DNA sequencing for *csaB* genes

Primers P1 (5'-GTGCGTTTAGTCTTATCAGGAT-3') and P2 (5'-CTTTCGCATCCCAATAMCKYACACT-3') were designed to amplify a DNA segment within the *csaB* gene with a length of 589 (for Group II) or 592 (for Group I) for each strain. For *Bacillus cereus* ATCC 14579, it represents the region of chromosome from 1,881,875 to 1,882,464.

Preparation of total DNA template for PCR was based on the method described by Gussow et al. (1989) with some modifications. The basic steps for this protocol were as follow: after being grown on LB plates overnight, a colony was picked with a sterile toothpick into a 1.5 mL tube with 50 μL TE buffer, boiled for 10 min, transferred on ice for 10 min and centrifuged at 12,000 rpm for 10 min. The supernatant was directly used as PCR template, together with primers P1 (5'-GTGCGTTTAGTCTTATCAGGAT-3') and P2 (5'-CTTTCGCATCCCAATAMCKYACACT-3'). For each amplification reaction mixture, 1 μL of bacterial DNA was subjected to PCR in a total volume of 25 μL, with 2.5 U Taq polymerase, 2.5 μL 10× PCR buffer, 0.5 μL dNTP mixture (25 mM) and 0.8 μM of each primer. PCR amplification involved an initial denaturation step of 95°C for 5 min and then 30 cycles of denaturation at 95°C for 30 s, primer annealing at 54°C for 30 s, extension at 72°C for 40 s, and a final extension step at 72°C for 5 min. PCR products were purified using a Gel Extraction Kit (OMIGA), and were sequenced in both directions. All of the sequences were submitted to GenBank, and their accessions numbers are showed in Table S1.