

SUPPLEMENTARY MATERIAL TO

Optimization of the slaughterhouse water treatment rate by a new *Marinobacter carbonoclasticus* SF and its biosurfactant

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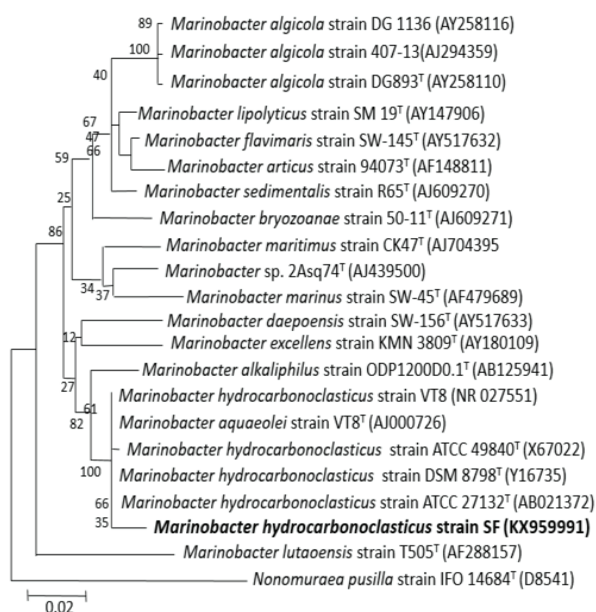


Fig. S-1. Phylogenetic tree based on 1500 nucleotides of the 16S rRNA gene sequence of the SF strain, showing its phylogenetic position among related species of the genus *Marinobacter*.

Bootstrap percentages are given at node level. Access numbers (Genbank) are given in brackets. Scale bar equals approximately 2 % nucleotide divergence.

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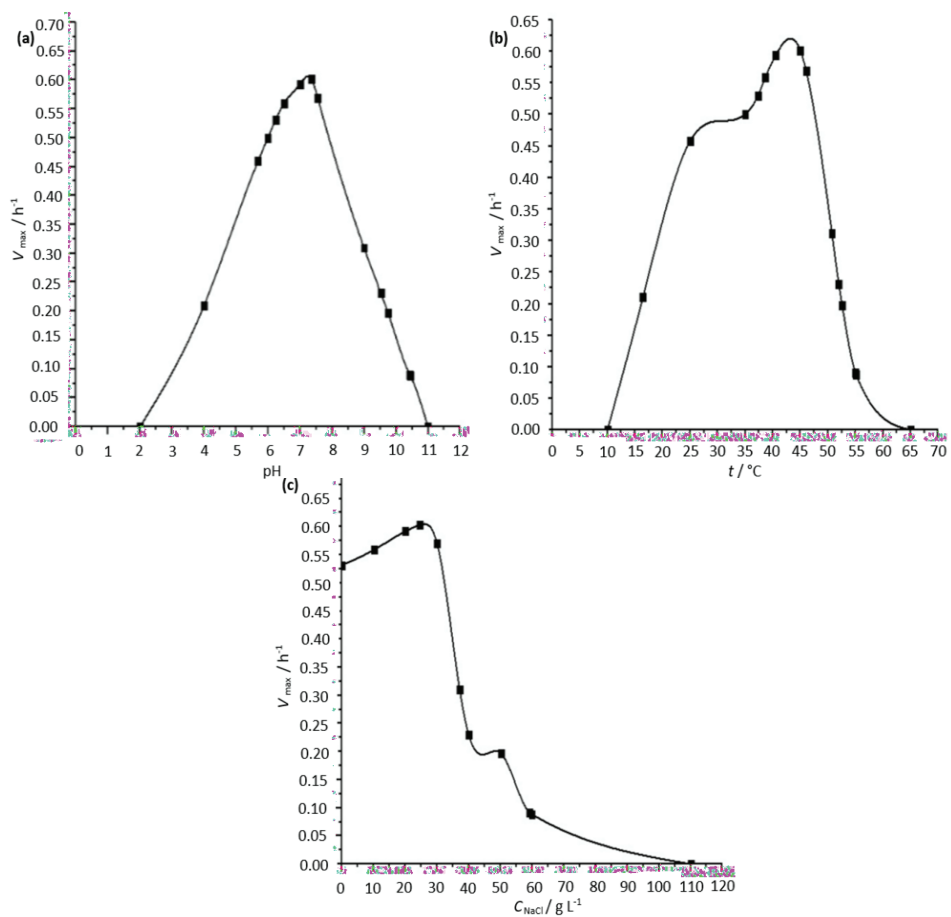


Fig. S-2. Influence of: a) pH, b) temperature and c) concentration of NaCl on bacterial growth.

