

Erratum

Erratum to “Analysis of Nucleotide Sequences of the 16S rRNA Gene of Novel *Escherichia coli* Strains Isolated from Feces of Human and Bali Cattle”

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In the paper titled “Analysis of Nucleotide Sequences of the 16S rRNA Gene of Novel *Escherichia coli* Strains Isolated from Feces of Human and Bali Cattle,” according to my data, there are too many nucleotides of both *S. dysenteriae* and *E. coli* O26:H11 different from the other strains. So logically both strains are placed as outgroup. This fact is difficult to explain from the point of view of the evolution. Taking this in mind I submit the erratum, that is, Figures 1 and 2 and Table 1 without *Shigella dysenteriae* and *E. coli* O26:H11 as a comparison. It is also completely concerned with the correction of some words in the specified paragraph. Figures 1 and 2 and Table 1 are corrected here.

Paragraph 4 of Results and Discussion is corrected as follows. The analysis of similarity or nucleotides different among *E. coli* SM-25(1) and KL-48(2) strains were studied against some strains of *E. coli*, that is, *E. coli* Sakai (BA000007), *E. coli* EDL 933 (AE005174), *E. coli* O104:H4 (AFOB02000112), *E. coli* O111:H-(GU237022), *E. coli* O121:H19 (JASV01000004), and *E. coli* ATCC 43894 as a bacterial control. The similarity analysis was also conducted on some strains of non-*E. coli*, that is, *Aeromonas* sp. (FM957460), *Vibrio* sp. (FM957459), *Shigella sonnei* (FR870445), *Streptomyces* sp. (AJ391832), and *Bacillus* sp. (AB851799) that are summarized in Table 1.

Paragraph 5 of Results and Discussion is corrected as follows. The summary of the 16S rRNA similarity analysis in Table 1 showed that *E. coli* KL-48(2) that originated

from human feces has nucleotide similarity to 16S rRNA gene closely against some strains. These strains, that is, *E. coli* SM-25(1), *E. coli* 121:H19, *E. coli* ATCC 43894, *E. coli* Sakai, *E. coli* EDL 933, *Shigella sonnei*, *E. coli* O111:H-, and *E. coli* O104:H4, are as high as 99.64, 99.56, 99.42, 99.35, 99.35, 99.20, and 99.13%, respectively. Furthermore, *E. coli* SM-25(1) that originated from cattle feces also has high nucleotides similarity to the data of 16S rRNA that are available in GenBank also. It has nucleotides similarity to *Shigella sonnei*, *E. coli* O121:H19, *E. coli* O104:H4, *E. coli* ATCC 43894, *E. coli* Sakai, and *E. coli* EDL 933 as high as 99.71, 99.64, 99.49, 99.20, 99.13, and 99.13%, respectively. On the other hand, both strains showed percentage of nucleotide similarity distinctly to *Bacillus* sp., *Streptomyces* sp., *Aeromonas*, and *Vibrio* sp.

Paragraph 11 of Results and Discussion is corrected as follows. Phylogenetic tree in Figure 2 showed that the *E. coli* KL-48(2) and SM-25(1) made close clade with some strains of pathogenic *E. coli*. On the contrary, both strains also showed distinct clade against some strains that are available in databank. Some of those strains are *Streptomyces* sp. isolated from Yogyakarta, *Bacillus* sp. isolated from Jepara, and *Vibrio* sp. and *Aeromonas* sp. isolated from Lampung. As a result, both strains are proved to be a strain of pathogenic *E. coli* potentially.

TABLE I: Similarity analysis and nucleotides different among 16S rRNA genes using PHYDIT program.

