

# Bacterial community structure in rhizosphere of barley at maturity stage

Siyu Zhang , Yue An, Yu Zhou, Xiaofang Wang, Yiqing Tang, Daorong Zhang, Genlou Sun, Qifei Wang and Xifeng Ren

Table S1. Valid sequences and lengths of the 35 samples.

Sample	Seq_num	Base_num	Mean_length	Min_length	Max_length
R1	41784	17421949	416.952637	232	482
R2	30681	12789607	416.857567	270	444
R3	39728	16546903	416.504808	232	461
R4	43369	18088579	417.085453	245	481
R5	36850	15372874	417.174328	274	499
R6	49107	20477649	417.000611	230	481
R7	44724	18629932	416.553349	230	496
R8	41465	17279872	416.73392	209	458
R9	40975	17120846	417.836388	203	530
R10	36965	15423983	417.25911	246	469
R11	40584	16916601	416.829317	202	470
R12	40637	16947760	417.05244	229	503
R13	46503	19396995	417.112767	230	482
R14	37669	15774141	418.756564	232	478
R15	39737	16569062	416.968115	202	490
R16	39025	16248234	416.354491	220	458
R17	38815	16155273	416.212109	300	472
R18	43757	18223366	416.467445	210	500
R19	40776	16959354	415.915097	223	493
R20	39809	16629425	417.730287	279	507
R21	38001	15874184	417.730691	230	458
R22	41993	17504545	416.844355	230	482
R23	43342	18080208	417.152139	248	458
R24	40114	16697082	416.240764	223	484
R25	38029	15882362	417.638171	214	463
R26	38103	15900153	417.293993	203	474
R27	41431	17261786	416.639376	203	507
R28	36109	15053155	416.880972	211	452
R29	41564	17307242	416.399817	222	503
R30	42264	17646523	417.53083	202	478
R31	36107	15054465	416.940344	203	504
R32	37041	15451763	417.152966	250	471
R33	41589	17307788	416.162639	245	497
R34	36589	15275629	417.492388	260	461
R35	45768	19056186	416.36484	230	450
Total	1411004	588325476	--	--	--
Average	40314.4	16809277	419.966	202	530

Table S2 Overview of percentage data of dominant bacteria at order level.

Class name	Range	Minimum	Maximum	Median	Average	Standard deviation	Coefficient of variation
Vicinamibacterales	0.1510	0.0146	0.1656	0.0671	0.0680	0.0300	0.4414
Rhizobiales	0.0707	0.0461	0.1168	0.0646	0.0682	0.0156	0.2289
Burkholderiales	0.0664	0.0479	0.1143	0.0607	0.0644	0.0135	0.2091
Chloroflexales	0.0557	0.0215	0.0772	0.0566	0.0539	0.0127	0.2352
Gaiellales	0.0662	0.0234	0.0896	0.0510	0.0524	0.0146	0.2792
Gemmatimonadales	0.0498	0.0297	0.0795	0.0660	0.0504	0.0099	0.1967
Micrococcales	0.0737	0.0161	0.0898	0.0462	0.0473	0.0180	0.3805
Solirubrobacterales	0.0343	0.0207	0.0550	0.0321	0.0345	0.0091	0.2632
Sphingomonadales	0.0354	0.0128	0.0482	0.0328	0.0333	0.0079	0.2368
Bacillales	0.0831	0.0163	0.0994	0.0295	0.0327	0.0167	0.5098

Table S3 Overview of percentage data of dominant bacteria at family level.

Class name	Range	Minimum	Maximum	Median	Average	Standard deviation	Coefficient of variation
Roseiflexaceae	0.0534	0.0207	0.0741	0.0539	0.0519	0.0122	0.2344
Gemmatimonadaceae	0.0498	0.0297	0.0795	0.0497	0.0504	0.0099	0.1967
f_norank_o_Vicinamibacterales	0.0831	0.0084	0.0915	0.0357	0.0367	0.0161	0.4398
Xanthobacteraceae	0.0293	0.0247	0.0540	0.0349	0.0364	0.0077	0.2119
f_norank_o_Gaiellales	0.0457	0.0147	0.0604	0.0342	0.0350	0.0100	0.2844
Sphingomonadaceae	0.0354	0.0128	0.0482	0.0328	0.0333	0.0079	0.2368
Bacillaceae	0.0833	0.0158	0.0991	0.0290	0.0323	0.0167	0.5171
Vicinamibacteraceae	0.0680	0.0061	0.0741	0.0285	0.0313	0.0146	0.4655
Chitinophagaceae	0.0478	0.0095	0.0573	0.0236	0.0244	0.0085	0.3486
Pyrinomonadaceae	0.0393	0.0059	0.0452	0.0234	0.0240	0.0101	0.4192

