

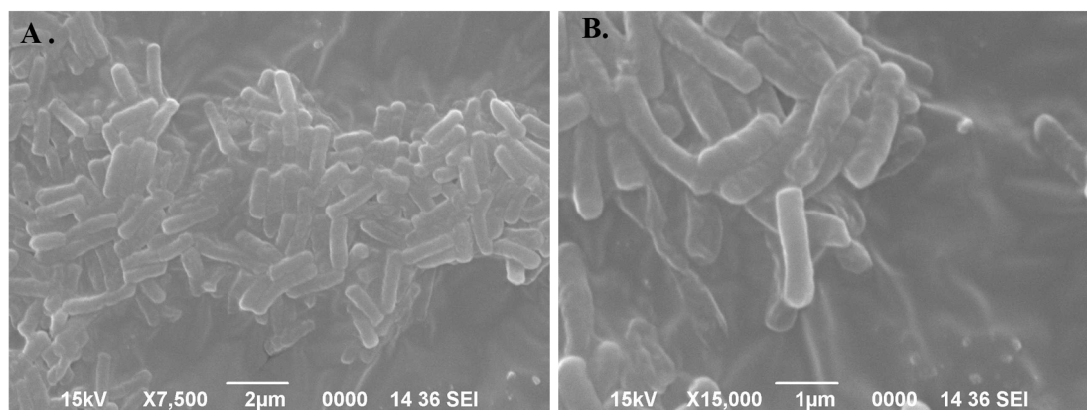


Figure S1: SEM micrographs of *pseudomonas aeruginosa* strain jbk1

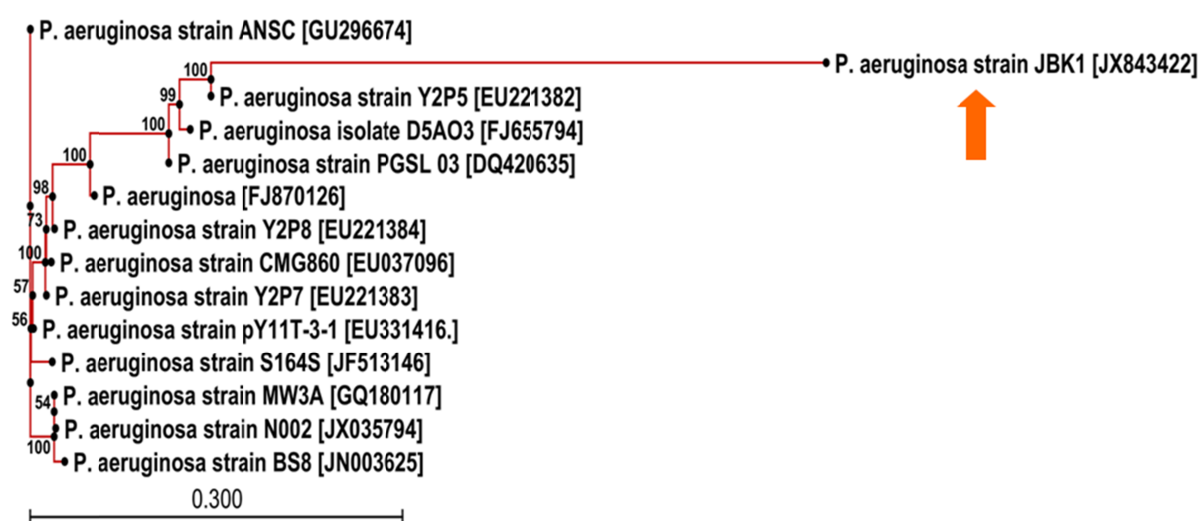


Figure S2: Phylogenetic tree generated using nj method showing the position of *pseudomonas aeruginosa* strain jbk1 compared to other highly similar 16s rRNA sequence of various *pseudomonas aeruginosa* strains.

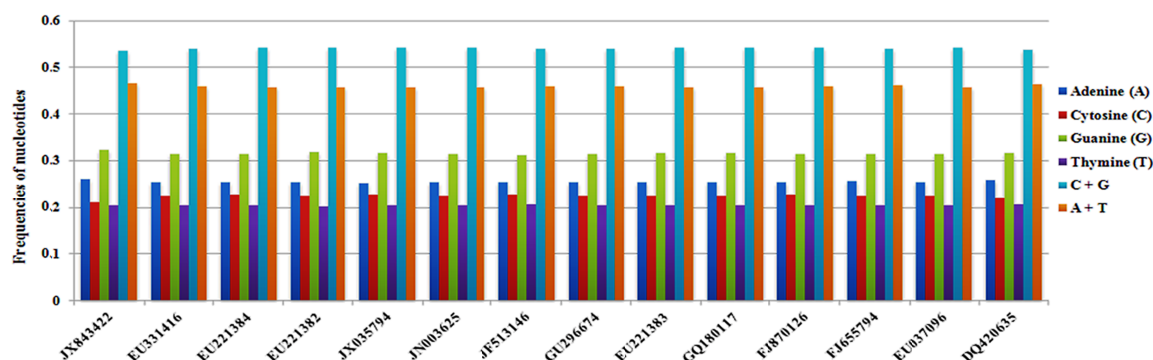


Figure S3: Frequency of nucleotide distribution for *pseudomonas aeruginosa* strain jbk1 and various strains of *pseudomonas aeruginosa* strain having maximum similarity with *pseudomonas aeruginosa* strain jbk1.

Supplementary Table 1. BLAST result of 16s rRNA of *Pseudomonas aeruginosa* strain JBK-1

S.No	Accession	Max Score	Total Score	Query coverage	E-value	Max Identity
1.	EU331416	1565	1565	100%	0.0	99%
2.	EU221384	1565	1565	100%	0.0	99%
3.	EU221382	1565	1565	100%	0.0	99%
4.	JX035794	1565	1565	100%	0.0	99%
5.	JN003625	1565	1565	100%	0.0	99%
6.	JF513146	1565	1565	100%	0.0	99%
7.	GU296674	1565	1565	100%	0.0	99%
8.	EU221383	1565	1565	100%	0.0	99%
9.	GQ180117	1565	1565	100%	0.0	99%
10.	FJ870126	1565	1565	100%	0.0	99%
11.	FJ655794	1565	1565	100%	0.0	99%
12.	EU037096	1565	1565	100%	0.0	99%
13.	DQ420635	1565	1565	100%	0.0	99%