

Supporting information 1 Chemical composition of Ferrosorp DGμ. n.d.=not detected

Methods:		
Water content	0.13%	DIN EN 14774-1 (2010): Solid biofuels - Determination of moisture content - Oven dry method - Part 1: Total moisture - Reference method.
Elementary analysis	[% _{TS}]	DIN EN 15104 (2011): Solid biofuels - Determination of total content of carbon, hydrogen and nitrogen - Instrumental methods.
Carbon	4.21	
Sulfur	0.77	
Nitrogen	0.23	
Hydrogen	0.29	
Elements	[mg kg _{TS} ⁻¹]	DIN EN 16170 (2012): Sludge, treated biowaste and soil - Determination of trace elements by inductively coupled plasma optical emission spectrometry (ICP-OES).
Aluminum	Al	5,940.00
Barium	Ba	49.20
Lead	Pb	5.20
Cadmium	Cd	n.d.
Calcium	Ca	118,000.00
Chrome	Cr	7.76
Cobalt	Co	53.50
Iron	Fe	334,000.00
Potassium	K	n.d.
Copper	Cu	7.02
Lithium	Li	2.21
Magnesium	Mg	8,410.00
Manganese	Mn	4,750.00
Molybdum	Mo	n.d.
Sodium	Na	390.00

Nickel	Ni	80.60
Phosphorus	P	245.00
Sulfur	S	18,800.00
Strontium	Sr	707.00
Thallium	Tl	n.d.
Titanium	Ti	241.00
Tungsten	W	n.d.
Zinc	Zn	253.00

Elements		[mg kg _{TS} ⁻¹]	DIN EN ISO 11969 (1996): Water quality - Determination of arsenic - Atomic absorption spectrometric method (hydride technique).
Arsenic	As	59.800	
Bismuth	Bi	n.d.	
Mercury	Hg	0.077	
Selenium	Se	0.130	

Supporting information 2 Overview of impurities of synthesized Fe(OH)₃ and Mn(OH)₂. n.d. = not detected.

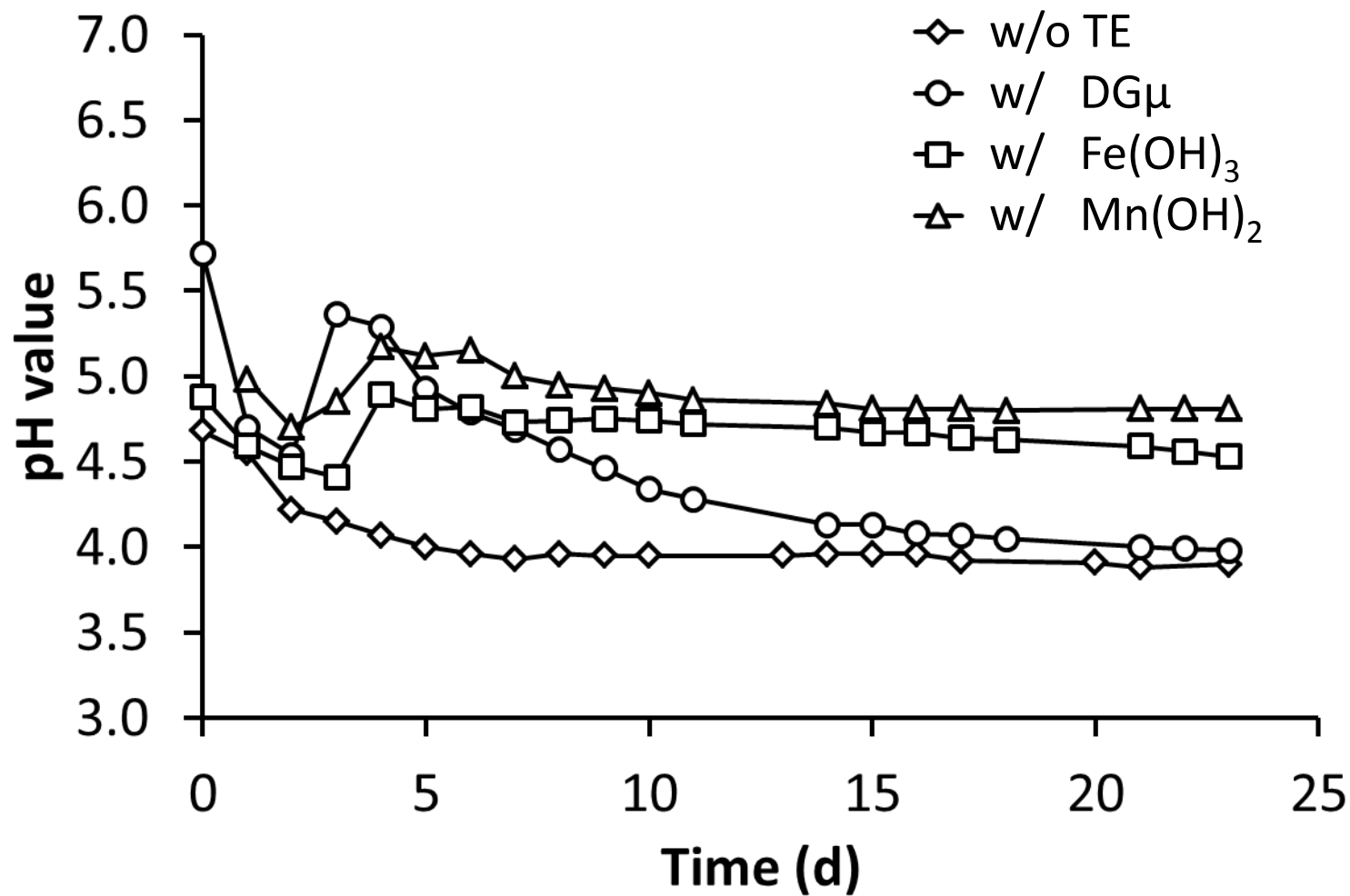
Anions (DIN EN 12457-4)	Impurities in Fe(OH) ₃ (mg kg _{TS} ⁻¹)	Impurities in Mn(OH) ₂ (mg kg _{TS} ⁻¹)
Br ⁻	0.05	57.7
Cl ⁻	1,720	30,800
NO ₃ ⁻	25.9	5.58
NO ₂ ⁻	1.44	1.65
PO ₄ ³⁻	0.058	0.18
SO ₄ ²⁻	21.9	1.93
Elements (DIN EN 16170)		
Al	327	n.d.
Ba	15.2	10.2
Pb	21.3	8.42
Ca	635	252
Cr	157	n.d.
Co	78.8	2.5
Fe	–	32.6
K	45,600	13,300
Cu	7.87	n.d.
Li	n.d.	n.d.
Mn	241	–
Mo	n.d.	3.18
Na	640	172
Ni	141	n.d.
P	n.d.	n.d.
S	43.7	2,270
Si	n.d.	n.d.
Sr	22.7	9.91
W	n.d.	n.d.
Zn	19.9	13.3
Sum of the impurities (mg kg _{TS} ⁻¹)	50,719.76	46,973.75
Percentage of the total weight (%)	5.07	4.70

