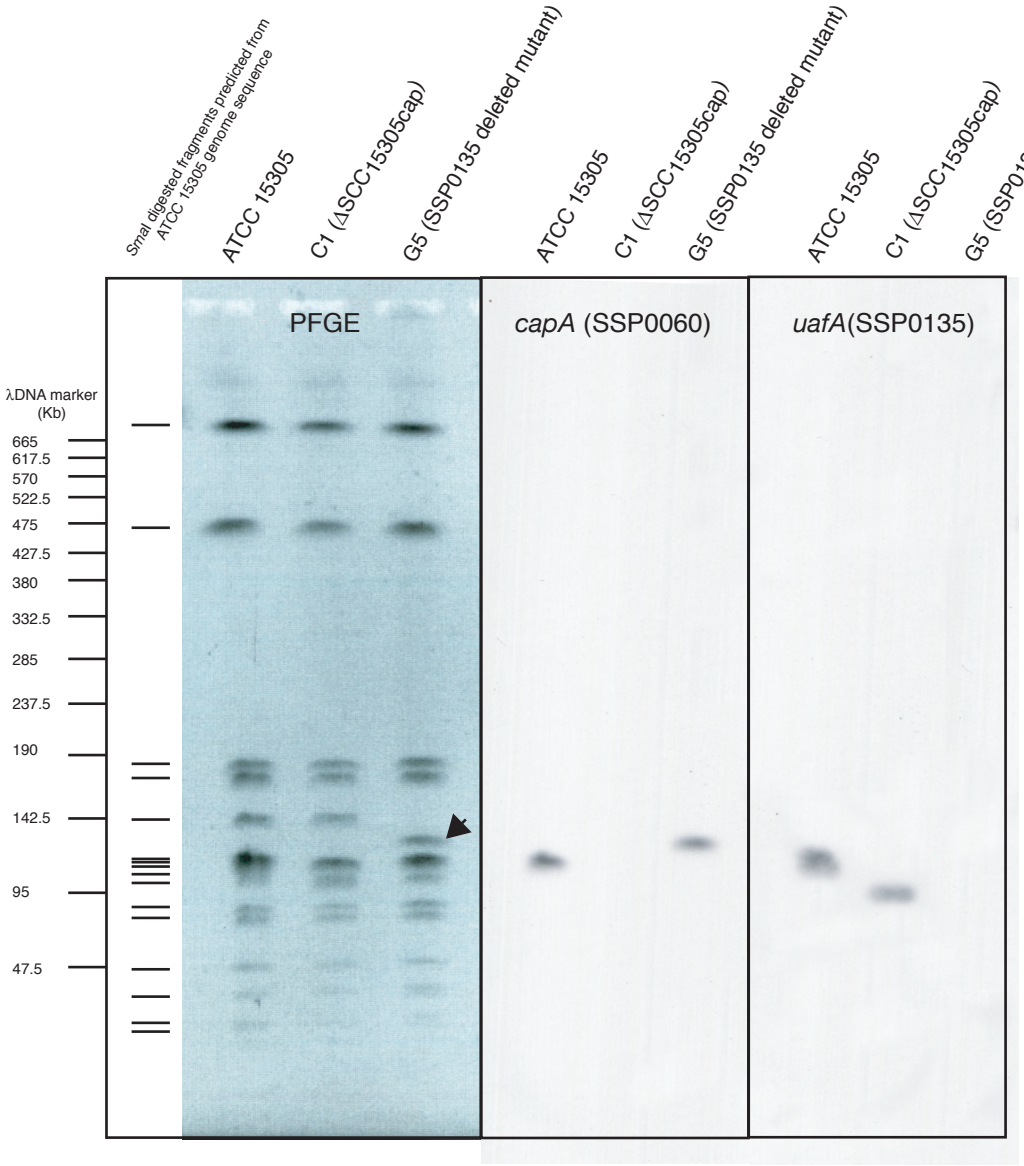

Positions at *Sma*I site		Length (bp)
964113	1667380	703268
1667381	2124803	457423
462069	646580	184512
2372032	29843	174387
169340	312168	142829
846017	961015	114999
57091	169339	112249
312169	419618	107450
2124804	2228382	103579
646581	745108	98528
748024	828212	80189
2228383	2301896	73514
419619	462068	42450
2310089	2339974	29886
2353694	2372031	18338
40489	57090	16602
828213	843102	14890
29844	40488	10645
2343941	2350779	6839
2339975	2343940	3966
961016	964112	3097
2307095	2310088	2994
745109	748023	2915
2350780	2353693	2914
843103	846016	2914
2301897	2304810	2914
2304811	2307094	2284
	Total	2516575

Fig. 6. Pulsed-field gel electrophoresis (PFGE) analysis was performed to verify the genome sequence of ATCC 15305. Predicted *Sma*I-digested fragments are consistent with a obtained PFGE profile of ATCC 15305. C1($\Delta SCC_{15305cap}$) and G5 (*uafA* deleted mutant) are confirmed as isogenic derivatives from ATCC 15305. The excised junction of $\Delta SCC_{15305cap}$ in C1 strain can be amplified by PCR, and definitely consistent with the consensus sequence of the attachment site for Ccr recombinases (the duplicated both *att* sequences are 5'-GAAGCGTATCACAAATAA-3'; the consensus sequence is referred to the report in ref. 1). Southern hybridization also shows no band with the *capA* gene specific probe in C1. Arrow indicates the DNA fragment in G5 including a deleted region, and Southern hybridization shows no band with the *uafA* gene specific probe in G5. PFGE analysis was done at the condition as follows: 6V/cm, ±60° angle, 5.3 sec initial time, 50 sec final time, running for 20 h with 0.5x TBE by Bio-Rad CHEF MAPPER.

1. Ito, T., Ma, X. X., Takeuchi, F., Okuma, K., Yuzawa, H. & Hiramatsu, K. (2004) *Antimicrob. Agents Chemother.* **48**, 2637-2651.