion found 4 bacterial isolates from 2 types of Lemea samples. Lemea made from betung	
106		bam	boo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found	
107		were	e coded B1, B2, S1 and S2 (Figure 3). The bacterial isolates found were lactic acid bacteria	
108		beca	use they were able to grow on MRSA specific media with cocci characteristics, a milky white	
109		color	r with a convex surface and smooth edges. The number of isolates obtained was less than	
110		that	of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang	
111		et al.	., 2008) <u>.(Tamang <i>et al.</i>, 2008).</u> The morphological characteristics of the isolates found in this	Formatted: Font: Italic
112		stud	y were almost the same as the previous findings isolated from <i>Lemea</i> produced by a cottage	
113		indu	stry in Kepahyang Regency, Bengkulu <u>(</u> Kurnia <i>et al.</i> , 2020) <u>. (Kurniaet al., 2020).</u>	Commented [Editor8]
114		3 2 Identi	fication of Lemea isolates	Formatted: Font: Italic
		·	results of genomic DNA amplification of the 4 isolates can be seen in Figures 4a and 4b.	
115		me	results of genomic Diva amplification of the 4 isolates can be seen in rightes 4d and 4D.	
116		Isola	tes B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size.	
117		Visu	alization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434	

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118 bp for isolate B1 (Figure 5a), 1424 bp for B2 (Figure 5b). The nucleotide sequence S1 isolate was 882 bp (Figure 5c) and 849 bp for the S2 isolate (Figure 5d). The results of the analysis using the 119 120 BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to 121 Lactobacillus plantarum while isolates S2 had Lactobacillus fermentum. The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% similar to the 122 partial sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of 123 124 Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree, isolate 125 B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure 6a), Isolate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA. (Figure 126 6b). S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal RNA 127 128 (Figure 6c), isolate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567 16S 129 ribosomal RNA. The type of isolate that was identified from Bekasam was lactobacillus 130 Lactobacillus_plantarum (Sukmarini et al., 2014).(Sukmarini et al., 2014).-All isolates have been Formatted: Font: Italic 131 homologous to the genus Lactobacillus. Bacillus subtilis, Lactobacillus brevis, and Lactobacillus 132 plantarum were found in dominating strains of Soidon fermented bamboo shoot food without 133 salt from Indian Manipur (Jeyaram et al., 2010). (Jeyaram et al., 2010). LAB strains in fermented Formatted: Font: Italic 134 Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) have been previously studied and 135 isolated as 2 species, namely Lactobacillus plantarum and Lactobacillus rossiae (Okfrianti et al., Formatted: Font: Italic 136 2019).(Okfrianti et al., 2019). Lactic acid bacteria isolated from Indonesian fermented foods are 137 dominated by Lactobacillus plantarum_(Rahayu, 2003)._-(Rahayu, 2003)..-This research is 138 expected to provide information on which LAB strains have been isolated from different types 139 of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the 140 bacterial community by increasing the abundance of Firmicutes, Actinobacteria and 141 Proteobacteria (Li et al., 2021). (Li et al., 2021). Formatted: Font: Italic Formatted: Font: Italic

142	Lactobacillus fermentum was only found in Lemeamade from yellow bamboo shoots (Bambusa
143	vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa
144	vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in
145	foodstuffs that trigger the growth of <i>Lactobacillus</i> ((Macfarlane_ _∧ _–Cummings, 1999) <u>.</u>
146	Macfarlane and Cummings, 1999). Oligosaccharides and fiber are prebiotics that promote the
147	growth of specific bacteria found in the gut. Bamboo shoots are a good source of fibre <u>(</u> Felisberto
148	et al., 2017) (Felisberto et al., 2017). At 100 g of fresh weight, bamboo shoots of B. vulgaris
149	contain 6.51 g of carbohydrates, 4.24 g of fibre, 4.90 g of <i>D. asper</i> , and 3.54 g of fibre_(Chongtham
150	et al., 2011). (Chongtham et al., 2011). Different bamboo species contain different Formatted: Font: Italic
151	macronutrients (Adebola <u>et al., 2014). (Adebola et al., 2014).</u> Differences in the content of Formatted: Font: Italic
152	bamboo shoots affect the types of bacteria found in <i>Lemea</i> products.

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153 4. Conclusion

- 154 Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus
- 155 plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 16S
- 156 rRNA. *Lactobacillus fermentum* was only found in the fermentation process of yellow bamboo shoots
- 157 (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots
- 158 (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).
- 159 Conflict of interest Disclose potential conflicts of interest appropriately.
- 160 The authors declare no conflict of interest.
- 161 Acknowledgments
- 162 This research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020

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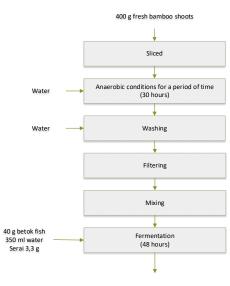
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Figure 1. Fermented bamboo shoot making process



Lemea

Figure 2. Isolation process

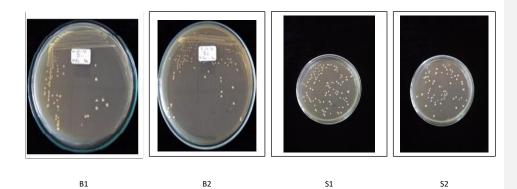
10 g sample homogenized ↓ serial dilution with 1% sterile NaCl ↓ Spread on MRSA ↓ Purification isolation ↓ isolate ↓ molecular identification

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298

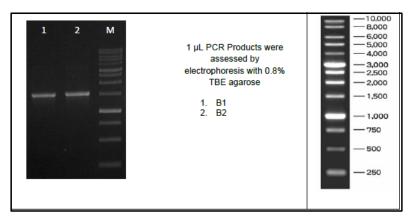
Figure 3. Isolate B1, B2,S1 dan S2



301

300

302 Figure 4a. Genomic DNA amplification of isolates B1 and B2

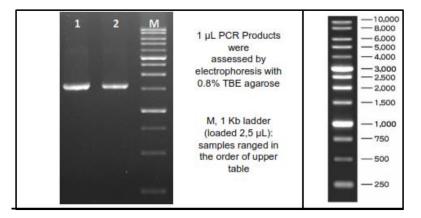


303

304 Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration

305 using the Kappa Universal ladder

306 Figure 4b. Genomic DNA amplification of isolates S1 and S2





308 Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose concentration

309 using the Kappa Universal ladder

Figure 5a. The nucleotide sequence B1 isolate

1	AGGCGGCTGG	TTCCTAAAAG	GTTACCCCAC	CGACTTTGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGI
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTI
301	GTCACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAI	GICCCCGAAG	GGAACGICIA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGI
661	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGI
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCO
781	CTACACATGG	AGTTCCACTG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTI
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCIGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTI
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTICI
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGI
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTICI	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCARATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTOGTTOG	ACTT

Figure 5b. The nucleotide sequence B2 isolate

Seque	ence Assembl	y 1424 bp				
1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GICACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGTATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTICACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CTTCGGTTGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGITTITA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GITGCICCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGTGTTATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGTGTT	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

315 Figure 5c. The nucleotide sequence S1 isolate

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGCGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTO
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACO
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGO
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

Figure 5d. The nucleotide sequence S2

1	ACCTTACCCC	CCTCCCTCCT	AAAAGGTTAC	CCCACCACT	TTCCCTCTTA	CAALCTCTCI
61			ACAAGGCCCG		CACCGCGGCA	
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGA
181	CGGTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGO
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
121	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGT
181	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
501	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
561	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTOTCAGO
21	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTO
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATO
841	CACTTCTCC					

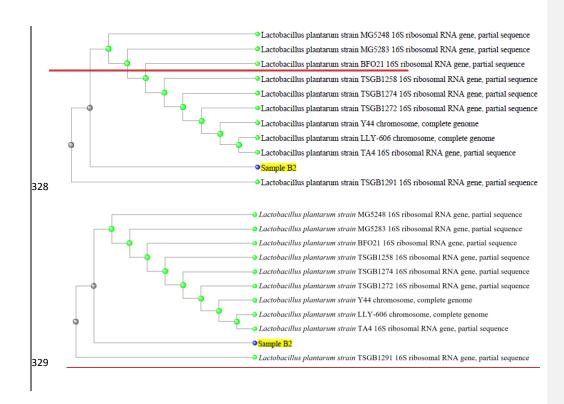
321 Table 1. Comparison of homology levels the 16S rRNA gene of BAL isolat with several sequences

Types of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung B1 Lactobacillus plantarum M N37236.01		99		
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

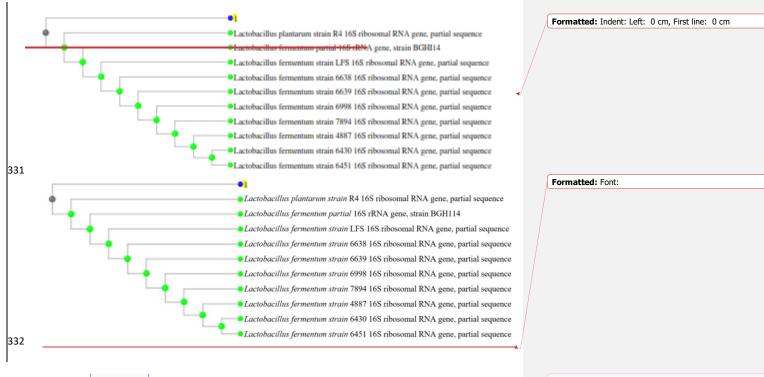
322

323 Figure 6a. Phylogenetic tree Isolate Code B1





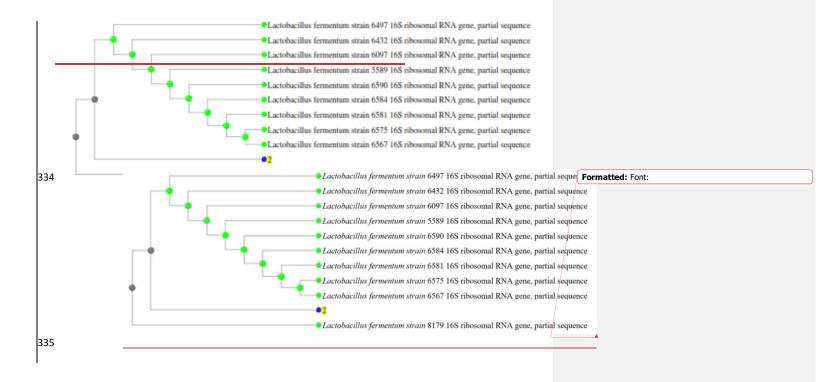




333 Figure 6d. Phylogenetic tree Isolate Code S2

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Commented [Editor12]: All species names must be in ITALICS,



1	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea"		
2	in Bengkulu, Indonesia		
3	^{1,2} *Okfrianti, Y., ² Herison, C., ² Fahrurrozi and ² Budiyanto		
4 5 6	¹ Department of Nutrition, Poltekkes Kemenkes Bengkulu Indragiri No 3 Padang Harapan, Bengkulu ² Department of Agriculture, Universitas Bengkulu WR. Supratman, Kandang Limun, Bengkulu		
7	*Corresponding author: yeni@poltekkesbengkulu.ac.id		
8	Author No.1: ORCID 0000-0001-7998-3633		
9	Author No.2: ORCID 0000-0002-8326-5105		
10	Author No.3: ORCID 0000-0002-3254-3013		
11	Author No.4: ORCID 0000-0002-2508-2351		
12			
13	Abstract		
14	Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The		
15	Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product		
16	known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid		
17	bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of Lemea.		
18	The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 h. Different types of		
19	bamboo shoots are expected to provide different types of LAB. Betung shoots (Dendrocalamus asper		
20	Schult) and yellow bamboo (Bambusa vulgaris Schrad) have been used. The isolation stage begins with 10		
21	gof homogenized Lemea sample, then 1 mL is taken and 9 mL of sterile 1% NaCl is added. Then serial		
22	dilutions were carried out starting from 10 ⁻¹ to 10 ⁻⁷ and spread on MRSA media for each dilution series.		
23	Incubate at 37 °C for 48 h to obtain isolates. The isolates were identified molecularly using the 16S rRNA		
24	method. The results of the study found 4 isolates from 2 types of Lemea. After identification, it was known		
25	that the four isolates were bacteria of the genus Lactobacillus. Lactobacillus fermentum was only found		
26	in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus		

27 plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus

28 asper Schult).

29 Keywords: Lemea, Bamboo shoot, 16S rRNA, LAB

30 1. Introduction

31 The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North 32 Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the 33 Rejang people live. Lemea is an ethnic food from the Rejang tribe. Ethnic foods are meals that have 34 their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are 35 fermented into Lemea by the Rejang people (Dewi et al., 2014). Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by the Rejang to produce Lemea. 36 37 Betok, kepala timah, and mujahir fish are the most common fish used. The odour and flavour are 38 unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 39 2011). Indigenous fermented foods have been extensively researched.

40 There are various fermented foods in the world, especially in Asia. Fermented foods made from bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially Lactobacillus 41 42 (Tomar, 2016) (Kiran et al., 2016). Meakri, from Meghalaya Indian fermented bamboo shoots as a source of Lactobacillus, has characteristics suitable for probiotics (Das et al., 2020). Lactobacillus is a 43 44 group of LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 2pathogenic microbes (Yang et al., 2021). LAB isolated from fermented bamboo shoots are 45 potential probiotic candidates that are beneficial for health (Mohamad et al., 2020). LAB strains are 46 47 selected for their decreased content of cholesterol, antioxidant activity, and anti-bacterial activity (Jitpakdee et al., 2022). Isolation of lactic acid bacteria from indegenous fermented foods is very 48 49 important (Mende *et al.,* 2022).

Commented [Editor1]: Not listed in the reference section?

Commented [LI2R1]: An error occurred in the author's name should be: (Kiran *et al.*, 2016)

Kiran, T., Rajani, C., Kumar, T.S., and Achun, P. (2016). Fermented Bamboo Shoots: A Riche Niche for Beneficial Microbes. Journal of Bacteriology &&& Mycology: Open Access, 2(4), 87–93. https://doi.org/10.15406/jbmoa.2016.02.00030

Already listed in the reference section.

Commented [Editor3]: Not listed in the reference section?

Commented [LI4R3]: Already listed in the reference section.

Das, S., Mishra, B.K., and Hati, S. (2020). Techno-functional characterization of indigenous Lactobacillus isolates from the traditional fermented foods of Meghalaya, India. Current Research in Food

Commented [Editor5]: Not listed in reference section?

Commented [LIGR5]: Already listed in the reference section. Yang, L., Huang, W., Yang, C., Ma, T., Hou, Q., Sun, Z., and Zhang, H. (2021). Using PacBio sequencing to investigate the effects of treatment with lactic acid bacteria or antibiotics on cow endometritis. Electronic Journal of Biotechnology, 51, 67–78.

Commented [Editor7]: Not listed in the reference section?

Commented [LIBR7]: Already listed in the reference section. Mohamad, N., Manan, H., Sallehhuddin, M., Musa, N., and Ikhwanuddin, M. (2020). Screening of Lactic Acid Bacteria isolated from giant freshwater prawn (Macrobrachium rosenbergii) as potential probiotics. Aquaculture Reports, 18(October 2019), 100523. https://doi.org/10.1016/j.agrep.2020.100523

Commented [Editor9]: Not listed in the reference section?

