Overall functional gene diversity of microbial communities in three full-scale activated sludge bioreactors

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Table S1 Data of wastewater characteristics and effluent qualities of LFA and LFB during January to September of 2011.

Time	CODcr (mg/l)					TP (mg/l)					NH4+-N (mg/l)					NO3--N (mg/l)					TN (mg/l)				
	Inf[a]		Eff[b]			Inf[a]		Eff[b]			Inf[a]		Eff[b]			Inf[a]		Eff[b]			Inf[a]		Eff[b]		
	LFA/LFB	BH	LFA	LFB	BH	LFA/LFB	BH	LFA	LFB	BH	LFA/LFB	BH	LFA	LFB	BH	LFA/LFB	BH	LFA	LFB	BH	LFA/LFB	BH	LFA	LFB	BH
Jan.	459.5	570.0	28.7	20.4	22.0	6.8	5.9	0.5	0.2	0.1	25.2	46.3	7.9	4.3	4.3	1.7	1.1	10.5	6.0	10.8	45.6	60.1	21.2	11.7	17.2
Feb.	371.7	647.1	23.4	17.4	24.1	5.6	8.4	0.5	0.6	0.1	25.3	46.6	7.9	3.0	2.9	0.7	1.1	8.5	6.8	13.1	41.3	60.7	22.1	10.1	18.5
Mar.	436.9	541.1	22.4	19.9	27.2	7.1	5.6	0.3	0.2	0.3	27.6	44.1	7.3	2.9	3.8	0.8	1.0	10.5	7.4	11.2	47.0	61.6	22.4	10.6	16.5
Apr.	370.1	506.2	26.8	21.2	20.1	5.5	5.7	0.3	0.6	0.1	25.0	44.5	7.9	0.4	3.5	0.5	1.0	9.8	3.6	10.4	40.4	63.3	20.2	5.2	15.4
May	319.0	498.0	24.0	21.0	19.9	4.6	5.7	0.4	0.9	0.1	21.5	42.4	7.4	0.6	3.2	0.5	0.9	8.8	5.7	9.2	34.7	60.0	18.2	7.3	15.2
Jun.	370.0	380.3	21.0	18.0	18.1	5.7	4.1	0.4	0.6	0.2	20.0	34.2	5.2	0.7	3.2	0.3	0.7	10.1	6.7	9.1	33.3	47.0	16.9	8.0	13.3
Jul.	360.0	362.1	23.0	15.0	20.0	4.4	4.0	0.6	0.4	0.1	21.1	33.3	2.7	0.8	3.6	0.6	0.9	13.1	6.9	9.5	34.5	46.4	16.5	8.1	14.0
Aug.	319.1	371.2	20.1	19.4	23.2	4.3	4.2	0.3	0.8	0.3	22.4	40.2	3.1	1.7	4.0	0.4	0.8	8.6	6.3	11.6	37.4	55.8	12.8	9.1	17.3
Sept.	284.7	482.2	18.4	17.4	21.1	4.1	5.1	0.4	1.3	0.2	22.6	37.1	3.1	1.1	3.9	0.4	0.6	7.3	4.8	11.1	34.5	56.6	10.2	6.6	16.4

a Inf is short for influent.

b Eff is short for effluent.

