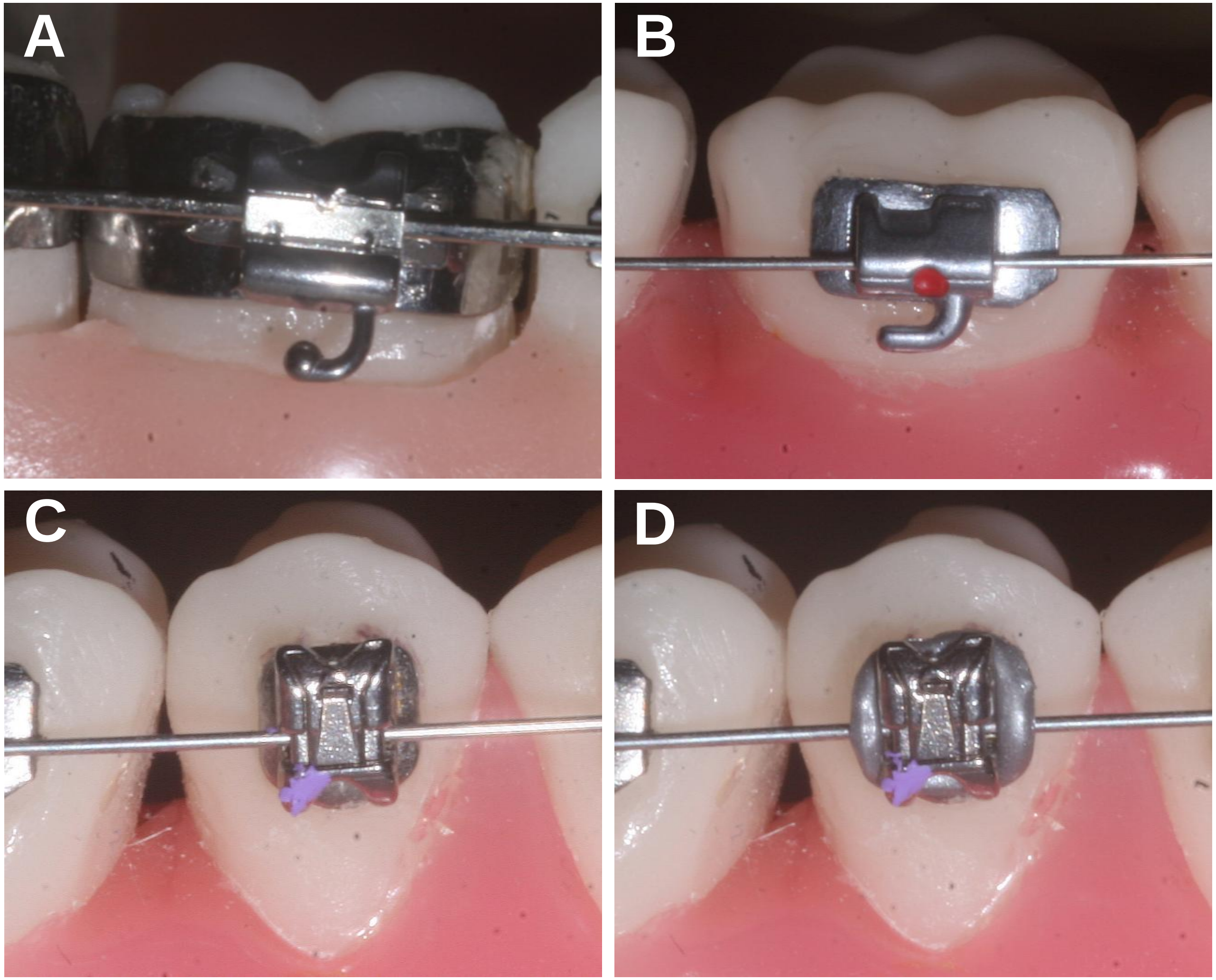

FIG. S1. Examples of the components of the orthodontic fixed appliances under test. A, molar band; B, bonded molar tube; C, self-ligating bracket without an elastomeric tie; D, self-ligating bracket with additional elastomeric tie.

