

Legends of the Figures:

Fig. 1. Consensus neighbor-joining phylogenetic tree based on 16S-rRNA gene sequences showing the phylogenetic positions of eleven biosurfactant producing isolates selected in this study and published biosurfactant isolates from literatures. Numbers at nodes indicate bootstrap values of neighbor-joining analysis for 1000 replicates. The scale bar indicates substitutions per nucleotide. The GenBank accession numbers for the 16S-rRNA gene sequences are given in parentheses after the strain name.

Fig. 2. Biosurfactant production profile (30°C, 120 rpm, 7 days):

(**A**) *Achromobacter* sp. (PS1), (**B**) *Bacillus* sp. (SLDB1),
(**C**) *Ochrobactrum* sp. (GREW1) and (**D**) *Bacillus* sp. (SB2).

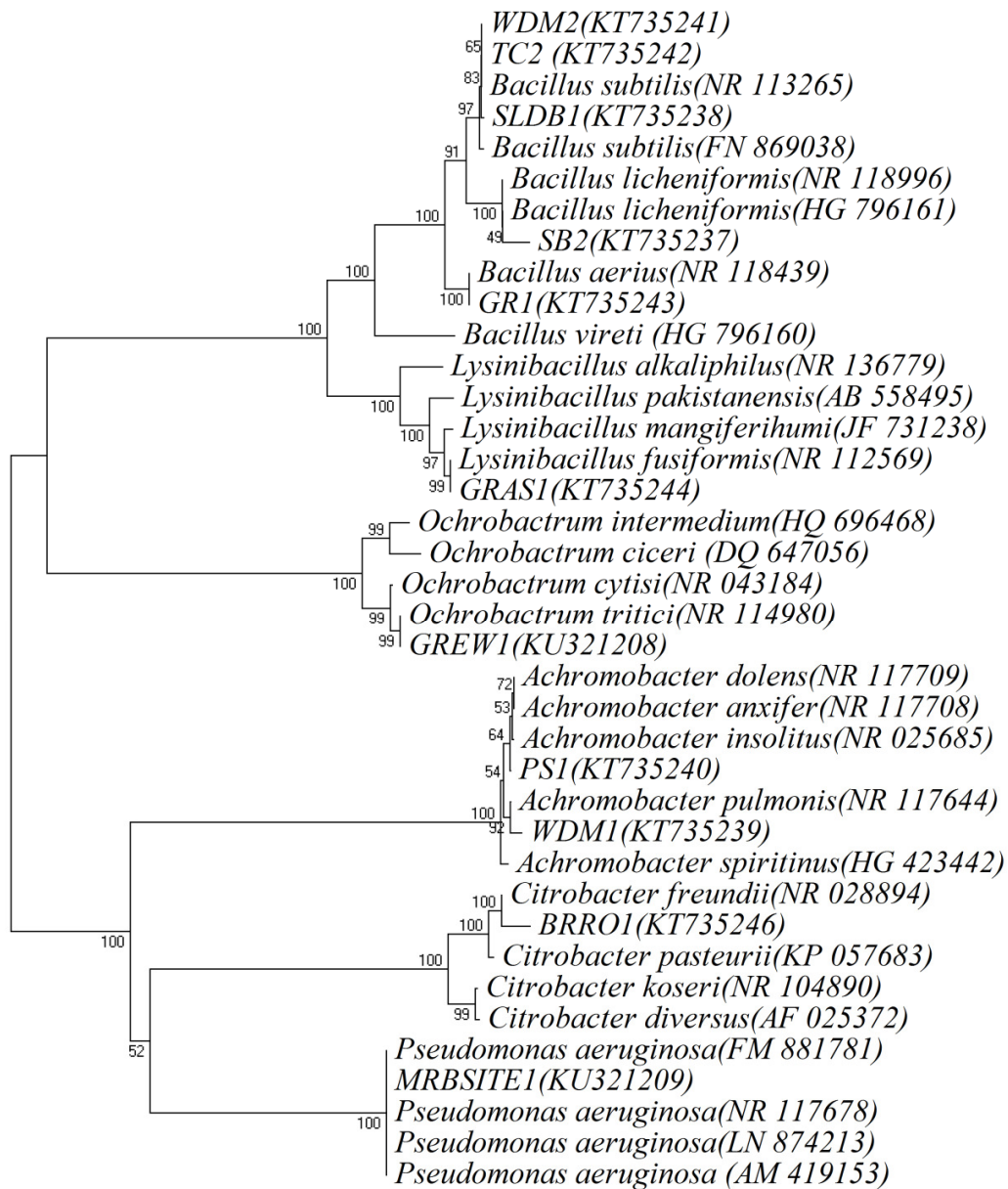
The standard deviations presented are based on triplicate (SD, n = 3)