Fig. S1

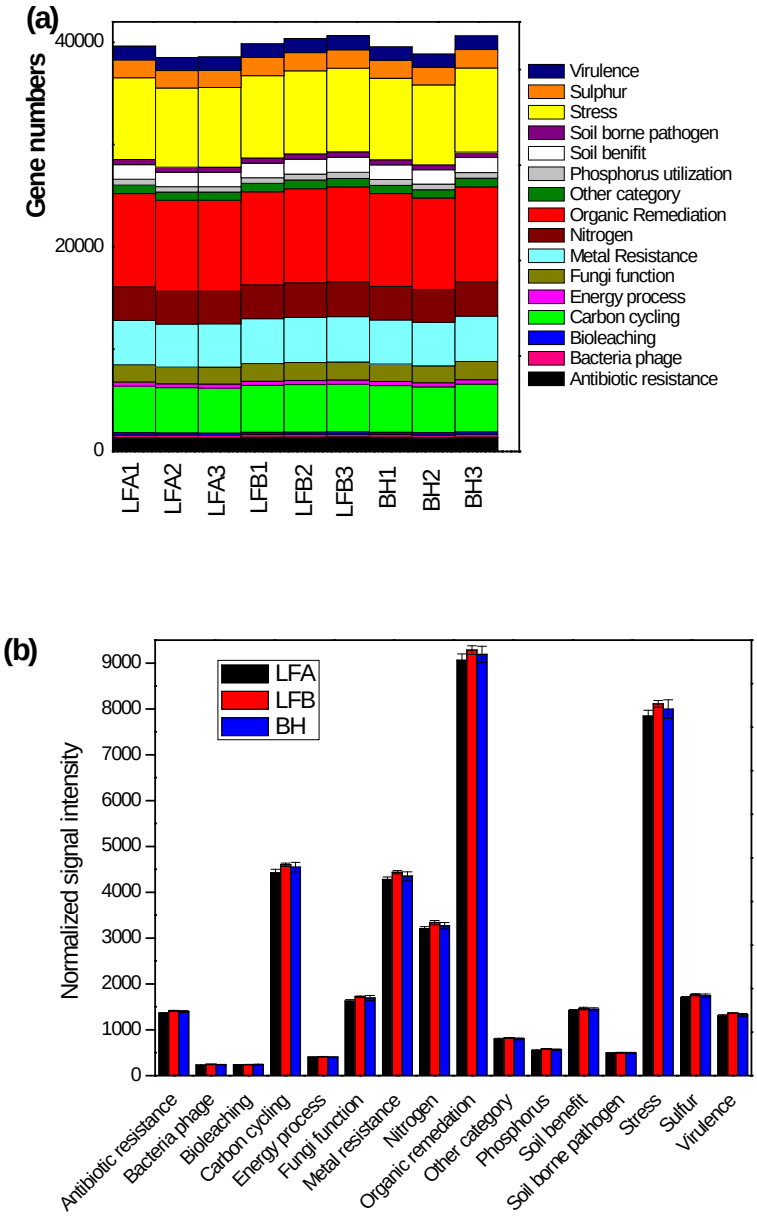

(a)
Gene numbers
40000
20000
0
LFA1
LFA2
LFA3
LFB1
LFB2
LFB3
BH1
BH2
BH3
Virulence
Sulphur
Stress
Soil borne pathogen
Soil benifit
Phosphorus utilization
Other category
Organic Remediation
Nitrogen
Metal Resistance
Fungi function
Energy process
Carbon cycling
Bioleaching
Bacteria phage
Antibiotic resistance
(b)
Normalized signal intensity
LFA
LFB
BH
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
Antibiotic resistance
Bacteria phage
Bioleaching
Carbon cycling
Energy process
Fungi function
Metal resistance
Nitrogen
Organic remedation
Other category
Phosphorus
Soil benefit
Soil borne pathogen
Stress
Sulfur
Virulence

