

**TABLES AND FIGURES**

**TABLE 1. Distribution of IST genotypes within clonal complexes by year.**

Clonal complex	IST type	1996	1997	1998	1999	2000	2001	2002	2003	2004	Total
IST1	IST1 <sup>a</sup>					66 (1)	449	180	13 (3)	2 (2)	710 (6)
	IST2					1					1
	IST23 <sup>b</sup>					1			8 (8)		9 (8)
	IST11 <sup>c</sup>	8	21	2	1				1 (1)	2	35 (1)
	IST30		1	1							2
	IST17 <sup>d</sup>									7 (7)	7 (7)
	IST18			10							10
	IST15						1				1
	IST20							1			1
	IST21			16							16
	IST22 <sup>e</sup>									3 (1)	3 (1)
	IST34 <sup>f</sup>									1 (1)	1 (1)
IST3	IST3						50	12			62
	IST4				1						1
	IST14						1				1
	IST25						15	1	1		17
	IST26						1				1
	IST5						1				1
	IST9		2								2
	IST10		1								1
	IST12								1		1
	IST13			1							1
	IST27								7	1	8
IST37							1	1		2	
IST6	IST6			4		1		3			8
	IST7					1	2		3	5	11
	IST8	1									1
	IST16	2									2
<b>Total</b>		<b>11</b>	<b>25</b>	<b>34</b>	<b>2</b>	<b>70 (1)</b>	<b>522</b>	<b>205</b>	<b>27 (12)</b>	<b>20 (11)</b>	<b>916 (24)</b>

<sup>a</sup>Imported from India (1 case) in 2000; Indonesia (2) in 2003, China (1) in 2003; Vietnam (1) in 2004, Indonesia (1) in 2004

<sup>b</sup>Indonesia (8) in 2003

<sup>c</sup>China (1) in 2003

<sup>d</sup>Vietnam (3) in 2004, Cambodia (4) in 2004

<sup>e</sup>Campodia (1) in 2004

<sup>f</sup>Thailand (1) in 2004

TABLE 2: Variation rates for 26 VNTR loci in 703 IST1 isolates derived from a common ancestor.

VNTR locus	No. repeat unit in SS26.66	No. new alleles	No. isolates with varied allele	Variation rate (%)	Total no. alleles <sup>a</sup>	Allele diversity <sup>a</sup>
SS3	20	10	533	75.82	16	0.81
SS6	20	12	253	35.99	18	0.85
SS11	6	3	56	7.97	6	0.61
SS9	7	3	43	6.12	9	0.7
SS10	8	2	6	0.85	5	0.64
SS5	4	2	2	0.28	2	0.49
SS26	4	1	2	0.28	2	0.19
SS1	2	1	1	0.14	10	0.63
SS8	1	1	1	0.14	2	0.09
SS13	3	1	1	0.14	4	0.52
SS2	2	0	0	0.00	3	0.51
SS4	2	0	0	0.00	2	0.5
SS7	3	0	0	0.00	2	0.5
SS12	2	0	0	0.00	4	0.6
SS14	2	0	0	0.00	2	0.5
SS15	2	0	0	0.00	3	0.5
SS16	2	0	0	0.00	3	0.53
SS17	2	0	0	0.00	2	0.49
SS18	2	0	0	0.00	2	0.5
SS19	2	0	0	0.00	3	0.5
SS20	2	0	0	0.00	2	0.49
SS21	1	0	0	0.00	2	0.49
SS22	2	0	0	0.00	2	0.49
SS23	3	0	0	0.00	5	0.67
SS24	2	0	0	0.00	2	0.49
SS25	1	0	0	0.00	2	0.41

<sup>a</sup>Observed in a collection of 206 diverse non-IST1 isolates.

TABLE 3. Distribution of distance (number of loci) to the ancestor genotype in the 703 IST1 isolates, the average evolutionary distance and evolutionary speed for clone defined with the 26-, 24- and 22- locus profiles.

No. loci difference	2000	2001	2002	2003	Total
<b>For 26 loci</b>					
0	52	42	11		105
1	11	270	57	5	343
2	2	128	83		213
3		9	27	3	39
4			1	2	3
Evolutionary distance <sup>a</sup>	0.23	1.23	1.72	2.2	1.28
Evolutionary speed					0.39
<b>For 24 loci<sup>b</sup></b>					
0	65	381	144	5	595
1		67	34	3	104
2		1	1	2	4
Evolutionary distance	0	0.15	0.2	0.7	0.16
Evolutionary speed					0.049
<b>For 22 loci<sup>c</sup></b>					
0	65	444	172	9	690
1		5	7	1	13
Evolutionary distance	0	0.011	0.039	0.1	0.018
Evolutionary speed					0.0055

<sup>a</sup>Average evolutionary distance of isolates collected in the year indicated to the ancestor genotype, SS26.66, SS24.1 and SS22.1

<sup>b</sup>Excluding the two hypervariable loci, SS3 and SS6 from the panel of 26 loci

<sup>c</sup>Excluding the two hypervariable loci and median variable loci, SS3, SS6, SS9 and SS11 from the panel of 26 loci.

