## **Appendix**

Table S1. Adjusted means and standard errors for treatments. Inverse of the link function with random effect =0. DGC (Alfa=0.05).

Treatments	PredLin	SE	Means	SE		
Control	-0.61	0.39	0.35	0.09	A	
221-Paenibacillus	-0.76	0.39	0.32	0.08	A	
182-Bacillus	-1.25	0.4	0.22	0.07		В
336-Pseudomonas	-1.42	0.4	0.19	0.06		В

Means with a common letter are not significantly different (P>0.05).

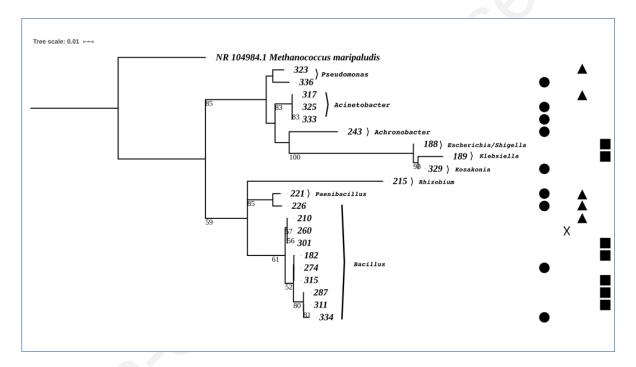


Figure S1. Phylogenetic tree of sugarcane bacteria and their habitat of isolation. The tree was generated using the RAxML method; the numbers at the branch nodes indicate the bootstrap percentage values obtained from 1000 resampling (only bootstraps > 50% are shown). Each symbol represents the site of isolation: ( $\bullet$ ) root, (X) stem, ( $\blacktriangle$ ) rhizosphere. Scale bar indicates substitutions per site. *Methanococcus maripaludis* (NR\_104984.1) was used as an outgroup.

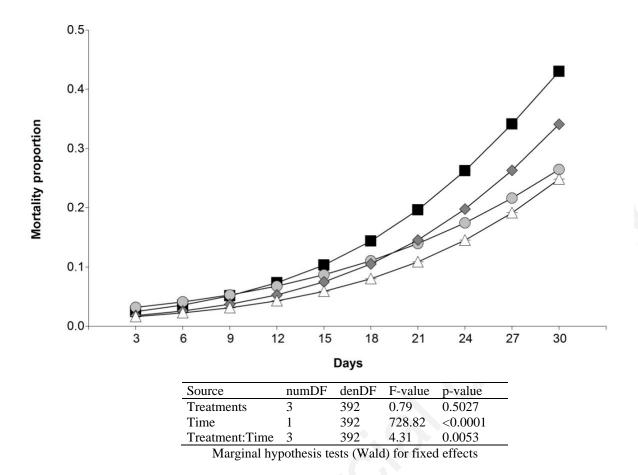


Figure S2. Mortality rate of micropropagated sugarcane seedlings in the *ex vitro* acclimatisation stage. *In vitro* grown sugarcane seedlings were treated with water (control) ( $\blacksquare$ ), 182-*Bacillus* ( $\blacktriangle$ ), 221-*Paenibacillus* ( $\blacklozenge$ ), and 336-*Pseudomonas* ( $\bullet$ ). After treatments, plant survival was evaluated for 30 days in a greenhouse.