Supporting information 3 Clone library obtained from bacterial 16S rRNA gene amplicons. Length and accession numbers of the partial sequences, their taxonomic affiliation as well as the experimental and calculated T-RF lengths of the respective clones obtained by *MspI* restriction are presented. BLASTn search was done against the NCBI database excluding environmental sequences. Taxonomic assignment is based on the RDP Classifier with 80% confidence threshold.

Clone	Sequence length (bp)	Acc. No.	Highest BLAST hit (Acc. no.) / Sequence identity	RDP Classifier	<i>MspI</i> T-RF (bp) calculated/experimental
8.13_13.11.12_B9	657	KT456558	<i>Lactobacillus</i> sp. IWT8 (AB894863) / 99 %	<i>Lactobacillus</i>	142/139
8.15_4.6.13_D3	703	KT456559	<i>Lactobacillus</i> sp. JCM 8674 (AB911515) / 96%	<i>Lactobacillus</i>	178/175
8.15_14.6.13_B12	684	KT456560	<i>Lactobacillus amylolyticus</i> (Y17361) / 94%	<i>Lactobacillus</i>	180/178
8.12S_18.12.12_D1	758	KT456561	<i>Lactobacillus amylovorus</i> GRL1118 (CP002609) / 95%	<i>Lactobacillus</i>	180/178
8.12S_1.12.12_F6	667	KT456562	<i>Lactobacillus perolens</i> strain JCM 8647 (AB690232) / 94%	<i>Lactobacillus</i>	215/214
8.12S_1.12.12_C1	753	KT456563	<i>Lactobacillus vini</i> (AY681131) / 96%	<i>Lactobacillus</i>	562/563
8.12S_1.12.12_F7	681	KT456564	<i>Lactobacillus vini</i> (NR_042196) / 99%	<i>Lactobacillus</i>	562/563
8.12S_1.12.12_E9	627	KT456565	<i>Lactobacillus porcinae</i> strain R-42633 (NR_108876) / 96%	<i>Lactobacillus</i>	567/567
8.17_8.6.13_A2	597	KT456566	<i>Lactobacillaceae</i> bacterium DJF_003 (EU728746) /96%	<i>Lactobacillus</i>	566/570
8.12S_18.12.12_C5	706	KT456567	<i>Lactobacillus silagei</i> strain IWT126 (NR_114388) / 99%	<i>Lactobacillus</i>	571/573
8.12S_1.12.12_C8	634	KT456568	<i>Lactobacillus porcinae</i> strain R-42633 (NR_108876) / 98%	<i>Lactobacillus</i>	571/574
8.15_4.6.13_A1	564	KT456569	<i>Lactobacillus coleohominis</i> (AB911496) / 98%	<i>Lactobacillus</i>	580/577
8.12S+8.13+8.15_B3	585	KT456570	<i>Lactobacillus camelliae</i> strain FQ060 (KF418823) / 99%	<i>Lactobacillus</i>	576/579
8.13_13.11.12_A3	714	KT456571	<i>Lactobacillus panis</i> strain GH1 (KP216208) / 99 %	<i>Lactobacillus</i>	579/580
8.15_4.6.13_D9	771	KT456572	<i>Lactobacillus pontis</i> strain M17-5 (KF030785) / 99%	<i>Lactobacillus</i>	580/580
8.12S_1.12.12_D6	645	KT456573	<i>Lactobacillus</i> sp. SW201 (JQ809688)/ 97%	<i>Lactobacillus</i>	580/582
8.15_4.6.13_F1	696	KT456574	<i>Lactobacillus buchneri</i> CD034 (CP003043) / 99%	<i>Lactobacillus</i>	581/582
8.12S_1.12.12_H7	699	KT456575	<i>Clostridium</i> sp. ZGM211 (KT000268) / 99%	<i>Clostridium sensu stricto</i>	508/506
8.12S_1.12.12_D5	772	KT456576	<i>Clostridium</i> sp. MB9-9 (KJ001789) / 100%	<i>Clostridium sensu stricto</i>	518/516
8.15+8.17+8.12S_D7	709	KT456577	<i>Clostridium tyrobutyricum</i> 5S (L08062) / 99%	<i>Clostridium sensu stricto</i>	518/517
8.12S_18.12.12_F3	510	KT456578	<i>Clostridium butyricum</i> (LC037212) / 99%	<i>Clostridium sensu stricto</i>	519/519
8.12S_1.12.12_E11	588	KT456579	<i>Clostridium</i> sp. L15 (AY337519) / 96%	<i>Clostridium sensu stricto</i>	524/521
8.12S_1.12.12_D12	691	KT456580	<i>Clostridium</i> sp. MSTE9 (JN091083) / 93%	<i>Clostridium IV</i>	281/276
8.12S_18.12.12_F5	554	KT456581	<i>Clostridiales</i> bacterium oral taxon F32 strain VO026 (HM099644) / 90%	<i>Clostridiales</i>	322/323

