

Table. S1 Sample ID and sampling location

Sample.no	Location	Region	Geographic coordinate	
			Latitude	Longitude
1	Dondoli	Upper West	010°03'00"N	002°29'00"W
2	Bilibao		010°17'06"N	001°57'36"W
3	Yepalsi	Upper East	09°35'54.6"N	000°43'02.9"W
4	Kike		010°47'00"N	000°51'00"W
5	Pwalugu		10°35'50.1"N	000°50'59.0"W
6	Gbrumani-Tibogu	Northern	09°41'40.4"N	001°12'77.3"W
7	Pagazaa		09°22'23.5"N	000°42'49.5"W
8	Fuu		09°15'15.0"N	000°37'45.0"W
9	Ngbanung		09°28'31.0"N	001°01'90.0"W
10	Aframso	Ashanti	007°03'75"N	001°03'67"W
11	Hiawoanwu		07°27'41.3"N	001°19'05.5"W
12	Darko farms		07°24'50.6"N	001°23'44.2"W
13	Ejura farms		07°24'29.6"N	001°23'48.4"W
14	Fante Newtown	Brong-Ahafo	07°36'50.6"N	001°60'41.0"W
15	Abour		07°36'18.3"N	001°07'53.4"W
16	Mempeasem		07°15'29.6"N	000°38'16.1"E
17	Jato-Zongo		07°40'02.5"N	001°03'52.4"W
18	Gbefi	Volta	07°00'13.3"N	000°20'08.6"E
19	Nywie-antokor		07°26'07.0"N	000°25'20.5"E
20	Peacebee		07°30'41.0"N	000°28'18.2"E

Rice roots were sampled at total 20 locatios in 6 regions in Ghana

Table. S2 α -diversity index.

Site	ReadBac	ObsBac	ShnBac	SimBac	ChaoBac	ObsFun	ReadFun	ShnFun	SimFun	ChaoFun
Don	88904	159	4.31084	0.97185	159	92	22790	3.69434	0.95449	92.083
Bib	75307	135	3.88184	0.93604	135	92	86903	3.61267	0.95307	93.333
Yep	94597	116	3.47168	0.92245	116	21	215941	0.85349	0.31736	21.500
Kike	55938	143	3.77085	0.92717	144	107	42642	3.8488	0.95345	107.900
Pw	79842	144	3.8602	0.93794	144	91	81151	3.72862	0.95986	92.125
GT	33821	151	4.04053	0.94314	151	31	151851	0.92653	0.29535	31.000
PAGA	57970	136	3.9913	0.95732	136	57	183604	2.77213	0.85287	57.500
FUU	22087	141	4.16769	0.97016	141	95	95196	3.45388	0.93825	95.562
Ngb2	20577	114	3.82387	0.95826	114	74	159085	3.17129	0.90781	74.125
AframsoU	30001	176	4.30082	0.97029	176	70	12241	3.2318	0.91898	70.071
Hia	57109	113	3.73533	0.94719	113	63	21146	2.60205	0.7728	63.000
Dar	26562	177	4.50895	0.97928	177	52	8843	3.08746	0.92883	53.499
Ejura	40845	144	4.15568	0.96642	144	14	51784	0.46002	0.18009	14.500
FanteN	28149	149	4.2279	0.97154	149	11	51786	0.52118	0.25297	11.500
Abour	84526	125	3.79313	0.94359	125	61	22180	3.00044	0.91637	61.083
Mem	29498	174	4.30801	0.96402	174	16	8081	0.42438	0.13885	16.000
Jato	37200	127	3.65003	0.9133	127	37	39294	1.45841	0.5245	38.125
Gbe	25166	181	4.55623	0.98194	181	49	138472	2.68582	0.87898	49.125
Ny1	8477	155	3.97199	0.95112	155	71	20762	3.10601	0.89763	75.165
Pea2	41294	148	4.25662	0.97358	148	35	170372	1.53979	0.54332	35.000

Bac = bacteria. Fun = fungi. Read = read counts. Obs =observed OTUs. Shn = Shannon index. Sim = Simpson index. Chao = Chao richness.