Commented [L110R9]: Already listed in the reference section. Mende, S., Rohm, H., and Aros, D. (2022). Lactic Acid Bacteria: Exopolysaccharides. In Encyclopedia of Dairy Sciences (Vol. 4). Elsevier. https://doi.org/10.1016/b978-0-08-100596-5.22982-x

50	Bekasam is an Indonesian fermented food that is similar to Lemea. Bekasam is a traditional
51	fermented food popular in Sumatera and Kalimantan (Desniar et al., 2013). The sour taste in Bekasam
52	is almost the same as in Lemea. The difference between these two products is the carbohydrate
53	source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play
54	a role in the fermentation process. The source of carbohydrates used for rice in Lemea is bamboo
55	shoots. Fermentation time for Lemea is 2-3 days, while Bekasam takes 10 days.

Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates
were found, and 3 of them had potential as probiotics (Wasis *et al.*, 2019). A total of 180 LAB isolates
have been isolated from Indonesian fermented foods (Sukmarini *et al.*, 2014). Research on the effect
of different types of bamboo shoots on strains of LAB produced during *Lemea* processing has not
been carried out.

Therefore, this research is very important to be carried out at this time because there is still a scarcity
of information. Studies on the molecular identification of *Lemea* isolates are still needed. This study
aims to identify and isolate LAB strains in fermented betung bamboo shoots (*Dendrocalamus Asper*Schult) and yellow bamboo shoots (*Bambusa Vulgaris* Schrad).

65 2. Materials and methods

66 2.1 Sample preparation

Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are
thinly sliced and soaked for 30 h. Then they were washed, filtered, and weighed as much as 400 g
and they added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for
48 h (Figure 1).

71

72

Commented [Editor11]: Not listed in the reference section?

Commented [LI12R11]: Already listed in the reference section. Wasis, N. O., Semadi Antara, N., and Wayan Gunam, I. B. (2019). Studi Viabilitas Isolat Bakteri Asam Laktat yang Diisolasi dari Asinan Rebung Bambu Tabah Terhadap pH Rendah dan Garam Empedu. Jurnal Rekayasa Dan Manajemen Agroindustri, 7(1), 1–10. https://doi.org/10.24843/jrma.2019.v07.i01.p01

73 2.2 LAB isolation

74	Isolation LAB was carried out using a device that was sterilized before hand and carried out			
75	aseptically where 10 g of the Lemea sample was homogenized and then serially diluted with 1			
76	percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was			
77	incubated at 37°C for 48 h. The isolates obtained need to be purified and identified. Purification			
78	was carried out by the plate scratch method, which was repeated so that pure isolates were found.			
79	The purification process is perfect and will produce separate colonies between strokes. The			
80	selected colonies are then identified to determine the strain of the colonies obtained.			
81	81 2.2 Identification of LAB			
82	Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA			
83	amplification, sequencing and analysis of nucleotide sequences in GenBank (Veljovic et al., 2007)			
84	2.2.1 DNA Isolation			
85	DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA			
86	Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.			
87	2.2.2 DNA amplification			
88	DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red			
89	Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA			
90	Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis			
91	as much as 1 uL of the PCR product was assessed with 0.8% TBE agarose.			
92	2.2.3 DNA sequenching and phylogenetic analysis			
93	Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping			
94	arrangement performed by comparing obtained (inquiry) with those already in the Gene			
95	Bank, with the information base hunted on the NCBI webpage			

96	(http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size
97	of the PCR amplification fragment was determined by comparing the position of the DNA
98	marker size (Marker) with the sample fragment size

99 3. Results and discussion

100 3.1 Isolation of lactic acid bacteria from Lemea

101 Isolation found 4 bacterial isolates from 2 types of Lemea samples. Lemea made from betung bamboo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found 102 were coded B1, B2, S1 and S2 (Figure 3). The bacterial isolates found were lactic acid bacteria 103 because they were able to grow on MRSA specific media with cocci characteristics, a milky white 104 105 color with a convex surface and smooth edges. The number of isolates obtained was less than 106 that of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang et al., 2008). The morphological characteristics of the isolates found in this study were almost 107 108 the same as the previous findings isolated from Lemea produced by a cottage industry in Kepahyang Regency, Bengkulu (Kurnia et al., 2020). 109

110 3.2 Identification of Lemea isolates

119

The results of genomic DNA amplification of the 4 isolates can be seen in Figures 4a and 4b. 111 112 Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size. 113 Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434 bp for isolate B1 (Figure 5a), 1424 bp for B2 (Figure 5b). The nucleotide sequence S1 isolate was 114 882 bp (Figure 5c) and 849 bp for the S2 isolate (Figure 5d). The results of the analysis using the 115 BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to 116 Lactobacillus plantarum while isolates S2 had Lactobacillus fermentum. 117 The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% similar to the 118

partial sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of

Commented [LI14R13]: Already listed in the reference section. Kurnia, M., Amir, H., and Handayani, D. (2020). Isolasi Dan Identifikasi Bakteri Asam Laktat Dari Makanan Tradisional Suku Rejang Di Provinsi Bengkulu: "Lemea." Alotrop, 4(1), 25–32. https://doi.org/10.33369/atp.v41.13705

Commented [Editor13]: Not listed in the reference section?

120	Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree, isolate
121	B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure 6a),
122	Isolate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA. (Figure
123	6b). S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal RNA
124	(Figure 6c), isolate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567 16S
125	ribosomal RNA. The type of isolate that was identified from Bekasam was lactobacillus
126	plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus Lactobacillus.
127	Bacillus subtilis, Lactobacillus brevis, and Lactobacillus plantarum were found in dominating
128	strains of Soidon fermented bamboo shoot food without salt from Indian Manipur (Jeyaram et
129	al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz)
130	have been previously studied and isolated as 2 species, namely Lactobacillus plantarum and
131	Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from Indonesian
132	fermented foods are dominated by Lactobacillus plantarum (Rahayu, 2003). This research is
133	expected to provide information on which LAB strains have been isolated from different types
134	of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the
135	bacterial community by increasing the abundance of Firmicutes, Actinobacteria and
136	Proteobacteria (Li et al., 2021).
137	Lactobacillus fermentum was only found in Lemeamade from yellow bamboo shoots (Bambusa
138	vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa
139	vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in
140	foodstuffs that trigger the growth of Lactobacillus (Macfarlane and Cummings, 1999).

Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in
the gut. Bamboo shoots are a good source of fibre (Felisberto *et al.*, 2017). At 100 g of fresh
weight, bamboo shoots of B. vulgaris contain 6.51 g of carbohydrates, 4.24 g of fibre, 4.90 g of

144	D. asper, and 3.54 g of fibre (Chongtham et al., 2011). Different bamboo species contain
145	different macronutrients (Adebola et al., 2014). Differences in the content of bamboo shoots
146	affect the types of bacteria found in <i>Lemea</i> products.

147 4. Conclusion

- Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 16S rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots
- 152 (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).

153 Conflict of interest - Disclose potential conflicts of interest appropriately.

- 154 The authors declare no conflict of interest.
- 155 Acknowledgments
- 156 This research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020
- 157

159 References

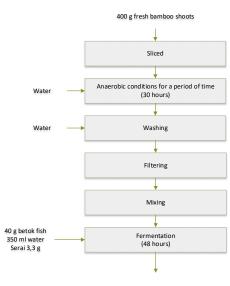
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Figure 1. Fermented bamboo shoot making process



Lemea

Figure 2. Isolation process

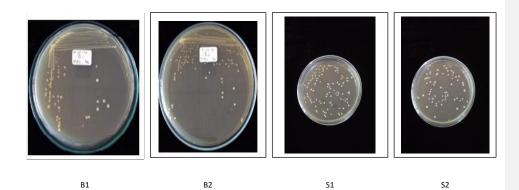
10 g sample homogenized ↓
serial dilution with 1% sterile NaCl
↓
Spread on MRSA
↓
Purification isolation
↓
isolate
↓
molecular identification

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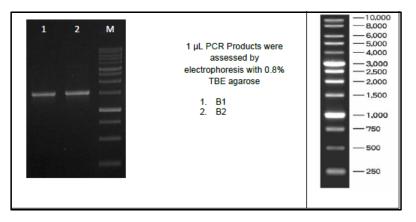
Figure 3. Isolate B1, B2,S1 dan S2



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249 Figure 4a. Genomic DNA amplification of isolates B1 and B2

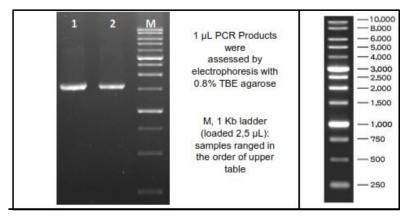


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251 Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration

252 using the Kappa Universal ladder

253 Figure 4b. Genomic DNA amplification of isolates S1 and S2





255 Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose concentration

256 using the Kappa Universal ladder

Figure 5a. The nucleotide sequence B1 isolate

	ence Assembl					
1	AGGCGGCTGG				TGTTACAAAC	
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATI
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGITCG	CAACICGIIG	TACCATCCAT	TGTAGCACGI
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTI
301	GICACCGGCA	GICTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGI
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGI
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCO
781	CTACACATGG	AGTTCCACTG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTI
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTARAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTTGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTI
961	AGCCGTGGCT	TICIGGTIAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGI
1141	GICICAGICC	CAATGTGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTO
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCABATGTA	AATCATGATG	CAAGCACCAA	TCANTACCAG	AGTTOGTTOG	ACTT

Figure 5b. The nucleotide sequence B2 isolate

Sequ	ence Assembly					
1			GITACCCCAC			
	TGACGGGCGG	TGTGTACAAG				
	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GTCACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCITCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCITIGAGIT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTITC	CGATGCACTT
841	CTTCGGTTGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGITITA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GITGCICCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCTTTCA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

262 Figure 5c. The nucleotide sequence S1 isolate

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGCGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTGA
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTO
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACO
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGO
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

Figure 5d. The nucleotide sequence S2

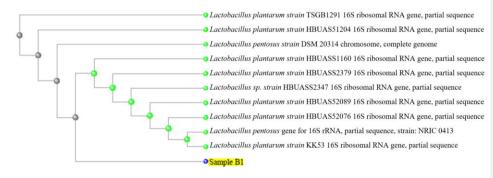
1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61		GGCGGTGTGT			CACCGCGGCA	
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGO
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCO
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTO
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

268 Table 1. Comparison of homology levels the 16S rRNA gene of BAL isolat with several sequences

Types o	f Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung	g B1	Lactobacillus plantarum	M N37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

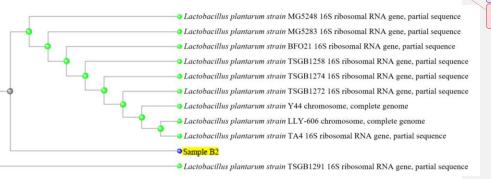
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270 Figure 6a. Phylogenetic tree Isolate Code B1



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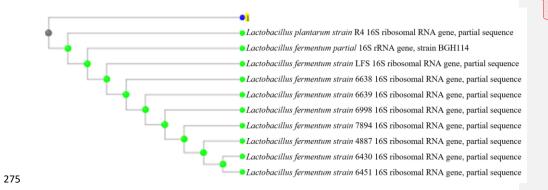
272 Figure 6b. Phylogenetic tree Isolate Code B2



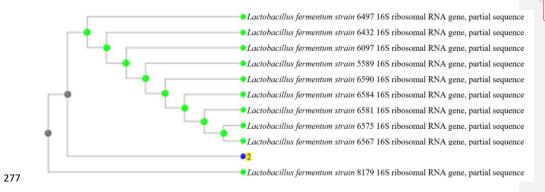
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274 Figure 6c. Phylogenetic tree Isolate Code S1



276 Figure 6d. Phylogenetic tree Isolate Code S2



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Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea" in Bengkulu, Indonesia

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Abstract

Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product known as *Lemea*, which is only found in Bengkulu province. *Lemea* is a source of indigenous lactic acid bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of *Lemea*. The bamboo shoots with betok fish (*Anabas testudineus*) were fermented for 48 h. Different types of bamboo shoots are expected to provide different types of LAB. Betung shoots (*Dendrocalamus asper Schult*) and yellow bamboo (*Bambusa vulgaris* Schrad) have been used. The isolation stage begins with 10 gof homogenized *Lemea* sample, then 1 mL is taken and 9 mL of sterile 1% NaCl is added. Then serial dilutions were carried out starting from 10⁻¹ to 10⁻⁷ and spread on MRSA media for each dilution series. Incubate at 37 °C for 48 h to obtain isolates. The isolates were identified molecularly using the 16S rRNA

method. The results of the study found 4 isolates from 2 types of *Lemea*. After identification, it was known that the four isolates were bacteria of the genus Lactobacillus. *Lactobacillus fermentum* was only found in the fermentation process of yellow bamboo shoots (*Bambusa vulgaris* Schrad), while *Lactobacillus plantarum* was found in yellow bamboo shoots (*Bambusa vulgaris* Schrad) and betung (*Dendrocalamus asper* Schult).

Keywords: Lemea, Bamboo shoot, 16S rRNA, Lactic acid bacteria

1. Introduction

The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the Rejang people live. *Lemea* is an ethnic food from the Rejang tribe. Ethnic foods are meals that have their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are fermented into *Lemea* by the Rejang people (Dewi *et al.*, 2014). Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by the Rejang to produce *Lemea* . Betok, kepala timah, and mujahir fish are the most common fish used. The odour and flavour are unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 2011). Indigenous fermented foods have been extensively researched.

There are various fermented foods in the world, especially in Asia. Fermented foods made from bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially *Lactobacillus* (Kiran *et al.*, 2016). *Meakri*, from Meghalaya Indian fermented bamboo shoots as a source of *Lactobacillus*, has characteristics suitable for probiotics (Das *et al.*, 2020). *Lactobacillus* is a group of LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 2 pathogenic microbes (Yang *et al.*, 2021). LAB isolated from fermented bamboo shoots are potential probiotic candidates that are beneficial for health (Mohamad *et al.*, 2020). LAB strains are selected for their

decreased content of cholesterol, antioxidant activity, and anti-bacterial activity (Jitpakdee *et al.*, 2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende *et al.*, 2022).

Bekasam is an Indonesian fermented food that is similar to *Lemea*. *Bekasam* is a traditional fermented food popular in Sumatera and Kalimantan (Desniar *et al.*, 2013). The sour taste in *Bekasam* is almost the same as in *Lemea*. The difference between these two products is the carbohydrate source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play a role in the fermentation process. The source of carbohydrates used for rice in *Lemea* is bamboo shoots. Fermentation time for *Lemea* is 2-3 days, while *Bekasam* takes 10 days.

Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates were found, and 3 of them had potential as probiotics (Wasis *et al.*, 2019). A total of 180 LAB isolates have been isolated from Indonesian fermented foods (Sukmarini *et al.*, 2014). Research on the effect of different types of bamboo shoots on strains of LAB produced during *Lemea* processing has not been carried out.

Therefore, this research is very important to be carried out at this time because there is still a scarcity of information. Studies on the molecular identification of *Lemea* isolates are still needed. This study aims to identify and isolate LAB strains in fermented betung bamboo shoots (*Dendrocalamus Asper* Schult) and yellow bamboo shoots (*Bambusa Vulgaris* Schrad).

