

Figure S1. Coordinates of the experimental field of experience 45.209483, 38.300953.



Figure S2. Growth of maize (*Zea mays* L.) Pioneer 9578 hybrid in phase 5-6 leaves (May, 27th, 2017).

Notes: A.- the control variant, with no mineral fertilizers and no BMF; B – the variant with ammophos addition (EuroChem Group); C- the variant with addition of bio- modified fertilizer BMF 1, the ammophos fertilizer with addition of spores of *Bacillus velezensis* BS89 on dry carrier (diatomite), D- BMF2, the “biocapsules”, ammophos granules treated with spores of *Bacillus velezensis* BS89 in cell suspension.

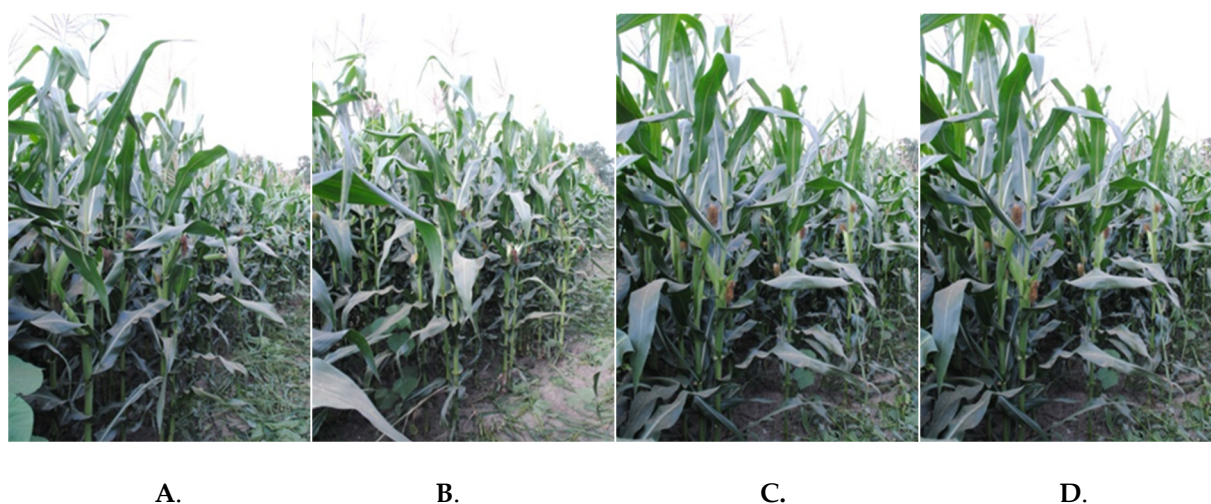


Figure S3. Growth of maize (Pioneer hybrid 9578) in flowering stage (16.07.2017).

Notes: A.- the control variant, with no mineral fertilizers and no BMF; B – the variant with ammophos addition (EuroChem Group); C- the variant with addition of bio- modified fertilizer BMF 1, the ammophos fertilizer with addition of spores of *Bacillus velezensis* BS89 on dry carrier (diatomite), D- BMF2, the “biocapsules”, ammophos granules treated with spores of *Bacillus velezensis* BS89 in cell suspension.

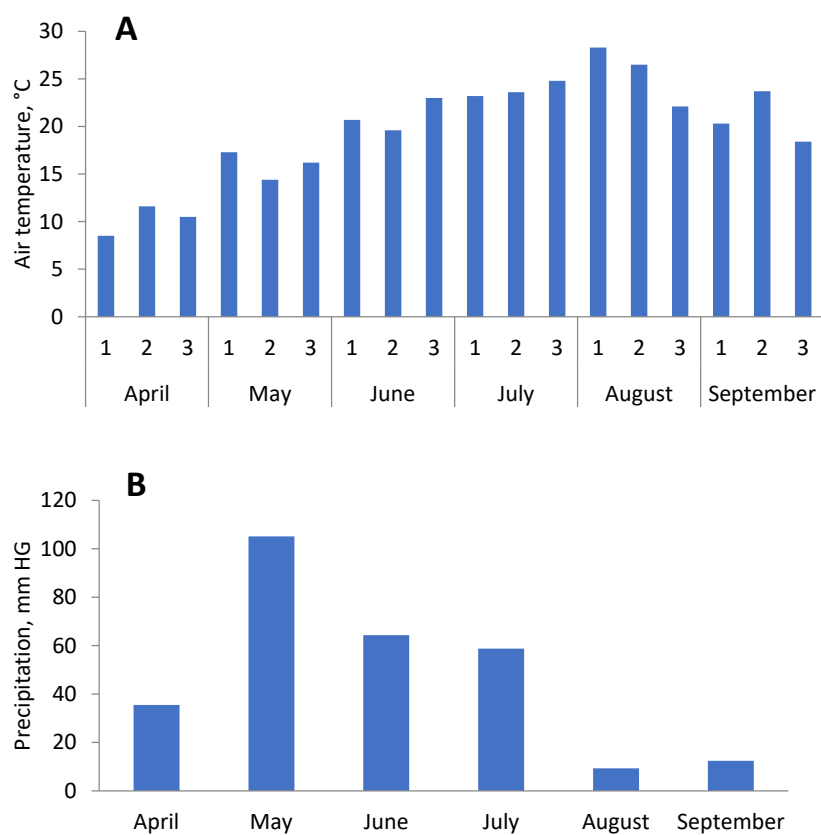


Figure S4. Meteorological data for the year of the field experiment (2017): **A** – air temperature, **B** – precipitation.