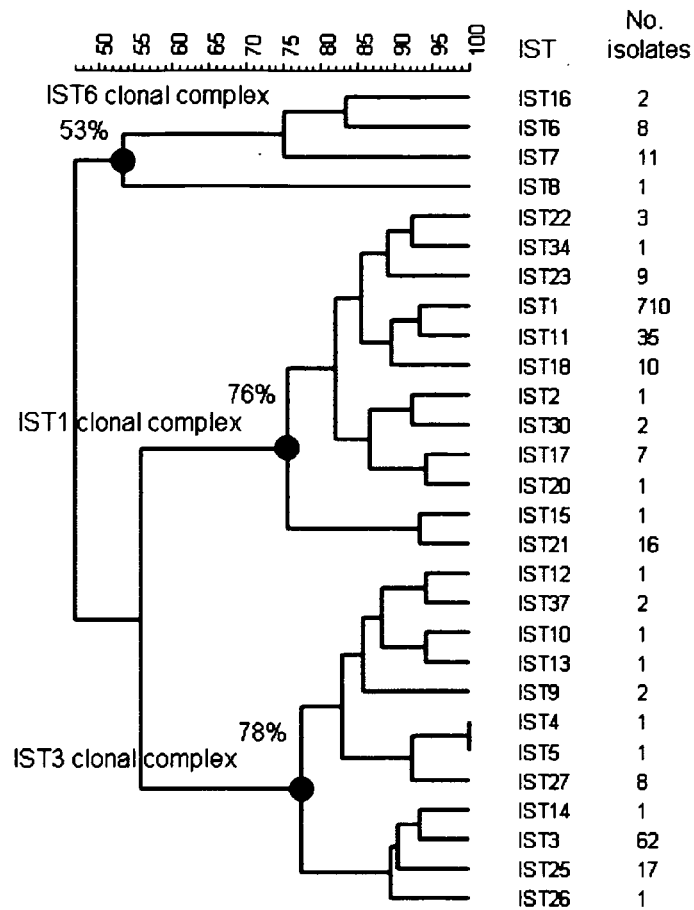


FIG. 1. Dendrogram constructed with the IST patterns found in 916 isolates and the associated number of isolates belonging to the IST genotype. The dendrogram was generated by the unweighted pair group method with arithmetic mean (UPGMA), using the Dice-predicted similarity value between two patterns. The statistic program was provided by BioNumerics version 4.5, with settings of 1% optimization and 0.95% tolerance.

