

Appendix A

Report of Microbial Identification by partial 16S rDNA sequence analysis

Sample Name: E1

700 bp Identification

Homology Search with BLASTn program from NCBI database

Sequences producing significant alignments:		SCORE	E VALUE
AB494716	Weissella cibaria	1263	0.0
GU138616	Weissella cibaria IMAU:10288	1263	0.0
GU138615	Weissella cibaria IMAU:10287	1263	0.0
GU138603	Weissella cibaria IMAU:10275	1263	0.0
GU138580	Weissella cibaria IMAU:10252	1263	0.0

BLASTN 2.2.24+

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A.

Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David

J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new

generation of protein database search programs", Nucleic

Acids Res. 25:3389-3402.

RID: FE7KC18P016

Query= E1 520F Length=700

>E1 520F

ATTTAAGTCTGAAGTGAAAGCCCTCAGCTCAACTGAGGAATTGCTTTGGAAACTGGATGA
CTTGAGTGCAGTAGAGGAAAGTGGAAGTCCATGTGTAGCGGTGAAATGCGTAGATATATG
GAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTAAGTACGTTGAGGCTCGAAAGT
GTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACACCGTAAACGATGAGTGCTAGG
TGTTTGAGGGTTTCCGCCCTTAAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGA
GTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCA
TGTGGTTTAATTTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTTGACAACT
CCAGAGATGGAGCGTTCCCTTCGGGGACAAGGTGACAGGTGGTGCATGGTTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATTACTAGTTGCC
AGCATTTAGTTGGGCACTCTAGTGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATG
ACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGCGTATACA
ACGAGTTGCCAACCCGCGAGGGTGAGCTAATCTCTTAAAG

Alignment and Phylogenic tree by MEGA 4

Unweighted pair-group method using arithmetic averages (UPGMA)



Report of Microbial Identification by partial 16S rDNA sequence analysis

Sample Name: E2

700 bp Identification

Homology Search with BLASTn program from NCBI database

Sequences producing significant alignments:		SCORE	E VALUE
AB494716	Weissella cibaria	1263	0.0
GU138616	Weissella cibaria IMAU:10288	1263	0.0
GU138615	Weissella cibaria IMAU:10287	1263	0.0
GU138603	Weissella cibaria IMAU:10275	1263	0.0
GU138580	Weissella cibaria IMAU:10252	1263	0.0

BLASTN 2.2.24+

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: FEC0PZB001N

Query= E2 520F Length=700

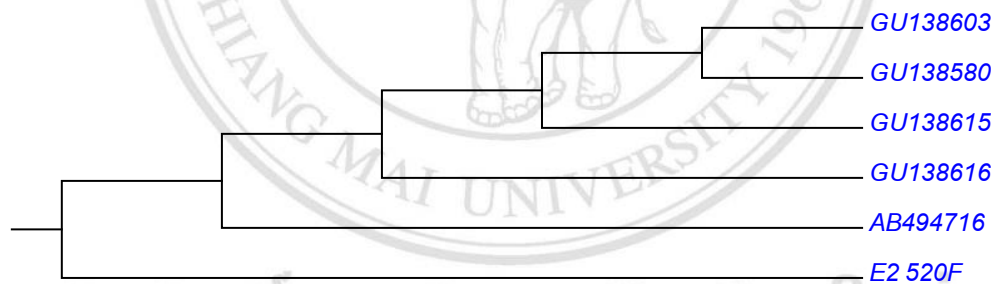
>E2 520F

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GTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACACCGTAAACGATGAGTGCTAGG
 TGTTTGAGGGTTTCCGCCCTTAAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGA
 GTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCA
 TGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTTGACAACT
 CCAGAGATGGAGCGTTCCTTCGGGGACAAGGTGACAGGTGGTGCATGGTTGTCGTCAGC
 TCGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATTACTAGTTGCC
 AGCATTTAGTTGGGCACTCTAGTGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATG
 ACGTCAAATCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGCGTATACA
 ACGAGTTGCCAACCCGCGAGGGTGAGCTAATCTCTTAAAG

Alignment and Phylogenic tree by MEGA 4

Unweighted pair-group method using arithmetic averages (UPGMA)



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Report of Microbial Identification by partial 16S rDNA sequence analysis

Sample Name: E3

700 bp Identification

Homology Search with BLASTn program from NCBI database

Sequences producing significant alignments:		SCORE	E VALUE
HQ441200	Lactobacillus plantarum strain LP-01	1263	0.0
HQ379175	Lactobacillus plantarum strain FHHMB120-8R-A3	1263	0.0
HQ286594	Lactobacillus plantarum strain H2	1263	0.0
HQ318714	Lactobacillus plantarum strain FJAT-CF7	1263	0.0
HQ293084	Lactobacillus plantarum strain NWL61	1263	0.0

BLASTN 2.2.24+

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A.

Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David

J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new

generation of protein database search programs", Nucleic

Acids Res. 25:3389-3402.