Table S4 Six alpha diversity indexes of the three clusters.

group	sobs	shannon	simpson	ace	chao	coverage
II	2227.714	6.453	0.00391	2978.783	3013.879	0.974
III	2308.643	6.504	0.00378	3091.230	3096.675	0.973
IV	2297.5	6.494	0.00418	3030.112	3033.650	0.973

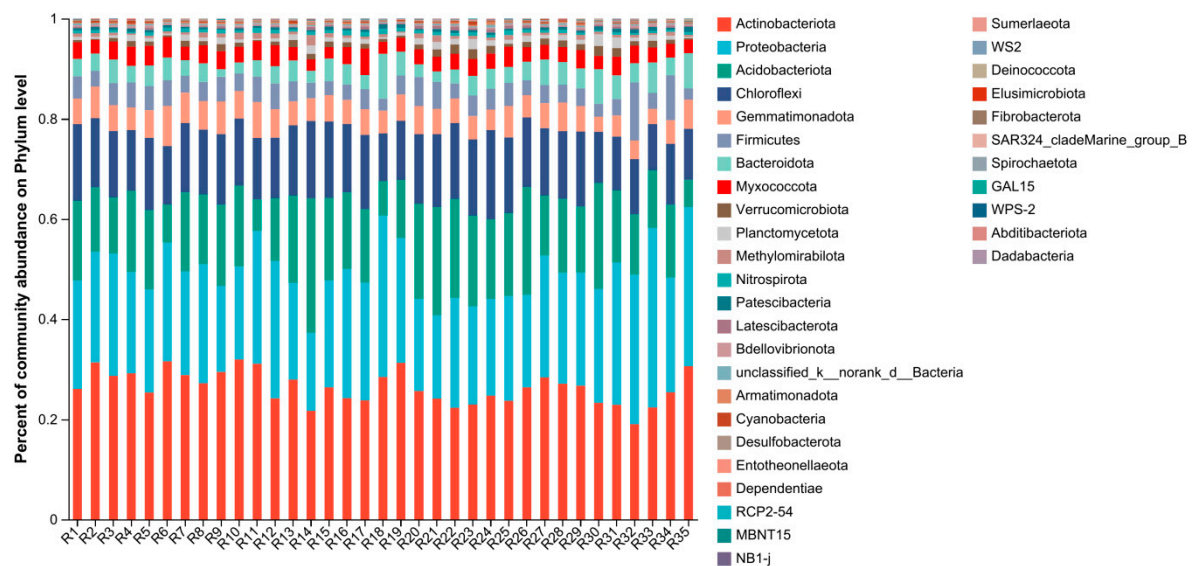


Figure S1 Community abundance at phylum level.

