

## Supplementary Information

### Nutrient availability shapes the microbial community structure in sugarcane bagasse compost-derived consortia

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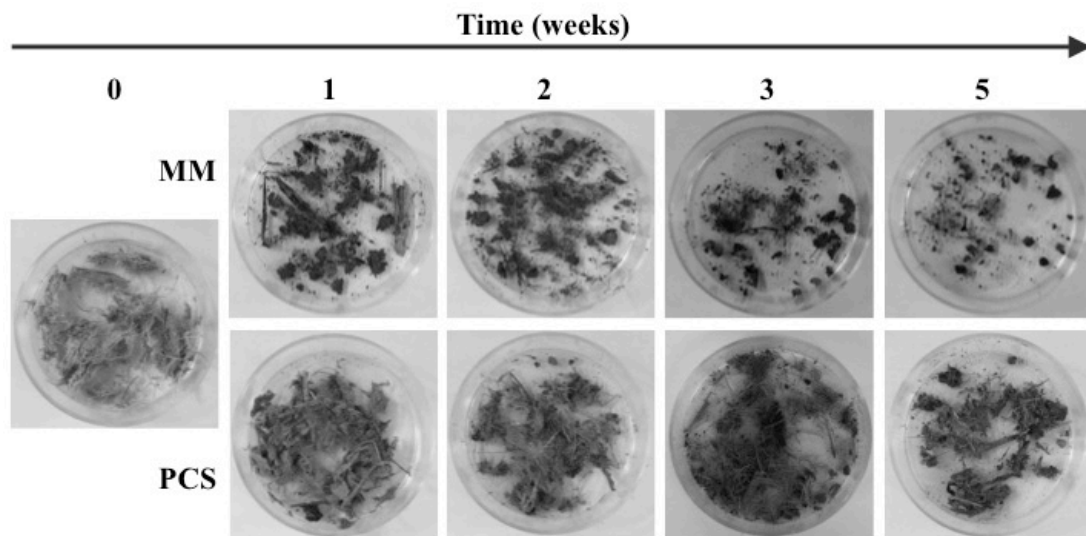
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### Supplementary Figure 1

Qualitative overview of sugarcane bagasse biomass collected from MM and PCS grown compost-derived consortia during five-week time course showing morphological changes such as particle size reduction, color darkening and biomass softening.



## Supplementary Table 1

Relative abundance values for twenty most abundant OTUs present in a) MM- and b) PCS-grown communities. Bolded taxa are present in both tables.

A)

phylum	class	order	family	genus	Mean abundance in MM community (%)	Mean abundance in PCS community (%)	Cumulative contribution to dissimilarity in MM (%)
Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Cellulomonas	6.7	0.0	6.7
Acidobacteria	<b>Chloracidobacteria</b>	<b>RB41</b>	<b>Ellin6075</b>	<b>unknown</b>	5.8	1.3	12.5
Actinobacteria	Actinobacteria	Actinomycetales	unknown	unknown	4.8	0.5	17.3
Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	unknown	3.6	0.0	21.0
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	3.2	0.1	24.1
Proteobacteria	$\gamma$ -proteobacteria	Alteromonadales	Alteromonadaceae	unknown	3.0	0.3	27.1
Bacteroidetes	<b>Saprospirae</b>	<b>Saprospirales</b>	<b>Chitinophagaceae</b>	<b>unknown</b>	2.6	5.5	29.7
Proteobacteria	$\gamma$ -proteobacteria	Xanthomonadales	Xanthomonadaceae	unknown	2.3	0.1	32.0
Proteobacteria	<b><math>\alpha</math>-proteobacteria</b>	<b>Caulobacterales</b>	<b>Caulobacteraceae</b>	<b>Asticcacaulis</b>	2.3	7.6	34.3
Proteobacteria	$\alpha$ -proteobacteria	Caulobacterales	Caulobacteraceae	unknown	2.3	0.8	36.6
Proteobacteria	$\alpha$ -proteobacteria	Rhizobiales	unknown	unknown	2.2	0.9	38.8
Proteobacteria	$\gamma$ -proteobacteria	Xanthomonadales	Sinobacteraceae	unknown	2.1	0.3	40.9
other kingdom	-	-	-	-	2.0	1.8	43.0
Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	unknown	2.0	0.6	45.0
Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	1.9	0.0	46.8
Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	unknown	1.8	0.9	48.7
Proteobacteria	<b><math>\alpha</math>-proteobacteria</b>	<b>Rhizobiales</b>	<b>Hyphomicrobiaceae</b>	<b>Devosia</b>	1.7	3.0	50.4
Bacteroidetes	<b>unknown</b>	<b>unknown</b>	<b>unknown</b>	<b>unknown</b>	1.7	2.0	52.1
Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	1.7	0.6	53.8
Proteobacteria	$\gamma$ -proteobacteria	Xanthomonadales	Xanthomonadaceae	unknown	1.6	0.5	55.4
Proteobacteria	$\alpha$ -proteobacteria	Rhodobacterales	Hyphomonadaceae	unknown	1.6	0.0	57.0