8.12S_18.12.12_G7	651	KT456582	<i>Clostridiales</i> bacterium canine oral taxon 123 clone OJ033 (JN713290) / 82%	<i>Clostridiales</i>	480/483
8.17_26.6.13_B4	661	KT456583	<i>Clostridium</i> sp. strain S6 (AY949858) /90%	<i>Ruminococcaceae</i>	69/62
8.17_26.6.13_C3	638	KT456584	<i>Clostridium</i> sp. strain S6 (AY949858) / 93%	<i>Ruminococcaceae</i>	76/69
8.17_26.6.13_A12	559	KT456585	<i>Clostridium</i> sp. strain S6 (AY949858) /93%	<i>Ruminococcaceae</i>	149/145
8.15+8.17+8.12S_C9	516	KT456586	Bacterium NLAE-zl-C147 (JQ607885) /99%	<i>Ruminococcaceae</i>	281/280
8.17_26.6.13_A10	625	KT456587	<i>Clostridium</i> sp. strain Z6 (AY949859) /93%	<i>Ruminococcaceae</i>	287/286
8.15+8.17+8.12S_A6	687	KT456588	<i>Clostridium</i> sp. MSTE9 (JN091083) /96%	<i>Ruminococcaceae</i>	383/372
8.15+8.17+8.12S_E4	719	KT456589	<i>Lachnospiraceae</i> bacterium 19gly4 (AF550610) /89%	<i>Ruminococcaceae</i>	285/284
8.17_26.6.13_C2	500	KT456590	<i>Clostridium</i> sp. MF18_Ns (HF675163) / 94%	<i>Lachnospiraceae</i>	159/157
8.15+8.17+8.12S_D2	644	KT456591	<i>Lachnospiraceae</i> bacterium A4 (DQ789118) /94%	<i>Lachnospiraceae</i>	210/209
8.12S+8.13+8.15_H2	727	KT456592	<i>Clostridiales</i> bacterium P3M-3 (KF931641) / 95%	<i>Lachnospiraceae</i>	296/296
8.12S_18.12.12_A10	657	KT456593	<i>Clostridium herbivorans</i> strain 54408 (NR_118669) / 95%	<i>Lachnospiraceae</i>	486/488
8.17_8.6.13_E6	632	KT456594	<i>Alicyclobacillus acidoterrestris</i> strain DSM 3922 (NR_118645) /83%	<i>Firmicutes</i>	204/202
8.15_14.6.13_A12	651	KT456595	<i>Megasphaera</i> sp. BLPYG-07 (HM990964) / 99%	<i>Megasphaera</i>	300/297
8.15_14.6.13_G9	557	KT456596	<i>Megasphaera elsdenii</i> (AB298908) / 99%	<i>Megasphaera</i>	300/298
8.15+8.17+8.12S_C8	683	KT456597	<i>Acetobacter syzygii</i> strain G4-4 (HM217935) /99%	<i>Acetobacter</i>	440/440
8.15_25.6.13_H9	683	KT456598	<i>Acetobacter pasteurianus</i> strain G3-12 (KF030748) /99%	<i>Acetobacter</i>	550/552
8.15+8.17+8.12S_C4	660	KT456599	Bacterium O61128-OL-KR37-AA 3-0 10000x -1A (FJ037613) /92%	<i>Acetobacteraceae</i>	90/84
8.17_8.6.13_H4	490	KT456600	<i>Bacillus oleronius</i> strain ATCC 700005 (NR_043325) /99%	<i>Bacillus</i>	146/142
8.15_14.6.13_A11	488	KT456601	<i>Bacillus</i> sp. KZ_AalM_Mm2 (GU726177) / 99%	<i>Bacillus</i>	153/147
8.15_14.+25.6.13_E8	555	KT456602	<i>Bacillus</i> sp. BO7 (KJ741217) / 100%	<i>Bacillus</i>	168/166
8.12S+8.13+8.15_G3	641	KT456603	<i>Bacteroides nordii</i> strain JCM 12987 (NR_112939) / 86 %	<i>Bacteroidales</i>	85/78
8.17_26.6.13_B8	731	KT456604	<i>Bacteroides heparinolyticus</i> strain SEQ218 (JN867293) /84%	<i>Bacteroidales</i>	361/362
8.15+8.17+8.12S_C1	628	KT456605	<i>Lutibacter aestuarii</i> strain MA-My1 (NR_108995) /84%	<i>Bacteroidetes</i>	208/206
8.15_14.6.13_H6	605	KT456606	<i>Coriobacteriaceae</i> bacterium 68-1-3 (CP009302) / 93%	<i>Coriobacteriaceae</i>	67/60
8.17_26.6.13_H12	654	KT456607	<i>Coriobacteriaceae</i> bacterium SNR48-350 (AB752502) / 94%	<i>Coriobacteriaceae</i>	131/125
8.15_4.6.13_A8	747	KT456608	<i>Paenibacillus</i> sp. AHK180-5 (AB306508) / 99%	<i>Paenibacillus</i>	137/131
8.15_25.6.13_E12	566	KT456609	<i>Paenibacillus lactis</i> strain SCTB114 (JN650279) / 99%	<i>Paenibacillus</i>	149/143
8.15_14.6.13_E1	629	KT456610	<i>Prevotella oulorum</i> strain F0390 (GU470906) / 88%	<i>Prevotella</i>	97/87
8.15_25.6.13_G2	421	KT456611	<i>Prevotella oulorum</i> strain F0390 (GU470906) /88%	<i>Prevotellaceae</i>	97/90

