

7. LAMPIRAN

Lampiran 1. Proses Identifikasi Sekuens Gen 16S rRNA Isolat Acar Rebung Bambu “Ampel”

Standard Nucleotide BLAST

BLASTn programs search nucleotide databases using a nucleotide query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Query subrange From To

Or, upload file No file chosen

Job Title

Align two or more sequences

BLAST results will be displayed in a new format by default
You can always switch back to the Traditional Results page.

Choose Search Set

Database Standard databases (nr, etc.) rRNA/ITS databases Genomic + transcript databases Betacoronavirus

16S ribosomal RNA sequences (Bacteria and Archaea)

Organism Optional

Exclude Optional Models (XM/XP) Uncultured/environmental sample sequences

Limit to Optional Sequences from type material

Entrez Query Optional

Lampiran 2. Hasil Identifikasi Sekuens Gen 16S rRNA Isolat Acar Rebung Bambu “Ampel”

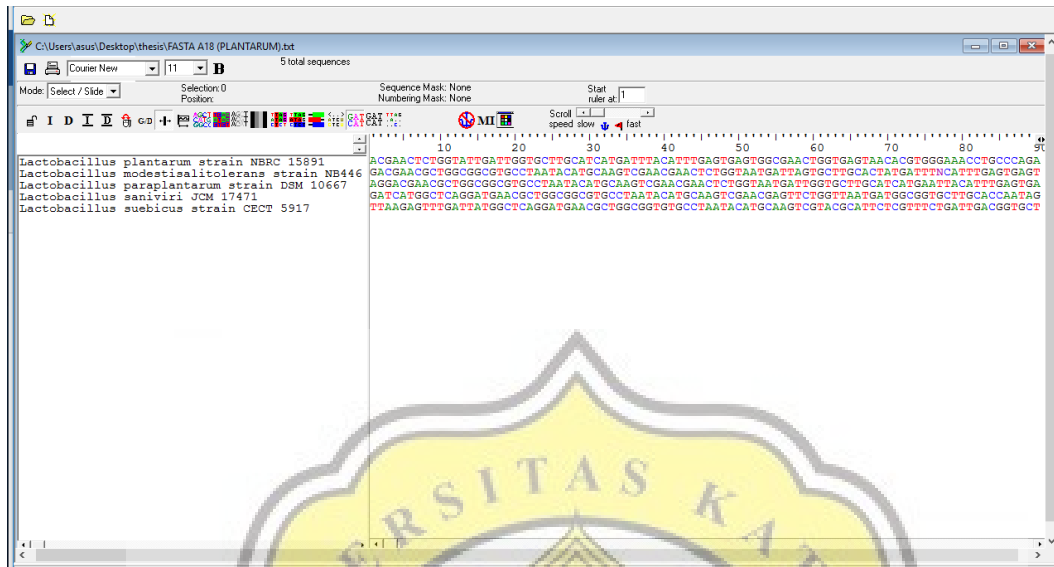
Accession	Score	Expect	Ident	Accession
Lactobacillus pentosus strain JCM 1149	1729	0.00	91.74%	NR_119192.1
Lactobacillus pentosus strain 124-2	1718	0.00	91.79%	NR_029133.1
Lactobacillus plantarum strain CIP 103151	1718	0.00	91.79%	NR_104573.1
Lactobacillus aquaticus strain IMCC1736	1718	0.00	93.16%	NR_115847.1
Lactobacillus plantarum strain NRRL B-14768	1718	0.00	91.79%	NR_042394.1
Lactobacillus plantarum strain NBRC 15891	1714	0.00	91.71%	NR_113338.1
Lactobacillus saniviri JCM 17471 = DSM 24301	1714	0.00	91.63%	NR_113289.1
Lactobacillus modestisalutolerans strain NB446	1714	0.00	91.72%	NR_136786.1
Lactobacillus plantarum strain JCM 1149	1712	0.00	91.71%	NR_115605.1
Lactobacillus paraplantarum strain DSM 10667	1712	0.00	91.71%	NR_025447.1
Lactobacillus wasatchensis strain WDC04	1711	0.00	91.55%	NR_147709.1
Lactobacillus porciniae strain R-42633	1711	0.00	93.00%	NR_108876.1
Lactobacillus mudanjiangensis strain 11050	1711	0.00	92.04%	NR_125561.1
Lactobacillus floricola DSM 23037 = JCM 16512	1711	0.00	91.64%	NR_113001.1
Pediococcus stillessii strain FAIR-F 180	1709	0.00	92.86%	NR_042401.1
Pediococcus pentosaceus strain DSM 20336	1707	0.00	93.05%	NR_042058.1
Lactobacillus succicola strain NRIC 0736	1707	0.00	92.99%	NR_112785.1
Lactobacillus rhamnosus strain NBRC 3426	1703	0.00	91.65%	NR_113332.1
Lactobacillus uvarum DSM 19971	1701	0.00	92.91%	NR_115308.1
Lactobacillus mali KCTC 3596 = DSM 20444	1701	0.00	92.77%	NR_112691.1
Lactobacillus plantarum strain NBRC 15891	1701	0.00	91.96%	NR_112680.1
Lactobacillus suebicus strain CECT 5917	1700	0.00	91.38%	NR_042190.1
Lactobacillus nasuensis JCM 17158	1696	0.00	92.83%	NR_113303.1
Lactobacillus hokkaidonensis JCM 18451	1696	0.00	92.81%	NR_114335.1