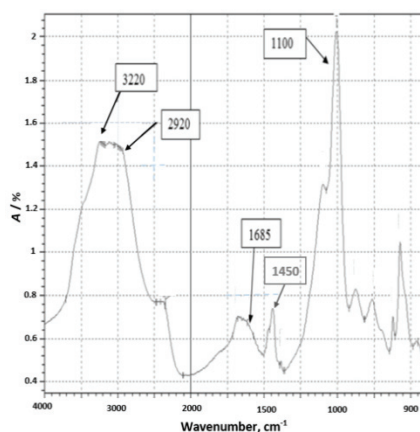
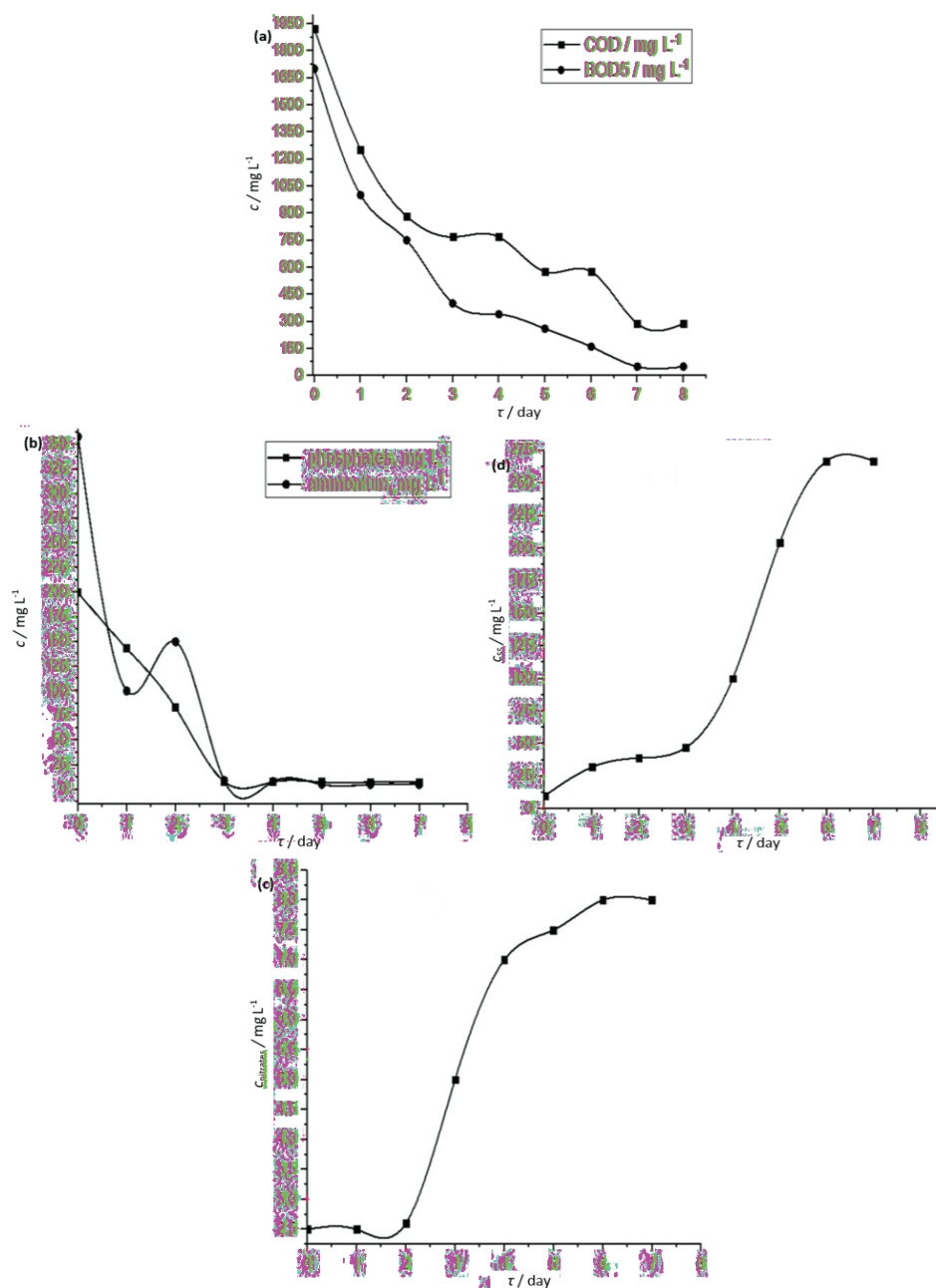