8.15_14.6.13_F2	659	KT456612	<i>Olsenella</i> sp. SK9K4 (JX905358) / 99%	<i>Olsenella</i>	62/54
8.17_26.6.13_G10	556	KT456613	<i>Stenotrophomonas</i> sp. BCBo8 (EU140962) / 99%	<i>Stenotrophomonas</i>	83/74
8.15_4.6.13_D12	712	KT456614	<i>Petrimonas</i> sp. ING2-E5A (KP233808) / 99%	<i>Petrimonas</i>	93/88
8.15_14.+25.6.13_E11	671	KT456615	<i>Rummeliibacillus pycnus</i> strain SCTB112 (JN650277) / 99%	<i>Rummeliibacillus</i>	152/149
8.15+8.17+8.12S_H7	615	KT456616	<i>Corynebacterium</i> sp. BBDP55 (DQ337519) /99%	<i>Corynebacterium</i>	162/159
8.15_14.+25.6.13_H11	674	KT456617	<i>Ureibacillus thermosphaericus</i> (AB300774) / 99%	<i>Ureibacillus</i>	167/164
8.15_25.6.13_B1	661	KT456618	<i>Pseudoclavibacter caeni</i> strain MJ28 (NR_109073) / 99%	<i>Micrococcineae</i>	281/282
8.15_14.6.13_H1	601	KT456619	<i>Dialister succinatiphilus</i> strain YIT 11850 (NR_041666) / 94%	<i>Veillonellaceae</i>	304/303
8.15_4.6.13_B4	694	KT456620	<i>Kerstersia gyiorum</i> strain HF2 (HM117848) / 99%	<i>Kerstersia</i>	448/447
8.15_4.6.13_D11	679	KT456621	<i>Acidovorax</i> sp. 98-63833 (AY258065) / 99%	<i>Comamonas</i>	489/490



