

Table 5. Representation of bacterial species in distal esophagus biopsies from four subjects

Species (n = 95)	Number of clones				
	A (n = 186)	B (n = 205)	C (n = 264)	D (n = 245)	Total (n = 900)
<i>Achromobacter piechaudii</i>	0	1	0	0	1
<i>Actinomyces graevenitzii</i>	1	0	1	0	2
<i>Actinomyces meyeri</i>	0	0	1	0	1
<i>Actinomyces odontolyticus</i>	1	1	1	2	5
<i>Atopobium parvulum</i>	0	0	3	1	4
<i>Atopobium rimae</i>	0	0	1	0	1
<i>Bulleidia moorei</i>	1	1	2	1	5
<i>Campylobacter concisus</i>	0	0	3	0	3
<i>Campylobacter showae</i>	1	0	0	0	1
<i>Centipeda periodontii</i>	0	1	0	0	1
<i>Comamonas testosteroni</i>	0	1	0	0	1
<i>Delftia acidovorans</i>	0	1	0	1	2
<i>Eubacterium sulsi</i>	0	1	0	1	2
<i>Filifactor alocis</i>	0	0	0	1	1
<i>Fusobacterium naviforme</i>	2	0	0	0	2
<i>Fusobacterium nucleatum</i>	3	0	2	1	6
<i>Fusobacterium simiae</i>	1	0	0	0	1
<i>Gemella haemolysans</i>	2	1	0	6	9
<i>Gemella morbillorum</i>	1	0	0	0	1
<i>Gemella sanguinis</i>	3	0	1	0	4
<i>Granulicatella adiacens</i>	7	1	2	5	15
<i>Granulicatella elegans</i>	0	2	0	0	2
<i>Haemophilus parainfluenzae</i>	1	0	0	0	1
<i>Haemophilus paraphrophilus</i>	1	0	0	2	3
† <i>Haemophilus segnis</i>	0	1	0	0	1
<i>Lactobacillus delbrueckii</i>	0	0	8	0	8

<i>Lactobacillus fermentum</i>	0	0	2	0	2
<i>Lactobacillus frumenti</i>	0	0	1	0	1
<i>Lactobacillus gasseri</i>	0	1	10	0	11
<i>Lactobacillus salivarius</i>	0	0	4	0	4
Megasphaera micronuciformis	3	8	7	1	19
<i>Mogibacterium vesicum</i>	0	0	1	0	1
<i>Neisseria pharyngis</i>	1	0	0	0	1
<i>Neisseria subflava</i>	1	0	0	0	1
<i>Porphyromonas endodontalis</i>	3	0	0	3	6
<i>Porphyromonas gingivalis</i>	0	0	0	2	2
<i>Prevotella denticola</i>	0	0	2	0	2
<i>Prevotella intermedia</i>	0	1	0	3	4
<i>Prevotella melaninogenica</i>	0	5	0	9	14
<i>Prevotella nigrescens</i>	0	0	0	1	1
<i>Prevotella oris</i>	0	0	2	0	2
Prevotella pallens	5	2	2	5	14
<i>Prevotella veroralis</i>	23	13	9	0	45
Rothia mucilagenosus	1	2	14	3	20
<i>Selenomonas sputigena</i>	0	0	0	1	1
<i>Shewanella baltica</i>	0	0	0	1	1
<i>Streptococcus anginosus</i>	0	0	0	1	1
<i>Streptococcus cristatus</i>	0	0	0	1	1
<i>Streptococcus gordonii</i>	0	1	0	1	2
<i>Streptococcus infantis</i>	0	0	6	2	8
<i>Streptococcus intermedius</i>	0	0	1	0	1
Streptococcus mitis	1	47	6	115	169
<i>Streptococcus oralis</i>	18	0	0	7	25
Streptococcus parasanguis	24	4	29	10	67
Streptococcus thermophilus	34	14	42	10	100
<i>Tennerella forsythensis</i>	1	0	0	0	1
<i>Haemophilus AB098612</i>	0	0	2	0	2
Veillonella atypica	8	22	21	15	66

Veillonella dispar	26	15	18	3	62
<i>Yersinia krist</i>	1	0	0	0	1
Subtotal	175	147	202	215	739
<i>Actinomyces AF385521</i>	0	0	4	0	4
Bacteroides AF385513	1	6	1	3	11
<i>Bacteroidetes AJ289174</i>	0	0	4	0	4
<i>Clostridiales AF201981</i>	0	0	2	2	4
<i>Clostridiales AF287770</i>	1	3	4	0	8
<i>Clostridiales AF287772</i>	0	0	0	1	1
<i>Clostridiales AF385508</i>	0	1	0	0	1
<i>Clostridiales AF385510</i>	2	0	0	0	2
<i>Clostridium AF385563</i>	0	1	0	0	1
Clostridium AY278618	1	1	7	1	10
<i>Fusobacterium AF287806</i>	0	0	0	1	1
<i>Haemophilus AB098612</i>	0	0	2	0	2
<i>Leptotrichia AF385571</i>	0	5	0	2	7
<i>Leptotrichia AY278621</i>	0	2	0	1	3
<i>Neisseria AY093465</i>	0	0	0	1	1
<i>Peptostreptococcus AF287763</i>	0	0	0	2	2
<i>Porphyromonas AY008310</i>	0	0	0	1	1
<i>Prevotella AF366269</i>	0	11	2	2	15
<i>Prevotella AF385512</i>	1	2	13	0	16
<i>Prevotella AF385551</i>	0	4	13	0	17
<i>Prevotella AF432133</i>	1	17	0	1	19
<i>Prevotella AJ012605</i>	0	0	0	1	1
<i>Prevotella AJ289182</i>	0	0	0	1	1
<i>Prevotella AY005064</i>	0	0	1	0	1
<i>Prevotella AY005065</i>	0	0	0	1	1
<i>Prevotella AY093466</i>	0	0	0	1	1
<i>Prevotella AY207061</i>	0	0	0	3	3
<i>Paenibacillus AY167820</i>	0	0	1	0	1
<i>Rothia AF543276</i>	0	0	0	2	2

	<i>Selenomonas AF287795</i>	0	1	0	0	1
	<i>Selenomonas AF385514</i>	0	1	0	1	2
	<i>TM7 AF385500</i>	0	1	0	0	1
	<i>TM7 AF385506</i>	0	0	0	1	1
	TM7 AF385520	4	1	5	1	11
	Subtotal	11	57	59	30	157
Unknowns [§] (n = 2)	<i>Selenomonas 9-1-7(92%)</i>	0	1	0	0	1
	<i>Veillonella 59-8-23 (95%)</i>	0	0	3	0	3
	Subtotal	0	1	3	0	4
	Total sequences	186	205	264	245	900
	Unique sequences	163	190	252	239	833
	Total species	35	40	45	51	94

Species/species-level operational taxonomic unites common to all four specimens are highlighted in yellow.

*Culture-defined sequences had similarity scores ≥ 0.873 with 16S rDNA of cultured-defined species.

[†]Species defined by similarity scores >0.873 with a cultivated non-type strain.

[‡]16S rDNA clones were defined as sequences with similarity scores ≥ 0.873 with 16S rDNA clones of uncultivated bacteria but not with cultured-defined species.

[§]Unknowns were defined as sequences with similarity scores <0.873 with 16S sequences in the RDP II database.