

Supplementary Materials

Table S1.1: Characteristics differentiating strain HW T2.11^T (*Acidisoma silvae*) from strain HW T5.17^T (*A. cellulositytica*) using Biolog GN2 microplate (adapted from Mieszkina *et al.* [17]). Characteristics are scored as: +, positive or –, negative.

Concerning the amino acids category, the two strains utilized L-Alanine and L-Asparagine but neither strain was capable of utilizing L-Histidine, Hydroxy-L-Proline, Inosine, L-Ornithine, L-Phenylalanine, L-Proline, L-Alanyl-glycine, D-Serine, L-Serine, D,L-Carnitine and L-Glutamic Acid.

Concerning the amines/amides category, the two strains utilized L-Alaninamide but neither strain was capable of utilizing Phenylethylamine, Putrescine, Glucuronamide, L-Threonine and 2-Aminoethanol.

Concerning the carbohydrates category, the two strains utilized i-Erythritol, D-Fructose, Dextrin, L-Fucose, D-Galactose, Alpha-D-Glucose, D-Sorbitol, D-Trehalose, Adonitol, D-Mannose, L-Arabinose, Xylitol, and D-Arabitol but neither strain was capable of utilizing Gentiobiose, L-Rhamnose, Alpha-D-Lactose, D-Mannitol, D-Melibiose, Beta-Methyl-D-Glucoside, D-Psicose, D-Raffinose, Sucrose, N-Acetyl-D-glucosamine, Lactulose, Turanose and Maltose.

Concerning the carboxylic acids category, the two strains utilized D,L-Lactic Acid and D-Gluconic-Acid but neither strain was capable of utilizing Urocanic-Acid, propionic acid, Glycyl-L-Glutamic Acid, Acetic Acid, p-Hydroxy-Phenylacetic-Acid, Bromo-Succinic-Acid, *Cis*-Aconitic-Acid, Itaconic-Acid, Succinamic-Acid, Citric-Acid, Alpha-Keto-Butyric-Acid, Formic-Acid, Alpha-Keto-Glutaric-Acid, Alpha-Keto-Valeric-Acid, D-Galacturonic-Acid, Malonic-Acid, L-Pyroglutamic-Acid, L-Aspartic-Acid, Quinic-Acid, Sebacic-Acid and Glycyl-L-Aspartic-Acid.

Concerning the miscellaneous category, the two strains utilized Glycreol, Mono-Methyl-Succinate and glucose-6-Phosphate but neither strain was capable of utilizing Glucose-1-Phosphate, Uridine, Glycogen, Thymidine, 2-Aminoethanol, 2,3-Butanediol and D,L-Alpha-Glycerol-Phosphate.

Concerning the polymer category, none of the strain was capable of hydrolyzing Alpha-Cyclodextrin.

		HW T2.11T	HW T5.17T
Amino acids			
	L Leucine	+	-
	D Alanine	-	+
Amines/Amides			
	N-Acetyl-D-galactosamine	-	+
Carbohydrates			
	L Fucose	-	+
	m-Inositol	-	+
	D cellobiose	-	+
Carboxylic acids			
	D-Glucosaminic-Acid	-	+
	D-Glucuronic-Acid	-	+
	Alpha-Hydroxy-Butyric-Acid	-	+
	D-Saccharic-Acid	-	+
	Beta-Hydroxy-Butyric-Acid	-	+
	Gamma-Hydroxy-Butyric-Acid	-	+
	Succinic-Acid	-	+
	Gamma-Amino-Butyric-Acid	-	+
	D-Galactonic-Acid-Lactone	-	+
Polymers			
	Tween 40	-	+
	Tween 80	-	+
Miscellaneous			
	Methyl-Pyruvate	-	+

Table S1.2: Classification of the CDS of strain HW T2.11^T (*Acidisoma silvae*) and strain HW T5.17^T (*A. cellulosilytica*) in COG categories.