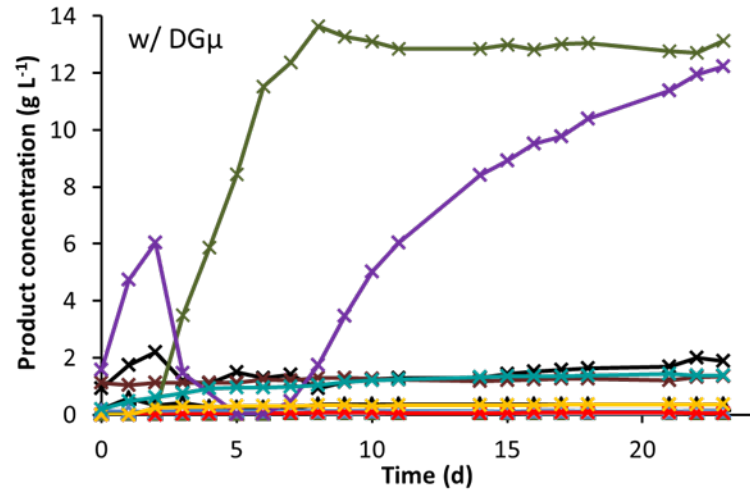
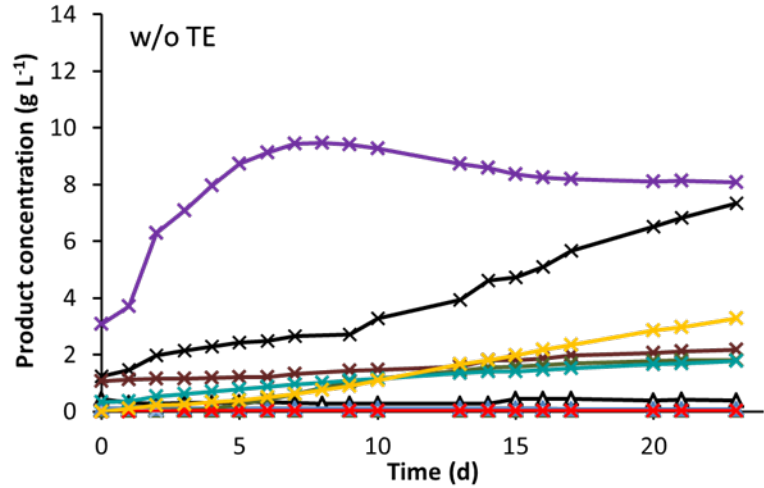
Supporting information 4 Development of the pH values in the replicate experiments.

Supporting information 5 Extended Weende forage analysis of maize silage before and after anaerobic fermentation without trace element supplementation (w/o TE) and with addition of DGμ (w/ DGμ). Conversion degrees were calculated for the single compounds. Mean values of the replicate experiments and the range are indicated. TS total solids, VS volatile solids.

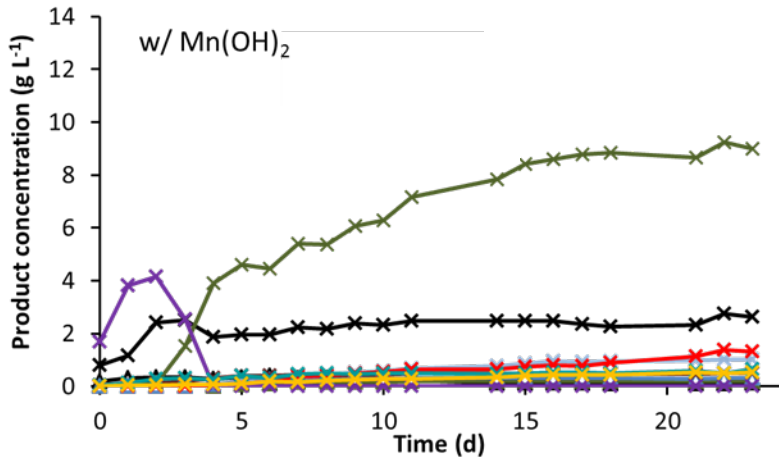
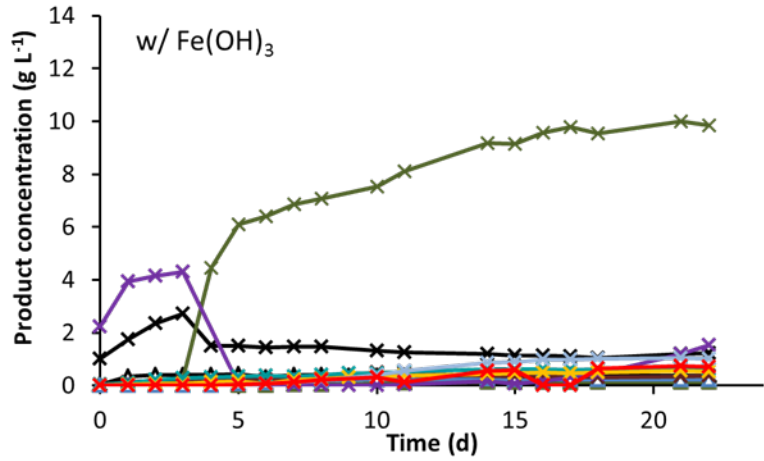
Sample	Fresh mass		TS		VS		Crude ash (g kg ⁻¹ TS ⁻¹)	Crude protein			Crude fat			Nitrogen free extractives			Cellulose			Hemicellulose			
	(g)	(% fresh mass)	(g)	Conversion degree (%)	(% TS)	(g)		Conversion degree (%)	(g kg ⁻¹ TS ⁻¹)	(g)	Conversion degree (%)	(g kg ⁻¹ TS ⁻¹)	(g)	Conversion degree (%)	(g kg ⁻¹ TS ⁻¹)	(g)	Conversion degree (%)	(g kg ⁻¹ TS ⁻¹)	(g)	Conversion degree (%)	(g kg ⁻¹ TS ⁻¹)	(g)	Conversion degree (%)
Maize silage	2000	35.4	707		95.4	675		45.7	94.1	67		12.3	9		649.8	459		194.4	137		368.8	261	
Solid digestate main experiment w/o TE	2515	20.6	517	25 ± 1.7	96.0	496	25 ± 1.6	40.5	75.5	39	39 ± 2.1	12.4	6	23 ± 3.0	625.4	323	27 ± 2.6	243.8	126	8 ± 0.7	349	181	37 ± 6.6
Solid digestate parallel experiment w/o TE	2503	21.6	541		95.6	518		43.7	77.2	42		12.8	7		641.1	347		236.6	128		269.7	146	
Solid digestate main experiment w/ DGμ	2416	18.6	449	35 ± 1.5	93.8	421	36 ± 1.7	62.3	88.4	40	38 ± 2.6	12.2	5	63 ± 26.4	589.6	265	39 ± 3.6	258.8	116	13 ± 2.9	251.6	113	54 ± 2.9
Solid digestate parallel experiment w/ DGμ	2619	18.0	471		94.4	444		56	91.6	43		1.9	1		631.8	297		263.7	124		272	128	