B)

phylum	class	order	family	genus	Mean abundance in MM community (%)	Mean abundance in PCS community (%)	Cumulative contribution to dissimilarity in PCS (%)
Bacteroidetes	Saprospirae	Saprospirales	Chitinophagaceae	unknown	0.9	10.2	10.2
Bacteroidetes	Saprospirae	Saprospirales	Saprospiraceae	unknown	0.6	10.0	20.2
Proteobacteria	<b><math>\alpha</math>-proteobacteria</b>	<b>Caulobacterales</b>	<b>Caulobacteraceae</b>	<b>Asticcacaulis</b>	2.3	7.6	27.9
Bacteroidetes	Cytophagia	Cytophagales	unknown	unknown	1.5	6.2	34.1
Bacteroidetes	<b>Saprospirae</b>	<b>Saprospirales</b>	<b>Chitinophagaceae</b>	<b>unknown</b>	2.6	5.5	39.6
Bacteroidetes	Sphingobacteriia	Sphingobacterales	Sphingobacteriaceae	unknown	0.1	4.5	44.1
Bacteroidetes	Sphingobacteriia	Sphingobacterales	Sphingobacteriaceae	Sphingobacterium	0.0	3.6	47.7
Proteobacteria	<b><math>\alpha</math>-proteobacteria</b>	<b>Rhizobiales</b>	<b>Hyphomicrobiaceae</b>	<b>Devosia</b>	1.7	3.0	50.7
Bacteroidetes	Flavobacteriia	Flavobacteriales	Weeksellaceae	unknown	0.0	3.0	53.6
Chloroflexi	Anaerolineae	SBR1031	A4b	unknown	0.7	2.7	56.3
Proteobacteria	$\gamma$ -proteobacteriia	Alteromonadales	Alteromonadaceae	Cellvibrio	1.5	2.6	58.9
Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.9	2.3	61.2
Bacteroidetes	<b>unknown</b>	<b>unknown</b>	<b>unknown</b>	<b>unknown</b>	1.7	2.0	63.2
other kingdom	-	-	-	-	2.0	1.8	65.0
Proteobacteria	$\alpha$ -proteobacteriia	BD7-3	unknown	unknown	0.1	1.7	66.8
Firmicutes	Bacilli	Bacillales	Planococcaceae	unknown	0.0	1.7	68.4
Verrucomicrobia	Spartobacteriia	Chthoniobacterales	Chthoniobacteraceae	heteroC45_4W	0.1	1.5	70.0
Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unknown	0.4	1.5	71.5
Acidobacteria	<b>Chloracidobacteria</b>	<b>RB41</b>	<b>Ellin6075</b>	<b>unknown</b>	5.8	1.3	72.8
Proteobacteria	$\alpha$ -proteobacteriia	Rhodobacterales	Rhodobacteraceae	unknown	1.2	1.2	74.0
Proteobacteria	$\alpha$ -proteobacteriia	Rhizobiales	Hyphomicrobiaceae	unknown	0.9	1.1	75.1