LLA18

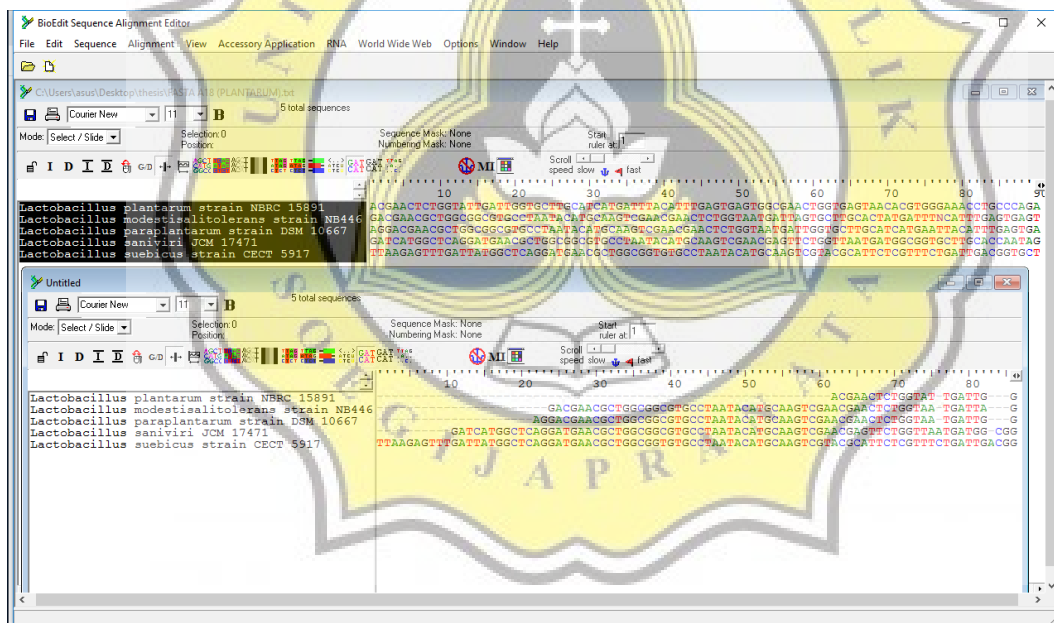
Description	Max Score	Total Score	Query Cover	E value	Percent Ident	Accession
Lactobacillus parabuchneri strain LMG 11457	1568	1568	65%	0.00	94.39%	NR_114962.1
Lactobacillus parabuchneri strain JCM 12493	1568	1568	65%	0.00	94.39%	NR_041294.1
Lactobacillus parabuchneri strain DSM 5707	1565	1565	65%	0.00	94.30%	NR_112755.1
Lactobacillus sunkii strain YIT 11061	1563	1563	65%	0.00	94.29%	NR_041656.1
Lactobacillus buchneri strain JCM 1115	1557	1557	65%	0.00	94.19%	NR_041293.1
Lactobacillus rapi strain YIT 11204	1557	1557	65%	0.00	94.19%	NR_041659.1
Lactobacillus otakiensis strain YIT 11163	1557	1557	65%	0.00	94.19%	NR_041657.1
Lactobacillus parakefiri strain JCM 8573	1552	1552	65%	0.00	94.09%	NR_112757.1
Lactobacillus kefir strain NBRC 15888	1552	1552	65%	0.00	94.09%	NR_113336.1
Lactobacillus kefir DSM 20587 = JCM 5818	1552	1552	65%	0.00	94.09%	NR_115271.1
Lactobacillus kefir strain AJK 16S	1552	1552	65%	0.00	94.09%	NR_042230.1
