

Applied Microbiology and Biotechnology

Supplementary Information

Characterization of a novel D-sorbitol dehydrogenase from *Faunimonas pinastri* A52C2

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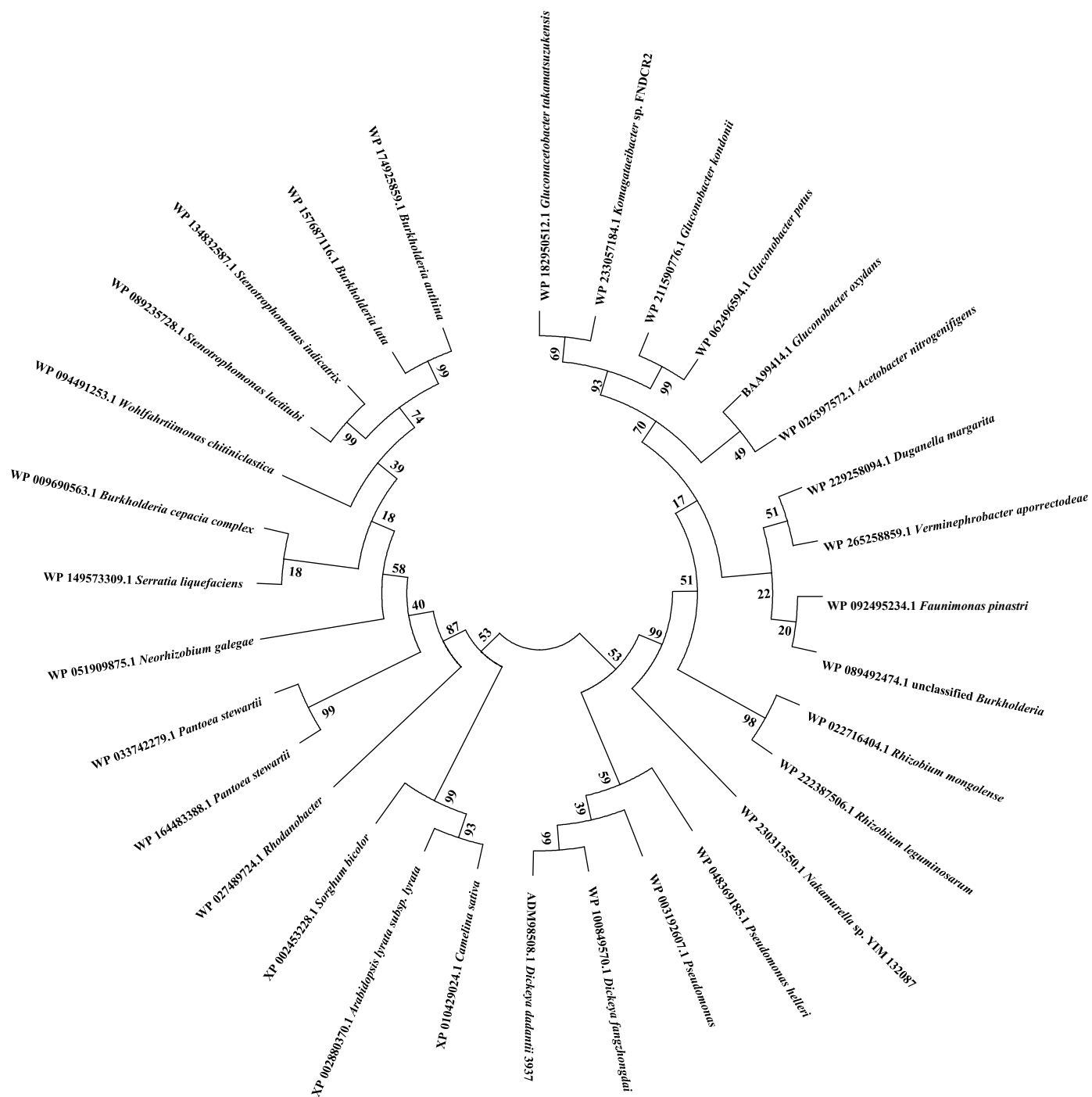


Fig. S1 Evolutionary relationships of taxa. The evolutionary history was inferred using the Neighbor-Joining method. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 31 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 107 positions in the final dataset.

Evolutionary analyses were conducted in MEGA7.

