

Table S2. Taxonomic structure of rhizosphere microbial communities of amaranths studied, %.

Associated OTUs	Background				Tulachermet				KGIW				Lenin Ave.			
	Valentina	Dyimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyimovochka	Bulava	Zelenaya Sosulka
p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_uncultured;g_uncultured	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.22	0.00	1.62	0.00	0.11	0.00	0.00	0.00
p_Acidobacteriota;c_Acidobacteriae;o_Bryobacteriales;f_Bryobacteraceae;g_Bryobacter	0.58	0.31	0.63	0.99	0.96	0.89	0.80	1.07	0.37	1.18	1.36	0.50	0.85	0.41	1.34	0.71
p_Acidobacteriota;c_Acidobacteriae;o_Solibacterales;f_Solibacteraceae;g_Candidatus_Solibacter	0.17	0.31	0.08	0.23	0.24	0.38	0.34	0.00	0.21	0.31	1.30	0.47	0.41	0.14	0.19	0.20
p_Acidobacteriota;c_Holophagae;o_Subgroup_7;f_Subgroup_7;g_Subgroup_7	0.49	0.17	0.40	0.70	0.29	0.66	0.41	0.39	0.41	0.46	0.57	1.13	0.53	0.46	0.44	1.43
p_Acidobacteriota;c_Thermoanaerobactria;o_Thermoanaerobactriales;f_Thermoanaerobactriae;g_Subgroup_10	0.90	0.69	2.13	0.83	1.25	1.57	2.03	2.39	2.61	2.36	1.63	1.19	0.41	0.81	2.81	1.35
p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterales;f_uncultured;g_uncultured	0.83	2.16	1.08	1.33	0.37	1.15	0.94	1.55	0.32	1.28	1.52	1.54	0.47	0.51	0.93	1.08
p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterales;f_Vicinamibacteraceae;g_Vicinamibacteraceae	1.47	2.15	1.73	1.50	0.54	1.04	1.47	1.97	0.55	1.74	1.62	3.21	0.94	1.18	1.58	2.62
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_uncultured;g_uncultured	0.84	1.56	0.61	0.51	0.91	1.28	0.97	0.65	1.36	1.03	0.49	0.99	0.22	0.79	1.27	1.20
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.39	0.17	0.30	0.03	0.00	0.00	0.64	0.00	0.26	0.00	1.10	1.11	0.29	0.19	0.71	0.64
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.57	0.84	0.42	0.85	0.15	0.84	0.48	1.06	0.53	0.50	0.63	1.01	0.11	0.39	0.27	0.81
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.67	0.75	0.56	0.66	0.35	0.52	0.44	0.92	0.72	0.51	0.61	1.07	0.13	0.97	0.64	1.30
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	1.90	2.41	2.37	0.88	1.45	1.61	3.38	2.34	1.25	1.03	2.06	2.13	0.70	1.38	1.36	2.43
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	3.26	3.70	1.85	2.37	1.83	2.06	2.15	2.07	3.30	1.61	2.40	4.74	1.30	2.12	2.26	4.42
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.59	1.02	1.22	1.40	0.88	1.25	1.76	1.46	0.85	1.23	1.35	0.71	1.14	1.18	1.42	0.73
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.67	1.11	0.90	0.74	0.22	0.75	0.83	0.92	0.43	0.55	0.55	0.39	1.13	0.99	0.75	0.00
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	1.07	1.07	0.85	0.66	0.52	0.59	0.87	1.11	0.93	0.64	0.83	0.86	0.67	0.53	0.00	0.35
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.70	0.65	0.51	0.79	0.38	0.28	0.53	0.60	0.37	0.44	0.47	1.69	0.56	0.56	0.57	0.72
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.20	0.86	4.21	1.65	0.05	0.92	0.87	1.63	1.30	0.85	0.78	0.27	1.87	0.96	4.74	2.00
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	1.65	0.47	0.59	0.40	1.99	0.57	0.00	0.00	1.00	0.90	0.28	0.14	1.04	0.86	0.48	0.00