			HW T2.11	HW T2.11	HW T5.17	HW T5.17
Processes	Class ID	Description	CDS (nb)	CDS (%)	CDS (nb)	CDS (%)
CELLULAR PROCESSES AND SIGNALING	D	Cell cycle control, cell division, chromosome partitioning	50	0.9089	46	0.761
	M	Cell wall/membrane/envelope biogenesis	293	5.3263	297	4.9132
	N	Cell motility	69	1.2543	49	0.8106
	O	Posttranslational modification, protein turnover, chaperones	147	2.6722	165	2.7295
	T	Signal transduction mechanisms	194	3.5266	165	2.7295
	U	Intracellular trafficking, secretion, and vesicular transport	95	1.727	92	1.5219
	V	Defense mechanisms	39	0.709	44	0.7279
	W	Extracellular structures	6	0.1091	7	0.1158
INFORMATION STORAGE AND PROCESSING	B	Chromatin structure and dynamics	4	0.0727	5	0.0827
	J	Translation, ribosomal structure and biogenesis	197	3.5812	209	3.4574
	K	Transcription	434	7.8895	508	8.4036
	L	Replication, recombination and repair	266	4.8355	265	4.3838
METABOLISM	C	Energy production and conversion	278	5.0536	310	5.1282
	E	Amino acid transport and metabolism	628	11.4161	696	11.5136
	F	Nucleotide transport and metabolism	91	1.6542	93	1.5385
	G	Carbohydrate transport and metabolism	520	9.4528	668	11.0505
	H	Coenzyme transport and metabolism	152	2.7631	155	2.5641
	I	Lipid transport and metabolism	231	4.1992	262	4.3342
	P	Inorganic ion transport and metabolism	331	6.0171	365	6.038
	Q	Secondary metabolites biosynthesis, transport and catabolism	206	3.7448	259	4.2845
POORLY CHARACTERIZED	R	General function prediction only	758	13.7793	857	14.177
	S	Function unknown	307	5.5808	347	5.7403

Table S1.3: Identification of enzymes involved in cellulose hydrolysis in the genome of strains HW T2.11^T (*Acidisoma silvae*) and HW T5.17^T (*A. cellulosilytica*) based on genes homology using PGAP and MaGe pipelines.

Enzymes	<i>Acidisoma silvae</i> (HW T2.11 ^T)			<i>Acidisoma cellulosilytica</i> (HW T5.17 ^T)		
	PGAP associated locus/EC number	gene associated locus/EC number	MaGe gene associated locus/EC number	PGAP associated locus/EC number	gene associated locus/EC number	MaGe gene associated locus/EC number
Cellulase	ASILVAE211_08965		ASILVAE211_v1_30210/EC 3.2.1.4			
Putative endoglucanase or cellulase (<i>cmcAX</i>)			ASILVAE211_v1_60021/EC 3.2.1.4			ACELLULO517_v1_130127/EC 3.2.1.4
Glucosidase	ASILVAE211_00975			ACELLULO_03405		
Amylo- α -1,6- glucosidase	ASILVAE211_03165	ASILVAE211_v1_10655		ACELLULO_23510		ACELLULO517_v1_120018
β -glucosidase				ACELLULO_11860/EC 3.2.1.23		
β -glucosidase A						ACELLULO517_v1_30664/EC 3.2.1.21
α -glucosidase or α -galactosidase				ACELLULO_14440 ACELLULO_16405 ACELLULO_20735		

Figure S1.1: Scheme of the experimental research procedure.