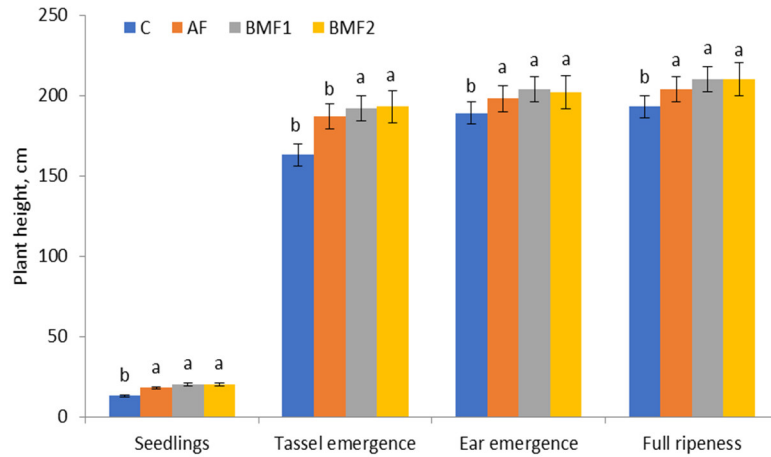


Figure S5. Plant height of maize plants (Pioneer P 9578 hybrid) at seedling, tassel emergence, ear emergence and full ripeness vegetation stages.

Notes: C – control plants (grown on fertilizer-free soil), AF – plants grown on soil fertilized with ammophos, BMF1 – plants grown on soil fertilized with BMF1 (ammophos with spores of *Bacillus velezensis* BS89 on dry carrier), BMF2 – plants grown on soil fertilized with BMF2 (ammophos pellets treated with spore suspension of *Bacillus velezensis* BS89). All data are presented as the mean \pm SE (standard error). Different letters indicate significant differences between treatments at $p < 0.05$ in Duncan test

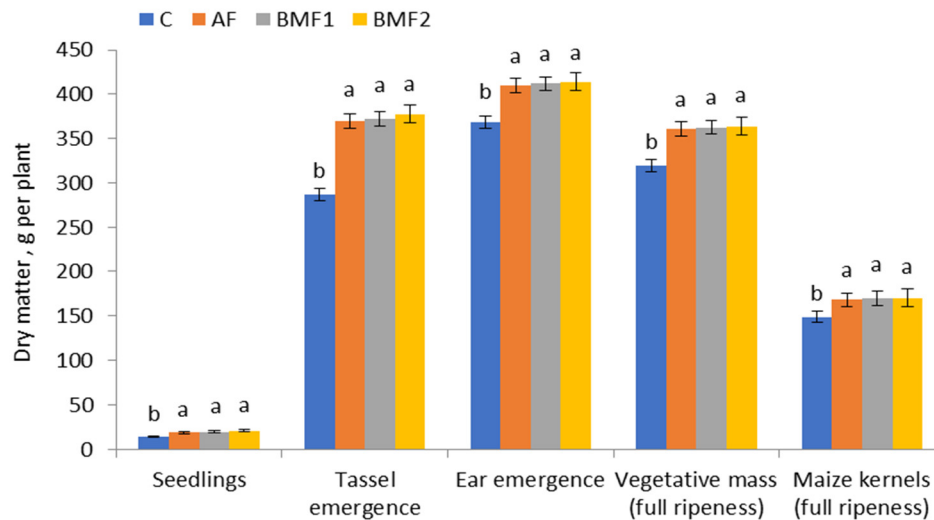


Figure S6. Dynamics of dry matter content in maize plants (Pioneer P 9578 hybrid) at seedling, tassel emergence, ear emergence and full ripeness vegetation stages.

Notes: C – control plants (grown on fertilizer-free soil), AF – plants grown on soil fertilized with ammophos, BMF1 – plants grown on soil fertilized with BMF1 (ammophos with spores of *Bacillus velezensis* BS89 on dry carrier), BMF2 – plants grown on soil fertilized with BMF2 (ammophos pellets treated with spore suspension of *Bacillus velezensis* BS89). All data are presented as the mean \pm SE (standard error). Different letters indicate significant differences between treatments at $p < 0.05$ in Duncan test

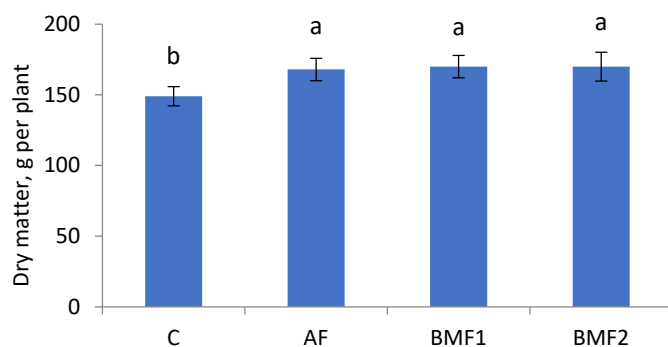


Figure S7. Dry matter content of maize (Pioneer P 9578 hybrid) kernels.