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	2.23	3.72	3.65	2.70	2.54	1.61	2.99	4.13	3.60	1.81	1.87	2.14	1.53	2.01	1.50	2.32
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.58	0.33	0.89	2.38	0.54	0.58	0.50	1.78	0.86	0.00	0.96	0.16	0.00	0.00	0.72	0.38
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	1.01	0.13	1.12	0.30	2.86	1.50	0.88	0.00	3.36	1.38	0.51	0.20	2.70	1.24	0.37	0.10
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.48	2.24	2.50	1.54	1.19	1.48	1.43	1.70	1.55	1.56	0.86	1.45	2.12	1.18	2.22	1.31
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	2.34	4.64	2.11	2.17	2.33	3.33	3.74	2.86	3.04	1.48	3.71	2.93	1.76	3.71	2.22	1.88
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	2.12	2.41	0.87	1.67	2.09	1.66	1.87	1.00	1.82	1.27	2.99	1.11	3.72	1.76	0.45	0.85
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	2.61	5.12	3.48	2.11	1.81	2.82	6.26	2.14	3.36	2.50	3.69	2.39	2.04	4.73	3.00	2.54
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.01	0.00	0.61	0.00	0.00	0.40	0.69	0.34	0.04	0.49	0.70	0.21	1.12	0.55	0.30	0.00
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.37	1.24	0.84	1.06	0.63	0.83	1.03	1.00	1.20	0.39	0.70	0.54	1.15	1.10	1.05	0.61
p_Actinobacteriota;c_Actinobacteriae;o_Actinomarinales;f_Actinomarinales;g_Actinomarinales	0.43	1.00	0.21	0.34	0.39	0.38	0.53	0.16	0.71	0.55	0.24	0.54	0.19	0.48	0.41	0.51
p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_uncultured	0.35	0.40	0.00	0.31	0.19	0.16	0.19	0.10	0.52	0.12	0.21	0.65	0.29	0.00	0.00	1.01
p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Terrimonas	0.00	0.27	0.95	0.77	0.06	0.16	0.16	0.51	0.07	0.34	0.10	0.58	0.00	0.10	1.77	0.68
p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Terrimonas	0.01	0.14	0.00	0.19	0.02	2.06	0.00	0.07	0.32	0.47	0.00	0.11	0.16	0.66	0.00	0.00
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	1.05	0.00	0.00	0.00	0.46	0.05	0.00	0.06	0.17	0.28	0.00	0.00	0.00	0.00	0.00	0.00
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	1.03	0.00	0.03	0.03	1.61	0.19	0.02	0.00	0.33	0.00	0.00	0.00	0.07	0.14	0.00	0.00
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	0.85	0.38	0.15	0.00	1.02	0.00	0.21	0.12	0.16	0.00	0.00	0.08	0.00	0.15	0.19	0.63
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	3.35	1.65	2.60	2.06	2.77	1.22	1.24	3.17	1.37	0.58	0.78	1.20	1.80	0.77	6.30	3.77
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	1.24	2.13	2.91	1.55	1.45	1.75	4.52	1.93	1.68	1.00	2.48	1.13	0.38	1.70	1.19	0.82
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	0.90	1.61	1.24	1.01	1.39	1.14	1.51	0.80	1.93	0.72	1.44	1.55	0.69	1.61	1.41	1.02
p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_Chloroflexia	2.65	4.38	1.59	2.82	2.46	2.55	2.65	1.79	4.43	1.28	2.52	3.24	2.38	3.03	1.64	3.71
p_Cyanobacteria;c_Cyanobacteriia;o_Cyanobacteriales;f_Coleofasciculaceae;g_Microcoleus_PCC-7113	4.12	0.00	0.47	0.00	8.19	3.81	0.07	0.00	0.63	13.54	0.00	0.00	0.95	0.19	0.00	0.00

Associated OTUs	Background				Tulachermet				KGIW				Lenin Ave.			
