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SURAT TUGAS

Nomor : 00208/A.1.5/ST.FTP/11/2020


Dekan Fakultas Teknologi Pertanian Universitas Katolik Soegijapranata, Semarang dengan ini memberikan tugas kepada:

- Nama : **Dr. Ir. Lindayani, MP.** dan Dr. Dra. Laksmi Hartajanie, MP
- Status : Dosen Fakultas Teknologi Pertanian Universitas Katolik Soegijapranata, Semarang.
- Tugas : Sebagai Presenter (Poster Presentation) ICSAF 2020 "**Study on Phylogenetic DNA of "Ampel" Bamboo (Bambusa vulgaris) Shoots Pickle**" dalam kegiatan 4th International Conference on Sustainable Global Agriculture and Food (ICSAF) in Taiwan via online conference.
- Tempat : Online.
- Hari/Tanggal : Jumat, 06 November 2020
- Lain-lain : Harap melaksanakan tugas dengan sebaik-baiknya dan penuh tanggung jawab, serta memberikan laporan setelah selesai melaksanakan tugas.

Semarang, 06 November 2020

Dekan,




Dr. R. Probo Y. Nugrahedhi, M. Sc.

NPP: 0581 2001244

SURAT KETERANGAN
No. 00412/A.1.5/FTP/02/2021

Nama-nama dosen Fakultas Teknologi Pertanian Universitas Katolik Soegijapranata, Semarang berikut ini :

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3. Mellia Harumi, S.Si., M.Sc
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9. Inneke Hantoro, STP, MSc.
10. Prof. Dr. Ir. Budi Widianarko, MSc.
11. Dr. Ir. Lindayani, MP.
12. Dr. Laksmi Hartayanie, MP.

Adalah benar-benar telah mengikuti the 4th International Conference on Sustainable Global Agriculture and Food pada 06 November 2020 sebagai Presenter oral maupun Poster yang diselenggarakan oleh Fu Jen Catholic University Taiwan secara daring.

Demikian surat keterangan ini dibuat sebagai pengganti sementara sertifikat yang belum diterbitkan oleh panitia.

Semarang, 09 Februari 2021

Dekan,



Dr. R. Probo Y. Nugrahedi, M. Sc.

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2020
November 6th to 7th
TAIWAN

ICSAF²⁰

FUTURE TRENDS IN FOOD SCIENCE AND TECHNOLOGY

4th International Conference on Sustainable
Global Agriculture and Food (ICSAF 2020)

Acceptance Letter

October 28, 2020

Dear Dr. Lindayani,

We are very pleased to confirm that your submission entitled below has been accepted for the 4th ICSAF in New Taipei City, Taiwan, November 6-7, 2020.

Study on Phylogenetic DNA of “Ampel” Bamboo (*Bambusa vulgaris*) Shoots Pickle

Paper ID: ICSAF-P003 [FM]

Presentation Type: Poster

Authors: Lindayani, Laksmi Hartayanie, Rose Marie Aldina

Affiliation: Soegijapranata Catholic University

Session/Topic: Food microbiology and safety

Please check the conference information given on the ICSAF 2020 in Taiwan website (<https://icsaf.org/>) for the details of registration and paper upload process. The presentation guideline and format was shown in the conference website. You can check the session you will be presenting from the conference program to be announced on the website soon.

We look forward to your presentation and participation in ICSAF 2020. Please do not hesitate to contact us should you require further information and/or guidance.

Yours Sincerely,



ICSAF

Prof. Bing-Huei Chen
Chairman of the Organizing Committee

Study on Phylogenetic DNA of "Ampel" Bamboo (*Bambusa vulgaris*)