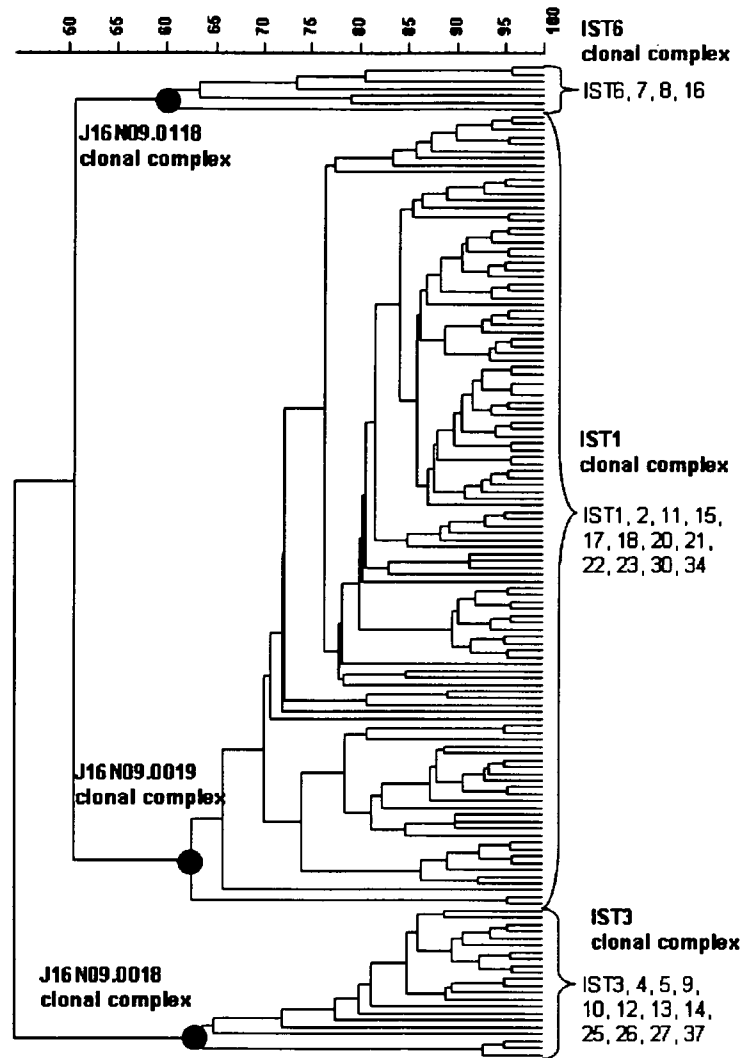


FIG 2. Dendrogram constructed with PFGE-NotI patterns. The dendrogram was generated by the unweighted pair group method with arithmetic mean (UPGMA), using the Dice-predicted similarity value of two patterns. The statistic program was provided by BioNumerics version 4.5, with settings of 1.0% optimization and 0.7% tolerance.