Notes: C – control plants (grown on fertilizer-free soil), AF – plants grown on soil fertilized with ammophos, BMF1 – plants grown on soil fertilized with BMF1 (ammophos with spores of *Bacillus velezensis* BS89 on dry carrier), BMF2 – plants grown on soil fertilized with BMF2 (ammophos pellets treated with spore suspension of *Bacillus velezensis* BS89). All data are presented as the mean \pm SE (standard error). Different letters indicate significant differences between treatments at $p < 0.05$ in Duncan test

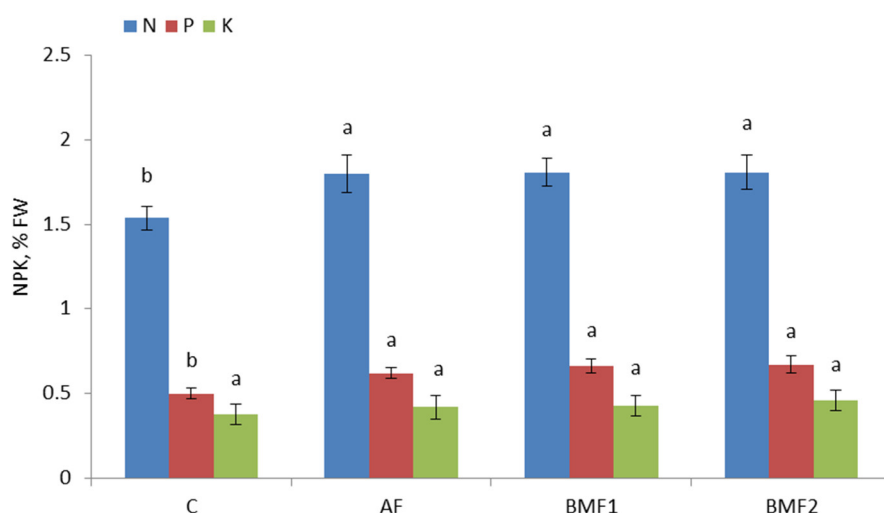


Figure S8. NPK content of maize (Pioneer P 9578 hybrid) kernels.

Notes: C – control plants (grown on fertilizer-free soil), AF – plants grown on soil fertilized with ammophos, BMF1 – plants grown on soil fertilized with BMF1 (ammophos with spores of *Bacillus velezensis* BS89 on dry carrier), BMF2 – plants grown on soil fertilized with BMF2 (ammophos granules treated with spore suspension of *Bacillus velezensis* BS89). All data are presented as the mean \pm SE (standard error). Different letters indicate significant differences between treatments at $p < 0.05$ in Duncan test

Table S1. Effects of different fertilizers on the contents of available N-NO₃, N-NH₄ and P₂O₅ in rhizosphere soil of maize (Pioneer hybrid 9578) under different vegetative stages

Vegetation Phase	Agrochemical Parameter	C	AF	BMF1	BMF2
Tassel emergence	NO ₃ , mg kg ⁻¹	19.6 \pm 1.1c	21.2 \pm 1.4b	22.8 \pm 0.9a	22.9 \pm 1.0a
	NH ₄ , mg kg ⁻¹	12.2 \pm 0.8c	15.8 \pm 0.7b	17.7 \pm 0.7a	17.8 \pm 0.8a
	P ₂ O ₅ , mg kg ⁻¹	56 \pm 3b	73 \pm 6a	76 \pm 5a	77 \pm 6a
Ear emergence	NO ₃ , mg kg ⁻¹	12.3 \pm 1.1c	17.2 \pm 1.0b	18.8 \pm 0.7a	18.9 \pm 0.7a

	NH ₄ , mg kg ⁻¹	7.3±0.4c	8.0±0.5b	9.2±0.4a	9.3±0.5a
	P ₂ O ₅ , mg kg ⁻¹	44±3b	56±3a	57±4a	57±5a
	NO ₃ , mg kg ⁻¹	5.0±0.5b	8.2±0.8a	9.1±0.5a	9.2±0.6a
	NH ₄ , mg kg ⁻¹	4.3±0.4c	6.1±0.5b	7.1±0.5a	7.1±0.7a
Full ripeness	P ₂ O ₅ , mg kg ⁻¹	25±3b	42±5a	44±3a	44±4a

Notes: C – control plants (grown on fertilizer-free soil), AF – plants grown on soil fertilized with ammophos, BMF1 - plants grown on soil fertilized with BMF1 - plants grown on soil fertilized with BMF1 (ammophos with spores of *Bacillus velezensis* BS89 on dry carrier), BMF2 – plants grown on soil fertilized with BMF2 (ammophos granules treated with spore suspension of *Bacillus velezensis* BS89). All data are presented as the mean ± SE (standard error). Different letters indicate significant differences between treatments at $p < 0.05$ in Duncan test