	Valentina	Dyuimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyuimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyuimovochka	Bulava	Zelenaya Sosulka	Valentina	Dyuimovochka	Bulava	Zelenaya Sosulka
p_Cyanobacteria;c_Cyanobacteriia;o_Cyanobacteriales;f_Phormidiaceae;g_Phormidium_IAM_M-71	4.94	0.00	1.07	0.12	4.97	2.55	0.13	0.01	1.94	1.15	0.06	0.00	1.19	3.41	0.00	0.00
p_Cyanobacteria;c_Cyanobacteriia;o_Cyanobacteriales;f_Phormidiaceae;g_Tychonema_CCAP_1459-11B	0.34	2.49	0.67	0.00	0.77	0.05	0.00	0.00	3.85	0.00	0.00	0.00	0.05	0.57	0.00	0.00
p_Cyanobacteria;c_Cyanobacteriia;o_Cyanobacteriales;f_Phormidiaceae;g_uncultured	1.02	0.00	0.00	0.11	1.08	0.40	0.08	0.08	0.82	1.12	0.17	0.00	1.15	1.55	0.00	0.00
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	1.09	1.14	1.00	1.32	1.22	0.70	1.61	1.99	0.51	0.43	2.48	2.12	2.42	0.31	2.04	0.90
p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_uncultured	0.67	1.32	0.77	1.33	0.17	1.39	1.02	1.06	0.26	1.10	1.31	2.96	0.31	0.37	1.00	2.45
p_Gemmatimonadota;c_Longimicrobia;o_Longimicrobiales;f_Longimicrobiaceae;g_YC-ZSS-LKJ147	0.89	0.00	0.57	0.07	2.21	0.49	0.41	0.23	0.80	0.65	0.54	0.00	2.35	1.63	0.15	0.00
p_Methylomirabilota;c_Methylomirabilia;o_Rokubacteriales;f_Rokubacteriales;g_Rokubacteriales	0.18	0.66	0.14	0.05	0.05	0.10	0.19	0.27	0.26	0.33	0.27	1.44	0.10	0.14	0.33	0.95
p_Myxococcota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_Haliangium	0.51	0.69	0.78	1.07	0.93	0.57	0.33	0.93	0.35	0.87	0.47	0.96	0.28	0.27	0.91	1.26
p_Myxococcota;c_Polyangia;o_Polyangiales;f_Blrii41;g_Blrii41	0.23	0.61	0.77	2.40	0.00	0.33	0.23	1.09	0.02	0.63	0.00	0.18	0.29	0.22	1.07	0.54
p_Plactomycetota;c_Phycisphaerae;o_Tepidisphaerales;f_WD2101_soil_group;g_WD2101_soil_group	0.23	0.46	0.26	0.49	0.05	1.02	0.55	0.51	0.32	0.80	0.58	1.10	0.59	0.13	0.43	0.58
p_Proteobacteria;c_Alphaproteobacteria;o_Azospirillales;f_Azospirillaceae;g_Skermanella	0.46	0.19	1.22	0.67	0.80	0.79	1.04	0.51	0.68	0.57	0.37	0.00	0.49	0.99	0.57	0.00
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_	0.89	0.73	0.86	1.06	0.54	0.77	1.12	0.86	2.22	0.69	0.09	0.60	0.78	0.89	0.60	1.05
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	1.84	2.66	1.90	2.87	1.10	1.33	2.34	2.08	2.07	0.62	1.01	3.04	1.71	2.73	2.16	2.82
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	0.62	0.29	0.67	0.95	1.20	1.69	0.89	1.33	2.14	0.57	1.16	0.56	2.14	0.80	0.71	0.29
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_	0.01	0.10	0.49	0.11	0.47	0.49	0.02	0.46	0.17	0.47	0.65	0.18	1.06	0.04	0.41	0.08
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium-Methylobacterium	0.15	0.00	0.00	0.00	1.36	0.00	0.00	0.01	0.65	0.00	0.00	0.00	5.19	0.26	0.00	0.00
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_	0.56	0.62	1.16	1.00	0.53	1.02	0.49	1.13	0.94	0.41	0.44	0.48	0.14	0.80	1.25	0.43
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.21	0.21	0.30	0.32	0.09	3.40	0.19	1.22	0.21	0.85	0.27	1.20	1.70	3.39	0.37	0.20
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_uncultured	0.00	0.95	0.38	0.82	0.23	0.14	0.52	0.77	0.14	0.39	1.40	0.43	0.39	0.00	0.24	0.00
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_	0.62	0.93	0.34	0.37	0.31	0.61	0.46	0.41	0.27	0.44	1.12	0.96	0.00	0.40	1.14	0.99
p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_	0.85	0.36	1.92	1.70	0.34	0.88	0.67	1.43	0.82	0.83	0.55	0.72	1.05	0.60	0.84	1.43
p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Nitrosomonadaceae;g_Ellin6067	0.46	0.66	0.81	0.94	0.16	0.67	0.58	0.87	0.27	0.86	1.34	0.89	0.36	0.24	1.32	1.91
p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Nitrosomonadaceae;g_MND1	0.29	0.48	0.30	0.47	0.42	0.89	0.75	0.72	0.54	0.72	0.53	0.97	0.47	0.00	0.85	1.10
p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Massilia	0.58	0.12	0.04	0.19	0.13	0.35	0.10	0.00	0.38	0.34	0.34	0.56	1.37	0.99	0.06	0.12
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	0.17	0.14	0.10	0.21	0.02	0.72	0.06	0.00	0.07	0.12	0.21	1.69	0.21	7.76	0.00	0.00
p_Proteobacteria;c_Gammaproteobacteria;o_Gammaproteobacteria_Incertae_Sedis;f_Unknown_Family;g_Acidibacter	0.52	0.77	0.43	0.70	0.09	0.36	0.45	1.15	0.18	0.76	0.37	0.44	0.39	0.19	0.58	0.61

Note: Only taxa, the share of which was $\geq 1\%$ are given in this table.