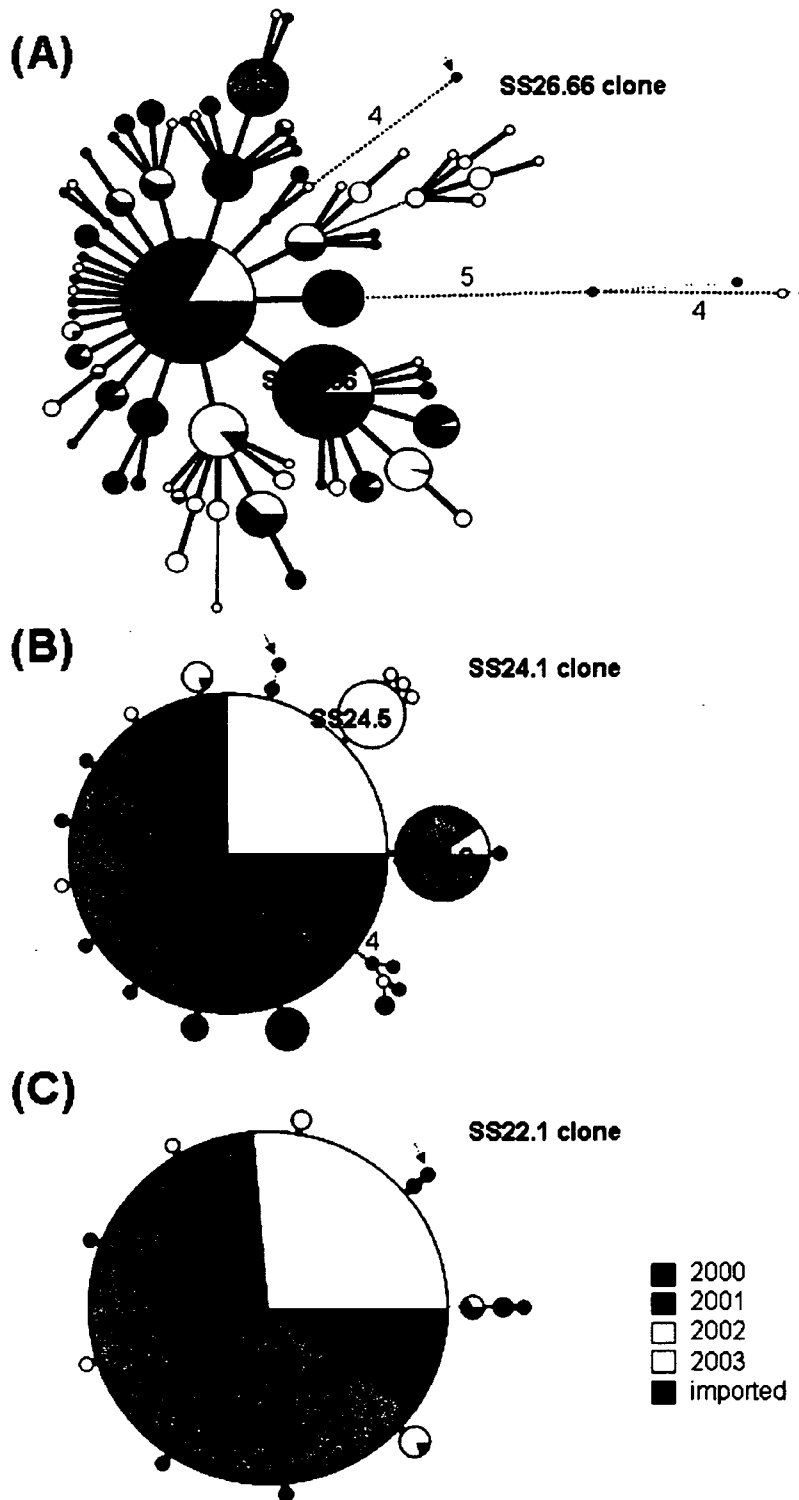


FIG. 3. Phylogenetic tree constructed with MLVA profiles in 710 IST isolates, consisting of (A) 26 VNTR loci (B), 24 loci and (C) 22 loci. The 24-locus combination was the 26 loci subtracting the 2 hypervariable loci, SS3 and SS6; the

22-locus combination was the 26 loci subtracting the 2 hypervariable and the 2 moderately variable loci, SS3, SS6, SS9 and SS11. Differences between the two MLVA types are marked by a bold line for 1 locus, a thin red line for 2 loci, and a red dashed line for 3 loci. MLVA types differing at more than 4 loci are marked by blue dashed line and numbered. Circle size is proportional to the number of isolates belonging to the MLVA type. MLVA types of a large clone are marked in gray shadow. The Indian strain is pointed out by a red arrow.



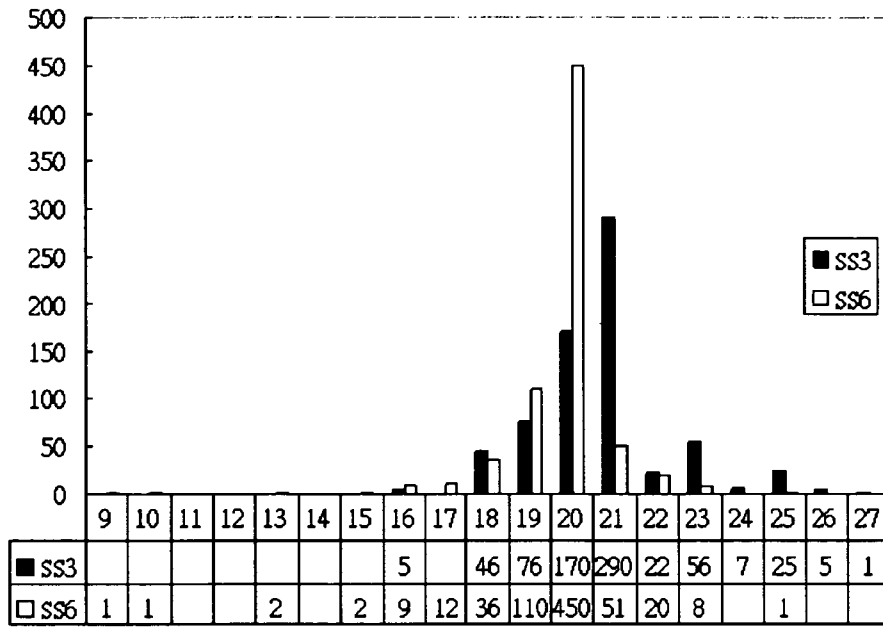


FIG. 4. Distribution of the alleles of SS3 and SS6 in the 703 IST1 isolates. The founder genotype, SS26.66, contained 20 repeat units in each of the SS3 and SS6 loci.