	<i>Vibrio</i>	<i>Aeromonas</i>	<i>E. coli</i> EDL 933 W	<i>E. coli</i> Sakai	<i>E. coli</i> ATCC 43894	<i>E. coli</i> O111:H-	<i>E. coli</i> O104:H4	<i>E. coli</i> O121:H19	<i>E. coli</i> SM-25(1)*	<i>E. coli</i> KL-48(2)*	<i>Shigella sonnei</i>	<i>Streptomyces</i> sp.	<i>Bacillus</i> sp.
<i>Aeromonas</i>	158/1500	—	151/1376	151/1376	150/1376	154/1503	149/1375	153/1529	147/1376	148/1376	161/1529	329/1445	357/1377
<i>Vibrio</i> sp.	—	89.47	131/1380	131/1380	130/1380	134/1501	141/1379	146/1506	140/1380	138/1380	252/1642	326/1418	458/1528
<i>E. coli</i> EDL 933 W	90.51	89.03	—	0/1380	1/1380	6/1380	19/1379	13/1379	12/1380	9/1380	16/1380	282/1346	305/1325
<i>E. coli</i> Sakai	90.51	89.03	100	—	1/1380	6/1380	19/1379	13/1379	12/1380	9/1380	16/1380	282/1346	305/1325
<i>E. coli</i> ATCC 43894	90.58	89.1	99.93	99.93	—	5/1380	18/1379	12/1379	11/1380	8/1380	15/1380	282/1346	305/1325
<i>E. coli</i> O111:H-	91.07	89.75	99.57	99.57	99.64	—	15/1379	11/1506	14/1380	11/1380	24/1506	301/1420	338/1378
<i>E. coli</i> O104:H4	89.78	89.16	98.62	98.62	98.69	98.91	—	6/1378	7/1379	12/1379	5/1379	280/1345	305/1324
<i>E. coli</i> O121:H19	90.31	89.99	99.06	99.06	99.13	99.27	99.56	—	5/1379	6/1379	21/1539	309/1447	342/1383
<i>E. coli</i> SM-25(1)*	89.86	89.32	99.13	99.13	99.2	98.99	99.49	99.64	—	5/1380	4/1380	284/1346	304/1325
<i>E. coli</i> KL-48(2)*	90	89.24	99.35	99.35	99.42	99.2	99.13	99.56	99.64	—	9/1380	285/1346	307/1325
<i>Shigella sonnei</i>	84.65	89.47	98.84	98.84	98.91	98.41	99.64	98.64	99.71	99.35	—	314/1449	511/1601
<i>Streptomyces</i> sp.	77.01	77.23	79.05	79.05	79.05	78.8	79.18	78.65	78.9	78.83	78.33	—	278/1298
<i>Bacillus</i> sp.	70.03	74.07	76.98	76.98	76.98	75.47	76.96	75.27	77.06	76.83	68.08	78.58	—

* Strain in this study.