RID: FEHD8TBJ011

Query= E3 520F Length=700

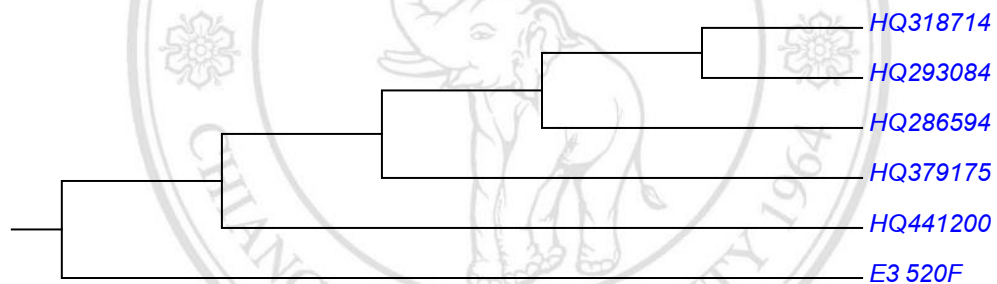
>E3 520F

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TATGGAAGAACACCAGTGCGAAGGCGGCTGTCTGGTCTGTAAGTACGCTGAGGCTCGA

AAGTATGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCATACCGTAAACGATGAATGC
 TAAGTGTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCTAACGCATTAAGCATTCCGCCTG
 GGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCCCGCACAAGCGGTGG
 AGCATGTGGTTTAATTCTGAAGCTACGCGAAGAACCTTACCAGGTCTTGACATACTATGCA
 AATCTAAGAGATTAGACGTTCCCTTCGGGGACATGGATACAGGTGGTGCATGGTTGTCGT
 CAGCTCGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATTATCAGT
 TGCCAGCATTAAAGTTGGGCACTCTGGTGAGACTGCCGGTGACAAACCGGAGGAAGGTGGG
 GATGACGTCAAATCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGATGG
 TACAACGAGTTGCGAACTCGCGAGAGTAAGCTAATCTCTT

Alignment and Phylogenetic tree by MEGA 4

Unweighted pair-group method using arithmetic averages (UPGMA)



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Report of Microbial Identification by partial 16S rDNA sequence analysis

Sample Name: E4

690 bp Identification

Homology Search with BLASTn program from NCBI database

Sequences producing significant alignments:		SCORE	E VALUE
AB470317	Enterococcus sp. SF-1	1245	0.0
AB596997	Enterococcus faecium	1245	0.0
HQ293070	Enterococcus faecium strain NWL47	1245	0.0
HQ293069	Enterococcus faecium strain NWL46	1245	0.0
HQ293030	Enterococcus faecium strain NWL07	1245	0.0

BLASTN 2.2.24+

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: FEM913R401S

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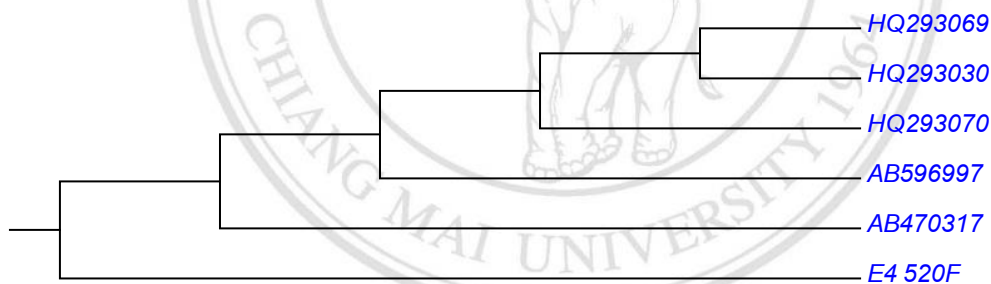
>E4 520F

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ATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAAGTACGCTGAGGCTCG

AAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTG
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 CCACTCTAGAGATAGAGCTTCCCCTTCGGGGGCAAAGTGACAGGTGGTGCATGGTTGTCTG
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 GGATGACGTCAAATCATCATGCCCTTATGACCTGGGCTACACACGTGCTACAATGGGAA
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Report of Microbial Identification by partial 16S rDNA sequence analysis

Sample Name: E5

700 bp Identification

Homology Search with BLASTn program from NCBI database

Sequences producing significant alignments:		SCORE	E VALUE
HQ441200	Lactobacillus plantarum strain LP-01	1263	0.0
HQ379175	Lactobacillus plantarum strain FHHMB120-8R-A3	1263	0.0
HQ286594	Lactobacillus plantarum strain H2	1263	0.0
HQ318714	Lactobacillus plantarum strain FJAT-CF7	1263	0.0
HQ293084	Lactobacillus plantarum strain NWL61	1263	0.0

BLASTN 2.2.24+

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A.

Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David

J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new

generation of protein database search programs", Nucleic

Acids Res. 25:3389-3402.