Supporting information 6 Ammonia nitrogen content ($\text{NH}_4^+\text{-N}$) during the anaerobic fermentation of maize silage without TE addition, with $\text{DG}\mu$, with $\text{Fe}(\text{OH})_3$, and with $\text{Mn}(\text{OH})_2$. Averages were calculated from values of all experiments (including the replicate experiments). The differences of average values from minimum and maximum are indicated in parentheses.

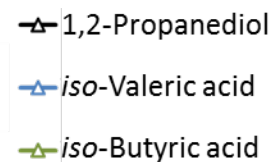
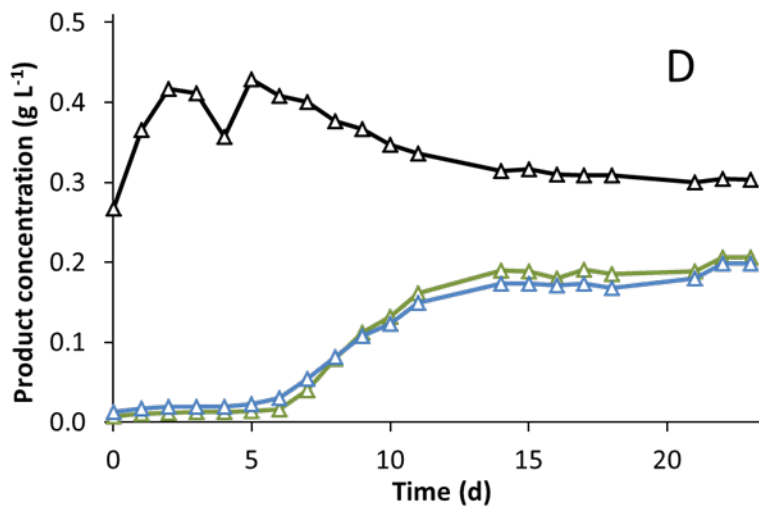
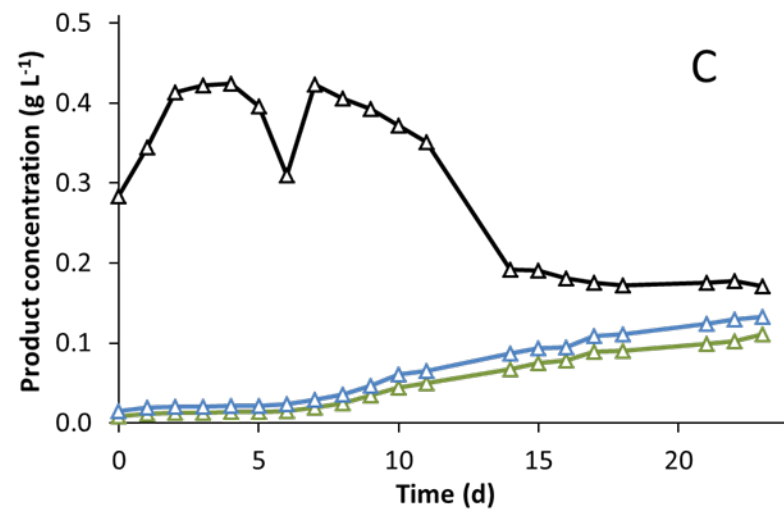
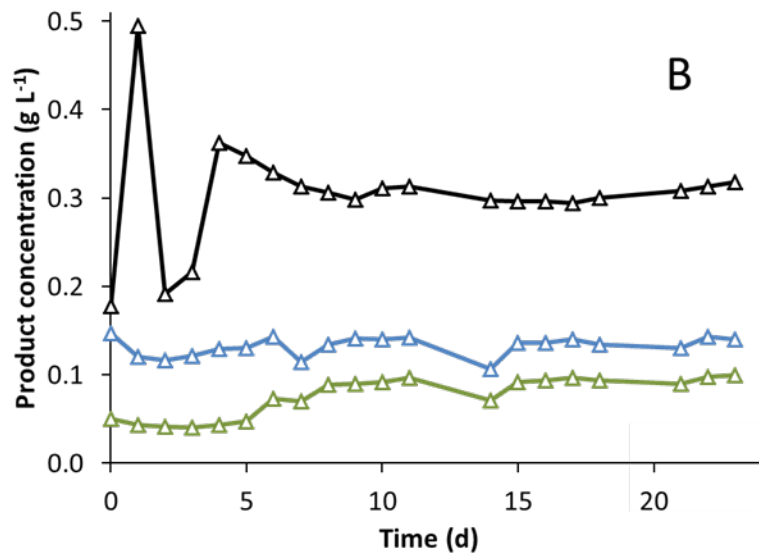
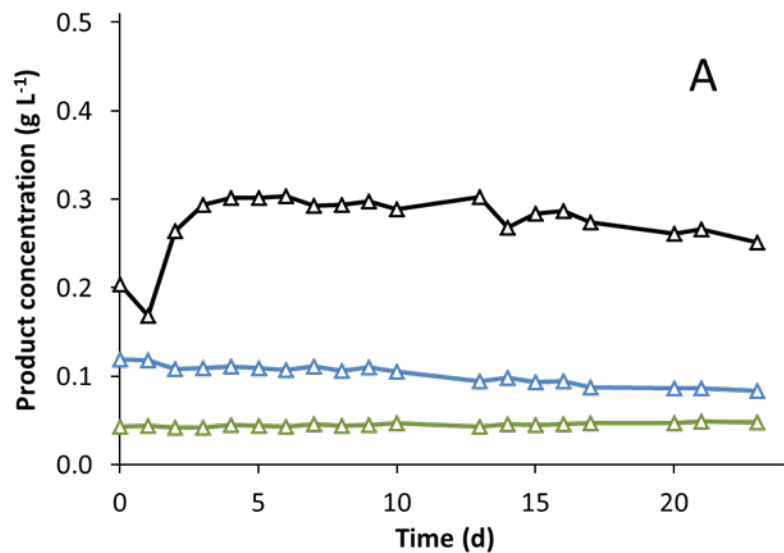
Experiment	$\text{NH}_4^+\text{-N}$ (g L^{-1})	
	Start	End
w/o TE	0.37 (± 0.08)	0.43 (± 0.00)
w/ $\text{DG}\mu$	0.36 (± 0.01)	0.49 (± 0.03)
w/ $\text{Fe}(\text{OH})_3$	0.25 (± 0.02)	0.43 (± 0.06)
w/ $\text{Mn}(\text{OH})_2$	0.27 (± 0.00)	0.49 (± 0.01)



