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Supplementary Material

The Complete Genome Sequence of *Bacillus safensis* BRM1 Isolated from Brazilian Mangrove Sediment: A Potential Source of Biomass Converting Enzymes

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Table S1. Clusters of orthologous groups (COG) analysis for *Bacillus safensis* BRM1.

COG Category	Code	Total	Total (%)
Information storage and processing			
RNA processing and modification	A	0	0,0%
Chromatin structure and dynamics	B	0	0,0%
Translation, ribosomal structure and biogenesis	J	169	5.1%
Transcription	K	286	8.6%
Replication, recombination and repair	L	129	3.9%
Cellular processes and signaling			
Cell cycle control, cell division, chromosome partitioning	D	33	1.0%
Cell wall/membrane/envelope biogenesis	M	177	5.3%
Cell motility	N	41	1.2%
Posttranslational modification, protein turnover, chaperones	O	98	2.9%
Signal transduction mechanisms	T	129	3.9%
Intracellular trafficking, secretion, and vesicular transport	U	25	0.8%
Defense mechanisms	V	56	1.7%
Extracellular structures	W	0	0.0%
Nuclear structure	Y	0	0.0%
Cytoskeleton	Z	0	0.0%
Metabolism			
Energy production and conversion	C	153	4.6%
Amino acid transport and metabolism	E	301	9.0%
Nucleotide transport and metabolism	F	74	2.2%
Carbohydrate transport and metabolism	G	222	6.7%
Coenzyme transport and metabolism	H	104	3.1%
Lipid transport and metabolism	I	92	2.8%
Inorganic ion transport and metabolism	P	169	5.1%
Secondary metabolites biosynthesis, transport and catabolism	Q	47	1.4%
Poorly Characterized			

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COG Category	**Code**	**Total**	**Total (%)**
General function prediction only	R	0	0,00%
Function unknown	S	818	24.6%
Total of ORFs Annotated		**3,326**	**100%**
ORFs unclassified		373	

Table S2. Putative cellulases and hemicellulases in *Bacillus safensis* BRM1, according to CAZY database [19].

Gene ID	**Conserved Domain**	**Localization Prediction**[1]	**Length in Amino Acids**
ARD54928.1	GH1	Cytoplasmic	473
ARD58015.1	GH1	Cytoplasmic	472
ARD56702.1	GH1	Cytoplasmic	468
ARD58075.1	GH1	Cytoplasmic	488
ARD57987.1	GH1	Cytoplasmic	477
ARD58091.1	GH1	Cytoplasmic	478
ARD54868.1	GH3	Cytoplasmic	639
ARD55290.1	GH4	Cytoplasmic	441
ARD55295.1	GH4	Cytoplasmic	442
ARD56363.1	GH4	Cytoplasmic	443
ARD57955.1	GH4	Cytoplasmic	442
ARD56165.1	GH5	Extracellular	377
ARD56162.1	GH9+CBM3	Extracellular	616
ARD56164.1	GH10	Extracellular	409
ARD56433.1	GH11	Extracellular	227
ARD55167.1	GH16	Extracellular	242
ARD56360.1	GH30	Extracellular	421
ARD58058.1	GH42	Cytoplasmic	688
ARD56361.1	GH43	Cytoplasmic	512
ARD56437.1	GH43	*Unknown*	535
ARD56163.1	GH48	Extracellular	701
ARD57051.1	GH51	Cytoplasmic	492
ARD58057.1	GH53	Membrane-ligated	402
ARD54864.1	CE4	Extracellular	254
ARD55371.1	CE4	Cytoplasmic	263
ARD55521.1	CE4	Cytoplasmic	284
ARD56186.1	CE4	Extracellular	317
ARD56538.1	CE4	Cytoplasmic	284
ARD56877.1	CE4	Cytoplasmic	246
ARD56884.1	CE4	Extracellular	466
ARD57608.1	CE4	Extracellular	469
ARD57984.1	CE4	Membrane-ligated	282
ARD55769.1	CE6	Membrane-ligated	276
ARD55018.1	CE7	Cytoplasmic	318
ARD55391.1	CE12	Extracellular	209

1 – Subcellular localization prediction by PSORTb v3.0 [24].

GH: Glycosyl Hydrolase Family. CE: Carbohydrate Esterase Family. CBM: Carbohydrate-Binding Module.