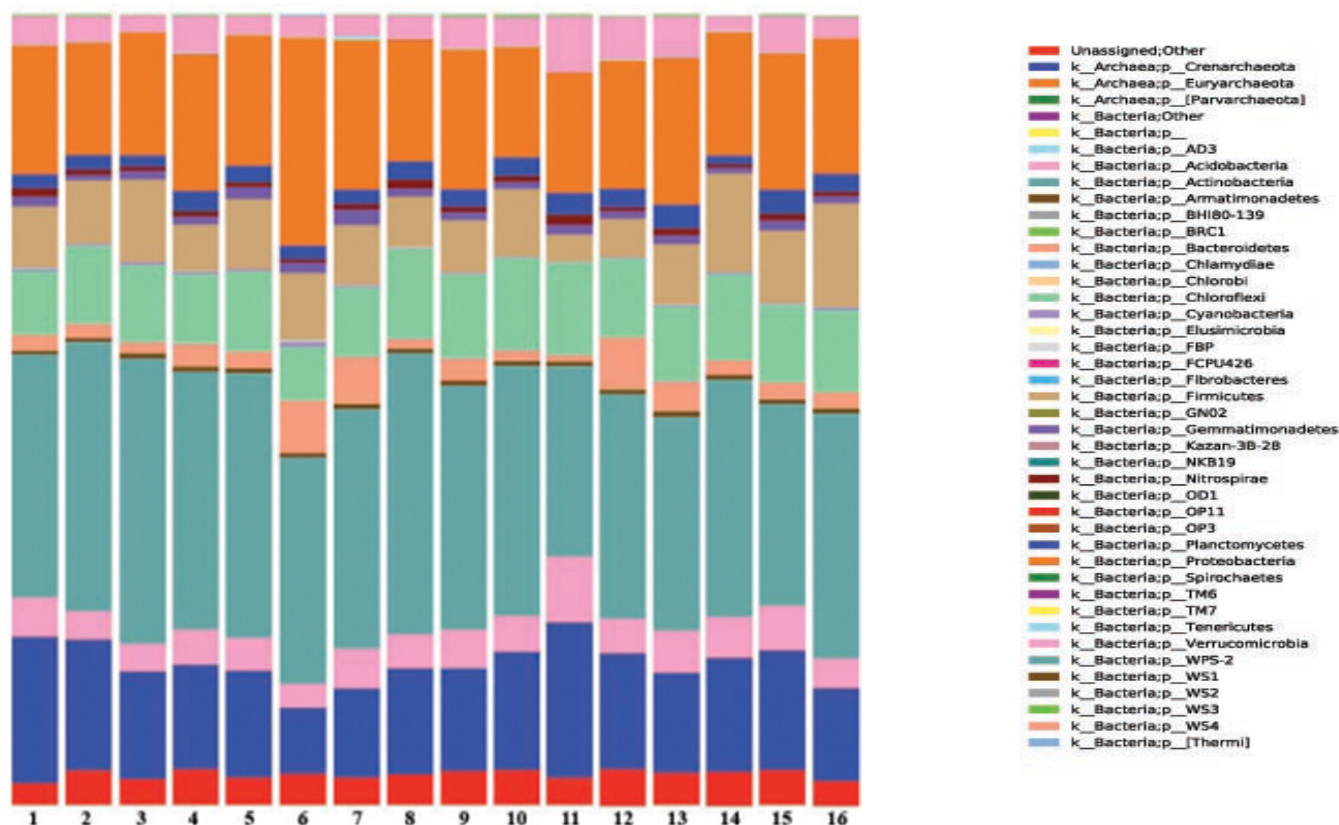


Figure S9. Taxonomic profile maize (Pioneer hybrid 9578) rhizosphere bacterial community when using various agricultural technologies. 1-4 control (C), 5-8 ammophos addition (AF), 9-12 ammophos with spores of *Bacillus velezensis* BS89 on dry carrier (BMF1); ammophos granules treated with a spore suspension of *Bacillus velezensis* BS89 (BMF2)

Table S2. The number of representatives of the main phyla of the microbiome of the rhizosphere of maize and bulk soil under different variants of fertilization

OTU ID	C	AF	BMF-1	BMF-2	Bulk
Unassigned	0.035776± 0.007757	0.035403± 0.002309	0.040194± 0.004268	0.040145± 0.00744	0.05308± 0.01233
Archaea _Crenarchaeota	0.184904± 0.02135	0.147627± 0.021852	0.189753± 0.020534	0.133408± 0.056758	0.127537± 0.01311
Archaea __Euryarchaeota	0.000253± 9.73E-05	0.000113± 3.8E-05	0.000149± 0.000102	0.000323± 0.000219	0
Archaea __Parvarchaeota	0	6.44E-06± 1.26E-05	0	0	0
Bacteria; Other	7.97E-05± 1.23E-05	2.17E-05± 2.11E-05	5.07E-05± 4.03E-05	2.26E-05± 1.58E-05	3.39E-05± 5.88E-06
Bacteria	5.53E-05± 3.17E-05	0	0	1.23E-05± 2.42E-05	0.000574± 0.001062
Bacteria_AD3	1.43E-05± 1.65E-05	3.56E-05± 4.82E-05	1.74E-05± 2.96E-05	2.47E-05± 2.48E-05	0
Acidobacteria	0.039652± 0.006709	0.039794± 0.007955	0.052983± 0.01562	0.049764± 2.86E-05	0.034654± 0.004017
Actinobacteria	0.32302± 0.020877	0.309742± 0.0299	0.27709± 0.026724	0.284945± 0.011066	0.297366± 0.039443
Armatimonadetes	0.005058± 0.001186	0.005253± 0.000397	0.005297± 0.000355	0.005816± 0.016961	0.002562 0.000498
BHI80-139	0	0	1.63E-05± 1.88E-05	9.27E-06± 0.000499	0
BRC1	0.000272± 6.99E-05	0.000189± 0.000151	0.00027± 0.000181	0.000254± 1.82E-05	0.000624± 0.000241
Bacteroidetes	0.018763± 0.005614	0.038171± 0.025804	0.027113± 0.020863	0.023835± 7.01E-05	0.081682± 0.047447