Lactobacillus parakefiri strain NBRC 15890	1548	1548	65%	0.00	94.00%	NR_113819.1
Lactobacillus kisonensis strain YIT 11168	1546	1546	65%	0.00	94.00%	NR_041658.1
Lactobacillus hilgardii strain NBRC 15886	1507	1507	65%	0.00	93.31%	NR_113817.1
Lactobacillus parafarraginis strain NRIC 0677	1507	1507	65%	0.00	93.31%	NR_041468.1
Lactobacillus parakefiri strain GCL 1731	1504	1504	64%	0.00	93.94%	NR_029039.1
Lactobacillus faraginis strain NRIC 0676	1496	1496	65%	0.00	93.11%	NR_041467.1
Lactobacillus diolivorans strain JKD6	1495	1495	64%	0.00	93.74%	NR_037004.1
Lactobacillus curieae strain S1119	1483	1483	65%	0.00	92.91%	NR_109538.1
Lactobacillus hilgardii strain DSM 20176	1471	1471	65%	0.00	92.33%	NR_044708.2
Lactobacillus senilis DSM 24302 = JCM 17472	1458	1458	65%	0.00	92.00%	NR_113339.1
Lactobacillus sniechdi strain ITH 5753	1434	1434	65%	0.00	92.00%	NR_113340.1

LLB3

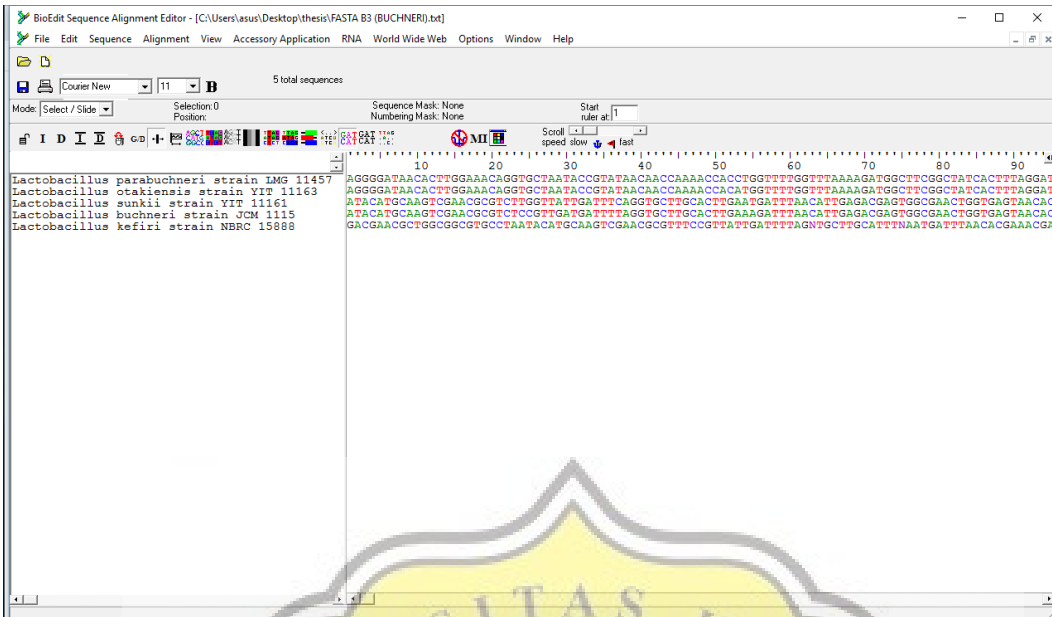
Lampiran 3. Proses Penjajaran Gen FASTA yang diperoleh dari situs GenBank menggunakan software BioEdit