Shoots Pickle



1

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ABSTRACT

Lactic acid bacteria from isolate of "Ampel" bamboo shoots pickle have the potential to be a source of probiotics. *Lactobacillus* is produced from fermentation processes, its beneficial properties for the human body. This study aims to analyses of the phylogenetic tree of "Ampel" bamboo shoots pickle isolates. The 16S rRNA gene sequences obtained from previously research were copied to the GenBank website database (NCBI) which consists of bacterial information for identification and then 5 figures having the highest percentage of the identity is and the FASTA gene is copied for alignment by BioEdit software. After being aligned by BioEdit, the data is stored and then copied to the MEGA X software for analyzing kinship relationships and making phylogenetic trees using the neighbor-joining method. The results of the identification of "Ampel" bamboo shoots pickle namely A18 isolate is *Lactobacillus plantarum* and B3 is *Lactobacillus buchneri*. The function of *Lactobacillus plantarum* on the health of the human body is that it can relieve irritation of the digestive tract, cure heart disease and respiratory tract and also maintain healthy skin. *Lactobacillus buchneri* also contributes to the health of the human body such as reducing cholesterol levels, antioxidant activity and high antimicrobial. The conclusion is *Lactobacillus plantarum* and *Lactobacillus buchneri* have good probiotic functions to be developed deeper.

Keys: Bamboo shoot pickle, A18, B3, *Lactobacillus*

Introduction

Lactic acid bacteria (LAB) have been isolated from various fermented food. The genus *Lactobacillus* is the largest group of family Lactobacteriaceae and have beneficial for human health (Wang et al., 2012). Various fermented foods are consumed by people in Indonesia such as tempeyak, mandai, dadih, sauerkraut (sayur asin), bamboo shoot pickles. Isolation of LAB from bamboo shoot pickles has been previously reported (Lindayani et al., 2018). Phylogenetic analysis based on 16S rRNA gene sequences is a method used to study such microbial biodiversity (Malik et al., 2015). This method used to help trace phylogenetic relationship from various sources.

Phylogeny is needed as a basic of systematic science in biological evolution to know the history of evolutionary an organism (Mount, 2001). Phylogenetic analysis can be carried out with the 16S rRNA gene sequence (Clarridge, 2004). This study aims to analyses of the phylogenetic tree of "Ampel" bamboo shoots pickle isolates.

In this research was used two isolates from "Ampel" bamboo shoots pickles, i.e. A18 and B3. Flow chart of this study can be seen at Figure 1.