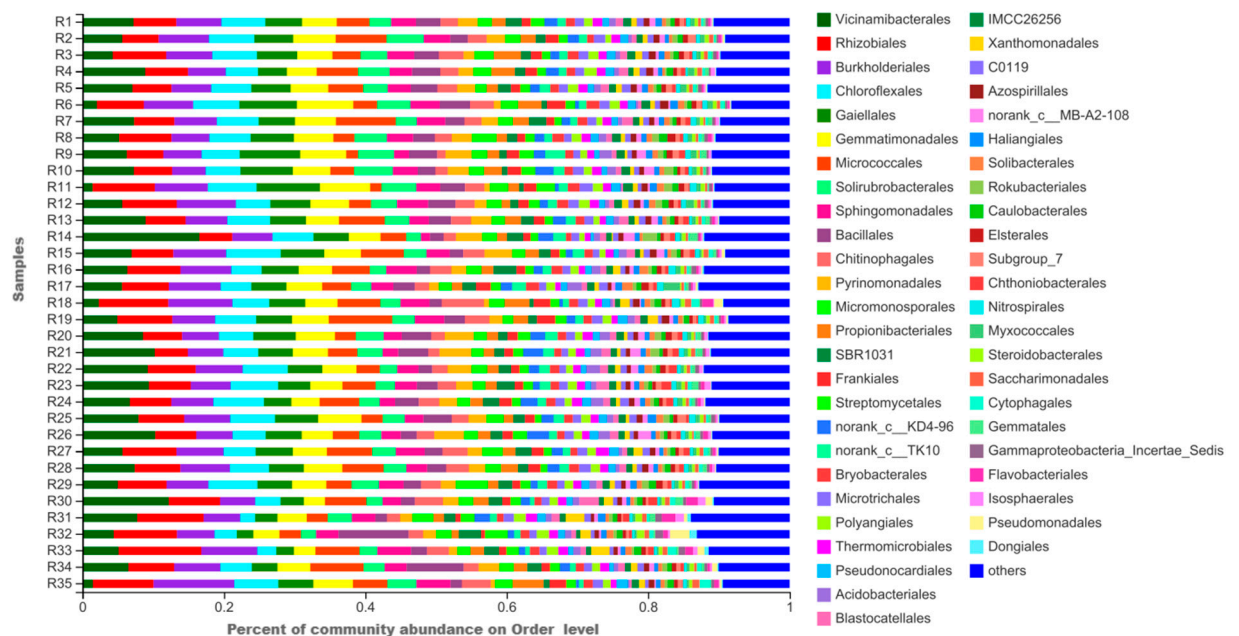


Figure S2 Abundance at the Order level of barley rhizosphere bacteria

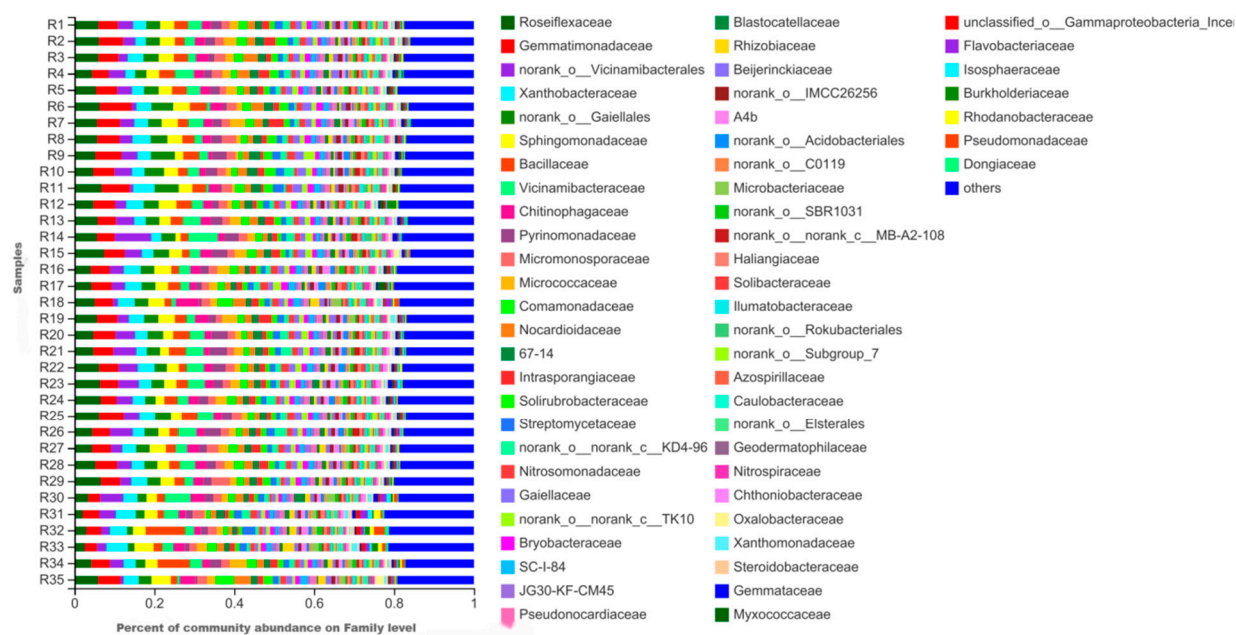


Figure S3 Abundance at the family level of barley rhizosphere bacteria