<i>E. coli</i> _Sakai	GGCTGGATCT TCGCGATCG ACCGGGGTCC GAGGAAGTCC AAAGGGCCGT TCCATCGGAA	[956]
<i>E. coli</i> _O104:H4A..TC	956
<i>E. coli</i> _EDL_933_W	956
<i>E. coli</i> _ATCC_43894	956
<i>E. coli</i> _SM25(1)	956
<i>E. coli</i> _KL48(2)CG..GC..GT.....CG.....TAC..CG.....T.....GG..TCC..ACGGA..GGA..A..CC.....	956
<i>Streptomyces</i> _sp.	CC..T.....C..A..TA.....A.....AC.....T.....GCC..TAAA.....GT..G..CC.....	956
<i>Bacillus</i> _sp.A.....TC	956
<i>S. sonnei</i>A..A..TC..C.....T..TT.....T..A.....T..CG.....CGA.....	956
<i>Vibrio</i> _sp.C..A.....T..C.....T..AC.....T..A.....G..CG.....CGT.....	956
<i>Aeromonas</i> _sp.	956
<i>E. coli</i> _O111:H-	956
<i>E. coli</i> _O121:H19	956
<i>E. coli</i> _Sakai	TTGGTCCATG AACATTGAAA ACAGAGACTA CCCGGGGGAA GCTGGCTTAC GGTAAAGTGT	[1136]
<i>E. coli</i> _O104:H4A.....	1136
<i>E. coli</i> _EDL_933_W	1136
<i>E. coli</i> _ATCC_43894	1136
<i>E. coli</i> _SM25(1)	1136
<i>E. coli</i> _KL48(2)T..A.....G..CC..G..G.....C.....	1136
<i>Streptomyces</i> _sp.A.....A.....CC..G..G.....C.....C..A.....G.....G.....	1136
<i>Bacillus</i> _sp.A.....G.....A.....	1136
<i>S. sonnei</i>A..G..A.....	1136
<i>Vibrio</i> _sp.A..T..A.....	1136
<i>Aeromonas</i> _sp.A.....A.....	1136
<i>E. coli</i> _O111:H-A.....	1136
<i>E. coli</i> _O121:H19A.....	1136
<i>E. coli</i> _Sakai	TAACCGGAGT ATCGGGCGA TCGGGGACA CCGTAGAAGC AGCGCGTGTG ATGACGCAAG	[1349]
<i>E. coli</i> _O104:H4	1349
<i>E. coli</i> _EDL_933_W	1349
<i>E. coli</i> _ATCC_43894	1349
<i>E. coli</i> _SM25(1)	1349
<i>E. coli</i> _KL48(2)T..A..G..G.....T.....T.....C..G.....	1349
<i>Streptomyces</i> _sp.TTT..A..A.....G..ACA..A.....T.....T.....T.....C.....	1349
<i>Bacillus</i> _sp.TT..T..G.....	1349
<i>S. sonnei</i>TT..T..G.....	1349
<i>Vibrio</i> _sp.TT..T..G.....	1349
<i>Aeromonas</i> _sp.G.....G.....	1349
<i>E. coli</i> _O111:H-	1349
<i>E. coli</i> _O121:H19	1349
<i>E. coli</i> _Sakai	AGTGAGACGT CAGGTATATA GGACAGGGT CTCACCCGCA CGGCGCACGG CAGTGACGGC	[1529]
<i>E. coli</i> _O104:H4	1529
<i>E. coli</i> _EDL_933_W	1529
<i>E. coli</i> _ATCC_43894	1529
<i>E. coli</i> _SM25(1)	1529
<i>E. coli</i> _KL48(2)T.....G..C..T.....T.....C.....AT.....G.....	1529
<i>Streptomyces</i> _sp.	GT.....A.....G..C.....T.....T.....G.....	1529
<i>Bacillus</i> _sp.T.....A.....A.....	1529
<i>S. sonnei</i>A.....C.....T.....	1529
<i>Vibrio</i> _sp.A.....C.....T.....	1529
<i>Aeromonas</i> _sp.C.....T.....	1529
<i>E. coli</i> _O111:H-	1529
<i>E. coli</i> _O121:H19	1529
<i>E. coli</i> _Sakai	GGAGGGTGGG CTGGGTGGAG TACCCGGTGC AGAACAAATCG CGGGGGCGGT TGGACAATCG	[1712]
<i>E. coli</i> _O104:H4	1712
<i>E. coli</i> _EDL_933_W	1712
<i>E. coli</i> _ATCC_43894	1712
<i>E. coli</i> _SM25(1)	1712
<i>E. coli</i> _KL48(2)A..T..A.....CG.....T.....AG.....	1712
<i>Streptomyces</i> _sp.T..T..G..CT..G.....A.....	1712
<i>Bacillus</i> _sp.T.....G.....A.....A.....	1712
<i>S. sonnei</i>T.....G.....A.....A.....	1712
<i>Vibrio</i> _sp.T.....	1712
<i>Aeromonas</i> _sp.T.....	1712
<i>E. coli</i> _O111:H-	1712
<i>E. coli</i> _O121:H19	1712
<i>E. coli</i> _Sakai	CGACATCGAG TCCGCTGATT AGGGATTGTA TGTGCCCGCC ACTTCCGTGC GACAACCGAA	[1907]
<i>E. coli</i> _O104:H4T..A.....	1907
<i>E. coli</i> _EDL_933_W	1907
<i>E. coli</i> _ATCC_43894	1907
<i>E. coli</i> _SM25(1)T..A.....	1907
<i>E. coli</i> _KL48(2)A.....TTTGT.....C.....G.....ACTA.....T.....	1907
<i>Streptomyces</i> _sp.A.....A.....C.....G..A.....A..AT.....T.....	1907
<i>Bacillus</i> _sp.T..A.....	1907
<i>S. sonnei</i>T..A.....	1907
<i>Vibrio</i> _sp.T..CG..C.....TGC.....C.....G.....TT.....G.....	1907
<i>Aeromonas</i> _sp.T..CG..C.....TGC.....C.....G.....A..TG.....G.....	1907
<i>E. coli</i> _O111:H-	1907
<i>E. coli</i> _O121:H19T..A.....	1907
<i>E. coli</i> _Sakai	TAAGGAATAC CGCTGGTAC GAAGCAAAGC CGAGAGCCAG CCACGTGTAT ACTACGTGCA	[2090]
<i>E. coli</i> _O104:H4	2090
<i>E. coli</i> _EDL_933_W	2090
<i>E. coli</i> _ATCC_43894	2090
<i>E. coli</i> _SM25(1)	2090
<i>E. coli</i> _KL48(2)C.....T.....G.....T.....G..T..T.....G..T.....	2090
<i>Streptomyces</i> _sp.C.....A.....GT.....A..T..CT..T..G..T..C.....G..T.....	2090
<i>Bacillus</i> _sp.C.....	2090
<i>S. sonnei</i>C.....	2090
<i>Vibrio</i> _sp.C.....T.....GGG.....T.....C.....	2090
<i>Aeromonas</i> _sp.C.....GGTA.....T.....C.....	2090
<i>E. coli</i> _O111:H-	2090
<i>E. coli</i> _O121:H19	2090
<i>E. coli</i> _Sakai	GGCACGGTGC GCT	[2132]
<i>E. coli</i> _O104:H4	2132
<i>E. coli</i> _EDL_933_W	2132
<i>E. coli</i> _ATCC_43894	2132
<i>E. coli</i> _SM25(1)CT.....	2132
<i>E. coli</i> _KL48(2)C.....	2132
<i>Streptomyces</i> _sp.C.....	2132
<i>Bacillus</i> _sp.C.....	2132
<i>S. sonnei</i>A..T.....	2132
<i>Vibrio</i> _sp.A..T.....	2132
<i>Aeromonas</i> _sp.A..T.....	2132
<i>E. coli</i> _O111:H-	2132
<i>E. coli</i> _O121:H19	2132