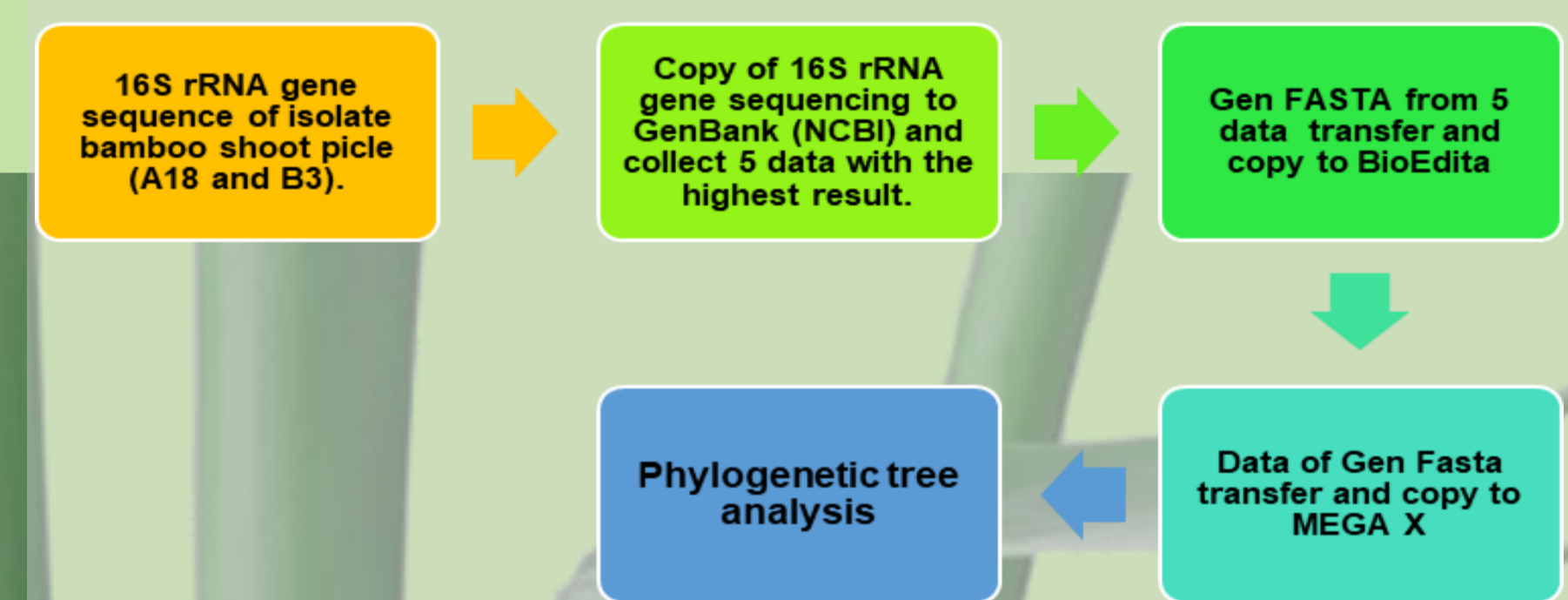


Figure 1. Flow chart of phylogenetic tree of bamboo shoot pickle isolate

Results and Discussion

Table 1. 16S rRNA gene sequencing of A18 (27F primer)

Sample	DNA Sequence
A18 (27F Primer)	NNNNTNNNGNNNGTACATCGAGTCCGAGTGGGCTGGTTGGTATTGATGTAG- GATGCTTCATTAAGTAACTTAACATTAAGACGAGTGGCGAAGTGGGTAACAGTGGTAACTGGCTTAAGAGTTAAGAGGATTAACCTGAACTGGAACAGGT GCTAATACCGTAAACAAACAACCACTGTGTTGGTTAAAAGATGGCTTCGCTGATCACTTAAGATGACCCGGCCGATTAGCTTGTGTAAGTAA ACCGCTTCAAAAGCAATGATAGCTAGGACCTGAGAGGTAATCGGCCACATGGGAGTGCAGCAGGCACTACCGGGAGCCAGTATGAGGA ATCTTCACAAGGAGTAACTGATGAGCAAGCCGCGTGAAGTGGAGGTTTCGGCTCGTAAAGTGGTTGGTTGGGAAAGAACTGATGAGTAACTG AACTGTTCACTTTCAGGATCAACCAAGAAAGCCGCTAACACTGCGCAGCAGCCGCTGATGAGTTGGGAGGCTTTCCCGCTTATTTGG CGTAAAGCAGCGACGCGGTTTCAGTTCTGATGTAAGCCTTCGGTTAACCAGGAAAGTGCATCGGAAACAGGAGACTTGAAGTGAAGAGGGA GTGAACTCCTATGTAGCCTGAAATCGTAGATATAGGAAGACCAAGTGGCAGGAGGCTGCTGGTCTGTAAGTCAAGCTGAGGCTGAAAGC GGGTAGCAGCAAGGATTAGATACCTGTAGCTAATCGCTGAAAGTGGTGAAGTGGTGAAGGTTCCGCTCAAGTGCAGCTAACGCATTAAG CACTCCGCTGGGGTACGAGCCAGGTTGAAGTAAAGTAAAGGAAAGTGGGGGGCCGCAAGCGGTGGAGCATGGGTTAAATCGATCAGCGAAG AACTTCACAGCTTCAGCATCTTTCGCAACCTAAGAGATTAGCGGTTCCCTCGGGANINGAATGAACAGTGGTGCATGGTTGCTGAGTGGTGTCT AGATGTTGGTAAAGTCCGCAAGAGCGCAACCCTTTATTGTTAGTTCAGCATTGAGTGGGCTCTGAGCAAGAGCTGCGTGCAGCAAGCGGAGGAG GGATAGCCTCAATTCATCTGCCCCTNNAGTGGGCTACAGNGCTAAATGGAGGTAAACAGGAGTCCGGAACGNNAGTCAACTAATCAGGAGGCGCAGCA GTGAAATGAGGNNACCCNNCNGMAATGGAAACCCGAAACCGGAAANNNCCGGAAACCTCCGCTTACCCGCCCTCCCGNNATTGTA CCCACCGGNNAGCTGGACCCCTAAGGGGAAANNNGGNNGTNNNNGGCTCTN

Table 2. 16S rRNA gene sequencing of A18 (1429R primer)

