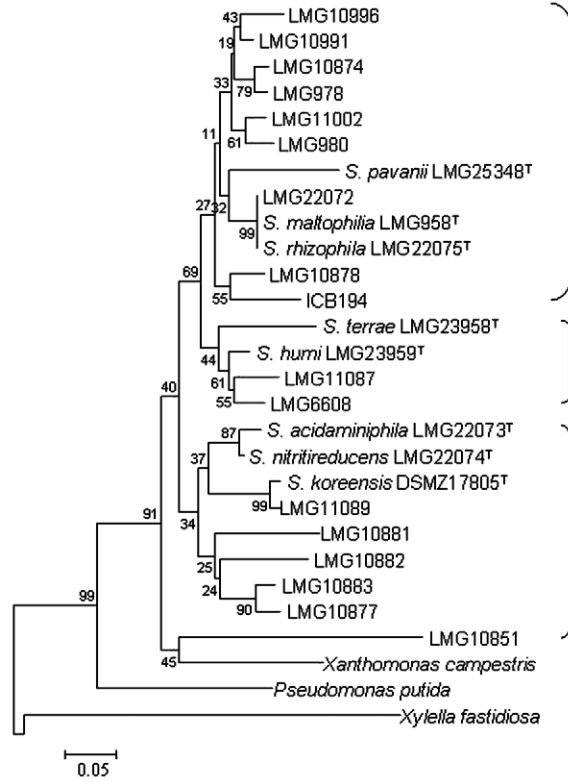


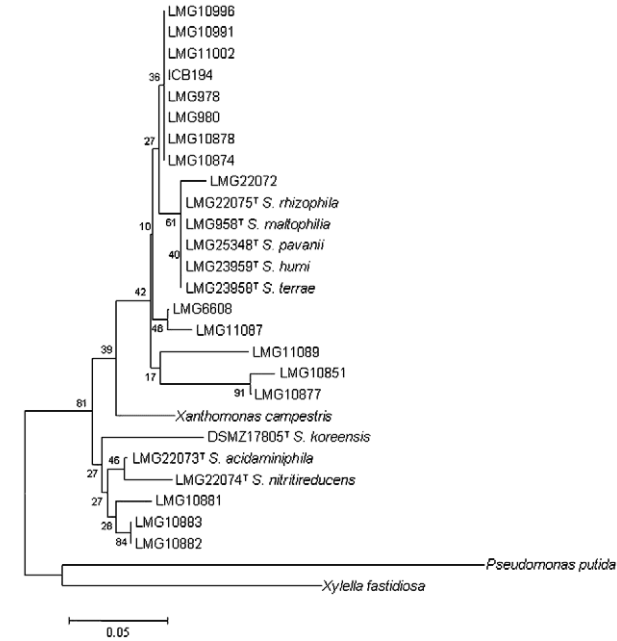
TABLE
Percentage DNA-DNA hybridization between *Stenotrophomonas* strains

	1 ^a	2 ^a	3 ^a	4 ^a	5 ^a	6 ^a	7 ^a	8 ^a	9 ^a	10 ^a	11 ^a	12 ^b	13 ^b	14 ^b	15 ^b	16 ^b	17 ^b	18 ^b	19 ^b
1 LMG 10996	100																		
2 LMG 10991	84	100																	
3 ICB 194	64.8	-	100																
4 LMG 25348 ^T <i>S. pavanii</i>	58.1	-	-	100															
5 LMG 22073 ^T <i>S. acidaminiphila</i>	17.7	-	-	-	100														
6 LMG 23369 ^T <i>S. koreensis</i>	12.3	-	-	-	-	100													
7 LMG 958 ^T <i>S. maltophilia</i>	56.6	-	77.1	55.1	-	-	100												
8 LMG 22074 ^T <i>S. nitritireducens</i>	26.3	-	-	31.2	66.9	-	-	100											
9 LMG 23958 ^T <i>S. terrae</i>	19.3	-	-	-	-	-	-	-	100										
10 LMG 23959 ^T <i>S. humi</i>	16	-	-	-	-	-	-	-	-	100									
11 LMG 24537 ^T <i>S. rhizophila</i>	24.5	-	-	30.7	-	-	-	-	-	-	100								
12 LMG 11004	65	89	-	-	-	-	-	-	-	-	-	100							
13 LMG 11000	71	-	-	-	-	-	-	-	-	-	-	-	100						
14 LMG 11111	-	76	-	-	-	-	-	-	-	-	-	-	-	100					
15 LMG 978	-	-	-	-	-	-	54	-	-	-	-	-	-	-	100				
16 LMG 980	53	-	-	-	-	-	55	-	-	-	-	-	-	-	-	100			
17 LMG 10874	-	-	-	-	-	-	60	-	-	-	-	-	-	-	-	-	100		
18 LMG 10878	-	-	-	-	-	-	49	-	-	-	-	-	-	-	-	-	-	100	
19 LMG 10877	-	-	-	-	-	-	51	-	-	-	-	-	-	-	-	-	-	-	100