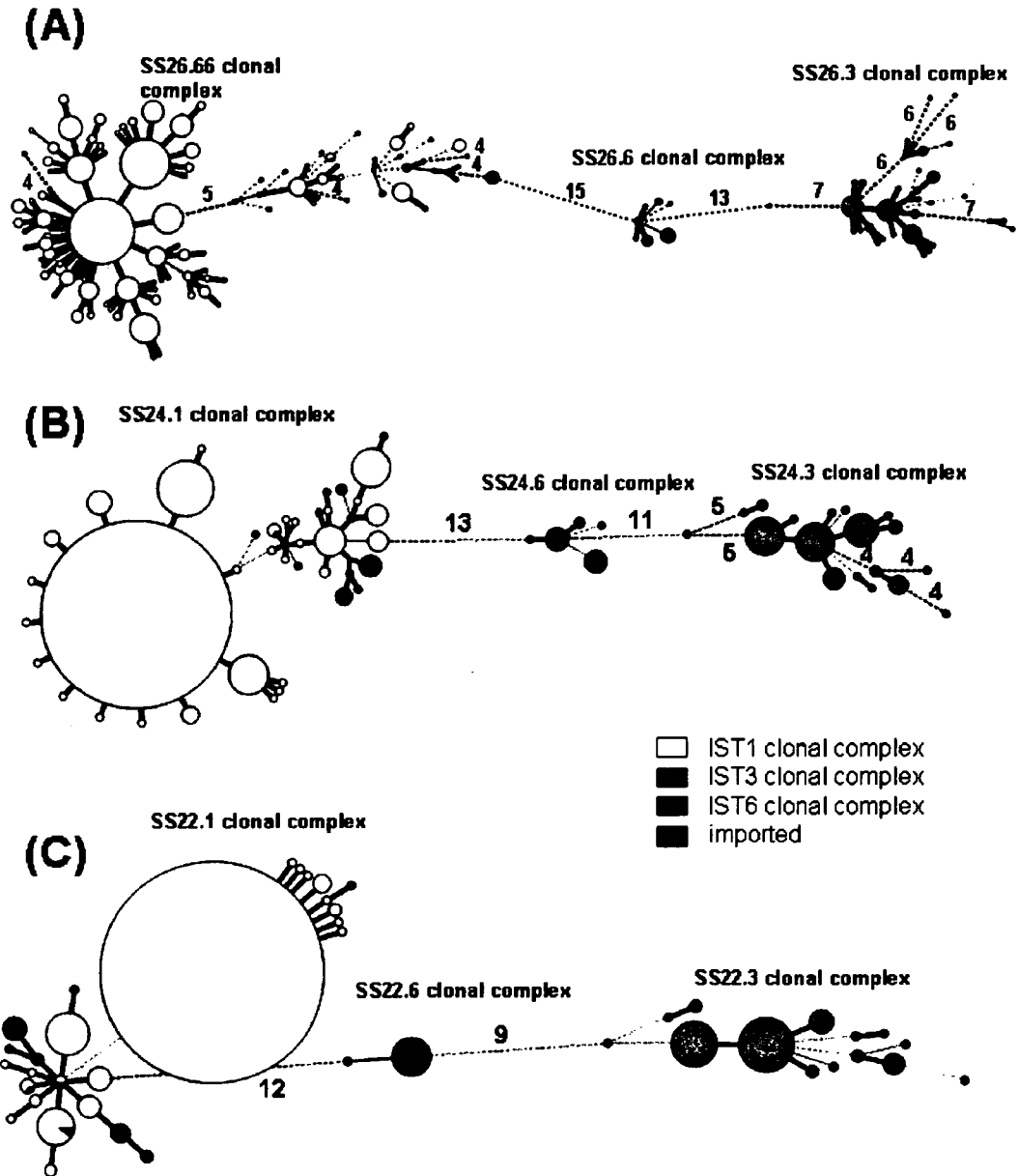


FIG 5. Phylogenetic tree constructed with MLVA profiles in 916 isolates, consisting of (A) 26 VNTR loci (B), 24 loci, and (C) 22 loci. The 24-locus combination (was) excluded the 2 hypervariable loci, SS3 and SS6 from the 26 loci; the 22-locus combination excluded the 4 highly variable loci, SS3, SS6, SS9 and SS11 from the 26 loci. Differences between two MLVA types are marked by a bold line for 1 locus, a thin red line for 2 loci, and a red dashed line for 3 loci. MLVA types differing at more than 4 loci are marked by a blue dashed line and numbered. Circle size is proportional to the number of isolates belonging to the MLVA type. MLVA types which share 19 or more loci are regarded as a group or as being within a clonal complex, and are marked by gray shadow.

研究成果の刊行に関する一覧表(平成19年度) プロジェクト1:細菌

執筆者氏名	刊行書籍又は雑誌名 (雑誌のときは雑誌名、 巻号数、論文名)	刊行書店名	巻名	ページ	刊行年
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<p>Kurokawa K., Itoh T., Kuwahara T., Oshima K., Toh H., Toyoda A., Takami H., Morita H., Sharma V.K., Srivastava T.P., Taylor T.D., Noguchi H., Mori H., Ogura Y., Ehrlich D.S., Itoh K., Takagi T., Sakaki Y., <u>Hayashi T.</u> &amp; Hattori M.</p>	<p>Comparative metagenomics revealed commonly enriched gene sets in human gut microbiomes.</p>	<p>DNA Res.</p>	<p>14.</p>	<p>169-181</p>	<p>2007</p>
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学会発表に関する一覧表 (平成19年度)

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三戸部治郎		第88回日本細菌学会総会	2007年3月	大阪
Mitobe J.		The 37th US-Japan Medical conference Cholera board	2007年12月	Austin Texas, USA
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## プロジェクト 2 : ウィルス