2. Materials and methods

2.1 Sample preparation

Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are thinly sliced and soaked for 30 h. Then they were washed, filtered, and weighed as much as 400 g

and they added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for 48 h (Figure 1).

2.2 LAB isolation

Isolation LAB was carried out using a device that was sterilized before hand and carried out aseptically where 10 g of the *Lemea* sample was homogenized and then serially diluted with 1 percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was incubated at 37°C for 48 hrs. The isolates obtained need to be purified and identified. Purification was carried out by the plate scratch method, which was repeated so that pure isolates were found. The purification process is perfect and will produce separate colonies between strokes. The selected colonies are then identified to determine the strain of the colonies obtained.

2.2 Identification of LAB

Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA amplification, sequencing and analysis of nucleotide sequences in GenBank (Veljovic *et al.*, 2007)

2.2.1 DNA Isolation

DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.

2.2.2 DNA amplification

DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis as much as 1 uL of the PCR product was assessed with 0.8% TBE agarose.

2.2.3 DNA sequenching and phylogenetic analysis

Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping arrangement performed by comparing obtained (inquiry) with those already in the Gene Bank, with the information base hunted on the NCBI webpage (http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size of the PCR amplification fragment was determined by comparing the position of the DNA marker size (Marker) with the sample fragment size.

3. Results and discussion

3.1 Isolation of lactic acid bacteria from Lemea

Isolation found 4 bacterial isolates from 2 types of *Lemea* samples. *Lemea* made from betung bamboo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found were coded B1, B2, S1 and S2 (Figure 2). The bacterial isolates found were lactic acid bacteria because they were able to grow on MRSA specific media with cocci characteristics, a milky white color with a convex surface and smooth edges. The number of isolates obtained was less than that of *mesu*, *soidon*, *soibum*, and *soijon* but the same as unfermented bamboo shoots (Tamang *et al.*, 2008). The morphological characteristics of the isolates found in this study were almost the same as the previous findings isolated from *Lemea* produced by a cottage industry in Kepahyang Regency, Bengkulu (Kurnia *et al.*, 2020).

3.2 Identification of Lemea isolates

The results of genomic DNA amplification of the 4 isolates can be seen in Figures 3a and 3b. Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size. Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434 bp for isolate B1 (Figure 4a), 1424 bp for B2 (Figure 4b). The nucleotide sequence S1 isolate was 882 bp (Figure 4c) and 849 bp for the S2 isolate (Figure 4d). The results of the analysis using the BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to *Lactobacillus plantarum* while isolates S2 had *Lactobacillus fermentum*.

The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% like the partial sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree, isolate B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure 5a), Isolate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA (Figure 5b). S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal RNA (Figure 5c), isolate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567 16S ribosomal RNA (Figure 5d). The type of isolate that was identified from Bekasam was lactobacillus plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus Lactobacillus. Bacillus subtilis, Lactobacillus brevis, and Lactobacillus plantarum were found in dominating strains of Soidon fermented bamboo shoot food without salt from Indian Manipur (Jeyaram et al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) have been previously studied and isolated as 2 species, namely Lactobacillus plantarum and Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from Indonesian fermented foods are dominated by Lactobacillus plantarum (Rahayu, 2003). This research is expected to provide information on which LAB strains have been isolated from different types of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the bacterial community by increasing the abundance of Firmicutes, Actinobacteria and Proteobacteria (Li et al., 2021).

Lactobacillus fermentum was only found in Lemeamade from yellow bamboo shoots (Bambusa vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in

foodstuffs that trigger the growth of *Lactobacillus* (Macfarlane and Cummings, 1999). Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in the gut. Bamboo shoots are a good source of fibre (Felisberto *et al.*, 2017). At 100 g of fresh weight, bamboo shoots of B. vulgaris contain 6.51 g of carbohydrates, 4.24 g of fibre, 4.90 g of *D. asper*, and 3.54 g of fibre (Chongtham *et al.*, 2011). Different bamboo species contain different macronutrients (Adebola *et al.*, 2014). Differences in the content of bamboo shoots affect the types of bacteria found in *Lemea* products.

4. Conclusion

Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 16S rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).

Conflict of interest - Disclose potential conflicts of interest appropriately.

The authors declare no conflict of interest.

Acknowledgments

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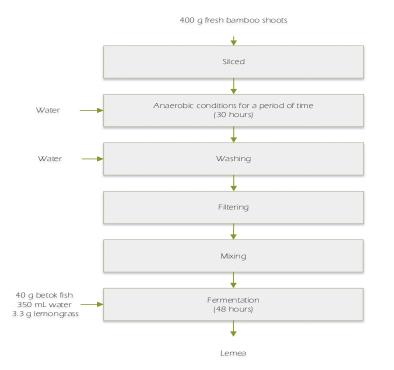


Figure 1. Fermented bamboo shoot making process

Figure 2. Isolate B1, B2,S1 and S2

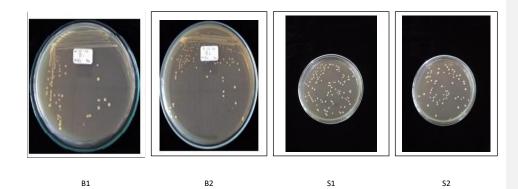
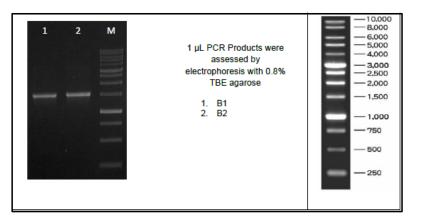
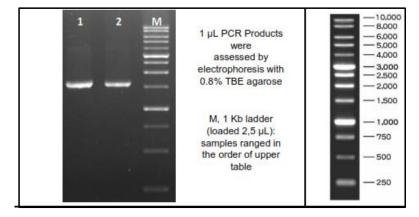


Figure 3a. Genomic DNA amplification of isolates B1 and B2 $\,$



Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration using the Kappa Universal ladder

Figure 3b. Genomic DNA amplification of isolates S1 and S2



Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose concentration using the Kappa Universal ladder

Figure 4a. The nucleotide sequence B1 isolate

1		у 1434 bp	GTTACCCCAC	CGACTITGGG	TGTTACABAC	TOTONTOGTO
61	TGACGGGCGG			GTATTCACCG		
121	ACTAGCGATT		GTAGGCGAGT		AATCCGAACT	GAGAATGGCT
181		AGCTTGCTCT		CAACTCGTTG		TGTAGCACGT
241		GGTCATAAGG		TTTGACGTCA		CCTCCGGTTT
301	GTCACCGGCA	GTCTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGTATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGICAGI
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGGCCGT
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCIA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT

Figure 4b. The nucleotide sequence B2 isolate

1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACICGITG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GICACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGITCTICCA	TATATCTACG	CATTICACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGITITA	CGAGCCGAAA	CCCTTCTTCA	CICACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

Figure 4c. The nucleotide sequence S1 isolate

order	nce Result Reve					
1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGCGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTG
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTO
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTO
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACO
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATO
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGO
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

Figure 4d. The nucleotide sequence S2

1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTO
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

Table 1. Comparison of homology levels the 16S rRNA gene of Lactid Acid Bacteria isolates BAL isolat with several sequences

Types of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
			GenBank Accession	
			Number	
Bamboo Betung	B1	Lactobacillus plantarum	M N37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

Figure 5a. Phylogenetic tree Isolate Code B1

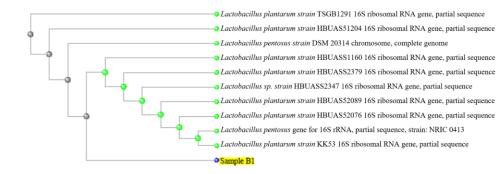
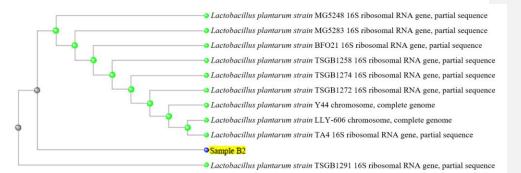


Figure 5b. Phylogenetic tree Isolate Code B2



Commented [A1]: ?

Commented [A2R1]: Comparison of homology levels of the 16S rRNA gene of Lactid Acid Bacteria isolates with several sequences

Commented [A3]: ?

Commented [A4R3]: GenBank Accession Number

Figure 5c. Phylogenetic tree Isolate Code S1

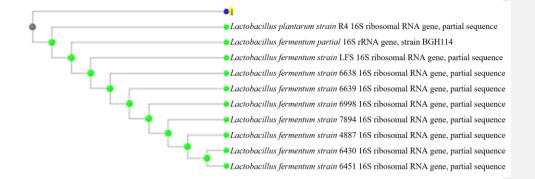
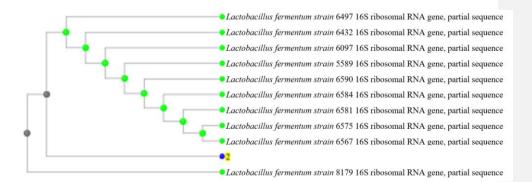


Figure 5d. Phylogenetic tree Isolate Code S2



1	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea"
2	in Bengkulu, Indonesia
3	^{1,2} *Okfrianti, Y., ² Herison, C., ² Fahrurrozi and ² Budiyanto
4 5 6	¹ Department of Nutrition, Poltekkes Kemenkes Bengkulu Indragiri No 3 Padang Harapan, Bengkulu ² Department of Agriculture, Universitas Bengkulu WR. Supratman, Kandang Limun, Bengkulu
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11	Author No.4: ORCID 0000-0002-2508-2351
12	
13	Abstract
14	Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The
15	Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product
16	known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid
17	bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of Lemea.
18	The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 h. Different types of
19	bamboo shoots are expected to provide different types of LAB. Betung shoots (Dendrocalamus asper
20	Schult) and yellow bamboo (Bambusa vulgaris Schrad) have been used. The isolation stage begins with 10
21	gof homogenized Lemea sample, then 1 mL is taken and 9 mL of sterile 1% NaCl is added. Then serial
22	dilutions were carried out starting from 10 ⁻¹ to 10 ⁻⁷ and spread on MRSA media for each dilution series.
23	Incubate at 37 °C for 48 h to obtain isolates. The isolates were identified molecularly using the 16S rRNA
24	method. The results of the study found 4 isolates from 2 types of <i>Lemea</i> . After identification, it was known
25	that the four isolates were bacteria of the genus Lactobacillus. Lactobacillus fermentum was only found
26	in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus

plantarum was found in yellow bamboo shoots (*Bambusa vulgaris* Schrad) and betung (*Dendrocalamus asper* Schult).

29 Keywords: Lemea, Bamboo shoot, 16S rRNA, LAB

30 **1.** Introduction

31 The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North 32 Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the 33 Rejang people live. Lemea is an ethnic food from the Rejang tribe. Ethnic foods are meals that have 34 their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are 35 fermented into Lemea by the Rejang people (Dewi et al., 2014). Betung, Tabah, Mayan, and Seik 36 bamboo are some of the most common bamboo varieties used by the Rejang to produce Lemea. 37 Betok, kepala timah, and mujahir fish are the most common fish used. The odour and flavour are 38 unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 39 2011). Indigenous fermented foods have been extensively researched.

40 There are various fermented foods in the world, especially in Asia. Fermented foods made from 41 bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially Lactobacillus (Kiran 42 et al., 2016). Meakri, from Meghalaya Indian fermented bamboo shoots as a source of Lactobacillus, has characteristics suitable for probiotics (Das et al., 2020). Lactobacillus is a group of LAB that are 43 44 gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 2 pathogenic 45 microbes (Yang et al., 2021). LAB isolated from fermented bamboo shoots are potential probiotic 46 candidates that are beneficial for health (Mohamad et al., 2020). LAB strains are selected for their 47 decreased content of cholesterol, antioxidant activity, and anti-bacterial activity (Jitpakdee et al., 2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende et 48 al., 2022). 49

50 Bekasam is an Indonesian fermented food that is similar to Lemea. Bekasam is a traditional 51 fermented food popular in Sumatera and Kalimantan (Desniar *et al.*, 2013). The sour taste in Bekasam 52 is almost the same as in Lemea. The difference between these two products is the carbohydrate 53 source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play 54 a role in the fermentation process. The source of carbohydrates used for rice in Lemea is bamboo 55 shoots. Fermentation time for Lemea is 2-3 days, while Bekasam takes 10 days.

Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates
were found, and 3 of them had potential as probiotics (Wasis *et al.*, 2019). A total of 180 LAB isolates
have been isolated from Indonesian fermented foods (Sukmarini *et al.*, 2014). Research on the effect
of different types of bamboo shoots on strains of LAB produced during *Lemea* processing has not
been carried out.

Therefore, this research is very important to be carried out at this time because there is still a scarcity of information. Studies on the molecular identification of *Lemea* isolates are still needed. This study aims to identify and isolate LAB strains in fermented betung bamboo shoots (*Dendrocalamus Asper* Schult) and yellow bamboo shoots (*Bambusa Vulgaris* Schrad).

- 65 2. Materials and methods
- 66 2.1 Sample preparation

67 Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are 68 thinly sliced and soaked for 30 h. Then they were washed, filtered, and weighed as much as 400 g 69 and they added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for 70 48 h (Figure 1).

71

2.2 LAB isolation

74	Isolation LAB was carried out using a device that was sterilized before hand and carried out
75	aseptically where 10 g of the Lemea sample was homogenized and then serially diluted with 1
76	percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was
77	incubated at 37°C for 48 h. The isolates obtained need to be purified and identified. Purification
78	was carried out by the plate scratch method, which was repeated so that pure isolates were found.
79	The purification process is perfect and will produce separate colonies between strokes. The
80	selected colonies are then identified to determine the strain of the colonies obtained.
01	2.2 Identification of LAB
81	
82	Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA
83	amplification, sequencing and analysis of nucleotide sequences in GenBank (Veljovic et al., 2007)
84	2.2.1 DNA Isolation
85	DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA
86	Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.
87	2.2.2 DNA amplification
88	DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red
89	Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA
90	Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis
91	as much as 1 uL of the PCR product was assessed with 0.8% TBE agarose.
92	2.2.3 DNA sequenching and phylogenetic analysis
93	Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping
94	arrangement performed by comparing obtained (inquiry) with those already in the Gene
95	Bank, with the information base hunted on the NCBI webpage

- 96 (http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size
 97 of the PCR amplification fragment was determined by comparing the position of the DNA
 98 marker size (Marker) with the sample fragment size.
- 99 3. Results and discussion

100 3.1 Isolation of lactic acid bacteria from Lemea

Isolation found 4 bacterial isolates from 2 types of Lemea samples. Lemea made from betung 101 102 bamboo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found 103 were coded B1, B2, S1 and S2 (Figure 2). The bacterial isolates found were lactic acid bacteria 104 because they were able to grow on MRSA specific media with cocci characteristics, a milky white 105 color with a convex surface and smooth edges. The number of isolates obtained was less than 106 that of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang et al., 2008). The morphological characteristics of the isolates found in this study were almost 107 108 the same as the previous findings isolated from Lemea produced by a cottage industry in Kepahyang Regency, Bengkulu (Kurnia et al., 2020). 109

110 *3.2 Identification of Lemea isolates*

111 The results of genomic DNA amplification of the 4 isolates can be seen in Figures 3a and 3b. 112 Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size. Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434 113 114 bp for isolate B1 (Figure 4a), 1424 bp for B2 (Figure 4b). The nucleotide sequence S1 isolate was 882 bp (Figure 4c) and 849 bp for the S2 isolate (Figure 4d). The results of the analysis using the 115 116 BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to 117 Lactobacillus plantarum while isolates S2 had Lactobacillus fermentum. 118 The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% like the partial

119 sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of

Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree, isolate 120 121 B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure 5a), 122 Isolate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA (Figure 5b). 123 S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal RNA (Figure 124 5c), isolate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567 16S 125 ribosomal RNA (Figure 5d). The type of isolate that was identified from Bekasam was 126 lactobacillus plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus 127 Lactobacillus. Bacillus subtilis, Lactobacillus brevis, and Lactobacillus plantarum were found in dominating strains of Soidon fermented bamboo shoot food without salt from Indian Manipur 128 129 (Jeyaram et al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) have been previously studied and isolated as 2 species, namely Lactobacillus 130 131 plantarum and Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from 132 Indonesian fermented foods are dominated by Lactobacillus plantarum (Rahayu, 2003). This research is expected to provide information on which LAB strains have been isolated from 133 134 different types of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the bacterial community by increasing the abundance of Firmicutes, Actinobacteria 135 136 and Proteobacteria (Li et al., 2021).