Sample	DNA Sequence
A18 (1429R Primer)	CHNNNNTCNGNCACCTAGACGGCTGCCCCGAGGTTACCTACCAGCTT- GGGTGTACAACTACTGTTGTGACCGGGGTGTGACAGCCCGGGAACCTATTACCGTGGCATCTGATCACCATTAGAGGATTCAAGGATTCCAATC ATGAGGCGAGTTCGAGCTAACTCCAAGTGAAGAGCTGTTAAAGATGATCTGAAGTGGACCGGGTTCGCGACTGTTACCGCTCAATTGATGACG TGTGACGCAAGTGAAGGCGGATGATGATGACCTACCCCACTCCTCCGTTGTGACCCGAGCTTGTAGATGGCCCACTGATGAGTGCATCCG AACTAACAATAGGTTGCTGCTGGGAACTAACCAACTCAGCACAGGAGTGAAGCACTGCAAGCAGCTGATCTGATCTGTCCCGAAGG AACCGCTAATCTTGTGTTGGAGAAAGTCAAGACTGGTAAGTCTTCGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT CAATCTCTTGAAGTTCAACTTTCGCGTGAAGTCCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT ACTCATCTGACCGTGAAGTCAAGGATCACTCACTGCTTCCGCTGCTTCAAGCTGCTTCAAGCTGCTTCCGCTGCTTCAAGCTGCTTCCGCTGCTT AGCCGAGGTTTCACATCAGACTAAGAAACCGCTGCTGCTTACGCCAATAAATCGGACAGCCTGCCACTAGTATACCGGGTCTGCTG GCACGTAGTAGCGGCTGCTTCTGGTTGAGTCAAGATGTGAACATCTCACTCACTGCTTCTTCAACAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT CTCATCANTAGCGGCTGCTCATCAACTTCTGCTCCTTGTGAAGATCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT GGCGGATAACCTTCAAGTGGTCACTNTCTGCT NTTAAACCCCGGGGTTGTTTAAACGGTAAACCCGCTTCAAGTTTCCCTTTTGGGGGGTCCCGGTTCCCGCTCCTCCCGCCTCCCGCCTCCCGCCT AAACCTTAAAGAACCTAACCAAAAAAGTTNNNNNTTANCCGCGGCCCCNNAGGAGTANTNACGNNAAAA

Table 3. 16S rRNA gene sequencing of B3 (27F primer)

Sample	DNA sequence
B3 (27F Primer)	NNNNNNNNNNNNNCATNANACATGAGTCCGTAACCAAGTAGCCAAAGTTCGNNNT- GTATCCCTCACTCCGAGTAGGTAACTCCGACCCAGCTTCTCCGGAAGTAAATGTTAAAAAAGGTTGAAGTGGATGAGCTTAAACGGGAGTCCG GTGNNATCCGGTTTCACTCAAACTCCGGGCTTGGATTAAAAGATGGCTCGGATATCACTTAAGATGAGCAGCCGGCGGCTTAACTTGTGGCA AGGTACTCTCAACAGGAAATGATCCATTGGCAGCTGAGAGGGTGTCCGCCACATTGGACTGAGCAGTATGATCACTCACTCACTCACTCACTCACT GTGGAAATCTCCCAAGTGAAGGAT GTGGAAATCTCCCAAGTGAAGGAT CGGATTATTTGGGCTAAAGGAGCGAGCGGTTCTTAGGTTGAT GAGTGCAGAGGAGCAGTGCAGTCCATCTGTGACGGTGAATGCGTAGATATGGAAGAACCAAGTGGCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCT ACGCTGAGCTCGAAAGCATGGTGAACAGGAT CAGTCTGACCTAACTAAGCTACCGCTGGGAGTACAGCAGCTAGTTGAACTAAGGAAATGACCGGCGCCGCAACAGCGGTGAGCA TGTTGGTTAAATCTGATCTACAGCACTACCGGCTTCCAGGCTTGGAACTCTTCGCAACCTAAGAAATGAGGCTTCCTCCCGGGAACGAATGA CAAGGCTGATAGTCTGTGCTG GAGTGGGCTNAGCAAAAAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT NNGGGCAAAATGGAGGGTAACCGCTGCGAAACCGGGGGCGCAAGCTTNTTTAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT NCCNNNAAGTGAAGACCNNAAGNANCCGGGGAACCCNNNCCGGGAAATTTCCCGGCTTNTTAAACCNNNNAAGGAGGAGGCA AGTTTTAACCCCGGGGGNNNTTTNNNNNNNCCNCTCGGGGAAANNATGAGTNTGNGTGGANNANAAACNNNTAAATT GTTTTTAANNA