Fig. S2

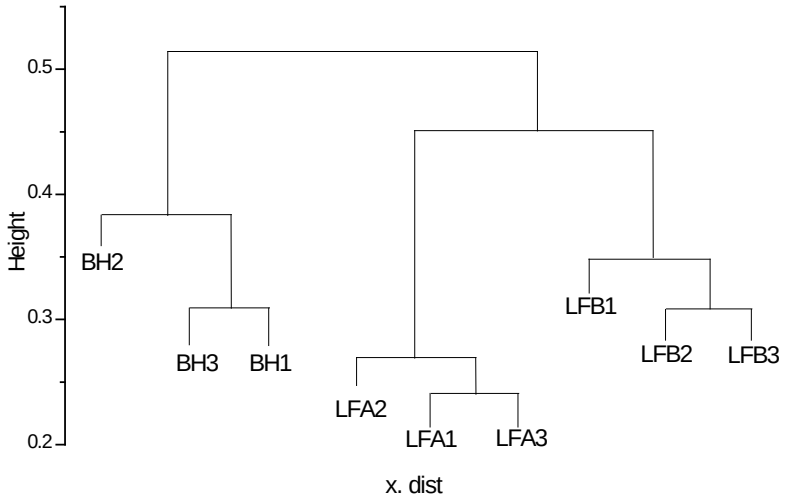

Height
0.5
0.4
0.3
0.2
BH2
BH3
BH1
LFA2
LFA1
LFA3
LFB1
LFB2
LFB3
x. dist

Fig. S3

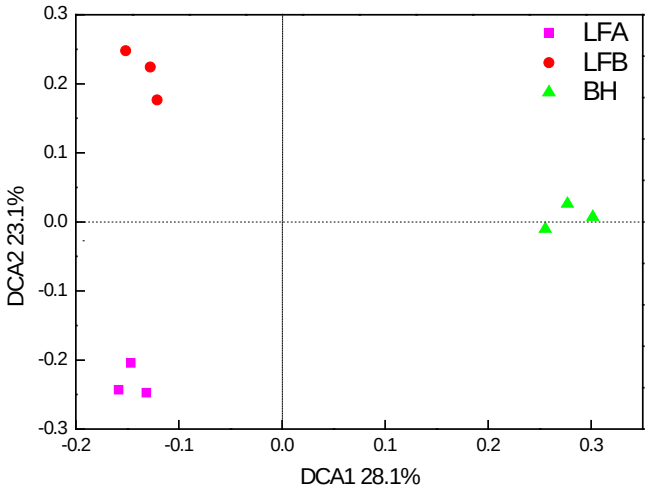
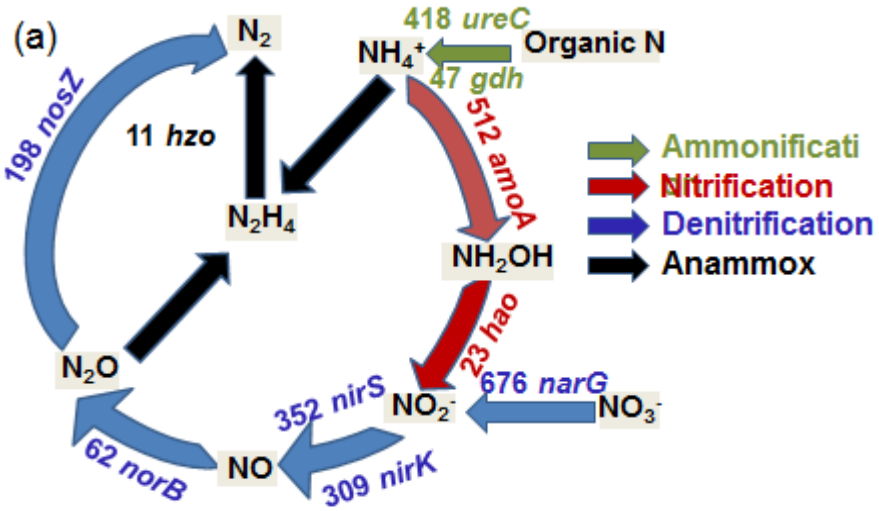


Fig. S4


(a)
N_2
418 ureC
NH_4^+
Organic N
47 gdh
512 amoA
198 nosZ
11 hzo
N_2H_4
NH_2OH
Ammonificati
Nitrification
Denitrification
Anammox
23 hao
N_2O
352 nirS
NO_2^-
676 narG
NO_3^-
62 norB
NO
309 nirK

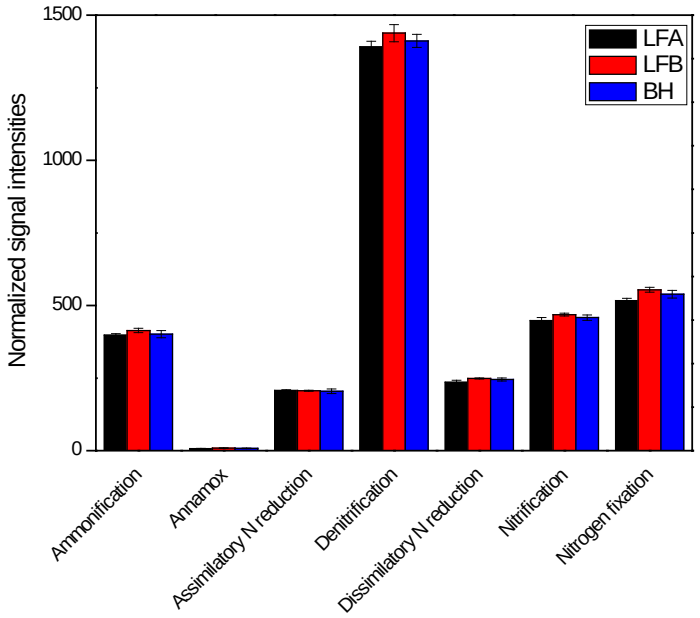

Normalized signal intensities
1500
1000
500
0
LFA
LFB
BH
Ammonification
Annamox
Assimilatory N reduction
Denitrification
Dissimilatory N reduction
Nitrification
Nitrogen fixation