Lactobacillus fermentum was only found in Lemeamade from yellow bamboo shoots (Bambusa
 vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa
 vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in
 foodstuffs that trigger the growth of Lactobacillus (Macfarlane and Cummings, 1999).
 Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in
 the gut. Bamboo shoots are a good source of fibre (Felisberto *et al.*, 2017). At 100 g of fresh
 weight, bamboo shoots of B. vulgaris contain 6.51 g of carbohydrates, 4.24 g of fibre, 4.90 g of

144 *D. asper*, and 3.54 g of fibre (Chongtham *et al.*, 2011). Different bamboo species contain 145 different macronutrients (Adebola *et al.*, 2014). Differences in the content of bamboo shoots 146 affect the types of bacteria found in *Lemea* products.

147 **4.** Conclusion

- 148 Four *Lactobacillus* isolates found in *Lemea* were from the *Lactobacillus* genus. *Lactobacillus*
- 149 *plantarum* and *Lactobacillus fermentum* were isolates which were identified molecularly by 16S
- 150 rRNA. *Lactobacillus fermentum* was only found in the fermentation process of yellow bamboo shoots
- 151 (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots
- 152 (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).

153 **Conflict of interest - Disclose potential conflicts of interest appropriately.**

154 The authors declare no conflict of interest.

155 Acknowledgments

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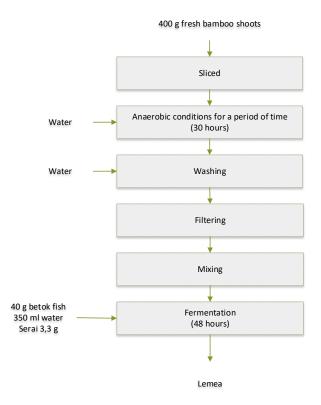
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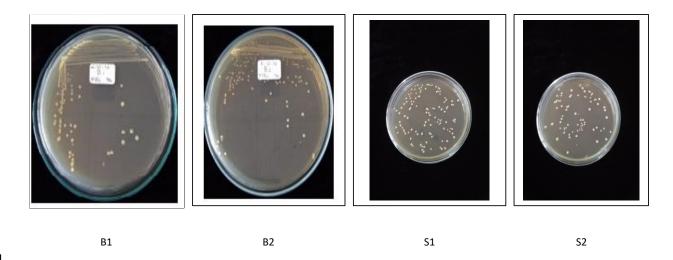
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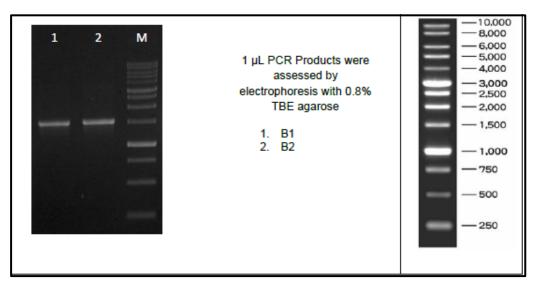
Figure 1. Fermented bamboo shoot making process





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245 Figure 3a. Genomic DNA amplification of isolates B1 and B2

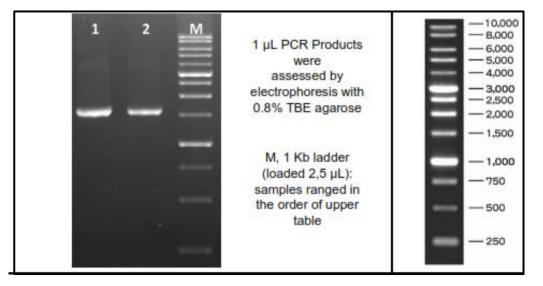


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247 Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration

248 using the Kappa Universal ladder

249 Figure 3b. Genomic DNA amplification of isolates S1 and S2



250

251 Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose concentration

252 using the Kappa Universal ladder

Sequi	ence Assembly	y 1434 Dp				
1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATICACCG	CGGCATGCTG	ATCCGCGATI
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGI
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTT1
301	GICACCGGCA	GICTCACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGG
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIAICCAT	GICCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATO
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGI
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCO
781	CTACACATGG	AGTTCCACTG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTI
841	CITCGGTIGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACO
901	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTI
961	AGCCGIGGCI	TICIGGITAA	ATACCGTCAA	TACCTGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCG1
1141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTO
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT

255 Figure 4b. The nucleotide sequence B2 isolate

Seque	ence Assembl	y 1424 bp				
1	AGGCGGCTGG	TICCTAAAAG	GTTACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGI
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
301	GICACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
421	CIGIATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCO
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTITC	CGATGCACTI
841	CTTCGGTTGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTI
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTAACAA	CAGAGITTIA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GITGCICCAI
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
1261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTIGTIATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGTGTTATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGIT	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

100000	nce Result Reve	CCCCCCTCCC	TOCTABAAACC	TTACCCCACC	CACTTROCCT	CTTACAAACT
1						
61	CTCATGGTGT	GACGGGCGGT	24	CCCGGGGAACG		
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTG
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTC
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACC
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATC
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGC
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

260 Figure 4d. The nucleotide sequence S2

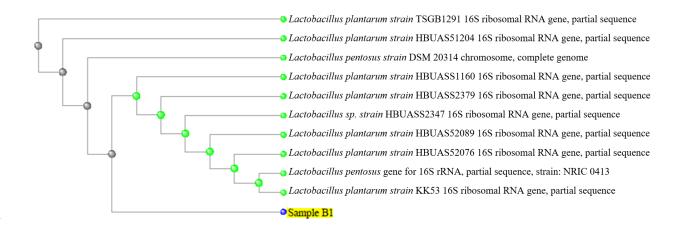
1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTO
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

Types of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung	B1	Lactobacillus plantarum	M N37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

264 Table 1. Comparison of homology levels the 16S rRNA gene of BAL isolat with several sequences

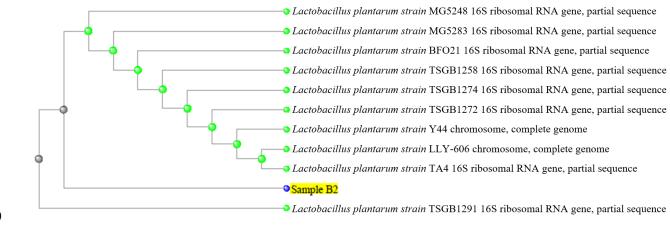
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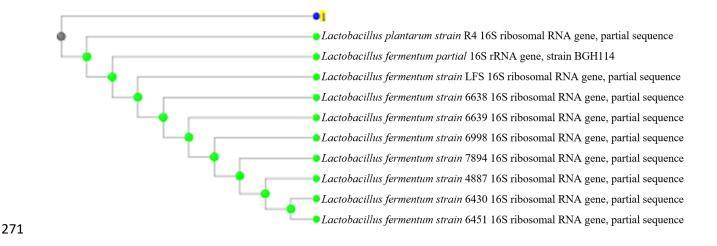
266 Figure 5a. Phylogenetic tree Isolate Code B1



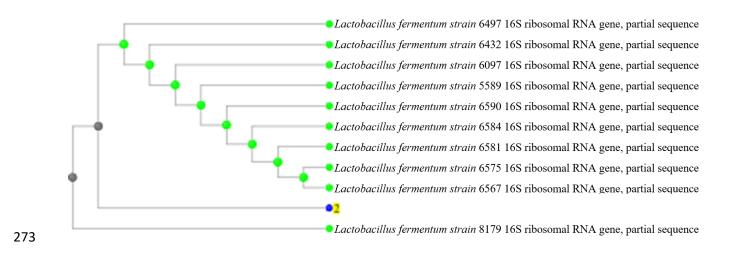
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268 Figure 5b. Phylogenetic tree Isolate Code B2





272 Figure 5d. Phylogenetic tree Isolate Code S2





27th June 2022

Dear Dr Okfrianti,

ACCEPTANCE LETTER

Food Research is pleased to inform you that the following manuscript has been accepted for publication in Food Research journal.

Manuscript Title	:	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea" in Bengkulu, Indonesia
Authors	:	Okfrianti, Y., Herison, C., Fahrurrozi and Budiyanto

We thank you for your fine contribution to the Food Research journal and encourage you to submit other articles to the Journal.

Yours sincerely,

Professor Dr. Son Radu **Chief Editor** Food Research



1	Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea" in Bengkulu, Indonesia
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12	Article history:
13	Received: 5 February 2022
14	Received in revised form: 3 April 2022
15	Accepted: 6 April 2022
16	Available Online: April 2022
17	
18	Abstract
19	Ethnic food is food inherited from ancestors whose process utilizes local food and distinctive tastes. The
20	Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product
21	known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid
22	bacteria (LAB). This study aims to find lactic acid bacteria (LAB) to isolate and identify strains of Lemea.
23	The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 h. Different types of
24	bamboo shoots are expected to provide different types of LAB. Betung shoots (Dendrocalamus asper
25	Schult) and yellow bamboo (Bambusa vulgaris Schrad) have been used. The isolation stage begins with 10
26	gof homogenized Lemea sample, then 1 mL is taken and 9 mL of sterile 1% NaCl is added. Then serial
27	dilutions were carried out starting from 10 $^{-1}$ to 10 $^{-7}$ and spread on MRSA media for each dilution series.

28 Incubate at 37 $^\circ\text{C}$ for 48 h to obtain isolates. The isolates were identified molecularly using the 16S rRNA method. The results of the study found 4 isolates from 2 types of *Lemea*. After identification, it was known that the four isolates were bacteria of the genus Lactobacillus. *Lactobacillus fermentum* was only found in the fermentation process of yellow bamboo shoots (*Bambusa vulgaris* Schrad), while *Lactobacillus plantarum* was found in yellow bamboo shoots (*Bambusa vulgaris* Schrad) and betung (*Dendrocalamus* asper Schult).

34 Keywords: Lemea, Bamboo shoot, 16S rRNA, Lactic acid bacteria

35 1. Introduction

36 The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North 37 Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the 38 Rejang people live. Lemea is an ethnic food from the Rejang tribe. Ethnic foods are meals that have 39 their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are 40 fermented into Lemea by the Rejang people (Dewi et al., 2014). Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by the Rejang to produce Lemea. 41 42 Betok, kepala timah, and mujahir fish are the most common fish used. The odour and flavour are 43 unique, and only the locals enjoy it. LAB that have an impact on the flavour of fermented foods (Fox, 44 2011). Indigenous fermented foods have been extensively researched.

There are various fermented foods in the world, especially in Asia. Fermented foods made from bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially *Lactobacillus* (Kiran *et al.*, 2016). *Meakri*, from Meghalaya Indian fermented bamboo shoots as a source of *Lactobacillus*, has characteristics suitable for probiotics (Das *et al.*, 2020). *Lactobacillus* is a group of LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 2 pathogenic microbes (Yang *et al.*, 2021). LAB isolated from fermented bamboo shoots are potential probiotic candidates that are beneficial for health (Mohamad *et al.*, 2020). LAB strains are selected for their

52	decreased content of cholesterol, antioxidant activity, and anti-bacterial activity (Jitpakdee et al.,
53	2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende et
54	al., 2022).

55	Bekasam is an Indonesian fermented food that is similar to Lemea. Bekasam is a traditional
56	fermented food popular in Sumatera and Kalimantan (Desniar et al., 2013). The sour taste in Bekasam
57	is almost the same as in Lemea. The difference between these two products is the carbohydrate
58	source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play
59	a role in the fermentation process. The source of carbohydrates used for rice in Lemea is bamboo
60	shoots. Fermentation time for <i>Lemea</i> is 2-3 days, while <i>Bekasam</i> takes 10 days.

Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates
were found, and 3 of them had potential as probiotics (Wasis *et al.*, 2019). A total of 180 LAB isolates
have been isolated from Indonesian fermented foods (Sukmarini *et al.*, 2014). Research on the effect
of different types of bamboo shoots on strains of LAB produced during *Lemea* processing has not
been carried out.

Therefore, this research is very important to be carried out at this time because there is still a scarcity
 of information. Studies on the molecular identification of *Lemea* isolates are still needed. This study
 aims to identify and isolate LAB strains in fermented betung bamboo shoots (*Dendrocalamus Asper* Schult) and yellow bamboo shoots (*Bambusa Vulgaris* Schrad).

70 2. Materials and methods

71 2.1 Sample preparation

Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are
thinly sliced and soaked for 30 h. Then they were washed, filtered, and weighed as much as 400 g

74	and they added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for
75	48 h (Figure 1).
76	
77	
78	2.2 LAB isolation
79	Isolation LAB was carried out using a device that was sterilized before hand and carried out
80	aseptically where 10 g of the Lemea sample was homogenized and then serially diluted with 1
81	percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was
82	incubated at 37°C for 48 hrs. The isolates obtained need to be purified and identified. Purification
83	was carried out by the plate scratch method, which was repeated so that pure isolates were found.
84	The purification process is perfect and will produce separate colonies between strokes. The
85	selected colonies are then identified to determine the strain of the colonies obtained.
86	2.2 Identification of LAB
87	Molecular identification based on 16S rRNA gene amplification with genomic DNA isolation, DNA
88	amplification, sequencing and analysis of nucleotide sequences in GenBank (Veljovic et al., 2007)
89	2.2.1 DNA Isolation
90	DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA
91	Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.
92	2.2.2 DNA amplification
93	DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red
94	Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA
95	Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis
96	as much as 1 uL of the PCR product was assessed with 0.8% TBE agarose.

97 2.2.3 DNA sequenching and phylogenetic analysis

98 Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping arrangement performed by comparing obtained (inquiry) with those already in the Gene 99 100 Bank, with the information base hunted on the NCBI webpage (http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size 101 102 of the PCR amplification fragment was determined by comparing the position of the DNA 103 marker size (Marker) with the sample fragment size.