RID: FEPXJEAS014

Query= E5 520F Length=700

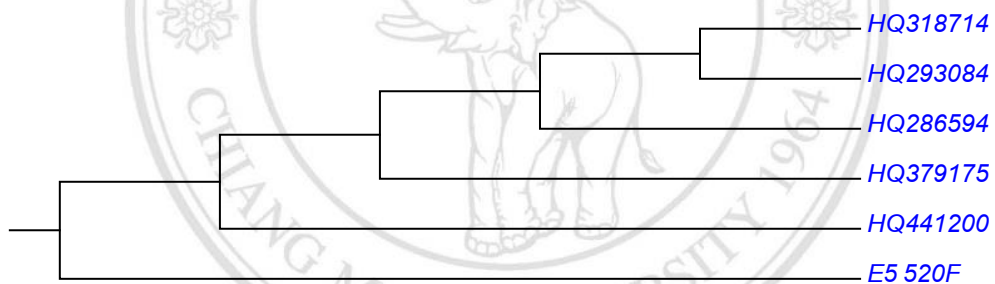
>E5 520F

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AAGTATGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCATACCGTAAACGATGAATGC
TAAGTGTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCTAACGCATTAAGCATTCCGCCTG
GGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGGCCGACACAAGCGGTGG
AGCATGTGGTTTAATTCGAAGCTACGCGAAGAACCTTACCAGGTCTTGACATACTATGCA
AATCTAAGAGATTAGACGTTCCCTTCGGGGACATGGATACAGGTGGTGCATGGTTGTCGT
CAGCTCGTGTCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATTATCAGT
TGCCAGCATTAAAGTTGGGCACTCTGGTGAGACTGCCGGTGACAAACGGAGGAAGGTGGG
GATGACGTCAAATCATCATGCCCTTATGACCTGGGCTACACACGTGCTACAATGGATGG
TACAACGAGTTGCGAACTCGCGAGAGTAAGCTAATCTCTT

Alignment and Phylogenetic tree by MEGA 4

Unweighted pair-group method using arithmetic averages (UPGMA)



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CURRICULUM VITAE

Name	Mr.Ronnachit Rungsri
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2010-Present	Master Degree in Pharmaceutical Science Chiang Mai University
1992-1998	D.V.M. Faculty of Veterinary Medicine, KhonKaen University, Thailand
1988-1992	SarakhamPittayakhom School, Mahasarakham
1983-1988	NongKo School, Mahasarakham
Professional Career	
2014-Present	Elephant Veterinarian specialist
2000-2014	Elephant Camp Veterinarian Maesa Elephant Camp, Chiang Mai, Thailand
1998-2000	Asian Elephant Foundation of Thailand
Professional Qualification	
2000-Present	Special Lecturer for Veterinary Student. Chiang Mai University, Chiang Mai, Thailand
2005-2009	Special Lecturer for “The Elephant Health Care Training Course” For Conservation Breeding Specialist Group (CB SG), Japan
2001-2007	Special Lecturer for “Veterinarian Intensive Course in Zoo and Wildlife Medicine” . KhaoKeaw Open Zoo, ChonBuri ,Thailand
2006-2008	Special Lecturer for Veterinary Student. KhonKaen University, KhonKaen, Thailand
Publications	

- Thongtip N1, Mahasawangkul S, Thitaram C, Pongsopavijitr P, Kornkaewrat K, Pinyopummin A, Angkawanish T, Jansittiwate S, **Rungsri R**, Boonprasert K, Wongkalasin W, Homkong P, Dejchaisri S, Wajjwalku W, Saikhun K. Successful artificial insemination in the Asian elephant (*Elephas maximus*) using chilled and frozen-thawed semen. *Reprod Biol Endocrinol*. 2009 Jul 19; 7:75.
- Thitaram C, Pongsopawijit P, Thongtip N, Angkavanich T, Chansittivej S, Wongkalasin W, Somgird C, Suwankong N, Prachsilpchai W, Suchit K, Clausen B, Boonthong P, Nimtrakul K, Niponkit C, Siritepsongklod S, **Roongsri R**, Mahasavankul S. Dystocia following prolonged retention of a dead fetus in an Asian elephant (*Elephas maximus*). *Theriogenology*. 2006 Sep 15; 66(5):1284-91.
- Thitaram C, Chansitthiwet S, Pongsopawijit P, Brown JL, Wongkalasin W, Daram P, **Roongsri R**, Kalmapijit A, Mahasawangkul S, Rojanasthien S, Colenbrander B, van der Weijden GC, van Eerdenburg FJ. Use of genital inspection and female urine tests to detect oestrus in captive Asian elephants. *Anim Reprod Sci*. 2009 Oct; 115 (1-4):267-78.
- Thitaram C, Brown JL, Pongsopawijit P, Chansitthiwet S, Wongkalasin W, Daram P, **Roongsri R**, Kalmapijit A, Mahasawangkul S, Rojansthien S, Colenbrander B, van der Weijden GC, van Eerdenburg FJ. Seasonal effects on the endocrine pattern of semi-captive female Asian elephants (*Elephas maximus*): timing of the anovulatory luteinizing hormone surge determines the length of the estrous cycle. *Theriogenology*. 2008 Jan 15; 69(2):237-44.