Fig. S5

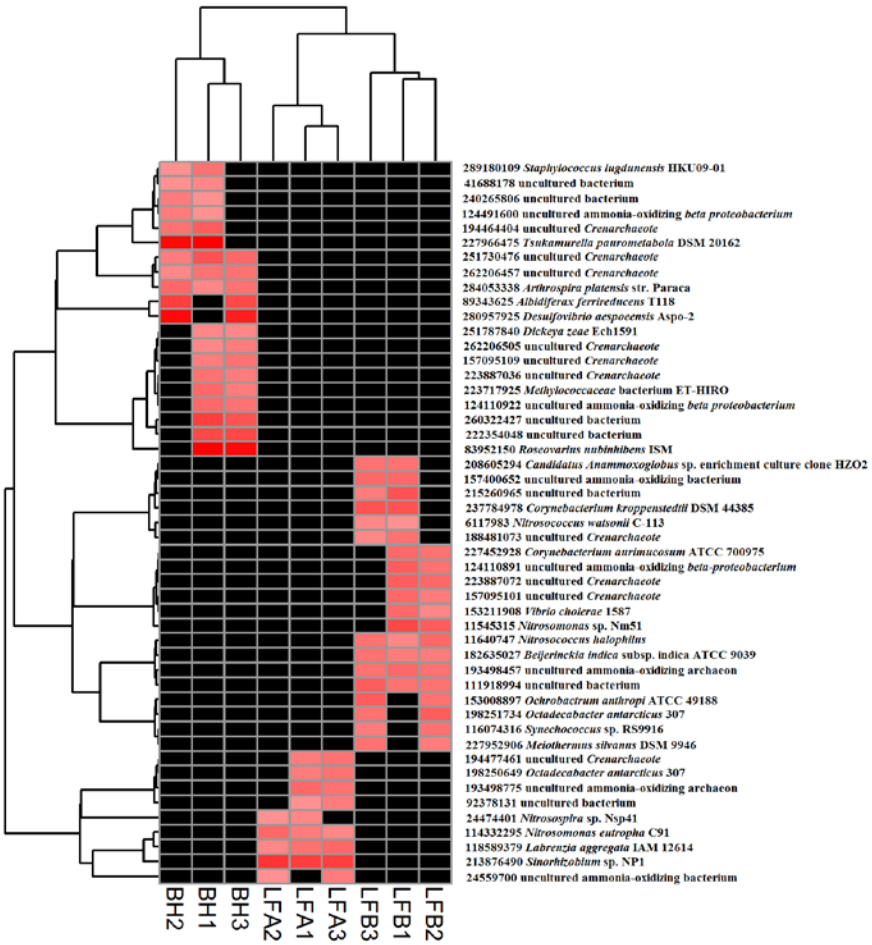
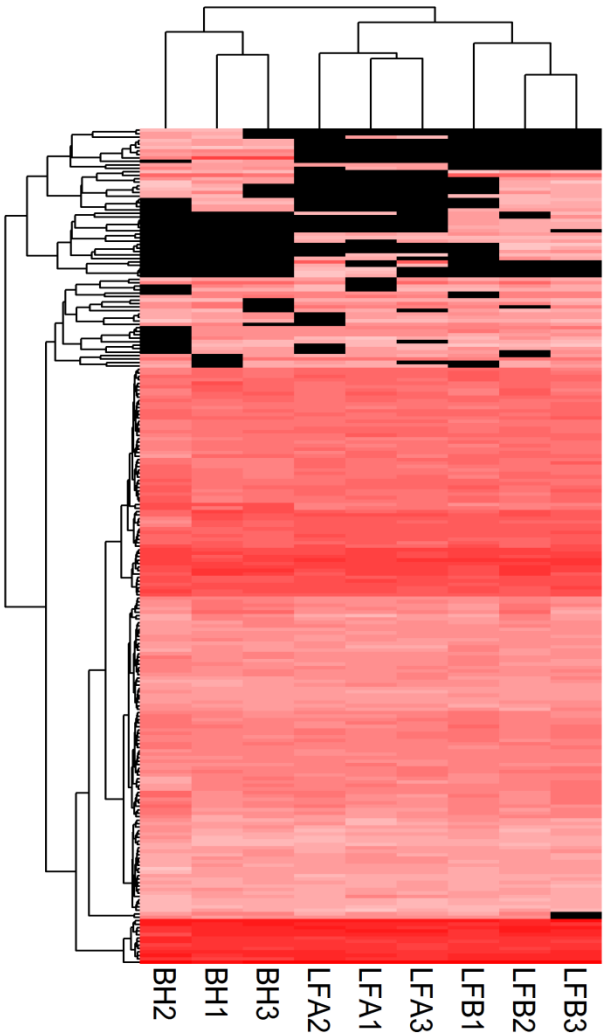

