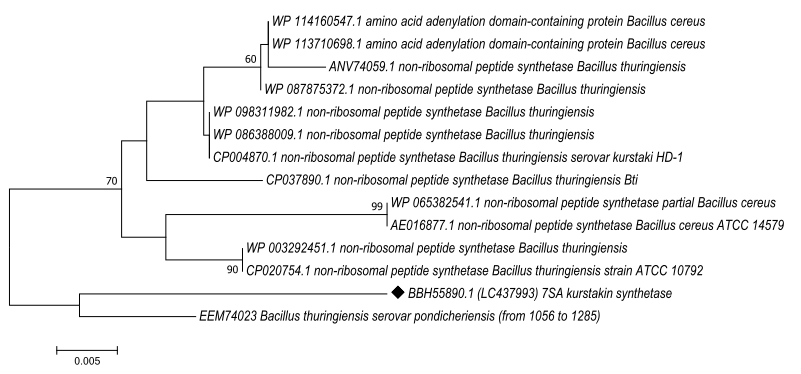


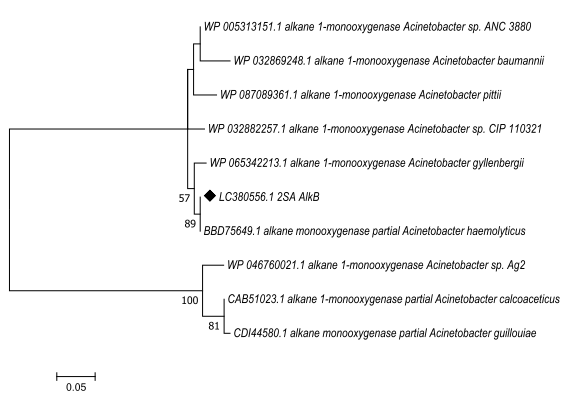
**Figure S1:** Critical micelle concentration (CMC) of kurstakin molecules produced by Bacillus thuringiensis strain 7SA



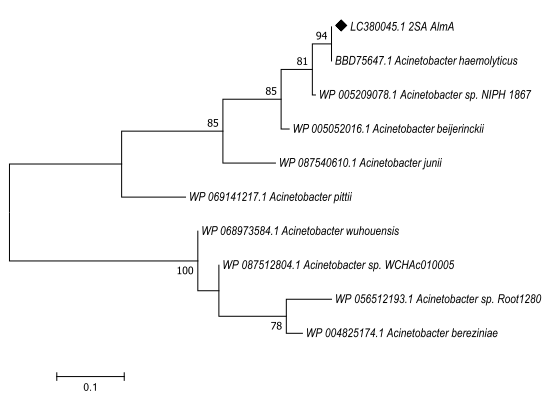
**Figure S2:** Maximum Likelihood phylogenetic trees based on the alignment of amino acid sequences of the kurstakin synthetase gene from strain 7SA. The reference sequences were retrieved from NCBI database.

C:\Users\bella\Desktop\Lipopeptides\Biodegradation\ENVIRONMENTAL TECHNOLOGY\trees\clustal.tif

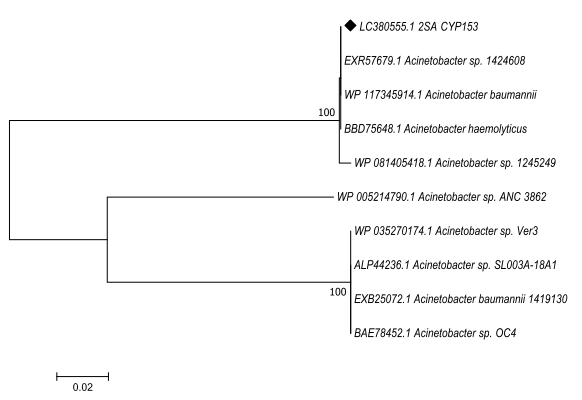
**Figure S3:** CLUSTAL O (1.2.4) multiple sequence alignment and comparison of amino acid sequences of the kurstakin synthetase gene from strain 7SA and reference sequences retrieved from NCBI database.



**Figure S4:** Maximum Likelihood phylogenetic trees based on the alignment of amino acid sequences of the alkB gene from strain 2SA. The reference sequences were retrieved from NCBI database.



**Figure S5:** Maximum Likelihood phylogenetic trees based on the alignment of amino acid sequences of the almA gene from strain 2SA. The reference sequences were retrieved from NCBI database.



**Figure S6:** Maximum Likelihood phylogenetic trees based on the alignment of amino acid sequences of the cyp153 gene from strain 2SA. The reference sequences were retrieved from NCBI database.