Chlamydiae	0.000457± 0.000198	0.0004± 0.000156	0.000529± 6.21E-05	0.000554± 0.008032	0.002037± 0.001845
Chlorobi	0.000348± 0.000179	0.000346± 0.000255	0.000215± 5.16E-05	0.00019± 0.000427	0.000531± 0.000272
Chloroflexi	0.087665± 0.007705	0.089182± 0.019127	0.1049± 0.007259	0.100922± 4.67E-05	0.040303± 0.01851
Cyanobacteria	0.002643± 0.000445	0.002943± 0.002385	0.001126± 0.000351	0.001714± 0.007939	0.000503± 0.000111
Elusimicrobia	0.000325± 0.000274	0.000344± 0.000166	0.00033± 5.76E-05	0.000266± 0.000703	0.000669± 0.000268
FBP	0.000344± 0.000196	0.000838± 0.000587	0.000254± 0.000142	0.000346± 6.97E-05	0.000273± 0.000293
FCPU426	7.17E-06± 8.24E-06	2.6E-05± 4.01E-05	1.37E-05± 2.32E-05	2.21E-05± 0.000173	2.15E-05± 4.21E-05
Fibrobacteres	0.000214± 0.000185	8.8E-05± 3.26E-05	0.000142± 6.91E-05	0.000276± 2.33E-05	0.000103± 9.52E-05
Firmicutes	0.077517± 0.017923	0.075179± 0.010496	0.056324± 0.018054	0.106139± 0.000192	0.060123± 0.005802
GN02	3.13E-06± 6.14E-06	4.51E-05± 5.96E-05	1.78E-05± 2.23E-05	9.4E-06± 0.023403	3.14E-05± 3.65E-05
Gemmatimonadetes	0.009605± 0.002248	0.014138± 0.003714	0.009993± 2.23E-05	0.01035± 1.06E-05	0.011181± 0.00393
Kazan-3B-28		1.28E-05± 1.61E-05	3.48E-06± 5.91E-06	4.64E-06± 0.002934	
NKB19	0 6.19E-06± 1.21E-05				0
Nitrospirae		0	0	0	0
	0.006502±	0.006238±	0.00697±	0.006172±	0.001115±

	0.002093	0.002801	0.002966	9.09E-06	0.001216
OD1				9.08E-05± 0.002563	0.000455± 0.000343
	0.000245± 0.000223	7.81E-05 2.36E-05 ±	9.34E-05± 7.17E-05		
OP11				1.93E-05± 1.48E-05	0.000205± 0.000175
	6.7E-05± 8.96E-05	0.000109± 7.64E-05	4.59E-05± 3.06E-05		
OP3				9.52E-06± 2.35E-05	5.52E-05± 6.01E-05
	1.52E-05± 2.24E-05	1.81E-05± 3.54E-05	3.57E-05± 3.67E-05		
Planctomycetes				0.02406± 1.87E-05	0.030126± 0.00957
	0.018307± 0.00418	0.019169± 0.002552	0.023374± 0.002111		
Proteobacteria				0.171611± 0.01003	0.200144± 0.025534
	0.152561± 0.012301	0.185906± 0.04603	0.151104± 0.012674		
Spirochaetes					8.18E-05± 8.55E-05
	0	0	0	0	
TM6				6.37E-05± 0.018325	0.00014 8.53E-05
	7.3E-05± 6.16E-05	3.45E-05± 1.19E-05	5.21E-05± 1.92E-05		
TM7				0.000564± 4.29E-05	0.002075± 0.001157
	0.000572± 0.000232	0.00064± 0.000156	0.000619± 0.000413		
Tenericutes				0.000356± 0.000283	0.001012± 0.001113
	0.000287± 0.000277	0.001123± 0.001957	0.000436± 0.000368		
Verrucomicrobia				0.035802± 0.000211	0.049877± 0.017286
	0.032559± 0.009767	0.025199± 0.001961	0.04811± 0.01254		
WPS-2				5.64E-05± 0.01644	0.000341± 0.000311
	1.15E-05± 2.25E-05	8.61E-06± 1.69E-05	2E-05± 1.34E-05		

WS1	2.3E-05± 4.51E-05				
		0	0	0	0
WS2				6.18E-05± 6.38E-05	7.55E-05± 7.76E-05
	8.5E-05± 8.15E-05	5.42E-05± 4.46E-05	2.76E-05± 2.71E-05		
WS3				0.001715± 3.62E-05	0.000146± 0.000205
	0.001575± 0.000426	0.001063± 0.000415	0.002301± 0.000621		
WS4				5.65E-05± 0.000629	
	8.74E-05± 5.22E-05	3.46E-05± 2.76E-05	2.67E-05± 1.85E-05		
[Thermi]_Deinococci					0
	4.78E-05± 6.71E-05		3.91E-06± 6.64E-06	7.72E-06± 5.46E-05	0.000263± 5.37E-05
		0.000427± 0.000769			
Total	1	1	1	1	1