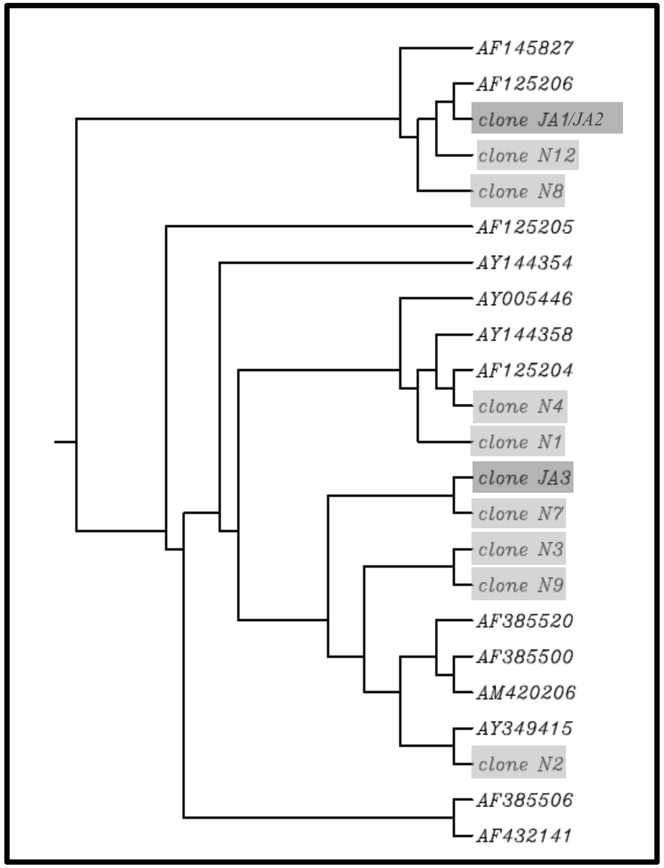

FIG. S2. Dendogram of oral candidate division TM7 phylotypes. The tree was derived from 16S rDNA sequences obtained from mixed cultures of dental plaque in FAB. The sequences were amplified by PCR, and cloned in *E. coli*. The 3 samples shown in this dendogram as JA1-2-3 were isolated from mixed broth cultures and were clustered in the same dendogram previously shown in Figure 1B.

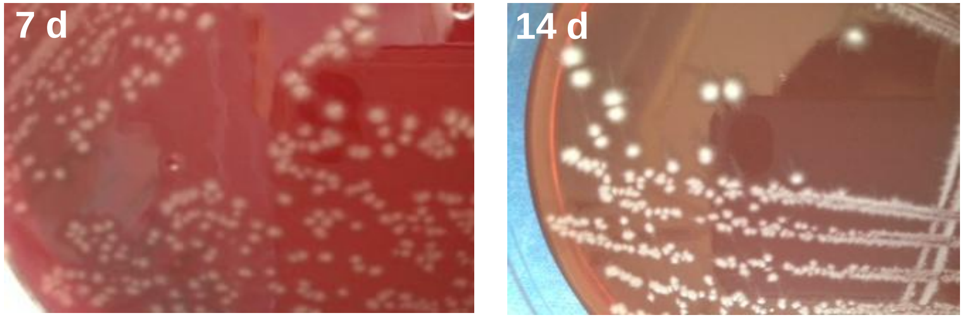

FIG. S3. Images of candidate division TM7 strain UB2523 bacterial colonies grown on FAA containing 5% horse blood and cultured anaerobically for 7 d or 14 d at 37°C.

Peptide sequence	Matching polypeptide in database	Accession no.	Query Cover. (%).	Max identity (%)
HYAHVDCPGHADYVK	Translation elongation factor Tu, partial [candidate division TM7 single-cell isolate TM7a]	10155636.1	100	100
VQLVGDDLFVTNTERLEK	Enolase [candidate division TM7 single-cell isolate TM7a]	10127055.1	88	94
AGYTAISSHR	Enolase [candidate division TM7 single-cell isolate TM7a]	10127055.1	100	80
FTAQVYVLTKDEGGR	GTPase - translation elongation factor [candidate division TM7 single-cell isolate TM7a]	10140889.1	100	80
TKNNPVLIGEPGVGK	ClpB protein [candidate division TM7 single-cell isolate TM7a]	10129174.1	100	100
TLSLLLK	Hypothetical protein, partial [candidate division TM7 single-cell isolate TM7a]	10142391.1	85	100
FTQAGSEVSALLGR	F_0F_1 ATP synthase subunit beta [candidate division TM7 genomosp. GTL1]	8578629.1	100	100
VADNTGAKEILTIR	50S ribosomal protein L14 [candidate division TM7 genomosp. GTL1]	8578359.1	100	86
NIALLFEKPSTR	Ornithine carbamoyltransferase, partial [candidate division TM7 single-cell isolate TM7a]	10128854.1	100	92
MKGIILAGGSGTR	TDP-Glucose pyrophosphorylase, partial [candidate division TM7 single-cell isolate TM7c]	10164824.1	100	100
EVTNLMHNAQSLVK *	AAA family ATPase, partial [candidate division TM7 single-cell isolate TM7a]	10131744.1	100	100
LGNIDATINLLTYFGEKSEK *	Hypothetical protein [candidate division TM7 single-cell isolate TM7a]	10128686.1	100	77
LWDIAQDSIKNNK *	Hypothetical protein [candidate division TM7 single-cell isolate TM7b]	10163984.1	100	100

TABLE S1. Identified peptides obtained from digestion of cell wall/membrane preparations from Candidate Division TM7 strain UB2523 cells. Each peptide analyzed was given the matching protein, accession number, query coverage (%) and maximum identity (%). * refers to peptides found in HOMD (http://www.homd.org/). The other peptides were identified using the BLAST program (http://blast.ncbi.nlm.nih.gov/Blast). The raw data files were processed using Proteome Discoverer software v1.2 (Thermo Scientific) and searched against the SwissProt Eubacteria database using the Mascot algorithm.