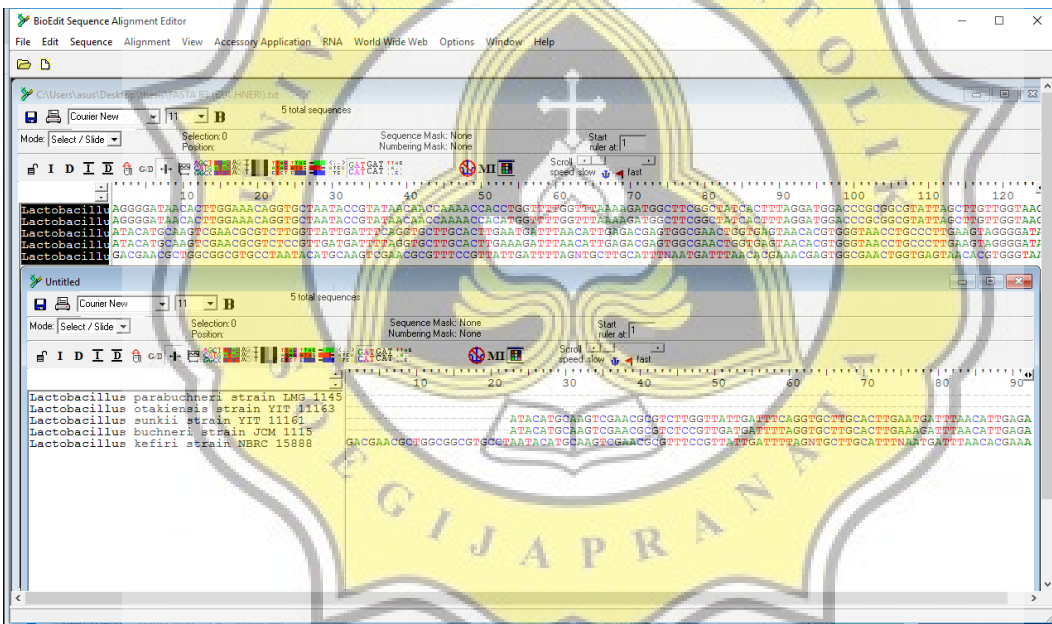
LLA18



Contoh yang sudah disejajarkan

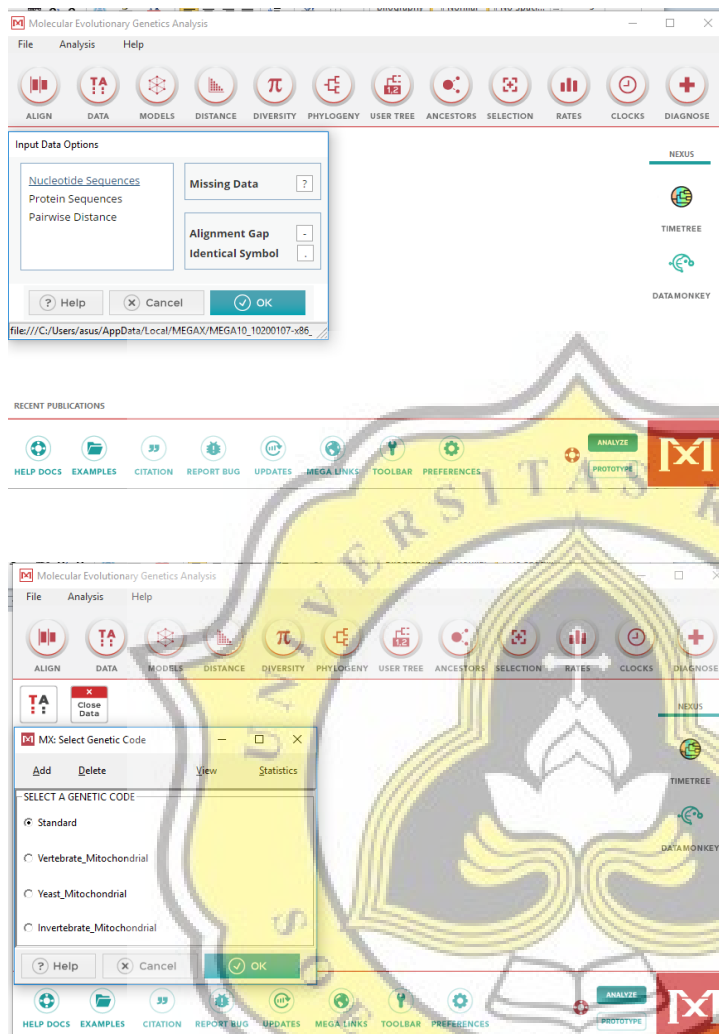


B3



Contoh yang sudah disejajarkan

Lampiran 4. Proses pembuatan pohon DNA filogenetika menggunakan software MEGA X.



Molecular Evolutionary Genetics Analysis

File Analysis Help

ALIGN DATA MODELS DISTANCE

Close Data

MX: Analysis Preferences

Phylogeny Reconstruction

Option	Setting
ANALYSIS	
Scope	All Selected Taxa
Statistical Method	Neighbor-joining
PHYLOGENY TEST	
Test of Phylogeny	Bootstrap method
No. of Bootstrap Replications	100
SUBSTITUTION MODEL	
Substitutions Type	Nucleotide
Genetic Code Table	Not Applicable
Model/Method	Maximum Composite Likelihood
Fixed Transition/Transversion Ratio	Not Applicable
Substitutions to Include	d: Transitions + Transversions
RATES AND PATTERNS	
Rates among Sites	Uniform Rates
Gamma Parameter	Not Applicable
Pattern among Lineages	Some (Homogeneous)
DATA SUBSET TO USE	
Gaps/Missing Data Treatment	Pairwise deletion
Site Coverage Cutoff (%)	Not Applicable
Select Codon Positions	<input checked="" type="checkbox"/> 1st <input checked="" type="checkbox"/> 2nd <input checked="" type="checkbox"/> 3rd <input checked="" type="checkbox"/> Non-coding Sites
SYSTEM RESOURCE USAGE	
Number of Threads	7

Help Cancel OK

RECENT PUBLICATIONS

HELP DOCS EXAMPLES CITATION REPORT BUG UPDATES MEGA LINKS TOOLBAR PREFERENCES

ANALYZE PROTOTYPE

MX: Tree Explorer: (A18 (1).fas)