- ✕ Acetic acid
- ✕ Propionic acid
- ✕ *n*-Butyric acid
- ✕ *n*-Valeric acid
- ✕ *n*-Caproic acid
- ✕ Lactic acid
- ✕ *iso*-Valeric acid
- ✕ *iso*-Butyric acid
- ✕ Ethanol
- ✕ 1-Propanol
- ✕ 1,2-Propanediol



Supporting information 7 Concentrations of organic acids and alcohols in the anaerobic fermentation of maize silage without TE additions (w/o TE), with DGμ (w/ DGμ), with Fe(OH)₃ (w/ Fe(OH)₃), and with Mn(OH)₂ (w/ Mn(OH)₂) in the replicate experiments.



Supporting information 8 Concentrations of *iso*-valeric and *iso*-butyric acid as well as 1,2-propanediol in the anaerobic fermentation of maize silage without TE additions (A), with DGμ (B), with Fe(OH)₃ (C), and with Mn(OH)₂ (D).

		H ₂	O ₂	N ₂	CH ₄	CO ₂
		in %				
w/o TE	experiment (end)	1.5 (± 0.1)	2.5 (± 0.5)	61.5 (± 0.2)	0.0 (± 0.0)	34.5 (± 0.2)
	replicate experiment (end)	4.3 (± 0.1)	1.0 (± 0.4)	48.0 (± 1.2)	0.0 (± 0.0)	46.7 (± 1.5)
w/ DGμ	experiment (days 9-10)	7.9 (± 0.3)	2.1 (± 0.2)	33.9 (± 0.4)	0.0 (± 0.0)	56.0 (± 0.1)
	experiment (end)	3.7 (± 1.0)	12.6 (± 1.8)	65.4 (± 3.1)	0.0 (± 0.0)	18.3 (± 3.8)
	replicate experiment (days 9-10)	8.5 (± 0.5)	2.3 (± 0.5)	32.5 (± 2.2)	0.0 (± 0.0)	56.7 (± 2.3)
	replicate experiment (end)	2.1 (± 1.7)	13.0 (± 2.1)	59.9 (± 2.1)	0.0 (± 0.0)	25.1 (± 2.4)
w/ Fe(OH) ₃	experiment (end)	11.7 (± 0.3)	4.1 (± 1.7)	43.5 (± 5.9)	0.0 (± 0.0)	40.6 (± 7.3)
	replicate experiment (end)	4.1 (± 3.0)	12.7 (± 4.8)	68.1 (± 8.4)	0.0 (± 0.0)	15.1 (± 10.3)
w/ Mn(OH) ₂	experiment (end)	6.1 (± 0.2)	4.7 (± 1.7)	38.8 (± 0.8)	0.0 (± 0.0)	50.4 (± 2.8)
	replicate experiment (end)	6.3 (± 1.2)	4.3 (± 1.5)	53.5 (± 4.5)	0.0 (± 0.0)	35.9 (± 4.8)

Supporting information 9 Gas composition in the last two or three days of anaerobic fermentation of maize silage without TE additions (w/o TE), with DGμ (w/ DGμ), with Fe(OH)₃ (w/ Fe(OH)₃), and with Mn(OH)₂ (w/Mn(OH)₂). For the experiments with DGμ, additionally values for the days 9-10 are shown. Mean values (± the range) are indicated.