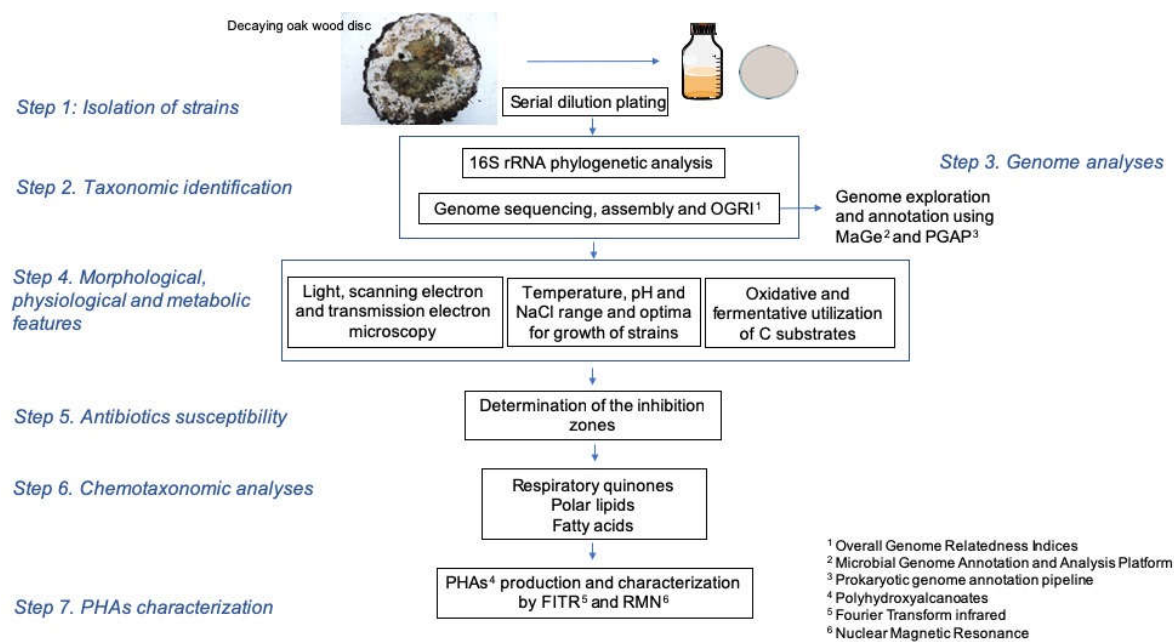


Figure S1.2: Growth kinetics under optimal growth conditions of strains HW T2.11^T (*Acidisoma silvae*) and HW T5.17^T (*A. cellulositytica*).

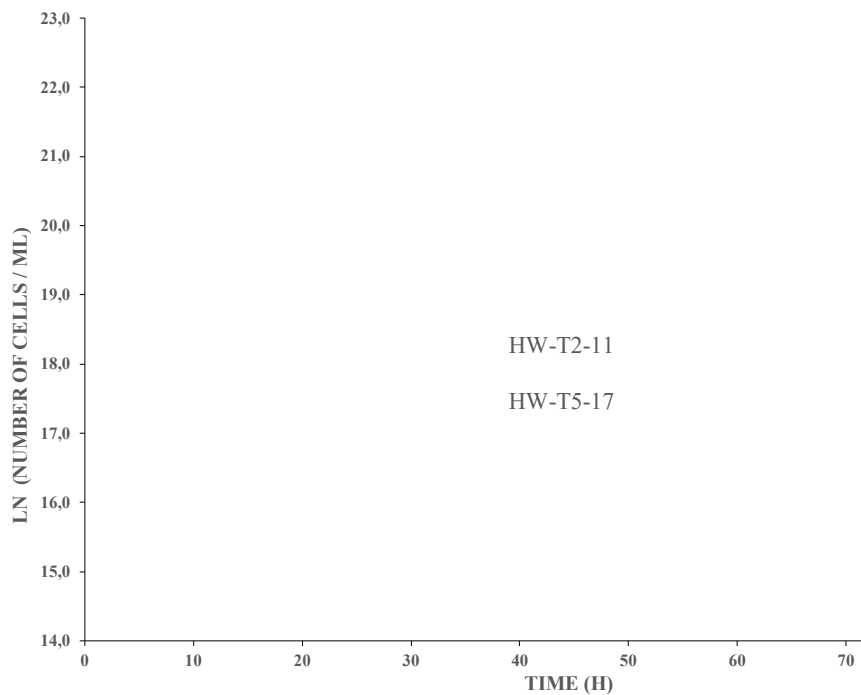


Figure SI.3: Location of the 4,156 georeferenced records (among the total 4,423 occurrences) for the genus *Acidisoma* in July 2021 based on the metagenomic 16S ribosomal RNA gene sequences from the GBIF database (<https://www.gbif.org/species/8071706>).