File Search Image Subtree View Compute Caption Help

Original Tree Bootstrap consensus tree

94

100

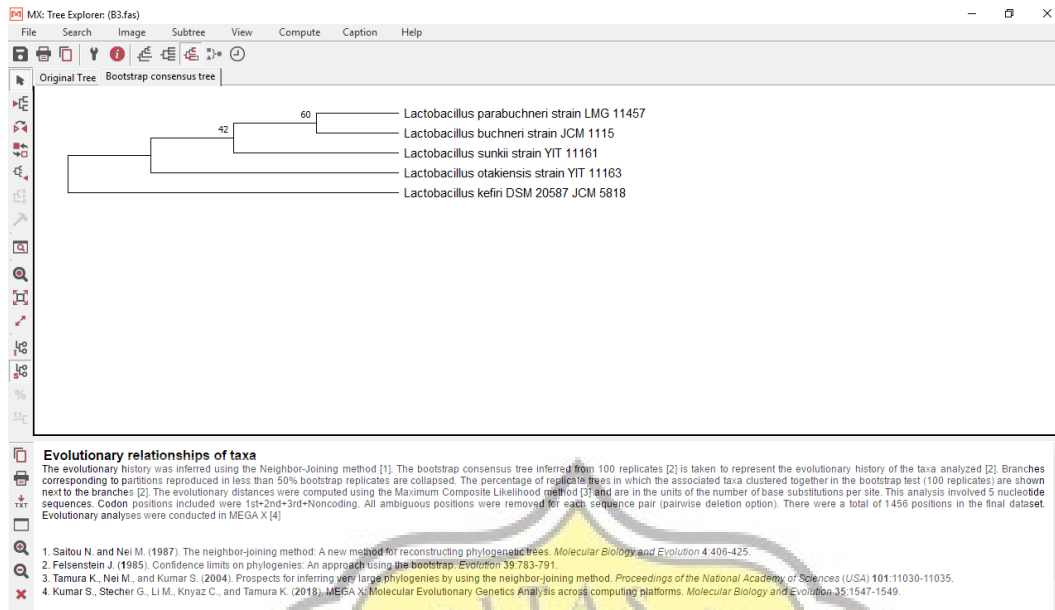
Lactobacillus plantarum strain NBRC 15891
 Lactobacillus paraplantarum strain DSM 10667
 Lactobacillus modestisaltolerans strain NB446
 Lactobacillus sanivini JCM 17471
 Lactobacillus subcicus strain CECT 5917

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method [1]. The bootstrap consensus tree inferred from 100 replicates [2] is taken to represent the evolutionary history of the taxa analyzed [2]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches [2]. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. This analysis involved 5 nucleotide sequences. Codon positions included were 1st-2nd-3rd-Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1574 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [4].

- Saitou N. and Nei M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.
- Felsenstein J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.
- Tamura K., Nei M., and Kumar S. (2004). Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)* 101:11030-11035.
- Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.

LLA18



LLB3





2.34% PLAGIARISM
APPROXIMATELY

1.2% IN QUOTES

Report #11089016

PENDAHULUAN Latar Belakang Pada jaman yang semakin maju ini, masyarakat modern semakin peka terhadap ancaman penyakit yang melanda dan peduli terhadap kesehatan mereka serta pola makan yang menentukan kualitas dari kehidupan mereka. Salah satu solusi untuk memperbaiki kesehatan secara rutin tanpa mengkonsumsi suplemen dan obat-obatan secara berlebihan yaitu adalah dengan mengkonsumsi produk pangan fungsional. Pangan fungsional merupakan produk pangan yang mengandung komponen aktif dan dapat memberikan manfaat yang baik bagi kesehatan. Selain itu, pangan fungsional menjadi salah satu penemuan yang selalu didapati kebaruan karena semakin hari, permintaan konsumen yang beragam dan selektif menjadi persaingan bagi para produsen pangan fungsional, terutama dalam pembuatan pangan fungsional tersebut, produsen mulai memakai bahan-bahan utama yang didapatkan dari tanaman dan buah-buahan lokal. Inovasi untuk mengembangkan sebuah produk menggunakan sumber alami lokal, salah satunya yaitu adalah memberdayakan tanaman-tanaman disekitar dan mencari tahu manfaat apa yang dapat diolah menjadi suatu penemuan baru contohnya seperti Bambu Ampel. Bagian tunas dari bambu ampel yaitu rebungnya dapat diolah menjadi olahan pangan berupa acar, isian dari makanan tradisional atau sebagai lauk yang biasa dikonsumsi