Supporting information 10 Correlation analysis (Spearman's rank correlation coefficient, $p < 0.05$) of lactic acid bacteria (LAB) and other bacteria (upper table) as well as of clostridia/*Megasphaera* and LAB (lower table). For the correlation analyses, only T-RF with phylogenetic affiliation were considered. Only correlation coefficients equal or higher than 0.40 or equal or lower than -0.40 are shown. Purple color indicates LAB T-RF with high abundance, while green color indicates clostridial/*Megasphaera* T-RF with high abundance.

Lactic acid bacteria		Other bacteria		Correlation coefficients	
T-RF	Phylogenetic affiliation	T-RF	Phylogenetic affiliation	Positive	Negative
175	<i>Lactobacillus</i>	286	<i>Ruminococcaceae</i>	0.61	
		297	<i>Megasphaera</i>	0.40	
		298	<i>Megasphaera</i>	0.55	
		303	<i>Veillonellaceae</i>	0.46	
178	<i>Lactobacillus</i>	516	<i>Clostridium s.s.</i>		-0.57
214	<i>Lactobacillus</i>	157	<i>Lachnospiraceae</i>	0.82	
563	<i>Lactobacillus</i>	506	<i>Clostridium s.s.</i>	0.58	
573	<i>Lactobacillus</i>	516	<i>Clostridium s.s.</i>		-0.59
		286	<i>Ruminococcaceae</i>		-0.46
574	<i>Lactobacillus</i>	506	<i>Clostridium s.s.</i>	0.51	
		517	<i>Clostridium s.s.</i>	0.40	
579	<i>Lactobacillus</i>	517	<i>Clostridium s.s.</i>	0.44	
		519	<i>Clostridium s.s.</i>	0.45	
580	<i>Lactobacillus</i>	516	<i>Clostridium s.s.</i>		-0.47
		286	<i>Ruminococcaceae</i>		-0.43
582	<i>Lactobacillus</i>	516	<i>Clostridium s.s.</i>		-0.43
		286	<i>Ruminococcaceae</i>		-0.56
		298	<i>Megasphaera</i>		-0.41
		303	<i>Veillonellaceae</i>		-0.44
53	<i>Olsenella</i>	506	<i>Clostridium s.s.</i>	0.42	
		286	<i>Ruminococcaceae</i>		-0.43
		297	<i>Megasphaera</i>		-0.42
		298	<i>Megasphaera</i>		-0.56
		303	<i>Veillonellaceae</i>		-0.45
60	<i>Coriobacteriaceae</i>	516	<i>Clostridium s.s.</i>	0.59	
		517	<i>Clostridium s.s.</i>	0.53	
125	<i>Coriobacteriaceae</i>	483	<i>Clostridiales</i>	0.48	
		69	<i>Ruminococcaceae</i>	0.61	
		286	<i>Ruminococcaceae</i>	0.61	
		298	<i>Megasphaera</i>	0.52	
		303	<i>Veillonellaceae</i>	0.41	

Clostridia		Lactic acid bacteria		Correlation coefficients	
T-RF	Phylogenetic affiliation	T-RF	Phylogenetic affiliation	Positive	Negative
506	<i>Clostridium s.s.</i>	563 574 53	<i>Lactobacillus</i> <i>Lactobacillus</i> <i>Olsenella</i>	0.58 0.51 0.42	
516	<i>Clostridium s.s.</i>	60 178 573 580 582	<i>Coriobacteriaceae</i> <i>Lactobacillus</i> <i>Lactobacillus</i> <i>Lactobacillus</i> <i>Lactobacillus</i>	0.59	-0.57 -0.59 -0.47 -0.43
517	<i>Clostridium s.s.</i>	574 579 60	<i>Lactobacillus</i> <i>Lactobacillus</i> <i>Coriobacteriaceae</i>	0.40 0.44 0.53	
519	<i>Clostridium s.s.</i>	579	<i>Lactobacillus</i>	0.45	
69	<i>Ruminococcaceae</i>	125	<i>Coriobacteriaceae</i>	0.61	
286	<i>Ruminococcaceae</i>	175 125 573 580 582 53	<i>Lactobacillus</i> <i>Coriobacteriaceae</i> <i>Lactobacillus</i> <i>Lactobacillus</i> <i>Lactobacillus</i> <i>Olsenella</i>	0.61 0.61	-0.46 -0.43 -0.56 -0.43
157	<i>Lachnospiraceae</i>	214	<i>Lactobacillus</i>	0.82	
297	<i>Megasphaera</i>	175 53	<i>Lactobacillus</i> <i>Olsenella</i>	0.40	-0.42
298	<i>Megasphaera</i>	175 125 582 53	<i>Lactobacillus</i> <i>Coriobacteriaceae</i> <i>Lactobacillus</i> <i>Olsenella</i>	0.55 0.52	-0.41 -0.56
483	<i>Clostridiales</i>	125	<i>Coriobacteriaceae</i>	0.48	