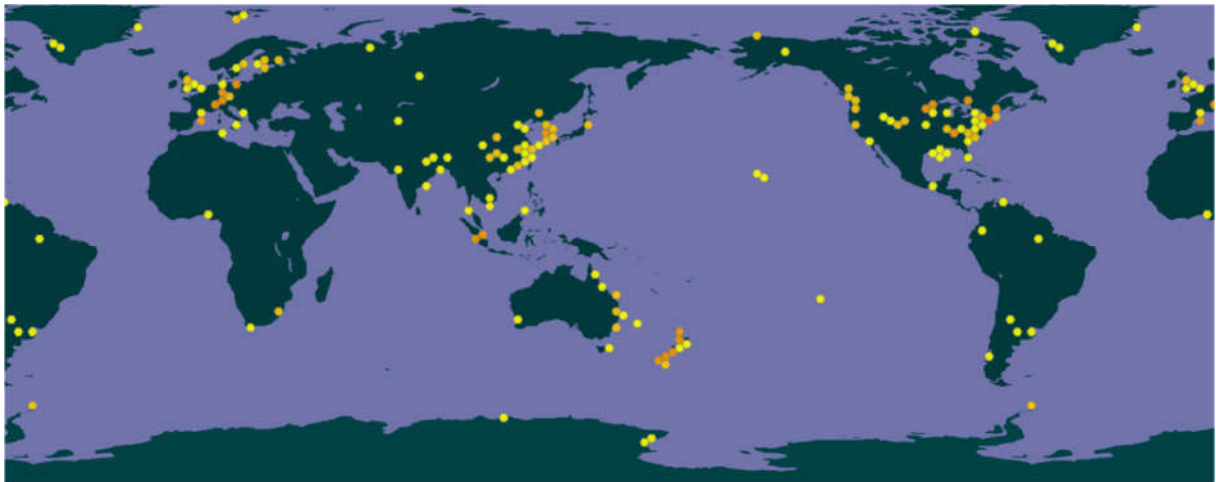
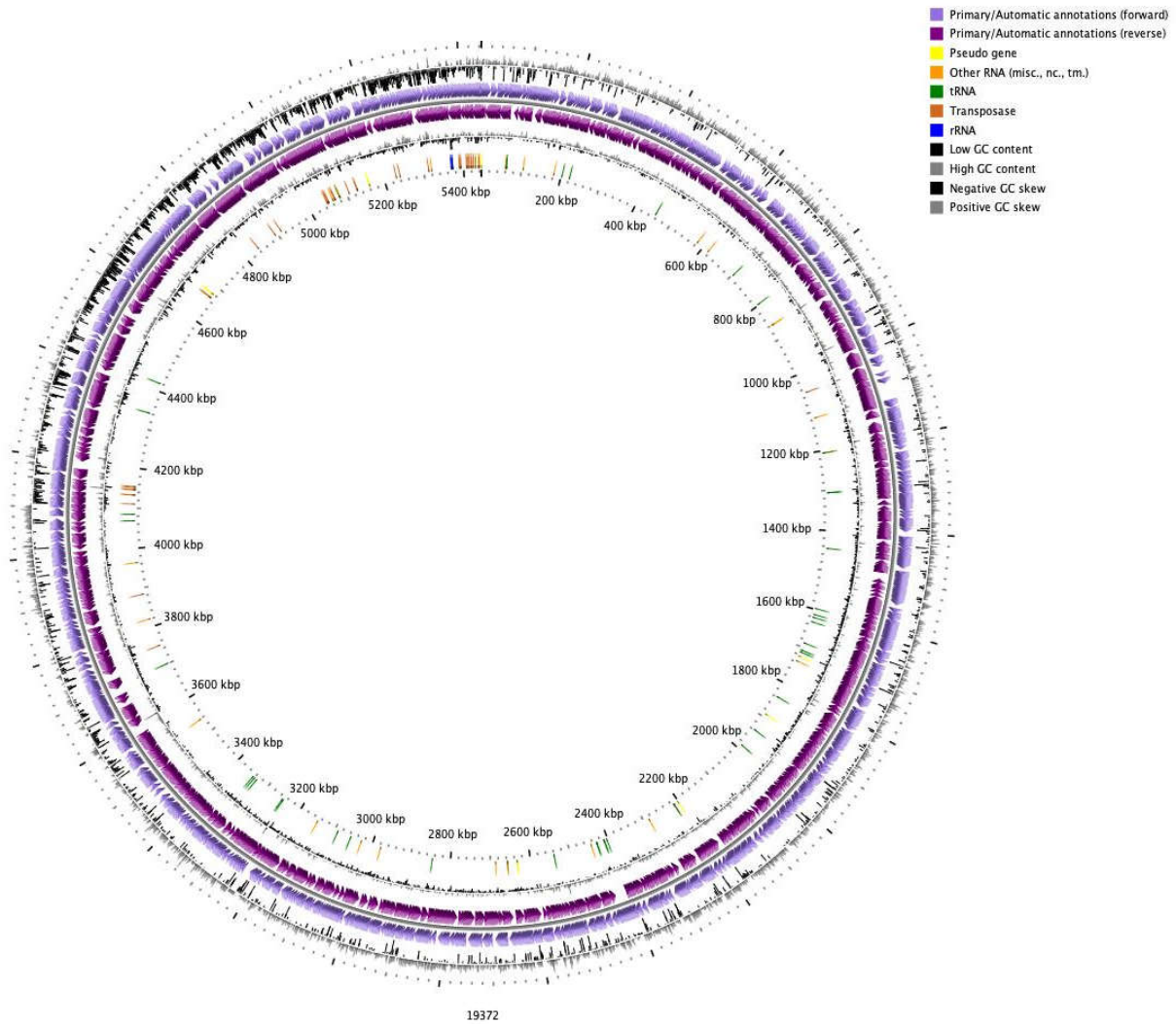


Figure S1.4: Circular mapping of the genome of strains (a) *Acidisoma silvae* (HW T2.11^T) and (b) *A. cellulosilytica* (HW T5.17^T) obtained from the circular genome viewer of the MaGe platform.

a.



b.

