

*Supplementary information*

**METAGENOMIC ANALYSIS OF MICROBIAL CONSORTIUM GF-20 IN  
CORN STOVER DEGRADATION AT LOW TEMPERATURE**

Bi-zhou ZHANG, Qinggeer BORJIGIN, Ju-lin GAO, Xiao-fang YU,  
Shu-ping HU, Fu-gui WANG, Xin ZHANG, Sheng-cai HAN

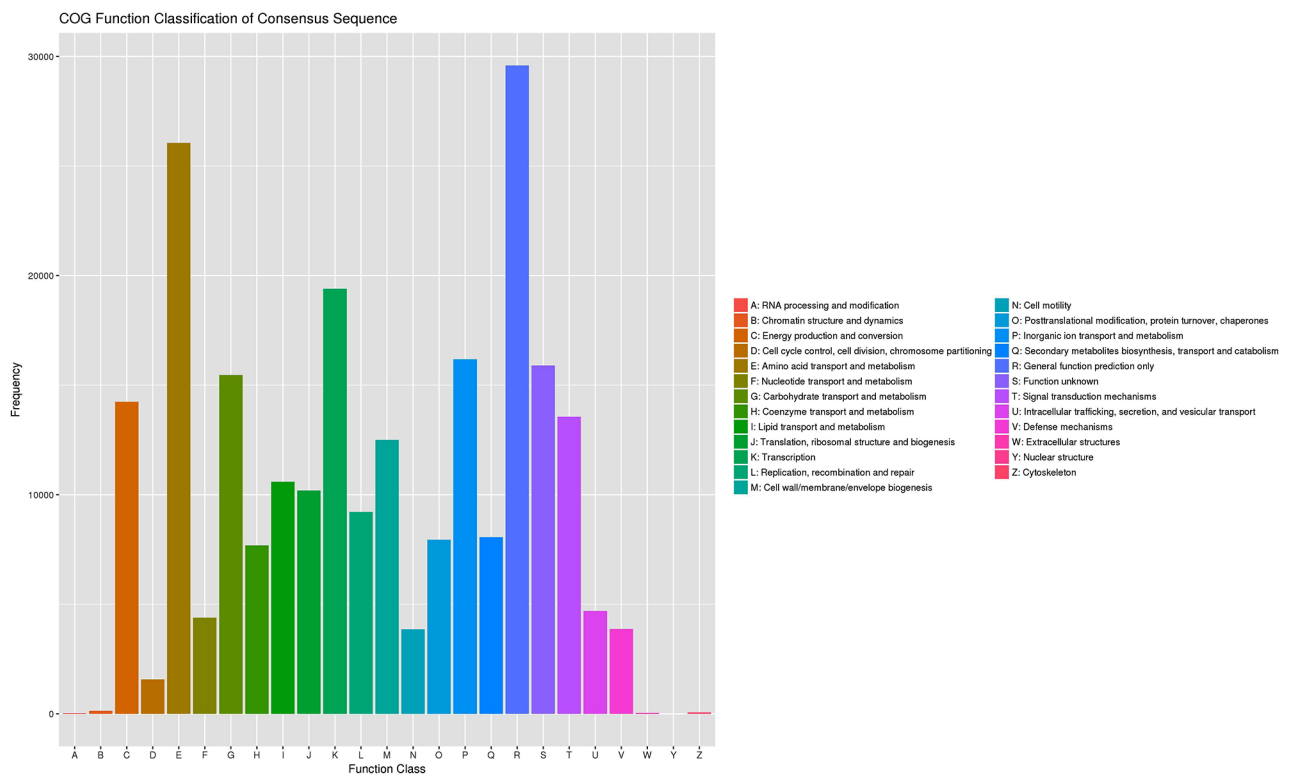


Figure S1. COG function classification of consensus sequence

Table S1. Species distribution for kingdom

Sample	Total_numbers	Bacterial	Eukaryota	Phage	Archaea	Viruses
GF-20	43,136,502	31,417,995	44,518	2,149	1,427	439

Table S2. Differential metabolic pathways with more metabolic active ability in the GF-20

Pathway id	I	II	III	Pathway name
ko02010	314	515	0.61	ABC transporters
ko02020	269	495	0.54	Two-component system
ko01200	200	356	0.56	Carbon metabolism
ko01230	167	237	0.7	Biosynthesis of amino acids
ko00190	127	218	0.58	Oxidative phosphorylation
ko00230	118	210	0.56	Purine metabolism
ko03010	118	143	0.83	Ribosome
ko02024	109	282	0.39	Quorum sensing
ko00520	98	147	0.67	Amino sugar and nucleotide sugar metabolism
ko01220	96	215	0.45	Degradation of aromatic compounds
ko00240	83	100	0.83	Pyrimidine metabolism
ko00680	78	190	0.41	Methane metabolism
ko00620	76	107	0.71	Pyruvate metabolism
ko00630	75	100	0.75	Glyoxylate and dicarboxylate metabolism
ko00640	73	110	0.66	Propanoate metabolism
ko00051	72	111	0.65	Fructose and mannose metabolism
ko00260	71	100	0.71	Glycine, serine and threonine metabolism
ko00650	68	99	0.69	Butanoate metabolism
ko00362	66	106	0.62	Benzoate degradation
ko03070	66	74	0.89	Bacterial secretion system
ko00010	65	105	0.62	Glycolysis / Gluconeogenesis
ko00270	63	117	0.54	Cysteine and methionine metabolism
ko00500	60	105	0.57	Starch and sucrose metabolism
ko00720	59	106	0.56	Carbon fixation pathways in prokaryotes
ko00860	58	129	0.45	Porphyrin and chlorophyll metabolism
ko00330	54	108	0.5	Arginine and proline metabolism
ko00920	53	109	0.49	Sulfur metabolism
ko05012	51	194	0.26	Parkinson's disease
ko05016	51	229	0.22	Huntington's disease
ko00020	50	61	0.82	Citrate cycle (TCA cycle)

Note: I: Represents the number of KO; II: Represent the KO number contained in the pathway; III: The proportion of the number of KO present to the total number of KO.

Table S3. The CAZy annotation of GF-20

Sample	GH	GTs	AA	CEs	CBM	PL
GF-20	1666	1091	215	862	532	99

Table S4. Related genes of GF-20 metabolism model

Metabolic process	Function annotation	Gene abbreviation
Starch and sucrose degradation	Alpha-amylase Glycogen phosphorylase Glycogen debranching enzyme beta-glucosidase Endoglucanase	Amy Pyg Agl bglX -
Glycolysis	Glucokinase Glucose-6-phosphate isomerase 6-Phosphofructokinase Fructose-bisphosphate aldolase Fructose1,6-bisphosphate aldolase Triosephosphate isomerase Glyceraldehyde-3-phosphate dehydrogenase  3-Phosphoglycerate kinase Enolase	Glk Pgi PfkA - - Tpi gapA gapA pgk eno
Pentose phosphate pathway	Pyruvate kinase 6-Phosphogluconolactonase 6-Phosphogluconate dehydrogenase Ribose-phosphate pyrophosphokinase Ribokinase Xylulokinase	Pyk Pgl Pgd prpS rbxK xylB
Galactose metabolism	Galactosidase 6-Phospho-beta-galactosidase Maltase-glucoamylase beta-fructofuranosidase	lacZ, GLA lacG MGAM sacA
Fructose and mannose metabolism	Mannan endo-1,4-beta-mannosidase	gmuG
Acetic acid metabolism	Acetyl CoA Acetokinase	Ack Ack