Similarity(%)	Vasldh	Rlsldh	Fpsldh	Ansldh	Dmsldh
Vasldh					
Rlsldh	53.33				
Fpsldh	55.53	50.20			
Ansldh	42.60	41.90	44.56		
Dmsldh	55.12	45.26	52.60	44.58	

Table S1 Amino acid sequence similarity among five new SLDHs

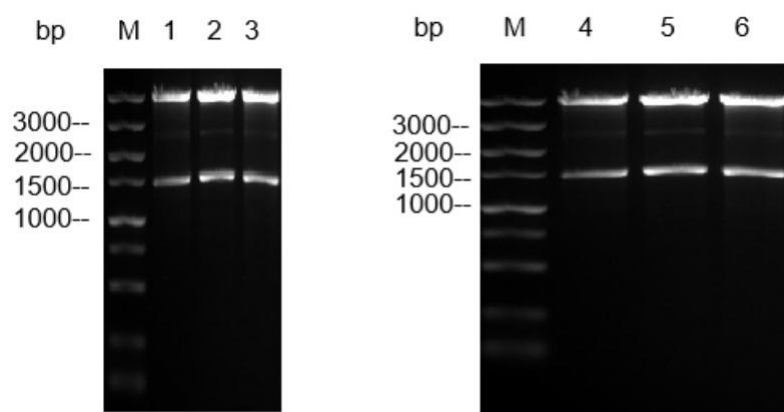


Fig. S2 Recombinant plasmids digested by the restriction enzymes *EcoRI* / *XhoI*. M1:DL5000 DNA marker,

1: pPG, 2: pPF, 3: pPA, 4: pPR, 5: pPV, 6: pPD

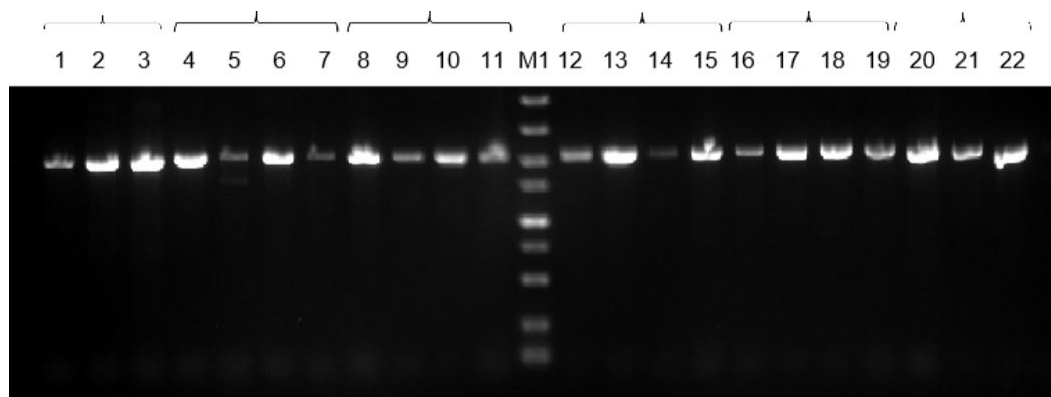


Fig. S3 Electrophoretic analysis of BL2 by PCR with electric transfer. M1: DL5000 DNA marker, 1, 2, 3:

BLpPG, 4, 5, 6, 7: BLpPF, 8, 9, 10, 11: BLpPA, 12, 13, 14, 15: BLpPR, 16, 17, 18, 19: BLpPV, 20, 21, 22: BLpPD

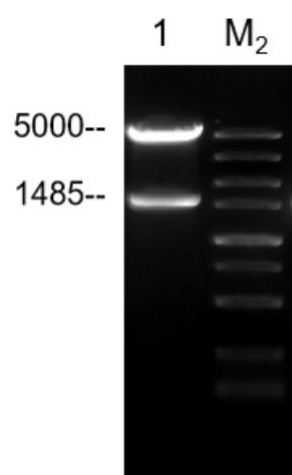


Fig. S4 pET28a-*fpsldh* digested by the restriction enzymes *EcoRI* / *XhoI*

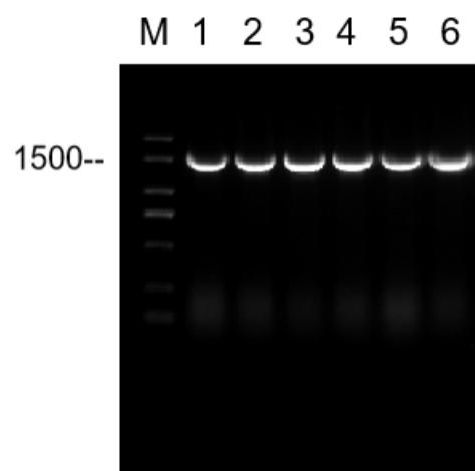


Fig. S5 pET28a-*fpsldh* conversion to *E. coli* BL21(DE3) colony PCR electrophoresis map