289180109 Staphylococcus lugdunensis HKU09-01
41688178 uncultured bacterium
240265806 uncultured bacterium
124491600 uncultured ammonia-oxidizing beta proteobacterium
194464404 uncultured Crenarchaeote
227966475 Tsukamurella paurometabola DSM 20162
251730476 uncultured Crenarchaeote
262206457 uncultured Crenarchaeote
284053338 Arthrospira platensis str. Paraca
89343625 Albidiferax ferrireducens T118
280957925 Desulfovibrio aespoeensis Aspo-2
251787840 Dickeya zeae Ech1591
262206505 uncultured Crenarchaeote
157095109 uncultured Crenarchaeote
223887036 uncultured Crenarchaeote
223717925 Methylococcaceae bacterium ET-HIRO
124110922 uncultured ammonia-oxidizing beta proteobacterium
260322427 uncultured bacterium
222354048 uncultured bacterium
83952150 Roseovarius nubinhibens ISM
208605294 Candidatus Anammoxoglobus sp. enrichment culture clone HZO2
157400652 uncultured ammonia-oxidizing bacterium
215260965 uncultured bacterium
237784978 Corynebacterium kroppenstedtii DSM 44385
6117983 Nitrosococcus watsonii C-113
188481073 uncultured Crenarchaeote
227452928 Corynebacterium aurimucosum ATCC 700975
124110891 uncultured ammonia-oxidizing beta-proteobacterium
223887072 uncultured Crenarchaeote
157095101 uncultured Crenarchaeote
153211908 Vibrio cholerae 1587
11545315 Nitrosomonas sp. Nm51
11640747 Nitrosococcus halophilus
182635027 Beijerinckia indica subsp. indica ATCC 9039
193498457 uncultured ammonia-oxidizing archaeon
111918994 uncultured bacterium
153008897 Ochrobactrum anthropi ATCC 49188
198251734 Octadecabacter antarcticus 307
116074316 Synechococcus sp. RS9916
227952906 Meiothermus silvanus DSM 9946
194477461 uncultured Crenarchaeote
198250649 Octadecabacter antarcticus 307
193498775 uncultured ammonia-oxidizing archaeon
92378131 uncultured bacterium
24474401 Nitrosospira sp. Nsp41
114332295 Nitrosomonas eutropha C91
118589379 Labrenzia aggregata IAM 12614
213876490 Sinorhizobium sp. NP1
24559700 uncultured ammonia-oxidizing bacterium
BH2
BH1
BH3
LFA2
LFA1
LFA3
LFB3
LFB1
LFB2

Fig. S6



Supplementary Figure Legends

Fig. S1 Detected numbers (a) and normalized signal intensities (b) of functional genes involved in each microbial process of the three wastewater treatment systems.

Fig. S2 Hierarchical clustering analysis of the overall functional genes from all investigated samples.

Fig. S3 Detrended correspondence analysis (DCA) of microbial community structures of the investigated nine samples. Triplicates of each treatment system grouped.

Fig. S4 (a) Numbers of the detected genes involved in important processes of nitrogen cycling. The names of the genes as well as their numbers were presented. (b) Normalized signal intensities of the genes associated with each process of nitrogen cycling.

Fig. S5 Clustering analysis of the nitrification genes unique to each system. Red indicates signal intensities above background, while black represents the ones below background. Brighter red coloring means higher signal intensities.

Fig. S6 Clustering analysis of *ppk* genes involved in poly P synthesis. See Fig. S5 legend for explanation.