Fig. 3. TLC chromatograms:

(**A**) Glycolipid biosurfactant (**a**, **b** & **c**): **a**- Jeneil JBR -215 (standard);
b- *Achromobacter* sp. (PS1); **c**- *Bacillus* sp. (SLDB1)

(**B**) Lipopeptide biosurfactant (**d** & **e**): **d**- *Ochrobactrum* sp. (GREW1);
e- *Bacillus* sp. (SB2)

Fig. 1.



0.02

Fig. 2.

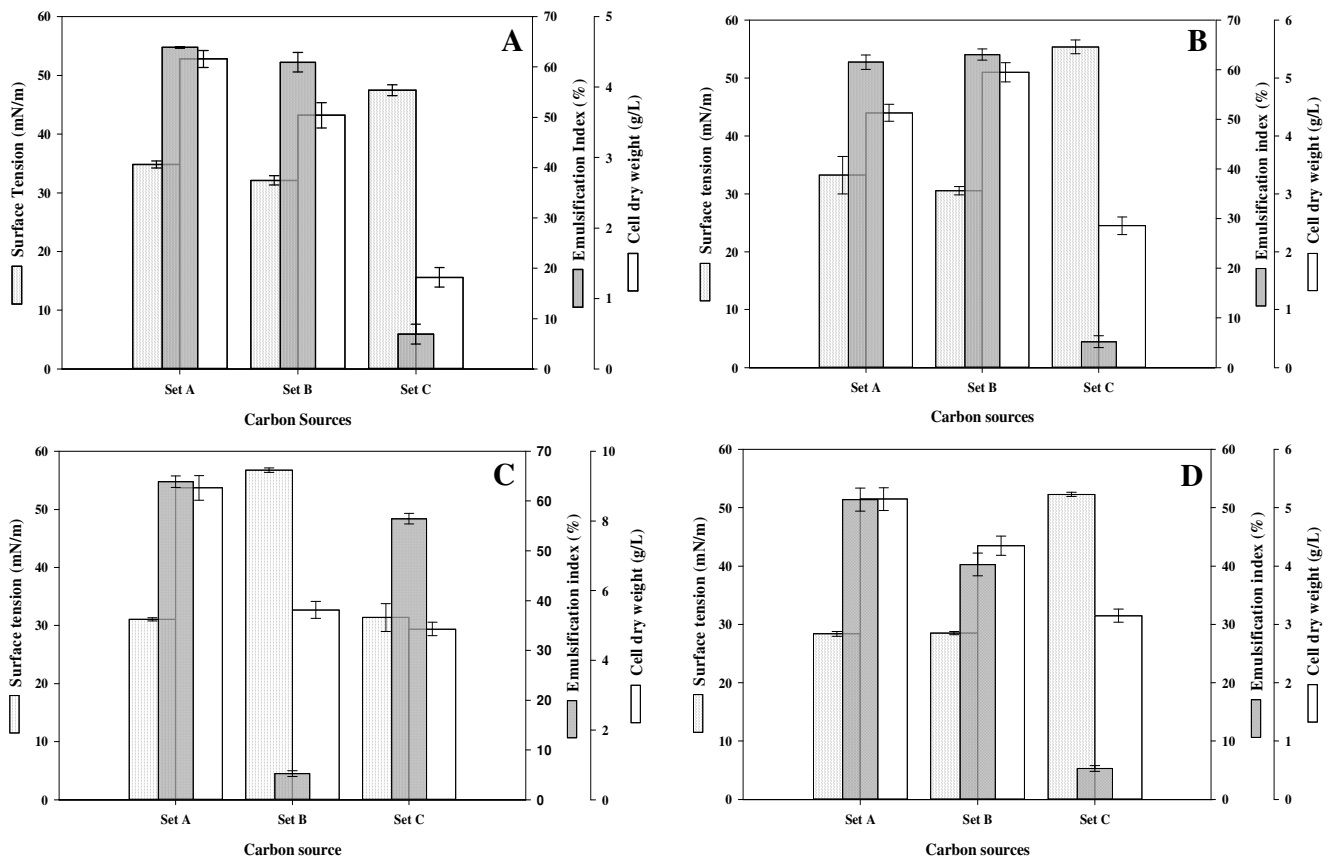
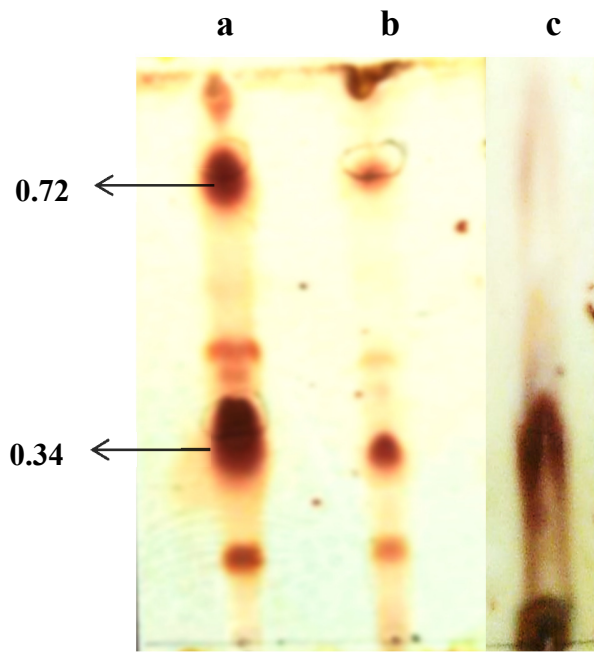
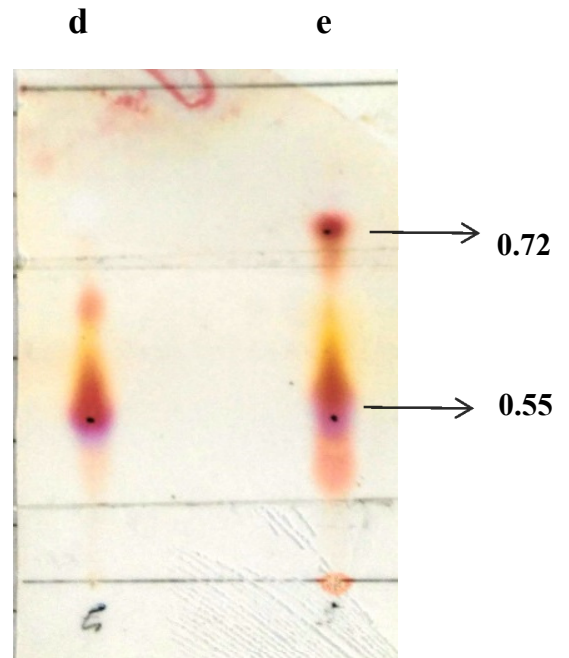


Fig. 3



A



B