

Genomic Insights Into A Novel, Alkalitolerant Nitrogen Fixing Bacteria, *Azonexus sp.* Strain ZS02.

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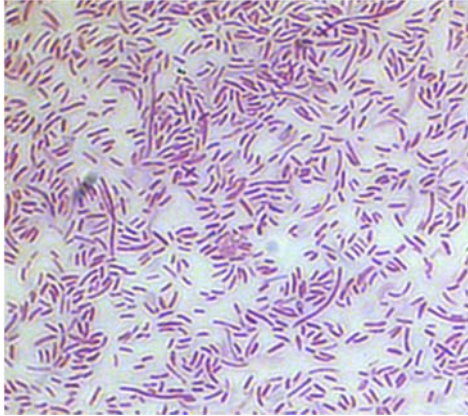
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Supplementary Material

Organism	Average Amino acid Identity (%)							
	1	2	3	4	5	6	7	8
Azonexus hydrophilus ZS-02 (1)	100	84.21	75.34	66.22	59.35	56.88	55.52	61.32
Azonexus hydrophilus DSM23864 (2)		100	74.48	66.56	59.85	56.43	55.69	61.62
Dechloromonas denitrificans ATCC BAA-841 (3)			100	66.01	58.97	57.87	56.07	62.18
Azovibrio restrictus DSM23866 (4)				100	59.60	57.22	55.23	60.60
Azoarcus sp BH72 (5)					100	62.84	54.97	57.25
Zoogloea sp LCSB751 (6)						100	52.37	55.15
Aquaspirillum sp LM1 (7)							100	52.98
Candidatus accumulibacter sp SK-02 (8)								100

Table S1: Amino acid identity comparisons suggested that strain ZS-02 showed greatest amino acid sequence homology with *Azonexus hydrophilus* d8-1.

A



B

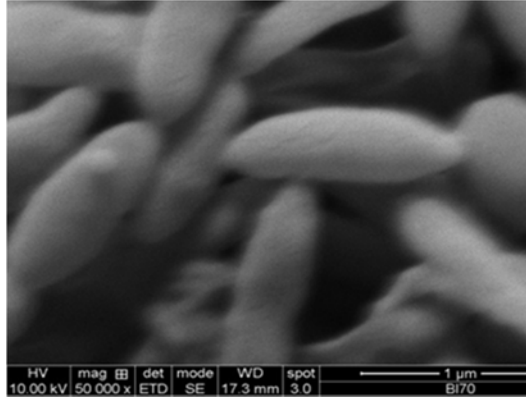


Figure S1: Microscopy investigation of morphology of *Azonexus hydrophilus* strain ZS-02[A] Gram stain at 1000x magnification. [B] SEM image.

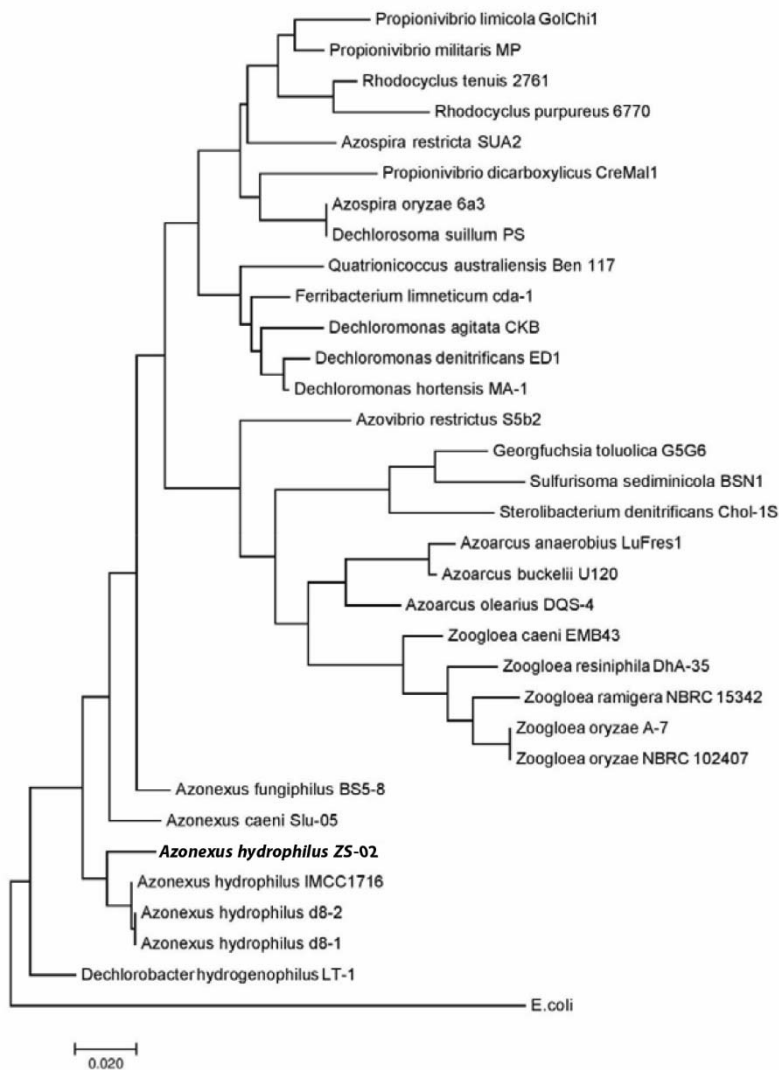


Figure S2: Maximum likelihood 16S rRNA phylogenetic tree showing distribution of closest relatives to *Azonexus hydrophilus* strain ZS-02.

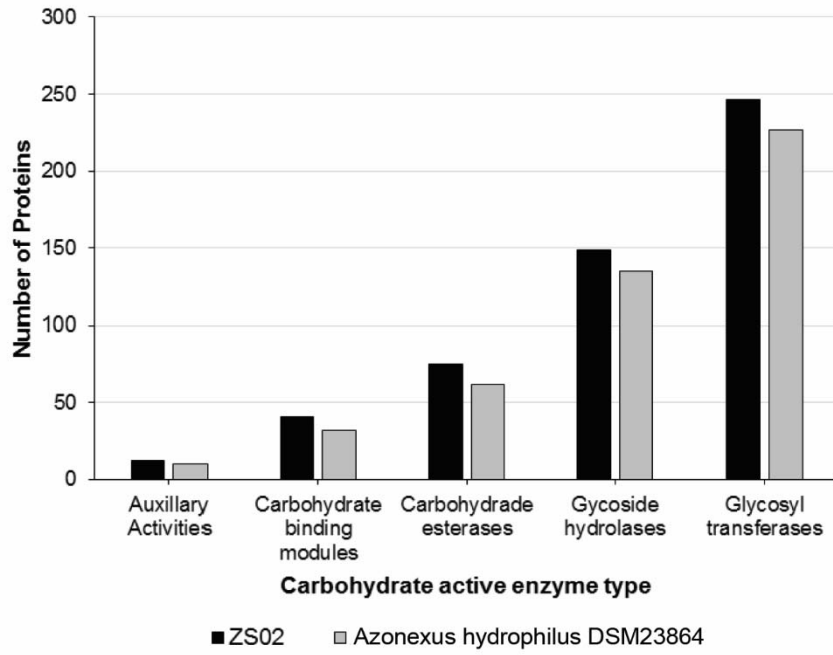


Figure S3: Identification of carbohydrate active enzymes through CAZy analysis indicated that isolate ZS02 had more proteins than *Azonexus hydrophilus* DSM2032 (d8-1) within each class.