104 3. Results and discussion

105 *3.1 Isolation of lactic acid bacteria from Lemea*

106	Isolation found 4 bacterial isolates from 2 types of Lemea samples. Lemea made from betung
107	bamboo shoots found 2 isolates and 2 isolates from yellow bamboo shoots. The isolates found
108	were coded B1, B2, S1 and S2 (Figure 2). The bacterial isolates found were lactic acid bacteria
109	because they were able to grow on MRSA specific media with cocci characteristics, a milky white
110	color with a convex surface and smooth edges. The number of isolates obtained was less than
111	that of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang
112	et al., 2008). The morphological characteristics of the isolates found in this study were almost
113	the same as the previous findings isolated from Lemea produced by a cottage industry in
114	Kepahyang Regency, Bengkulu (Kurnia <i>et al.</i> , 2020).

115 3.2 Identification of Lemea isolates

116The results of genomic DNA amplification of the 4 isolates can be seen in Figures 3a and 3b.117Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size.118Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434119bp for isolate B1 (Figure 4a), 1424 bp for B2 (Figure 4b). The nucleotide sequence S1 isolate was120882 bp (Figure 4c) and 849 bp for the S2 isolate (Figure 4d). The results of the analysis using the

121	BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to
122	Lactobacillus plantarum while isolates S2 had Lactobacillus fermentum.
123	The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% like the partial
124	sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of
125	Lactobacillus plantarum but not Lactobacillus fermentum. Based on the phylogeny tree, isolate
126	B1 was closely related to Lactobacillus plantarum strain KK53 16S ribosomal RNA (Figure 5a),
127	Isolate B2 with Lactobacillus plantarum strain TA4 and TSGB1291 16S ribosomal RNA (Figure 5b).
128	S1 isolate was closely related to Lactobacillus plantarum strain R4 16S ribosomal RNA (Figure
129	5c), isolate S2 was closely related to Lactobacillus fermentum strain 8179 and 6567 16S
130	ribosomal RNA (Figure 5d). The type of isolate that was identified from Bekasam was
131	lactobacillus plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus
132	Lactobacillus. Bacillus subtilis, Lactobacillus brevis, and Lactobacillus plantarum were found in
133	dominating strains of Soidon fermented bamboo shoot food without salt from Indian Manipur
134	(Jeyaram et al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata
135	buse-kurz) have been previously studied and isolated as 2 species, namely Lactobacillus
136	plantarum and Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from
137	Indonesian fermented foods are dominated by Lactobacillus plantarum (Rahayu, 2003). This
138	research is expected to provide information on which LAB strains have been isolated from
139	different types of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the
140	diversity of the bacterial community by increasing the abundance of Firmicutes, Actinobacteria
141	and Proteobacteria (Li et al., 2021).
142	Lactobacillus fermentum was only found in Lemeamade from yellow bamboo shoots (Bambusa
143	vulgaris Schrad) and Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa

vulgaris Schrad) and betung (Dendrocalamus asper Schult). Prebiotics are contained in

145	foodstuffs that trigger the growth of Lactobacillus (Macfarlane and Cummings, 1999).
146	Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in
147	the gut. Bamboo shoots are a good source of fibre (Felisberto et al., 2017). At 100 g of fresh
148	weight, bamboo shoots of B. vulgaris contain 6.51 g of carbohydrates, 4.24 g of fibre, 4.90 g of
149	D. asper, and 3.54 g of fibre (Chongtham et al., 2011). Different bamboo species contain
150	different macronutrients (Adebola et al., 2014). Differences in the content of bamboo shoots
151	affect the types of bacteria found in Lemea products.

152 4. Conclusion

- 153Four Lactobacillus isolates found in Lemea were from the Lactobacillus genus. Lactobacillus154plantarum and Lactobacillus fermentum were isolates which were identified molecularly by 16S155rRNA. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots156(Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots157(Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).158Conflict of interest Disclose potential conflicts of interest appropriately.159The authors declare no conflict of interest.
- 160 Acknowledgments
- 161 This research was funded by the Poltekkes Kemenkes Bengkulu, Indonesia in 2020
- 162
- 163

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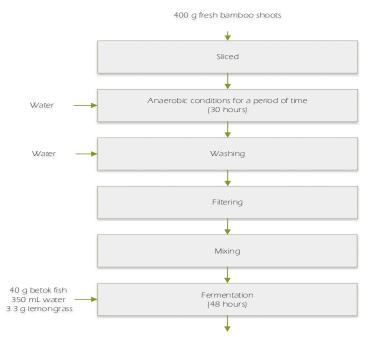
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Lemea

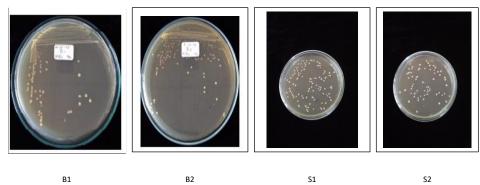
Figure 1. Fermented bamboo shoot making process

Commented [A1]: Serai 3.3 g (comma change) ml=mL

Commented [A2R1]: Is Serai = Lemon grass?

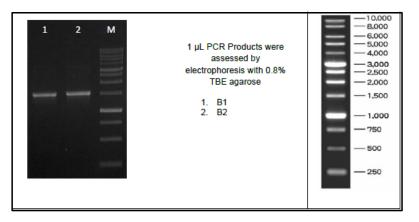
Commented [A3R1]: It has been fixed as suggested 350 mL water 3.3 lemongrass

260 Figure 2. Isolate B1, B2,S1 and S2



B1 B2 S1 261

262 Figure 3a. Genomic DNA amplification of isolates B1 and B2

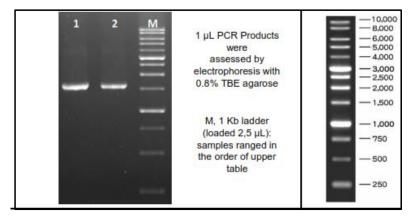


263

264 Visualization of 16 S rRNA gene amplification of isolates B1 and B2 at 0.8% TBE agarose concentration

265 using the Kappa Universal ladder

266 Figure 3b. Genomic DNA amplification of isolates S1 and S2





268 Visualization of 16 S rRNA gene amplification of isolates S1 and S2 at 0.8% TBE agarose concentration

269 using the Kappa Universal ladder

270	Figure 4a.	The nucleotide sequence B1 isolate
270	inguic 4u.	The nucleonal sequence by isolate

- 30		у 1434 bp	GTTACCCCAC	CGACTITIGGE	TGTTACAAAC	TETCATOGTO
1					CGGCATGCTG	
21					AATCCGAACT	
81	TTAAGAGATT	AGCTTGCTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
41	GTGTAGCCCA	GGTCATAAGG	GGCATGATGA	TTTGACGTCA	TCCCCACCTT	CCTCCGGTTT
801	GTCACCGGCA	GTCTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
861	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
21	CIGIAICCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
81	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
501	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
61	ATGGACTACC	AGGGTATCTA	ATCCIGITIG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
21	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATITCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCACTT
41	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
01	CCCAATAAAT	CCGGACAACG	CITGCCACCI	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
61	AGCCGTGGCT	TICIGGITAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
021	TCTTTAACAA	CAGAGTTTTA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TITGGGCCGT
141	GICICAGICC	CAATGIGGCC	GATTACCCTC	TCAGGICGGC	TACGTATCAT	TGCCATGGTG
201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
381	CICAAAIGIA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT

272 Figure 4b. The nucleotide sequence B2 isolate

1	AGGCGGCTGG	TICCTAAAAG	GITACCCCAC	CGACTITGGG	TGTTACAAAC	TCTCATGGTG
61	TGACGGGCGG	TGTGTACAAG	GCCCGGGAAC	GTATTCACCG	CGGCATGCTG	ATCCGCGATT
121	ACTAGCGATT	CCGACTTCAT	GTAGGCGAGT	TGCAGCCTAC	AATCCGAACT	GAGAATGGCT
181	TTAAGAGATT	AGCTTACTCT	CGCGAGTTCG	CAACTCGTTG	TACCATCCAT	TGTAGCACGT
241	GIGIAGCCCA	GGTCATAAGG	GGCATGATGA	TITGACGICA	TCCCCACCTT	CCTCCGGTTT
301	GTCACCGGCA	GICICACCAG	AGIGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTTGC
361	GCTCGTTGCG	GGACTTAACC	CAACATCTCA	CGACACGAGC	TGACGACAAC	CATGCACCAC
121	CIGIATCCAT	GTCCCCGAAG	GGAACGTCTA	ATCTCTTAGA	TTTGCATAGT	ATGTCAAGAC
481	CIGGIAAGGI	TCTTCGCGTA	GCTTCGAATT	AAACCACATG	CTCCACCGCT	TGTGCGGGGCC
541	CCCGTCAATT	CCTTTGAGTT	TCAGCCTTGC	GGCCGTACTC	CCCAGGCGGA	ATGCTTAATG
601	CGTTAGCTGC	AGCACTGAAG	GGCGGAAACC	CTCCAACACT	TAGCATTCAT	CGTTTACGGT
661	ATGGACTACC	AGGGTATCTA	ATCCTGTTTG	CTACCCATAC	TTTCGAGCCT	CAGCGTCAGT
721	TACAGACCAG	ACAGCCGCCT	TCGCCACTGG	TGTTCTTCCA	TATATCTACG	CATTTCACCG
781	CTACACATGG	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTITC	CGATGCACTT
841	CITCGGITGA	GCCGAAGGCT	TTCACATCAG	ACTTAAAAAA	CCGCCTGCGC	TCGCTTTACG
901	CCCAATAAAT	CCGGACAACG	CTIGCCACCT	ACGTATTACC	GCGGCTGCTG	GCACGTAGTT
961	AGCCGTGGCT	TTCTGGTTAA	ATACCGTCAA	TACCIGAACA	GTTACTCTCA	GATATGTTCT
1021	TCTTTARCAA	CAGAGITITA	CGAGCCGAAA	CCCTTCTTCA	CTCACGCGGC	GTTGCTCCAT
1081	CAGACTITCG	TCCATTGTGG	AAGATTCCCT	ACTGCTGCCT	CCCGTAGGAG	TTTGGGCCGT
1141	GTCTCAGTCC	CAATGTGGCC	GATTACCCTC	TCAGGTCGGC	TACGTATCAT	TGCCATGGTG
1201	AGCCGTTACC	CCACCATCTA	GCTAATACGC	CGCGGGGACCA	TCCAAAAGTG	ATAGCCGAAG
261	CCATCITICA	AACTCGGACC	ATGCGGTCCA	AGTTGTTATG	CGGTATTAGC	ATCTGTTTCC
1321	AGGIGITATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
1381	CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	

275 Figure 4c. The nucleotide sequence S1 isolate

1	GTCCACCTTA	GGCGGCTGGC	TCCTAAAAGG	TTACCCCACC	GACTTTGGGT	GTTACAAACT
61	CTCATGGTGT	GACGGGGGGGT	GTGTACAAGG	CCCGGGGAACG	TATTCACCGC	GGCATGCTG
121	TCCGCGATTA	CTAGCGATTC	CGACTTCGTG	CAGGCGAGTT	GCAGCCTGCA	GTCCGAACTO
181	AGAACGGTTT	TAAGAGATTT	GCTTGCCCTC	GCGAGTTCGC	GACTCGTTGT	ACCGTCCATT
241	GTAGCACGTG	TGTAGCCCAG	GTCATAAGGG	GCATGATGAT	CTGACGTCGT	CCCCACCTTO
301	CTCCGGTTTG	TCACCGGCAG	TCTCACTAGA	GTGCCCAACT	TAATGCTGGC	AACTAGTAAC
361	AAGGGTTGCG	CTCGTTGCGG	GACTTAACCC	AACATCTCAC	GACACGAGCT	GACGACGACO
421	ATGCACCACC	TGTCATTGCG	TTCCCGAAGG	AAACGCCCTA	TCTCTAGGGT	TGGCGCAAGA
481	TGTCAAGACC	TGGTAAGGTT	CTTCGCGTAG	CTTCGAATTA	AACCACATGC	TCCACCGCTT
541	GTGCGGGCCC	CCGTCAATTC	CTTTGAGTTT	CAACCTTGCG	GTCGTACTCC	CCAGGCGGAG
601	TGCTTAATGC	GTTAGCTCCG	GCACTGAAGG	GCGGAAACCC	TCCAACACCT	AGCACTCATO
661	GTTTACGGCA	TGGACTACCA	GGGTATCTAA	TCCTGTTCGC	TACCCATGCT	TTCGAGTCTC
721	AGCGTCAGTT	GCAGACCAGG	TAGCCGCCTT	CGCCACTGGT	GTTCTTCCAT	ATATCTACGO
781	ATTCCACCGC	TACACATGGA	GTTCCACTAC	CCTCTTCTGC	ACTCAAGTTA	TCCAGTTTCC
841	GATGCACTTC	TCCGGTTAAG	CCGAAGGCTT	TCACATCATA	CT	

277 Figure 4d. The nucleotide sequence S2

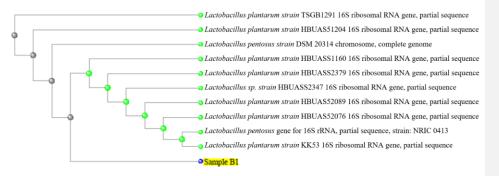
1	ACCTTAGGCG	GCTGGCTCCT	AAAAGGTTAC	CCCACCGACT	TTGGGTGTTA	CAAACTCTCA
61	TGGTGTGACG	GGCGGTGTGT	ACAAGGCCCG	GGAACGTATT	CACCGCGGCA	TGCTGATCCG
121	CGATTACTAG	CGATTCCGAC	TTCGTGCAGG	CGAGTTGCAG	CCTGCAGTCC	GAACTGAGAA
181	CGGTTTTTAAG	AGATTTGCTT	GCCCTCGCGA	GTTCGCGACT	CGTTGTACCG	TCCATTGTAG
241	CACGTGTGTA	GCCCAGGTCA	TAAGGGGCAT	GATGATCTGA	CGTCGTCCCC	ACCTTCCTCC
301	GGTTTGTCAC	CGGCAGTCTC	ACTAGAGTGC	CCAACTTAAT	GCTGGCAACT	AGTAACAAGG
361	GTTGCGCTCG	TTGCGGGACT	TAACCCAACA	TCTCACGACA	CGAGCTGACG	ACGACCATGO
421	ACCACCTGTC	TTTGCGTTCC	CGAAGGAAAC	GCCCTATCTC	TAGGGTTGGC	GCAAGATGTC
481	AAGACCTGGT	AAGGTTCTTC	GCGTAGCTTC	GAATTAAACC	ACATGCTCCA	CCGCTTGTGC
541	GGGCCCCCGT	CAATTCCTTT	GAGTTTCAAC	CTTGCGGTCG	TACTCCCCAG	GCGGAGTGCT
601	TAATGCGTTA	GCTCCGGCAC	TGAAGGGCGG	AAACCCTCCA	ACACCTAGCA	CTCATCGTTT
661	ACGGCATGGA	CTACCAGGGT	ATCTAATCCT	GTTCGCTACC	CATGCTTTCG	AGTCTCAGCG
721	TCAGTTGCAG	ACCAGGTAGC	CGCCTTCGCC	ACTGGTGTTC	TTCCATATAT	CTACGCATTC
781	CACCGCTACA	CATGGAGTTC	CACTACCCTC	TTCTGCACTC	AAGTTATCCA	GTTTCCGATG
841	CACTTCTCC					