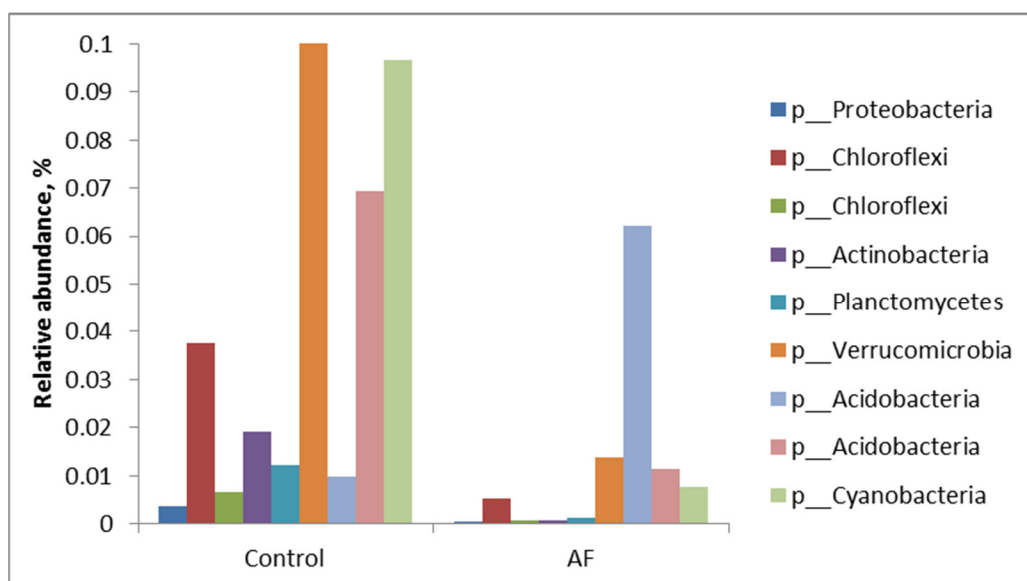


Figure S10. Changes in the composition of the minor microbial community in the control and ammophos (AF) experimental variants.

Notes (Figure S10):

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bosea

k__Bacteria;p__Chloroflexi;c__TK17;o__mle1-48;f__g__

k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__WCHB1-50;f__g__

k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__koll13;g__

k__Bacteria;p__Planctomycetes;c__o__f__g__

k__Bacteria;p__Verrucomicrobia;c__[Pedosphaerae];o__[Pedosphaerales];f__auto67_4W;g__

k__Bacteria;p__Acidobacteria;c__Solibacteres;o__Solibacterales;f__Solibacteraceae;g__

k__Bacteria;p__Acidobacteria;c__o__f__g__

k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Nostocales;f__Nostocaceae;g__

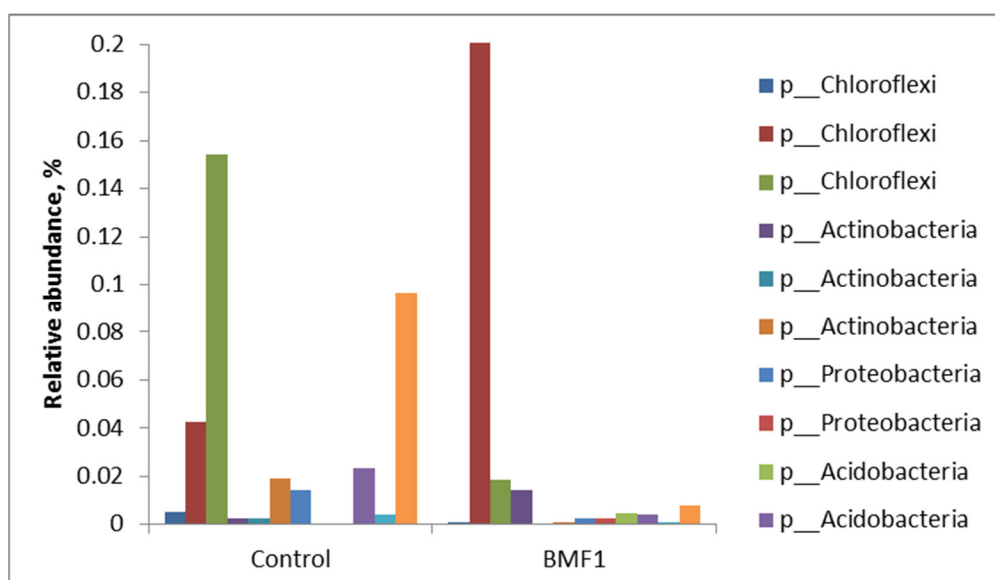


Figure S11. Changes in the composition of the minor microbial community in the control and BMF1 experimental variants.