Table 4. 16S rRNA gene sequencing of B3(1429R primer)

Sample	DNA sequence
B3 (1429R Primer)	NNNNNTNNNNNNCTCNATNGCAGGTTNGTGGCAGNNANATACATCAAGTCG- TAAACNGGTAACTCACTCATGTTGTACGGCGGGGTACAAGCCGGGGAACGTATTACCGTGGCATGCTGAGCCATGATTCAAGCTAA GCCAAATCAAGTACCCTAATGACGCTAAATCCGAAGTGAAGAGCCCTTAAGAGAAAGCTTGAACCTGCGGTTTCGCGACTGTTGACCG TCATTTAGCACTGTGTAGCCAGGCTAAGGGGCTGATGATTTGACTCACCCTTCCCTGGTTGTACCGGCACTTCTGATGAG TGCCCACTGAATCTGGAACAATCAAGGGTGGCGTCTGGGGAGCTAACCAACTCTCAGCAGCAGGCTGACGCAACCAAGTAAACC ACTGTCTATGCTCCGAAGGAAAGCCTAATCTTAGTTGGCAGGAAGTAAAGCACTGGAAGGTTGCTCGCTAGATCGAATTAAC CACATGCTCACCGCTGTGCGGGCCCGCTCAATCTTTGGTTCACCTGGCTGACTCCAGGCGGAGTCTAAATCGTTAGCTGAC GCATGGAAGGCGGAAACCTCCAACTTAGCACTCATCTGTTTACGGATGGACCAAGGTTATCTAAGTCTGCTGCTCAATCTTCGAG CTCAGGCTCAGTTACAGCACAGCAGCCGCTTCCGCTGCTTCTTCATATATCTACGATTTTCACCGTACACAGGAGTCCACCTGCT CTTCGCACTCAAGTCTCGGTTCCCGATGCACTTTCGGTTAAGCGGAGGCTTTCNNATCAGAATAAAGAAACCGCGCTCCCTCCTTCAC GCCAAAAAATCCGCAACNNTTCCACTACGTTTACCGCGCTGCTGGCANNANSTAAAGCTTGGCTTCTGTTGGAAAAACCGCAAA GNHTGAAAGTTCCTCCCTGCTTCTTNCAAAAGAGATTTTACAGCCGAAACCTCANNATTTNNGGGGCTTCCCTCC CAGAAATTCGGCATTGGAATACTTAACCGCCCTCCGGGAAATTTGGCCGGTNNNAANNNNAAGTGGCAATTTCC TTCAENNGNNAACCTTNACTTTCCTTTGGGCGGTTACTTTCACAAAGCANNNAAGCCCGGGCCTACCACAAAGGTGAC CAACNCTTTTTAAACCAACCGGGGTTTGGGGTTTAAACGGCTTNAAGCCCTNNNTTCAAGGTTTCCCGCATTAAGGGGGGG GTTTNNAGGTTTAAACCCCTNTNNCCCTTCCCTTTTAAAAANNNTAAAGCCNNAACAAAAAAAGGGGTGTTCTTTTATATC CNCCGCGGNNAANNAATAATATTAGTNTTATGATTANN

Based on the results obtained from MEGA X analysis, the lactic acid bacteria found in bamboo shoots pickled isolate A18 is *Lactobacillus plantarum* (91.96%). Meanwhile, for the comparison of other lactic acid bacteria are *Lactobacillus paraplantarum* (91.71%), *Lactobacillus modestisalitolers* (91.72%), *Lactobacillus sanviri* (91.63%) and *Lactobacillus subebicus* (91.38%). *Lactobacillus plantarum* which has the highest percentage as the identity of the bamboo shoot isolate fermentation A18.