281 Table 1. Comparison of homology levels the 16S rRNA gene of BAL isolat with several sequences

Types of	Isolate	Species	Comparison Squen	Similarity (%)
Bamboo Shoots	Code		Access Number	
Bamboo Betung	B1	Lactobacillus plantarum	M N37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

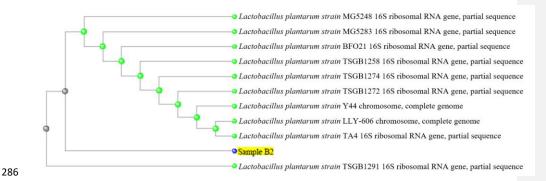
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283 Figure 5a. Phylogenetic tree Isolate Code B1

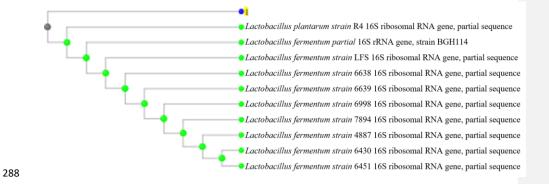


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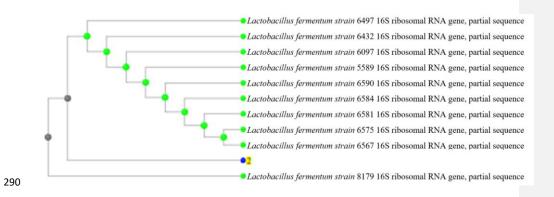
285 Figure 5b. Phylogenetic tree Isolate Code B2



287 Figure 5c. Phylogenetic tree Isolate Code S1



289 Figure 5d. Phylogenetic tree Isolate Code S2





Yenni Okfrianti <yeni@poltekkesbengkulu.ac.id>

FR-IFC-029 - Article Production

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Food Research Production <fr.production@outlook.com> Kepada: "yeni@poltekkesbengkulu.ac.id" <yeni@poltekkesbengkulu.ac.id> 7 Juni 2023 pukul 20.47

Dear Dr Yeni

Manuscript ID: FR-IFC-029 Manuscript Title: Identification of LAB isolated from ethnic fermented bamboo shoot "Lemea" in Bengkulu, Indonesia

Before we can proceed with the article production, I would like to clarify a few points that I have commented in the manuscript. Please refer to the attachment. Please address the issues raised in the comments.

Please use the attached copy to make your revisions as it has been corrected to the Journal's format. Do not delete the comments. Once you have done, kindly revert the copy to me as soon as possible. Please note the faster you respond, the quicker we will process your manuscript.

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Dear Vivian New, PhD Editor

The article has been revised in the comments section (attachment).

Thanks & Regards

Yenni Okfrianti

[Kutipan teks disembunyikan]

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Food Research Production <fr.production@outlook.com> Kepada: Yenni Okfrianti <yeni@poltekkesbengkulu.ac.id> 8 Juni 2023 pukul 18.31

Dear Dr Yenni

Received with thanks.

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You are welcome. [Kutipan teks disembunyikan]

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8 Juni 2023 pukul 18.36

Dear Dr Yenni

Please address the comments raised in the manuscript.

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Sent: 08 June 2023 7:36 PM

[Kutipan teks disembunyikan]

[Kutipan teks disembunyikan]

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Yenni Okfrianti <yeni@poltekkesbengkulu.ac.id> Kepada: Food Research Production <fr.production@outlook.com>

Dear Vivian New, PhD Editor

has been repaired according to the suggestions

Thanks & Regards

Yenni Okfrianti

[Kutipan teks disembunyikan]

FR-IFC-029_08062003.docx 3735K 8 Juni 2023 pukul 20.57

Food Research Production <fr.production@outlook.com> Kepada: Yenni Okfrianti <yeni@poltekkesbengkulu.ac.id>

Dear Yenni

Please refer to the attachment for the galley proof of your manuscript FR-IFC-029 entitled ' Identification of lactic acid bacteria isolated from ethnic fermented bamboo shoot "Lemea" in Bengkulu, Indonesia'. Please check the content of the galley proof. If there are any mistakes on the typesetting, please comment and highlight them in the PDF itself and revert to us within five (5) days of receipt. Change or addition of data/results is strictly prohibited. Please note that you are allowed one (1) revision of the galley proof.

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[Kutipan teks disembunyikan]

PR-IFC-029.pdf 1365K

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Dear Vivian New, PhD Editor

I have checked the contents of the kitchen evidence, and there is no correction from me. It's clear

Thanks & Regards

Yenni Okfrianti

[Kutipan teks disembunyikan]

Identification of lactic acid bacteria isolated from ethnic fermented bamboo shoot "*Lemea*" in Bengkulu, Indonesia

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Abstract

Ethnic food is inherited from ancestors who utilizes local food and that have distinctive tastes. The Rejang tribe is a native Bengkulu community who processes bamboo shoots into a fermented product known as Lemea, which is only found in Bengkulu province. Lemea is a source of indigenous lactic acid bacteria (LAB). This study aimed to isolate and identify lactic acid bacteria (LAB) strains in Lemea. The bamboo shoots with betok fish (Anabas testudineus) were fermented for 48 hrs. Different types of bamboo shoots were expected to contain different types of LAB. Betung shoots (Dendrocalamus asper Schult) and yellow bamboo shoots (Bambusa vulgaris Schrad) have been used. Isolation of the LAB was performed through serial dilution of 10 g homogenized *Lemea* sample and spread on MRSA plates for each dilution series. Plates were incubated at 37°C for 48 hrs to obtain isolates. The isolates were identified molecularly using the 16S rRNA method. The results of the study found four isolates from two types of *Lemea*. After identification, it was known that the four isolates were bacteria of the genus Lactobacillus. Lactobacillus fermentum was only found in the fermentation process of yellow bamboo shoots (Bambusa vulgaris Schrad), while Lactobacillus plantarum was found in yellow bamboo shoots (Bambusa vulgaris Schrad) and betung (Dendrocalamus asper Schult).

1. Introduction

The Rejang are the third-largest tribe in Bengkulu Province, after the Serawai and Basema. North Bengkulu, Central Bengkulu, Rejang Lebong, Lebong, and Kepahyang are the five districts where the Rejang people live. Lemea is an ethnic food from the Rejang tribe. Ethnic foods are meals that have their origins in an ethnic group's history and culture (Kwon, 2015). Bamboo shoots and river fish are fermented into Lemea by the Rejang people (Dewi et al., 2014). Betung, Tabah, Mayan, and Seik bamboo are some of the most common bamboo varieties used by the Rejang to produce Lemea. Betok, kepala timah, and mujahir fish are the most common fish used. The odours and flavours are unique, and only the locals enjoy it. LAB has an impact on the flavour of fermented foods (Fox, 2011). Indigenous fermented foods have been extensively researched.

There are various fermented foods in the world, especially in Asia. Fermented foods made from bamboo shoots from India, Indonesia, and Taiwan are a source of LAB, especially *Lactobacillus* (Kiran *et al.*, 2016).

Meakri, from Meghalaya Indian fermented bamboo shoots as a source of *Lactobacillus*, has characteristics suitable for probiotics (Das *et al.*, 2020). *Lactobacillus* is a group of LAB that are gram-positive bacteria. LAB have the potential to inhibit the infection and growth of 2 pathogenic microbes (Yang *et al.*, 2021). LAB isolated from fermented bamboo shoots are potential probiotic candidates that are beneficial for health (Mohamad *et al.*, 2020). LAB strains are selected for their decreased content of cholesterol, antioxidant activity, and antibacterial activity (Jitpakdee *et al.*, 2022). Isolation of lactic acid bacteria from indegenous fermented foods is very important (Mende *et al.*, 2022).

Bekasam is an Indonesian fermented food that is similar to *Lemea*. *Bekasam* is a traditional fermented food popular in Sumatera and Kalimantan (Desniar *et al.*, 2013). The sour taste in *Bekasam* is almost the same as in *Lemea*. The difference between these two products is the carbohydrate source and fermentation time. Carbohydrate sources are a source of nutrition for bacteria that play a role in the fermentation process. The source of carbohydrates used for rice in *Lemea* is bamboo shoots. Fermentation time for *Lemea* is 2-3 days, while *Bekasam* takes 10 days.

Isolates from several bamboo shoot products have been found. In pickled bamboo shoots, 88 isolates were found, and 3 of them had potential as probiotics (Wasis *et al.*, 2019). A total of 180 LAB isolates have been isolated from Indonesian fermented foods (Sukmarini *et al.*, 2014). Research on the effect of different types of bamboo shoots on strains of LAB produced during *Lemea* processing has not been carried out.

Therefore, this research is very important to be carried out at this time because there is still a scarcity of information. Studies on the molecular identification of *Lemea* isolates are still needed. This study aimed to identify and isolate LAB strains in fermented betung bamboo shoots (*Dendrocalamus Asper* Schult) and yellow bamboo shoots (*Bambusa Vulgaris* Schrad).

2. Materials and methods

2.1 Sample preparation

Bamboo shoot samples were obtained from Lebong Regency. The peeled bamboo shoots are thinly sliced and soaked for 30 hrs. Then they were washed, filtered, and weighed as much as 400 g and they added 40 g of betok fish, 350 mL of water, and 3.3 g of lemongrass, and fermented for 48 hrs (Figure 1).

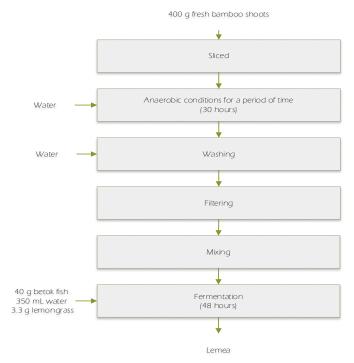


Figure 1. Fermented bamboo shoots making process

2.2 Lactic acid bacteria isolation

Isolation LAB was carried out using a device that was sterilized before hand and carried out aseptically where 10 g of the *Lemea* sample was homogenized and then serially diluted with 1 percent sterile NaCl. And each dilution series was spread on MRSA media and then petridish was incubated at 37°C for 48 hrs. The isolates obtained need to be purified and identified. Purification was carried out by the plate scratch method, which was repeated so that pure isolates were found. The purification process is perfect and will produce separate colonies between strokes. The selected colonies are then identified to determine the strain of the colonies obtained.

2.3 Molecular identification of lactic acid bacteria

Molecular identification was based on 16S rRNA gene amplification with genomic DNA isolation, DNA amplification, sequencing and analysis of nucleotide sequences in GenBank following the method by Veljovic *et al.* (2007).

2.3.1 Deoxyribonucleic acid isolation

DNA isolation was done using the Genomic DNA extraction with Presta TM Mini GDNA Bacteria Kit (Geneaid, GBB100). Stages of isolation based on the procedure kit.

2.3.2 Deoxyribonucleic acid amplification

DNA amplification 16S rDNA sequence amplification was performed using MyTaqHS Red Mix (Bioline, BIO-25047). PCR Products were purified with ZymocleanTM Ge; DNA Recovery Kit (Zymo Research, D4001). The PCR results were visualized by electrophoresis as much as 1 μ L of the PCR product was assessed with 0.8% TBE agarose.

2.3.3 Deoxyribonucleic acid sequencing and phylogenetic analysis

Sequencing and analysis of nucleotide sequences in GenBank. Analysis of grouping arrangement performed by comparing obtained (inquiry) with those already in the Gene Bank, with the information base hunted on the NCBI webpage (http://www.ncbi.nlm.nih.gov) using Impact (Basic Local Alignment Search Tool). The size of the PCR amplification fragment was determined by comparing the position of the DNA marker size (Marker) with the sample fragment size.

3. Results and discussion

3.1 Isolation of lactic acid bacteria from Lemea

Isolation found four bacterial isolates from the two types of *Lemea* samples. *Lemea* made from betung bamboo shoots found two isolates and two isolates from yellow bamboo shoots. The isolates found were coded

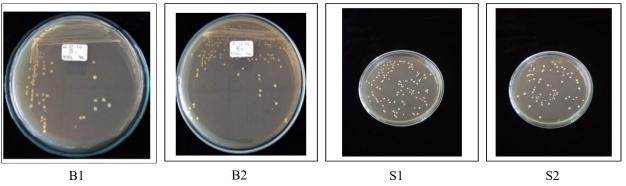


Figure 2. Isolate B1, B2, S1 and S2.

B1, B2, S1 and S2 (Figure 2). The bacterial isolates found were lactic acid bacteria because they were able to MRSA specific media with grow on cocci characteristics, a milky white color with a convex surface and smooth edges. The number of isolates obtained was less than that of mesu, soidon, soibum, and soijon but the same as unfermented bamboo shoots (Tamang et al., 2008). The morphological characteristics of the isolates found in this study were almost the same as the previous findings isolated from Lemea produced by a cottage industry in Kepahyang Regency, Bengkulu (Kurnia et al., 2020).

3.2 Identification of lemea isolates

The results of genomic DNA amplification of the 4 isolates can be seen in Figures 3a and 3b. Isolates B1, B2 produced 1500 bp amplicons and S1, S2 amplicons with 1400 bp size. Visualization of PCR results by electrophoresis on 0.8% agarose. Nucleotide sequence at 1434 bp for isolate B1 (Figure 4a), 1424 bp for B2 (Figure 4b). The nucleotide sequence S1 isolate was 882 bp (Figure 4c) and 849 bp for the S2 isolate (Figure 4d). The results of the analysis using the BLAST algorithm on other isolates showed that isolates B1, B2 and S1 have been close to *Lactobacillus plantarum* while isolates S2 had *Lactobacillus fermentum*.

The 16S rRNA gene sequences of each isolate B1, B2, S1 and S2 have been 99% like the partial sequences of the comparison isolates (Table 1). The bacteria were found to be a strain of L. plantarum but not L. fermentum. Based on the phylogeny tree, isolate B1 was closely related to L. plantarum strain KK53 16S ribosomal RNA (Figure 5a), Isolate B2 with L. plantarum strain TA4 and TSGB1291 16S ribosomal RNA (Figure 5b). S1 isolate was closely related to L. plantarum strain R4 16S ribosomal RNA (Figure 5c), isolate S2 was closely related to L. fermentum strain 8179 and 6567 16S ribosomal RNA (Figure 5d). The type of isolate that was identified from Bekasam was L. plantarum (Sukmarini et al., 2014). All isolates have been homologous to the genus Lactobacillus. Bacillus subtilis, Lactobacillus brevis, and L. plantarum were found in dominating strains of Soidon fermented bamboo shoot food without salt from Indian Manipur (Jeyaram et al., 2010). LAB strains in fermented Tabah bamboo shoots (Gigantochloa nigrociliata buse-kurz) have been previously studied and isolated as 2 species, namely L. plantarum and Lactobacillus rossiae (Okfrianti et al., 2019). Lactic acid bacteria isolated from Indonesian fermented foods are dominated by L. plantarum (Rahayu, 2003). This research is expected to provide information on which LAB strains have been isolated

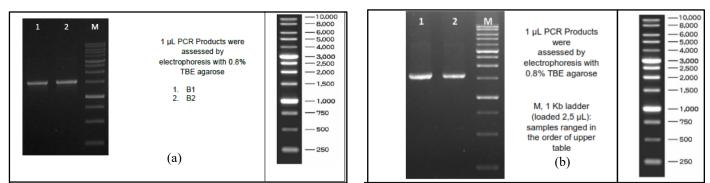


Figure 3. Genomic 16S rRNA amplification of (a) isolates B1 and B2 and (b) isolates S1 and S2. M: Kappa universal ladder.