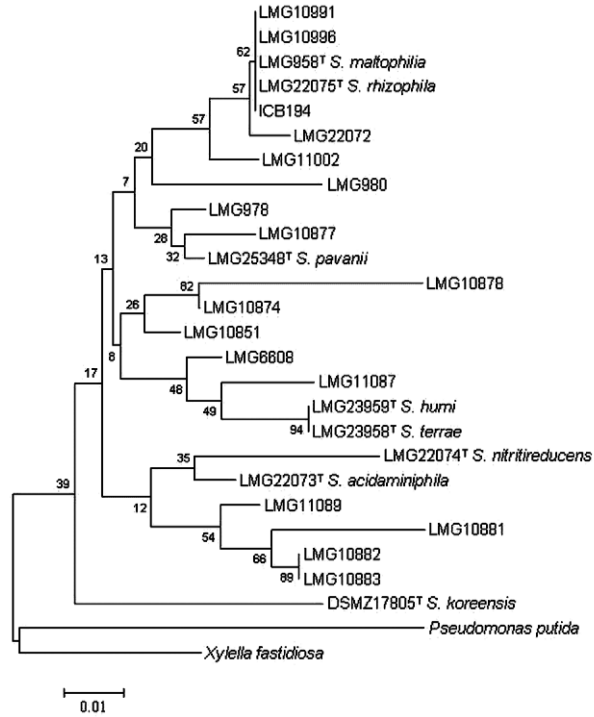
a: data from our study; b: data from Hauben et al. (1999).



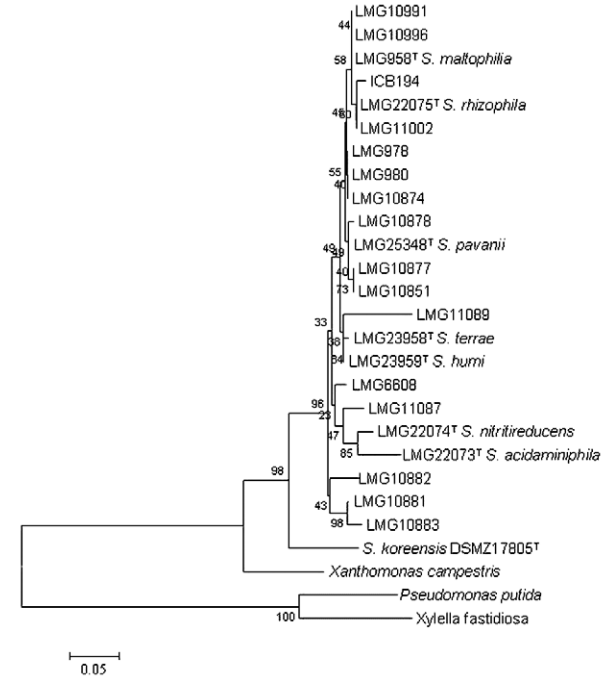
Neighbour-Joining phylogenetic tree based on the *atpA* gene sequences. Values of bootstrap after 1,000 repetitions are shown at the nodes. *Pseudomonas putida*, *Xanthomonas campestris* and *Xylella fastidiosa* were used as out-groups.



Neighbour-Joining phylogenetic tree based on the *recA* gene sequences. Values of bootstrap after 1,000 repetitions are shown at the nodes. *Pseudomonas putida* and *Xylella fastidiosa* were used as out-groups.



Neighbour-Joining phylogenetic tree based on the *rpoA* gene sequences. Values of bootstrap after 1,000 repetitions are shown at the nodes. *Pseudomonas putida*, *Xanthomonas campestris* and *Xylella fastidiosa* were used as out-groups.



Neighbour-Joining phylogenetic tree based on the *uvrB* gene sequences. Values of bootstrap after 1,000 repetitions are shown at the nodes. *Pseudomonas putida*, *Xanthomonas campestris* and *Xylella fastidiosa* were used as out-groups.