

# Effect of Sugarcane Straw and Goat Manure on Soil Nutrient Transformation and Bacterial Communities

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Sample Name	Total tag	Taxon Tag	Unclassified Tag	Unique Tag	OTU number
CK1.1	83,997	78,937	0	5060	5385
CK1.2	71,008	66,650	0	4358	5119
CK1.3	78,417	73,501	0	4916	5163
M1.1	59,686	57,057	0	2629	3805
M1.2	69,619	66,261	0	3358	4338
M1.3	74,443	70,713	0	3730	4381
MS1.1	65,640	62,390	0	3250	4347
MS1.2	49,364	46,458	0	2906	3969
MS1.3	72,845	68,040	0	4805	5137
S1.1	75,490	69,089	0	6401	5416
S1.2	66,104	59,947	0	6157	5511
S1.3	78,937	72,652	0	6285	5935
CK2.1	75,002	69,385	0	5617	4817
CK2.2	76,883	68,522	0	8361	5120
CK2.3	73,185	67,061	0	6124	5009
M2.1	48,798	40,135	0	8663	3733
M2.2	82,445	76,103	0	6342	4925
M2.3	69,604	64,138	0	5466	4726
MS2.1	75,566	70,328	1	5237	4894
MS2.2	66,179	60,620	5	5554	4654
MS2.3	77,750	72,701	1	5048	4972
S2.1	80,879	74,640	0	6239	4991
S2.2	49,696	43,394	0	6302	4504
S2.3	72,139	66,913	0	5226	4893

**Table S1.** Statistics of the operational taxonomic units (OTU) clusters and species annotation of every replication of treatment. Total Tag indicates the number of total effective tags. Unique Tag indicates the total number of singletons which were removed for further analysis from the dataset. Taxon Tag displays the total number of tags which were subjected to OTU clusters along species annotation. Unclassified Tag represents the total number of tags without species annotation. OTU number show the number of OTUs for each replication of treatment. CK1, CK2 = soil without amendment; M1, M2: goat-amended soil; MS1, MS2: goat manure + straw-amended soil; and S1, S2: straw-amended soil of different time phases.

**Table S2.** Dominant genus possible roles on soil fertility and plant growth.

<b>Genus</b>	<b>Function</b>	<b>References</b>
<i>Pseudomonas</i>	PGPR	[1,2]
	Degrade of lignin	[3,4]
	SOC sequestration	[5]
<i>Acinetobacter</i>	N <sub>2</sub> -fixation , PGPR , siderophore production	[1,6]
<i>Sphingomonas</i>	Degrade cellulose and lignin	[7,8]
<i>Dyella</i>	Degrade cellulose	[9,10]
	Nitrogen cycling	[11,12]
<i>Rhizomicrobium</i>	PGPR and nitrogen fixation.	[13,14]
<i>Luteimonas</i>	N <sub>2</sub> -fixation and PGPR	[15]
<i>Azoarcus</i>	N <sub>2</sub> -fixation	[16,17]
<i>SMIA02</i>	Nitrogen cycling	[18]
<i>Denitratisoma</i>	Nitrogen cycling	[11,12]
<i>Anaeromyxobacter</i>	Iron reducers, and important for carbon and iron dynamics plant rhizosphere.	[19]
<i>Hydrogenophaga</i>	Positive effects on soil nutrient cycling	[20,21]
	Degrade high molecular weight organic compounds as starch, cellulose, proteins, xylan, and chitin.	
<i>Geobacter</i>	<i>Geobacter</i> spp. can oxidize organic pollutants.	[22,23]
	Beneficial for the uranium reduction in uranium in uranium contaminated environment	
<i>Bacteroides</i>	Bactericides make the way to enter inside the root building up endophytic population, which ultimately benefits the crop plants.	[24]
<i>Haliangium</i>	Some species of this can produce haliangicin, which can be biocontrol agents against fungal pathogens, which can suppress <i>Fusarium</i> wilt in organic farming.	[25,26]
<i>Candidatus</i>	Strains of this genus are known to be adapted for low-nutrient conditions.	[27–29]
<i>Koribacter and</i>		
<i>Candidatus Solibacter</i>		
<i>Flavisolibacter</i>	Removes polycyclic aromatic hydrocarbons	[30]
<i>Proteiniphilum</i>	Removes polycyclic aromatic hydrocarbons.	[31]

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