Table 1. Comparison of homology levels	s of the 16S rRNA gene of LAE	B isolates with several sequences.
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Types of Bamboo Shoots	Isolate Code	Species	GenBank Accession Number	Similarity (%)
Bamboo Betung	B1	Lactobacillus plantarum	MN37236.01	99
	B2	Lactobacillus plantarum	MN972325.1	99
Yellow Bamboo	S1	Lactobacillus plantarum	KM350169.1	99
	S2	Lactobacillus fermentum	MT538927.1	99

61		1434 bp				(a)
	AGGCGGCTGG	TTCCTAAAAG		CGACTTTGGG		
121 .				GTATTCACCG		
				TGCAGCCTAC		
				CAACTCGTTG TTTGACGTCA		
				TTAATGCTGG		
				CGACACGAGC		
				ATCTCTTAGA		
				AAACCACATG		
				GGCCGTACTC		
				CTCCAACACT CTACCCATAC	TAGCATTCAT	
				TGTTCTTCCA		
				CACTCAAGTT		
				ACTTAAAAAA		TCGCTTTACG
				ACGTATTACC		
				TACCTGAACA		
				CCCTTCTTCA		
				ACTGCTGCCT TCAGGTCGGC		
				CGCGGGGACCA		
				AGITGTTATG		
1321 /	AGGTGTTATC	CCCCGCTTCT	GGGCAGGTTT	CCCACGIGII	ACTCACCAGT	TCGCCACTCA
1381 (CTCAAATGTA	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTTCGTTCG	ACTT
						(c)
Seque	nce Result Re	everse Prime	r 882bp			(c)
	nce Result Re			S TTACCCAC	GACTTTGGGT	~ /
1	GTCCACCT	TA GGCGGCTG	GC TCCTAAAAA	G TTACCCCACC		GTTACAAACT
1 61	GTCCACCT CTCATGGT	TA GGCGGCTG GT GACGGGCG	GC TCCTAAAAAG GT GTGTACAAG	G CCCGGGAACO	G TATTCACCGC	GTTACAAACT GGCATGCTGA
1 61 121	GTCCACCT CTCATGGT TCCGCGAT	TA GGCGGCTG GT GACGGGGCG TA CTAGCGAT	GC TCCTAAAAAG GT GTGTACAAG TC CGACTTCGT	G CCCGGGAACO	G TATTCACCGC GCAGCCTGCA	GTTACAAACT GGCATGCTGA GTCCGAACTG
1 61 121 181	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT	TA GGCGGCTG GT GACGGGCG TA CTAGCGAT TT TAAGAGAT	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT	GG CCCGGGAACO NG CAGGCGAGTT NC GCGAGTTCGO	G TATTCACCGC GCAGCCTGCA GACTCGTTGT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCATT
1 61 121 181 241	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG	TA GGCGGCTG GT GACGGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG	GG CCCGGGAACO NG CAGGCGAGTT NC GCGAGTTCGO GG GCATGATGAT	G TATTCACCGC GCAGCCTGCA GACTCGTTGT CTGACGTCGT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCATT CCCCACCTTC
1 61 121 181 241 301	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT	TA GGCGGCTG GT GACGGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC, TG TCACCGGC.	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG	GG CCCGGGAACC TG CAGGCGAGTT TC GCGAGTTCGC GG GCATGATGAT GA GTGCCCAACT	G TATTCACCGC GCAGCCTGCA GACTCGTTGT CTGACGTCGT TAATGCTGGC	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCATT CCCCACCTTC AACTAGTAAC
1 61 121 181 241 301 361	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG	TA GGCGGCTG GT GACGGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC, TG TCACCGGC, CG CTCGTTGC	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACC	GG CCCGGGAACC TG CAGGCGAGTT TC GCGAGTTCGC GG GCATGATGAT GA GTGCCCAACT TC AACATCTCAC	G TATTCACCGC GCAGCCTGCA GACTCGTTGT CTGACGTCGT TAATGCTGGC GACACGAGCT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCATT CCCCACCTTC AACTAGTAAC GACGACGACC
1 61 121 181 241 301 361 421	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA	TA GGCGGCTG GT GACGGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC CG CTCGTTGC CC TGTCATTG	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACC CG TTCCCGAAG	GG CCCGGGAACC NG CAGGCGAGTT NC GCGAGTTCGC GG GCATGATGAT GA GTGCCCAACT CC AACATCTCAC GG AAACGCCCTA	G TATTCACCGC GCAGCCTGCA GACTCGTTGT CTGACGTCGT TAATGCTGGC GACACGAGCT TCTCTAGGGT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCATT CCCCACCTTC AACTAGTAAC GACGACGACC TGGCGCAAGA
1 61 121 181 241 301 361 421 481	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCAAGA	TA GGCGGCTG GT GACGGCGG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CG CTCGTTGC CC TGTCATTG CC TGGTAAGG	GC TCCTAAAAG GT GTGTACAAG TC GACTTCGT TG GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACC CG TTCCCGAAG TT CTTCGCGTA	GG CCCGGGAACC TC CAGGCGAGTT TC GCGAGTTCGC GG GCATGATGAT GA GTGCCCAACT CC AACATCTCAC GG AAACGCCCTP AG CTTCGAATTP	G TATTCACCGC GCAGCCTGCA GACTCGTTGT CTGACGTCGT TAATGCTGGC GACACGAGCT A TCTCTAGGGT A AACCACATGC	GTTACAAACT GGCATGCTCA ACCGCACCTG ACCGCCACTT CCCCACCTTC AACTAGTAAC GACGACGACC TGGCGCAAGA TCCACCGCTT
1 61 121 241 301 361 421 481 541	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCCAGA GTGCGGGC	TA GGCGGCTG GT GACGGCGG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CG CTCGTTGC CC TGCTTGC CC TGGTAAGG CC CCGTCAAT	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACG CG TCCCCGAAG TT CCTCGCGTA TC CTTCGCGTA	G CCCGGGAACC C GCGAGTTCGC GCGAGTTCGC GGGATTCGC GGGATGATGAT GGGCCCAACT C AACATCTCAC GG AAACGCCCTM GG CTTCGAATTM TT CAACCTTGCC	GACTCGTGA GACTCGTGG CGACCCGTGT CGACCGCGTGT TAATGCTGGC GACACGAGCT ACCCTAGGGT AACCACATGC GCGTACTCC	GTTACAAACT GCCATCCTGA GTCCGAACTG ACCGTCCAAT CCCCCACCTTC AACTAGTAAC GACGACGAACA TCCACCGCTT CCACGGCGAAGA
1 61 121 181 241 301 361	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCCAGA GTGCGGGC	TA GGCGGCTG GT GACGGCGG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CG CTCGTTGC CC TGCTTGC CC TGGTAAGG CC CCGTCAAT	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACG CG TCCCCGAAG TT CCTCGCGTA TC CTTCGCGTA	GG CCCGGGAACC TC CAGGCGAGTT TC GCGAGTTCGC GG GCATGATGAT GA GTGCCCAACT CC AACATCTCAC GG AAACGCCCTP AG CTTCGAATTP	GACTCGTGA GACTCGTGG CGACCCGTGT CGACCGCGTGT TAATGCTGGC GACACGAGCT ACCCTAGGGT AACCACATGC GCGTACTCC	GTTACAAACT GCCATCCTGA GTCCGAACTG ACCGTCCAAT CCCCCACCTTC AACTAGTAAC GACGACGAACA TCCACCGCTT CCACGGCGAAGA
1 61 121 241 301 361 421 481 541	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCAAGA GTGCGGGC TGCTTAAT	TA GGCGCCG GT GACGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CC CTGCTTGC CC TGCTTGC CC TGGTAAGG CC CCGTCAAT GC GTTAGCTC	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG TCTCACTAG GG GACTTAACG CG TCCCCGAAG TT CCTCGCGTA TC CTTCGCGTA CC TTTGAGTT CG GCACTGAAG	G CCCGGGAACC C GCGAGTTCGC GCGAGTTCGC GGGATTCGC GGGATGATGAT GGGCCCAACT C AACATCTCAC GG AAACGCCCTM GG CTTCGAATTM TT CAACCTTGCC	G TATTCACCGC CCAGCCTGCA CGAGCCGTGT CTGACGCGTGT TAATGCTGGC GACACGAGCT ACTCTAGGGT AACCACATGC GTCGTACTCC TCCAACACCT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCAACT CCCCACCTC AACTAGTAAC GACGACGACC TGCCGCAGAGA TCCACCGCTT CCAGGCGGAG AGCACTCATC
1 61 121 241 301 361 421 481 541 601	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCAAGA GTCCGGGC TGCTAAT GTTTACGG	TA GGCGGCTG GACGGGGG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CC TGTCATCG CC TGTCATCG CC TGGTAAGG CC CCGTCAAT GC GTTAGCTCC CA TGGACTAC	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG GTCTAACG GG GACTTAACG GTCCCCGAAG TC CTCCGGAA TC CTTCGAGT CC GCACTGAAG CA GGGTATCTA	G CCCGGAACC CAGGCGAGTI C GCGAGTCGC G GCATGATGAT G GTGCCCAACT C AACATCTCAC G AAACGCCCTM AACCGCCCTM G CTCGAATTM T CAACCTTCCC G GCGGAAACCC	G TATTCACCGC GCAGCCTGCA GACTCGTTGT TAATGCTGGC GACACGAGCT ACTCTAGGGT AACCACATGC GTCGTACTCC TCCAACACCT TACCCATGCT	GTTACAAACT GGCATGCTGA GTCCGAACTG ACCGTCCAAT CCCCACCTTC AACTAGTAAC GACGACGACC TGCCCCAAGA TCCACCGCT TCCACGCGAG ACCACTCATC TTCGAGTCTC
1 61 121 241 301 361 421 481 541 601 661	GTCCACCT CTCATGGT TCCGCGAT AGAACGGT GTAGCACG CTCCGGTT AAGGGTTG ATGCACCA TGTCAAGA GTCCGGGC TGCTAAT GTTTACGG AGCGTCAG	TA GGCGGCTG GT GACGGCG TA CTAGCGAT TT TAAGAGAT TG TGTAGCCC. TG TCACCGGC. CC TGTCACTGC. CC TGGTAGG CC CGCTAAGG CC CGCTAAGG CC CGCTCAAT GC GTTAGCTC CA TGGACTAC TGGACCAC	GC TCCTAAAAG GT GTGTACAAG TC CGACTTCGT TT GCTTGCCCT AG GTCATAAGG AG GTCTAACG GG GACTTAACG GTCTCCCGAAG TC CTCCGGAA TC CTTCAGTT CG GCACTGAAG CA GGGTATCTA GG TAGCCGCCT	G CCCGGGAACC CAGGCGAGTI C GCGAGTCGC G GCATGATGAT G GCGCCAACI CAACTCCAAC G AAACGCCCT G CTCGAATT/ C AACCTGGC G CGGGAAACCC G CGGGAAACCC A TCCTGTCGC	G TATTCACCGC CCAGCCTGCA CCAGCCTGCA CTGACGCGTGT TATGCTGGC GACACGACGC CGACACGACGA AACCAACACGC CTCCTAACACCT CTCCAACACCT CTCCAACACCT CTCCCATGCT GTCCTTCCAT	GTTACAAACT GGCATGCTGA GTCCGAACTG GTCCGAACTA CCCCCACTTC AACTAGTAAC GACGACGACC TGGCGCAAGA TCCACCGCTT CCAGCGCGAG AGCACTCATC TTCGAGTCTC ATATCTACGC