Fig. S-3 FTIR spectra (500-4000 cm^{-1}) of biosurfactant product.Fig. S-4. Variation in the level of a) COD, BOD₅, b) phosphates, ammonium, c) nitrates and d) suspended matter; after 120 h of treatment with isolated *marinobacter* SF.

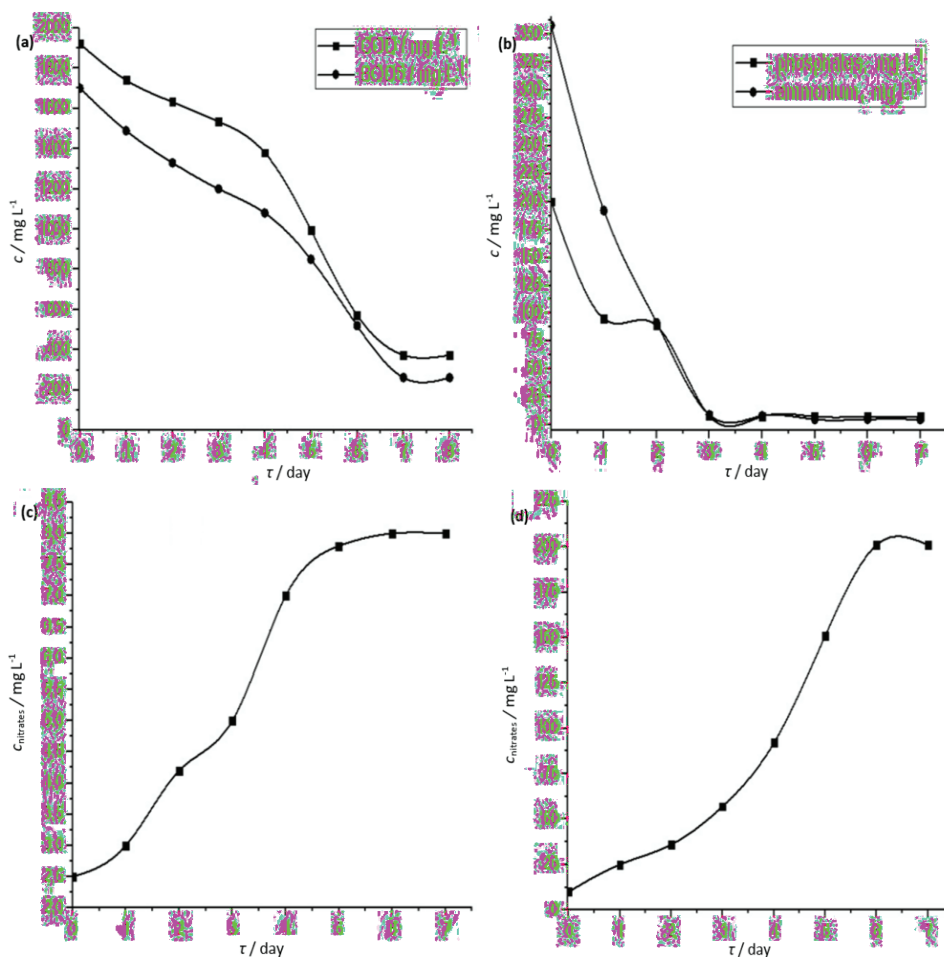


Fig. S-5. Variation in the level of: a) *COD*, *BOD*₅, b) phosphates, ammonium, c) nitrates and d) suspended matter; after 120 h of treatment with the biosurfactant.