Notes (Figure S11):

k__Bacteria;p__Chloroflexi;c__TK10;o__AKYG885;f__g__

k__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Thermogemmatisporales;f__Thermogemmatisporaceae;g__

k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__Caldilinea

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Frankiaceae;Other

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Cellulomonadaceae;g__Actinotalea

k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__koll13;g__

k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__34P16;f__g__

k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__Acidobacteriaceae;g__

k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__11-24;f__g__

k__Bacteria;p__Firmicutes;c__Clostridia;o__SHA-98;f__g__

k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Nostocales;f__Nostocaceae;g__

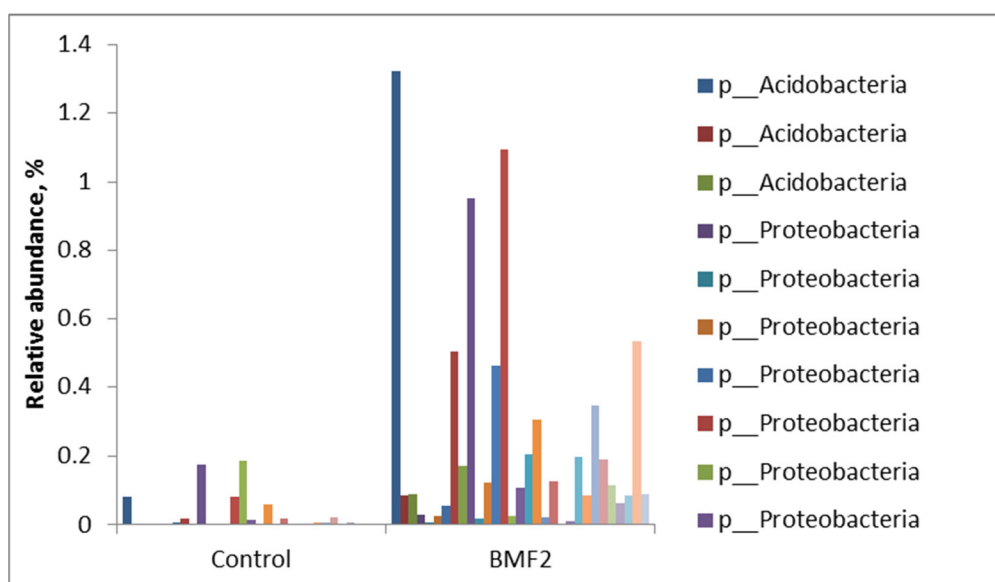


Figure S12. Changes in the composition of the minor microbial community in the control and BMF2 experimental variants.

Notes (Figure S12):

k__Bacteria;p__Acidobacteria;c__Solibacteres;o__Solibacterales;f__Solibacteraceae;g__
k__Bacteria;p__Acidobacteria;c__iii1-8;o__32-20;f__g__
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__11-24;f__g__
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;Other;Other
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Hyphomonadaceae;g__
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__mitochondria;g__Vermamoeba
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__BD7-3;f__g__
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Ramlibacter
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__IS-44;f__g__
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;Other;Other
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylobacter
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;Other
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Tatlockia
k__Bacteria;p__Chloroflexi;c__Chloroflexi;o__[Roseiflexales];f__g__
k__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Thermogemmatissporales;f__Thermogemmatissporaceae;g__
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__GCA004;f__g__
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__f__g__
k__Bacteria;p__Chloroflexi;c__o__f__g__
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Microbispora
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Microlunatus
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nakamurellaceae;g__
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiaceae;g__
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__koll13;g__
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Conexibacteraceae;g__Conexibacter
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__C114;f__g__
k__Bacteria;p__Gemmatimonadetes;c__Gemm-5;o__f__g__
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planomicrobium
k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Nostocales;f__Nostocaceae;g__
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia
k__Bacteria;Other;Other;Other;Other;Other
k__Bacteria;p__c__o__f__g__

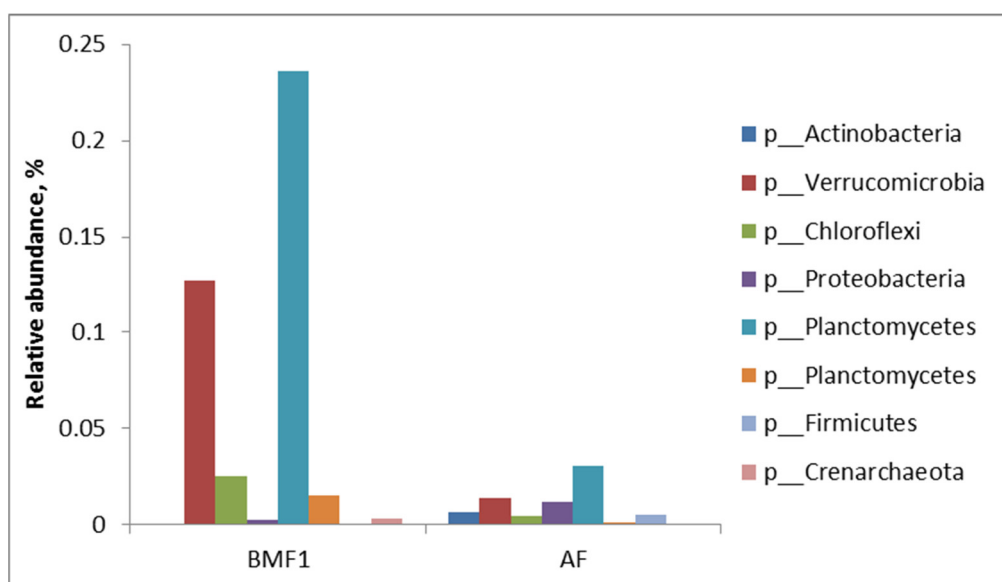


Figure S13. Changes in the composition of the minor microbial community in the BMF1 and ammophos experimental variants.