1		1424 bp				
61	AGGCGGCTGG 1 TGACGGGCGG 1					
121	ACTAGCGATT (
181	TTAAGAGATT A					
241	GIGIAGCCCA (
301	GTCACCGGCA (GTCTCACCAG	AGTGCCCAAC	TTAATGCTGG	CAACTGATAA	TAAGGGTT
361	GCTCGTTGCG (
421	CIGIATCCAT (
481 541	CIGGIAAGGI : CCCGICAAII (
541 601	CGTTAGCTGC A					
661	ATGGACTACC J					
721	TACAGACCAG					
781	CTACACATGG 2	AGTICCACIG	TCCTCTTCTG	CACTCAAGTT	TCCCAGTTTC	CGATGCA
841	CTTCGGTTGA (
901	CCCAATAAAT (
961	AGCCGTGGCT					
	CAGACTITCG 1					
	GICICAGICC (
	AGCCGTTACC (
	CCATCITICA J					
1321	AGGTGTTATC (CCCCGCTTCT	GGGCAGGTTT	CCCACGTGTT	ACTCACCAGT	TCGCCAC
1381	CTCAAATGTA A	AATCATGATG	CAAGCACCAA	TCAATACCAG	AGTT	
Com	ence Pasult P	ouero e Drima	ar 940km			
	ence Result Re					
1	ACCTTAGG	CG GCTGGCTC	CT AAAAGGTTA	AC CCCACCGAC		
1	ACCTTAGG	CG GCTGGCTC	CT AAAAGGTTA	AC CCCACCGAC		
1 61	ACCTTAGG TGGTGTGA	CG GCTGGCTC CG GGCGGTGT	CT AAAAGGTTA	G GGAACGTAT	CACCGCGGCA	TGCTGAT
1 61 121	ACCTTAGG TGGTGTGA CGATTACT	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG	CT AAAAGGTTA GT ACAAGGCCC AC TTCGTGCAC	CG GGAACGTAT	CACCGCGGGCA CCTGCAGTCC	TGCTGAT GAACTGA
1 61 121 181	ACCTTAGG TGGTGTGA CGATTACT CGGTTTTA	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTGC	CT AAAAGGTTA GT ACAAGGCCO AC TTCGTGCAO TT GCCCTCGCO	CG GGAACGTAT GG CGAGTTGCA GA GTTCGCGAC	CACCGCGGGCA CCTGCAGTCC CGTTGTACCG	TGCTGAT GAACTGA TCCATTG
1 61 121 181 241	ACCTTAGG TGGTGTGA CGATTACT CGGTTTTA CACGTGTG	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT	CT AAAAGGTT/ GT ACAAGGCCC AC TTCGTGCAC TT GCCCTCGCC CA TAAGGGGC/	CG GGAACGTAT GG CGAGTTGCA GA GTTCGCGAC AT GATGATCTG	CACCGCGGGCA CCTGCAGTCC CGTTGTACCG CGTCGTCCCC	TGCTGAT GAACTGA TCCATTG ACCTTCC
1 61 121 181 241	ACCTTAGG TGGTGTGA CGATTACT CGGTTTTA CACGTGTG	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT	CT AAAAGGTT/ GT ACAAGGCCC AC TTCGTGCAC TT GCCCTCGCC CA TAAGGGGC/	CG GGAACGTAT GG CGAGTTGCA GA GTTCGCGAC	CACCGCGGGCA CCTGCAGTCC CGTTGTACCG CGTCGTCCCC	TGCTGAT GAACTGA TCCATTG ACCTTCC
1 61 121 181 241 301	ACCTTAGG TGGTGTGA CGATTACT CGGTTTA CACGTGTG GGTTTGTC	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT AC CGGCAGTC	CT AAAAGGTTA GT ACAAGGCCC GAC TTCGTGCAC TT GCCCTCGCC TCA TAAGGGGCA TC ACTAGAGTC	CG GGAACGTAT GG CGAGTTGCAG GA GTTCGCGAC AT GATGATCTGJ GC CCAACTTAA	CACCGCGGGA CCTGCAGTCC CGTTGTACCG CGTCGTCCCC CGTCGTCCCCC	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA
1 61 121 181 241 301 361	ACCTTAGG TGGTGTGA CGATTACT CGGTTTAI CACGTGTG GGTTTGTC GTTGCGCT	CG GCTGGCTG CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA	CT AAAAGGTTA GT ACAAGGCCO AC TTCGTGCAO TT GCCCTCGCO CA TAAGGGGCA TC ACTAGAGTO ACT TAACCCAAO	CG GGAACGTAT SG CGAGTTGCA SA GTTCGCGAC MT GATGATCTG/ GC CCAACTTAA CA TCTCACGAC	CACCGCGCGCA CCTGCAGTCC CGTTGTACCG CGTCGTCCCCC CGTCGCCAACT CGAGCTGACG	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA
1 61 121 181 241 301 361 421	ACCTTAGG TGGTGTGAI CGGTTTAL CACGTGTG GGTTTGCC GTTGCGCT ACCACCTG	CG GCTGGCTG CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTTGCGTT	CT AAAAGGTTA GT ACAAGGCCO AC TTCGTGCAO TT GCCCTCGCO CA TAAGGGGCA TC ACTAGAGTO CC TAACCCAAO CC CGAAGGAA	CG GGAACGTAT" GG CGAGTTGCA GA GTTCGCGAC AT GATGATCTG GC CCAACTTAA CA TCTCACGAC AC GCCCTATCT	CACCGCGGGCA CCTGCAGTCC CGTTGTACCG CGTCGTCCCCC GCTGGCAACT CGAGCTGACG TAGGGTTGGC	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT
1 61 121 181 241 301 361 421	ACCTTAGG TGGTGTGAI CGGTTTAL CACGTGTG GGTTTGCC GTTGCGCT ACCACCTG	CG GCTGGCTG CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTTGCGTT	CT AAAAGGTTA GT ACAAGGCCO AC TTCGTGCAO TT GCCCTCGCO CA TAAGGGGCA TC ACTAGAGTO CC TAACCCAAO CC CGAAGGAA	CG GGAACGTAT SG CGAGTTGCA SA GTTCGCGAC MT GATGATCTG/ GC CCAACTTAA CA TCTCACGAC	CACCGCGGGCA CCTGCAGTCC CGTTGTACCG CGTCGTCCCCC GCTGGCAACT CGAGCTGACG TAGGGTTGGC	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT
1 61 121 181 241 301 361 421 481	ACCTTAGG TGGTGTGA CGATTACT CGGTTTTA CACGTGTG GGTTTGCC GTTGCGCT ACCACCTG AAGACCTG	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTGC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTTGCGTT GT AAGGTTCT	CT AAAAGGTTA GT ACAAGGCCC GAC TTCGTGCAG CT GCCCTCGCC CC TAAGGGGCA CT AACGGGCA CC CGAAGGAA TC GCGTAGCT	CG GGAACGTAT GG CGAGTTGCAG GA GTTCGCGAC AT GATGATCTG GC CCAACTTAA CA TCTCACGAC AC GCCCTATCT TC GAATTAAACO	CACCGCGCGCA CCTGCAGTCC CCTTGTACCG CCTGCTCCCC GCTGGCAACT CGAGCTGACG TAGGGTTGGC CACATGCTCCA	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG
1 61 121 181 241 301 361 421 481 541	ACCTTAGG TGGTGGA CGATTACT CGGTTTAC GGTTTGTC GGTTGCC GTTGCGCT ACCACCTG AGACCTG GGGCCCCC	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTGCC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTGCGGTT GT AAGGTTCT GT CAATTCCT	ICT AAAAGGTI/ ICT ACAAGGCCC AC TTCGTGCAC ICT GCCCTCGCC ICT ACAGGGCC/ ICT AAAGGGCC/ ICT TAACCCAAC ICT CAACCCAAC ICC CGAAGGAA/ ICT GAGTTCA/ ICT GAGTTCA/	CG GGAACGTAT GG CGAGTTGCA(SA GTTCGCGAC AT GATGATCTGJ GC CCAACTTAA CC TCTCACGAC AC GCCCTATCT(FC GAATTAAAC(AC CTTGCGGTC(<pre>P CACCGCGGCA G CCTGCAGTCC G CGTTGTACCG A CGTCGTCCCC G GCTGGCACCT A CGAGCTGACG C TAGGGTTGGC C ACATGCTCCA G TACTCCCCAG</pre>	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG GCGGAGT
1 61 121 241 301 361 421 481 541 601	ACCTTAGG TGGTGTGA CGATTACT, CGGTTTAL CACGTGTG GGTTGCCG ACCACCTG ACCACCTG GGGCCCCC TAATGCGT	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTGCC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTTGCGTT GT AAGGTTCT GT CAATTCCT TA GCTCCGGC	AAAAGGTT/ GT ACAAGGCCC AC TTCGTGCAC TT GCCCTGCC CCA TAAGGGCC CC ACTAGAGGTC CC CGAAGGAC TC CCAAGGAC CC CGAAGGAC TC GCCTACT TT GAGTTCAJ AC TGAAGGCC	CG GGAACGTAT GG CGACTTGCA GATGATCTGJ CCAACTTAA CCACTCACGACJ AC GCCCTATCT CGAATTAAACC AC CTTGCGGTC GG AAACCCTCCJ	<pre>CACCGCGGCA CCTGCAGTCC CGTTGTACCG CGTGGCACCCC GCTGGCAACT CGAGCTGACG TAGGGTTGGC ACATGCTCCA ACATGCTCCAG ACACCTAGCA</pre>	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG GCGGAGT CTCATCG
1 61 121 181 241 301 361 421 481 541	ACCTTAGG TGGTGTGA CGATTACT, CGGTTTAL CACGTGTG GGTTGCCG ACCACCTG ACCACCTG GGGCCCCC TAATGCGT	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTGCC TA GCCCAGGT AC CGGCAGTC CG TTGCGGGA TC TTTGCGTT GT AAGGTTCT GT CAATTCCT TA GCTCCGGC	AAAAGGTT/ GT ACAAGGCCC AC TTCGTGCAC TT GCCCTGCC CCA TAAGGGCC CC ACTAGAGGTC CC CGAAGGAC TC CCAAGGAC CC CGAAGGAC TC GCCTACT TT GAGTTCAJ AC TGAAGGCC	CG GGAACGTAT GG CGAGTTGCA(SA GTTCGCGAC AT GATGATCTGJ GC CCAACTTAA CC TCTCACGAC AC GCCCTATCT(FC GAATTAAAC(AC CTTGCGGTC(<pre>CACCGCGGCA CCTGCAGTCC CGTTGTACCG CGTGGCACCCC GCTGGCAACT CGAGCTGACG TAGGGTTGGC ACATGCTCCA ACATGCTCCAG ACACCTAGCA</pre>	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG GCGGAGT CTCATCG
1 61 121 241 301 361 421 481 541 601	ACCTTAGG TGGTGTGA CGATTACT CGGTTTAL GGTTGTG GGTTGGC ACCACCTG AAGACCTG GGGCCCCC TAATGCGT ACGGCATG	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTTCC TA GCCCAGGT AC CGGCAGTC GTGCGGGA TC TTGCGGGA TC TTGCGGTCT GT CAATTCCT TA GCTCCGGC GA CTACCAGG	CT AAAAGGTT/ GT ACAAGGCCC AC TTCGTGCAC TT GCCCTGCC CCA TAAGGGCC/ TC ACTAGAGTC CC CAAAGGAC CC CGAAGGAA TC GCCTACTT TT GACTTCAJ AC TGAAGGCC GT ATCTAATCC	G GGAACGTAT GG CGAGTTGCA GATCGCGAC AT GATCATCTG CCCAACTTAA CC TCTCACGAC GCCCTATCT CC GAATTAAAC CC GCCCTATCT CC GAATTAAAC CC CTTGGGTC GG AAACCCTCCI CT GTTCGCTAC	<pre>CACCGCGGCA CCTGCAGTCC CGTTGTACCG A CGTCGTCCCC GCTGGCAACT A CGAGCTGACG TAGGGTGGC A ACATGCTCCA A ACACCTAGCA CATGCTTCG CATGCTTCG</pre>	TGCTGAT GAACTGAI TCCATTG' ACCTTCC' AGTAACAI ACGACCA' GCAAGAT CCGCTTG' GCGGAGT CTCATCG' AGTCTCA
1 61 121 181 241 301 361 421 481 541 601 661 721	ACCTTAGG TGGTGTA CGATTACT, CGGTTTACT, CACGTGTG GGTTTGTC, GTTGCGCT ACCACCTG AAGACCTG GGGCCCCC TAATGCGT ACGGCATG TCAGTGC	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTGC TA GCCCAGGT CCG TGCGGAGTC CTGCGGGA GT AAGGTTCT GT CAATTCCT TA GCTCCGGC GA CTACCAGG AG ACCAGGTA	AAAAGGTT/ GT ACAAGGCCC AC TTCGTCCAC TTCGTCCAC TTCGTCCAC ATAAGGGCC/ TC ATAAGGGCC/ TC ACTAAGGGCC CC CGAAGGAA/ TC GCCTACCTI TT GAGTTCCA/ CC TGAAGGCC GT ATCTAATCC GC CGCCTCGC	G GGAACGTAT GG CGAGTGCAC GATGATCTGI GATGATCTGI CCAACTTAA CCCCTACTGAC GCCCTATCTGI GGCCCTATCTGI GGCCCTATCTGI GG AAACCCTCCI CTGCGGGTCI CC ACTGGTGTTI	CACCGCGCGCA CCTGCAGTCC CGTTGTACCG CGTGGCACC CGTGGCAACT CGGGCTGACC TAGGGTGGC ACATGCTCCA ACATGCCCAA ACACCTAGCA CATGCTTCG TTCCATATAT	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG GCGGAGT CTCATCG AGTCTCA CTACGCA
1 61 121 181 241 301 361 421 481 541 601 661	ACCTTAGG TGGTGTA CGATTACT, CGGTTTACT, CACGTGTG GGTTTGTC, GTTGCGCT ACCACCTG AAGACCTG GGGCCCCC TAATGCGT ACGGCATG TCAGTGC	CG GCTGGCTC CG GGCGGTGT AG CGATTCCG AG AGATTGC AG AGATTGC CG TGCCAGGT CG TGCGGGA TC TTGCGGGA TC TTGCGGT GT AAGGTTCT GT CAATTCCT A GCTCCGGC AG CTACCAGG AG ACCAGGTA CA CCAGGAGT	AAAAGGTT/ GT ACAAGGCCC AC TTCGTCCAC TTCGTCCAC TTCGTCCAC ATAAGGGCC/ TC ATAAGGGCC/ TC ACTAAGGGCC CC CGAAGGAA/ TC GCGTACCTI TT GAGTTCAA CC TGAAGGGCC GT ATCTAATCC GC CGCCTCGC	G GGAACGTAT GG CGAGTTGCA GATCGCGAC AT GATCATCTG CCCAACTTAA CC TCTCACGAC GCCCTATCT CC GAATTAAAC CC GCCCTATCT CC GAATTAAAC CC CTTGGGTC GG AAACCCTCCI CT GTTCGCTAC	CACCGCGCGCA CCTGCAGTCC CGTTGTACCG CGTGGCACC CGTGGCAACT CGGGCTGACC TAGGGTGGC ACATGCTCCA ACATGCCCAA ACACCTAGCA CATGCTTCG TTCCATATAT	TGCTGAT GAACTGA TCCATTG ACCTTCC AGTAACA ACGACCA GCAAGAT CCGCTTG GCGGAGT CTCATCG AGTCTCA CTACGCA

Figure 4. Nucleotide sequences of (a) B1, (b) B2, (c) S1 and (d) S2 isolates.

from different types of bamboo shoots. Bamboo Shoot Polysaccharide fermentation increases the diversity of the bacterial community by increasing the abundance of *Firmicutes*, *Actinobacteria* and *Proteobacteria* (Li *et al.*, 2021).

Lactobacillus fermentum was only found in Lemea made from yellow bamboo shoots and L. plantarum was found in yellow bamboo shoots and betung. Prebiotics in foodstuffs can trigger the growth of Lactobacillus (Macfarlane and Cummings, 1999). Oligosaccharides and fiber are prebiotics that promote the growth of specific bacteria found in the gut. Bamboo shoots are a good source of fibre (Felisberto *et al.*, 2017). At 100 g of fresh weight, the yellow bamboo shoots contain 6.51 g of carbohydrates, 4.24 g of fibre while betung contained 4.90 g of carbohydrates and 3.54 g of fibre (Chongtham *et al.*, 2011). Different bamboo species contained different macronutrients (Adebola *et al.*, 2014). The differences in the content of bamboo shoots may affect the types of bacteria found in Lemea products.

4. Conclusion

A total of four *Lactobacillus* isolates were found in *Lemea* were from the *Lactobacillus* genus. *L. plantarum* and *L. fermentum* were isolates which were identified molecularly by 16S rRNA. *Lactobacillus fermentum* was only found in the fermentation process of yellow bamboo

shoots while *L. plantarum* was found in yellow bamboo shoots and betung.

Conflict of interest

The authors declare no conflict of interest.

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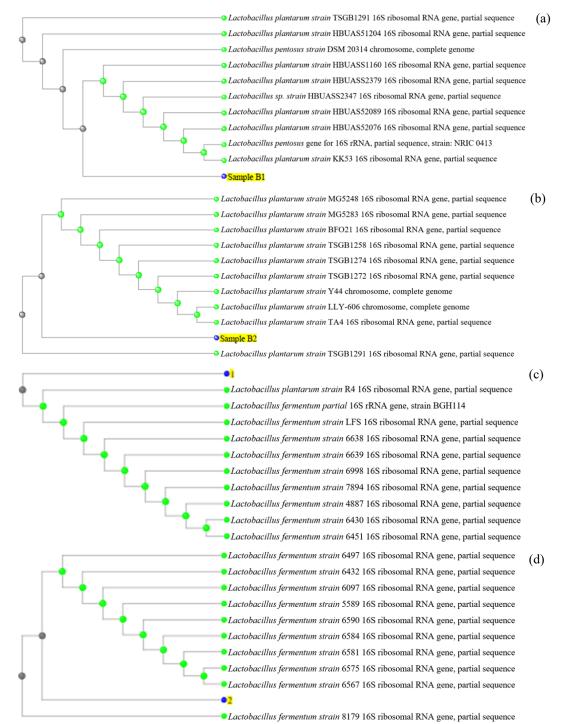


Figure 5. Phylogenetic tree of (a) B1, (b) B2, (c) S1 and (d) S2 isolates

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