FIGURE 1: Nucleotides sequence of the 16S rRNA gene of the isolates *E. coli* SM-25(1) and *E. coli* KL-48(2) among nucleotides sequence of those available in databanks. Data indicated the position of nucleotides different among isolates and identical data for all isolates are not shown.

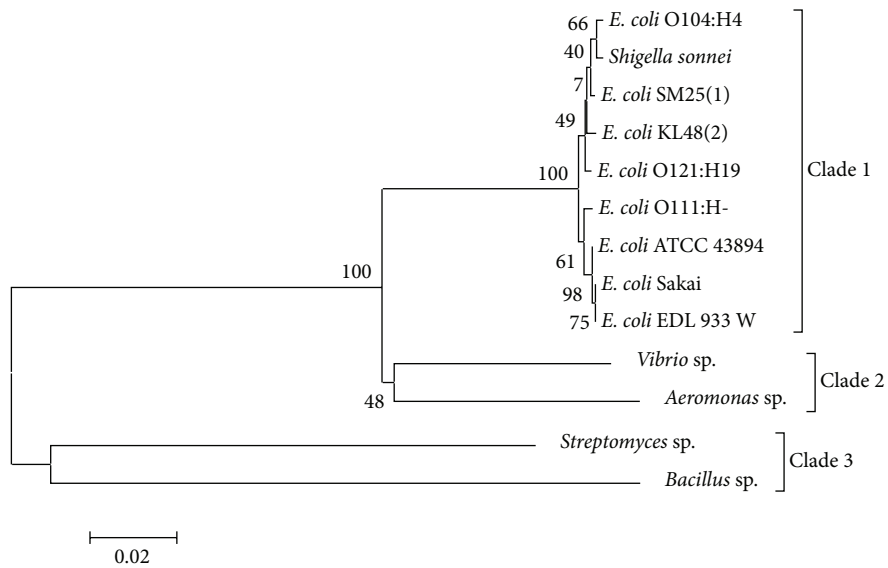


FIGURE 2: Phylogenetic tree was constructed using neighbor-joining algorithm [14] of nucleotides sequence of 16S rRNA gene. The number in the branch of phylogram indicates bootstrap value (%) by 1000-replication multiple and scale indicates one per 1000 substitutions of nucleotides sequence of 16S rRNA gene.



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