Notes (Figure S13):

k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Actinotalea
k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_auto67_4W;g_
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_H39;f_g_
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_
k_Bacteria;p_Planctomycetes;c_OM190;o_CL500-15;f_g_
k_Bacteria;p_Planctomycetes;c_o_;f_g_
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Marinibacillus
k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaeraceae;g_

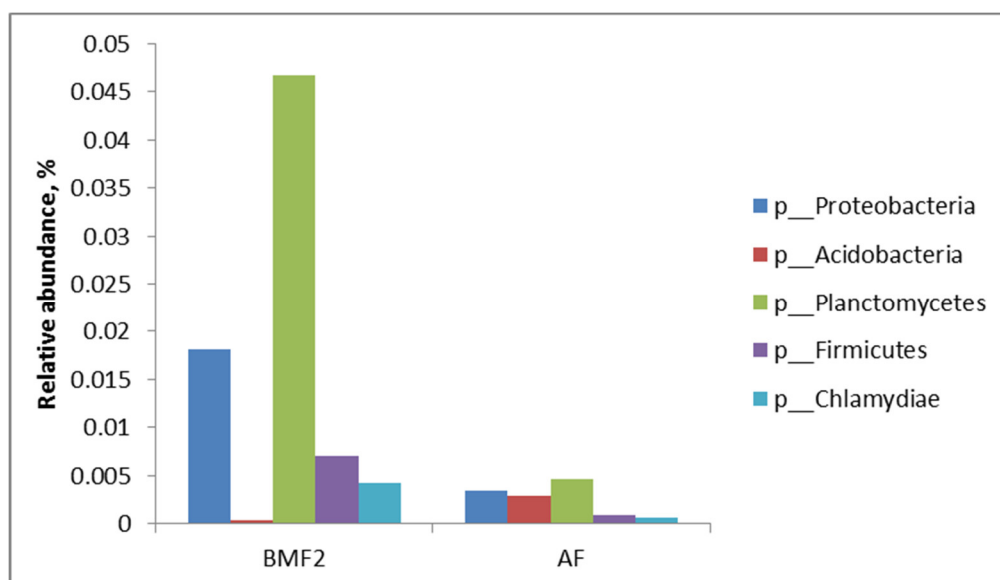


Figure S14. Changes in the composition of the minor microbial community in the BMF2 and ammophos experimental variants.

Notes (Figure S14):

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Phyllobacterium
 k__Bacteria;p__Acidobacteria;c__Solibacteres;o__Solibacterales;f__[Bryobacteraceae];g__
 k__Bacteria;p__Planctomycetes;c__C6;o__MVS-107;f__g__
 k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Anaerobacillus
 k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia

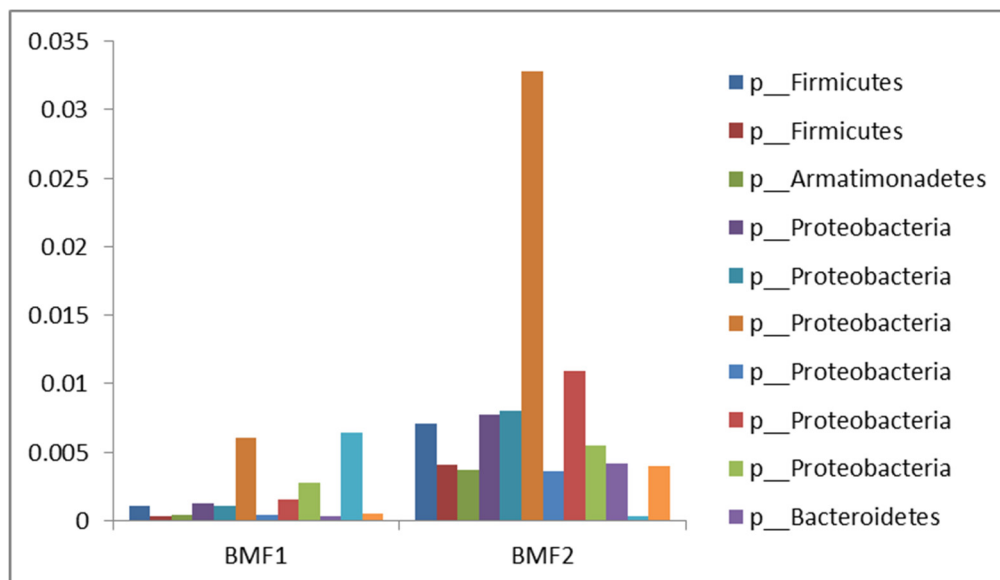


Figure S15. Changes in the composition of the minor microbial community in the BMF1 and BMF2 experimental variants.

Notes (Figure S15):

k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Anaerobacillus
 k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Marinibacillus
 k__Bacteria;p__Armatimonadetes;c__Chthonomonadetes;o__Chthonomonadales;Other;Other
 k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rubellimicrobium
 k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Kaistia
 k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__mitochondria;g__Acanthamoeba
 k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__g__
 k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Myxococcaceae;g__
 k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas
 k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__[Amoebophilaceae];g__Candidatus Amoebophilus
 k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium
 k__Bacteria;p__OD1;c__ZB2;o__f__g__