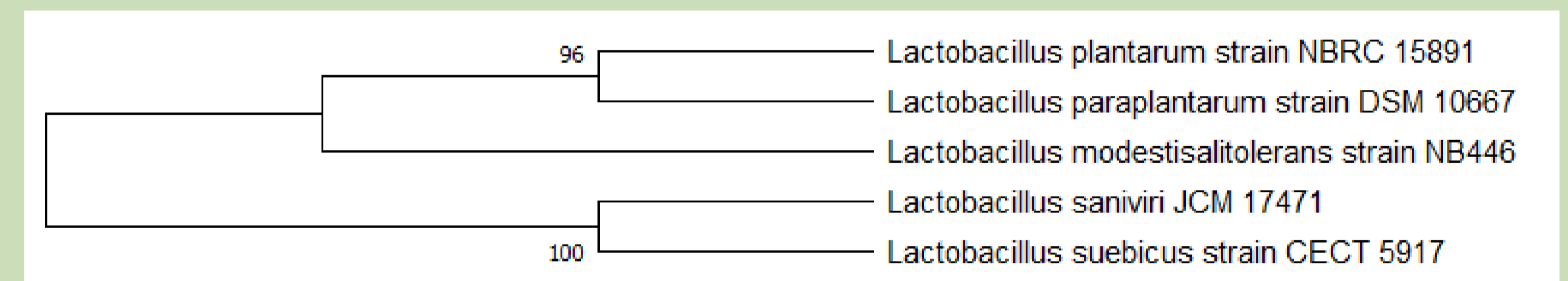


Figure 2. Phylogenetic tree of A18 analysis results from MEGA-X software on the relationship of *Lactobacillus plantarum* compare to other lactic acid bacteria.

Based on phylogenetic tree described by MEGA X software, isolate B3 is *Lactobacillus parabuchneri* (94.39%). Meanwhile, lactic acid bacteria for other comparisons were *Lactobacillus buchneri* (94.19%), *Lactobacillus sunkii* (94.19%), *Lactobacillus otakiensis* (94.19%) and *Lactobacillus kefir* (94.09%). *Lactobacillus parabuchneri* which had the highest percentage as the identity of the lactic acid bacteria owned by fermentation of bamboo shoots pickle LLB3.

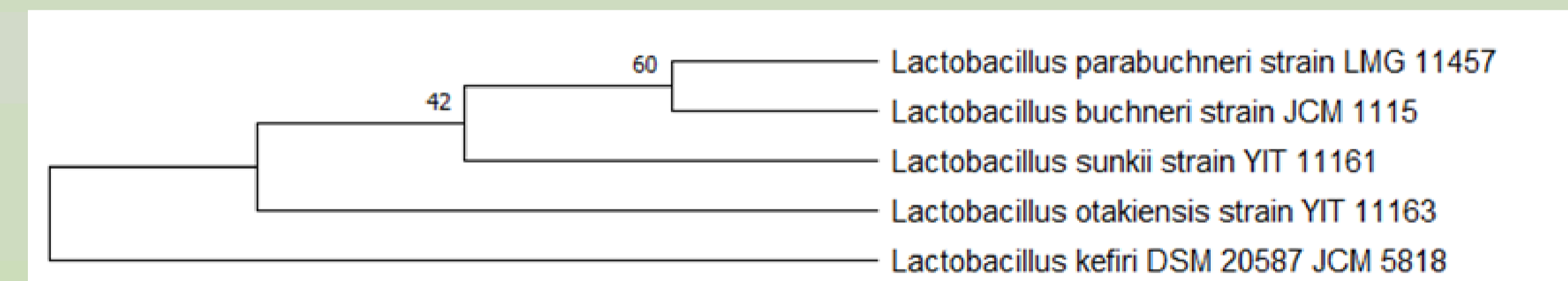


Figure 3. Phylogenetic tree of B3 analysis results from MEGA-X software on the relationship of *Lactobacillus parabuchneri* compare to other lactic acid bacteria

Based on GenBank, it is known that A18 bamboo shoots pickle isolates are *Lactobacillus plantarum* and *Lactobacillus paraplantarum* and B3 are *Lactobacillus parabuchneri* and *Lactobacillus buchneri*. Followed by phylogenetic trees, A18 and B3 that are most closely related have almost the same characteristics and functions that they contribute (Mc Donald & Kreitman, 1991). Both of them have a potential probiotic (Lindayani et al, 2018).

Conclusion

- "Ampel" bamboo shoot pickles A18 isolate contains *Lactobacillus plantarum* and *Lactobacillus paraplantarum*; bamboo shoot pickles B3 isolate contains *Lactobacillus parabuchneri* and *Lactobacillus buchneri*.
- Lactobacillus plantarum* and *Lactobacillus buchneri* have the potential of probiotics.

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