Table. S3 Correlation between bacterial community and environmental factors.

	NMDS1	NMDS2	r2	Pr(>r)
pH	0.09015	0.99593	0.1207	0.340166
Moisture	0.97732	0.21177	0.3112	0.040496*
NO3	0.05833	0.9983	0.1906	0.164984
P	-0.41793	-0.90848	0.0349	0.754425
TC	0.40601	0.91387	0.2194	0.121688
TN	0.23113	0.97292	0.2428	0.091491.
CN	0.59178	0.8061	0.1689	0.20348
CEC	0.49169	0.87077	0.1728	0.20088
ReadFun	0.72452	-0.68926	0.4304	0.007799**
ObsFun	0.15572	-0.9878	0.2625	0.073993.
SimFun	-0.74071	-0.67183	0.315	0.040396*
ShnFun	-0.80609	-0.59179	0.3374	0.029197*
ChaoFun	0.32171	-0.94684	0.1276	0.310769

Abiotic and biotic environmental factors involved in the assembly of bacterial community by vector analysis. Fun = fungi. Read = read counts. Obs =observed OTUs. Shn = Shannon-Weaver. Sim = Simpson. Chao = Chao richness. Significance codes; 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1

Table. S4 Correlation between fungal community and environmental factors

	NMDS1	NMDS2	r2	Pr(>r)
pH	0.45535	0.89031	0.4114	0.010399*
Moisture	-0.40573	0.91399	0.1053	0.3816618
NO3	0.75628	0.65425	0.5797	0.0005999***
P	-0.95315	-0.30249	0.0547	0.6307369
TC	0.38695	0.9221	0.5601	0.0007999***
TN	0.62472	0.78085	0.2796	0.0628937.
CN	0.99999	0.0044	0.0545	0.6249375
CEC	0.38942	0.92106	0.3546	0.0225977*
ReadBac	-0.08821	-0.9961	0.3546	0.0250975*
ObsBac	0.39321	0.91945	0.1459	0.2647735
ShnBac	0.45567	0.89015	0.1737	0.1981802
SimBac	0.42934	0.90314	0.1487	0.2521748
ChaoBac	0.38435	0.92319	0.1442	0.2685731

Abiotic and biotic environmental factors involved in the assembly of fungal community by vector analysis. Bac = bacteria. Read = read counts. Obs =observed OTUs. Shn = Shannon-Weaver. Sim = Simpson. Chao = Chao richness. Significance codes; 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1.

Table. S5 Correlation between abiotic and biotic factors.

R	pH	Moisture	NO3	P	TC	TN	CN	CEC	ReadBac	ObsBac	ShnBac	SimBac	ChaoBac	ObsFun	ReadFun	ShnFun	SimFun	ChaoFun
pH		-0.040	0.0662	-0.187	0.647	0.491	0.456	0.559	-0.200	0.06	0.393	0.350	0.073	-0.118	-0.129	-0.188	-0.124	-0.017
Moisture			0.224	-0.216	0.447	0.288	0.166	0.387	-0.347	-0.252	0.053	-0.042	-0.314	-0.121	0.004	-0.239	-0.217	-0.104
NO3				-0.436	0.790	0.649	0.393	0.682	-0.350	-0.033	0.312	0.198	0.027	-0.408	-0.447	-0.476	-0.404	-0.094
P					-0.366	-0.491	-0.596	-0.220	-0.099	-0.204	-0.096	-0.001	-0.208	0.231	0.430	0.017	0.064	0.177
TC						0.754	0.446	0.933	-0.490	-0.280	0.338	0.347	-0.250	-0.220	-0.251	-0.222	-0.128	-0.114
TN							0.638	0.632	-0.224	-0.018	0.258	0.143	0.020	-0.315	-0.278	-0.214	-0.166	-0.229
CN								0.397	0.169	0.206	0.206	0.206	0.169	-0.146	-0.076	-0.163	-0.179	-0.170
CEC									-0.534	-0.357	0.284	0.351	-0.310	-0.205	-0.165	-0.228	-0.137	-0.074
ReadBac										0.817	-0.430	-0.523	0.805	0.135	0.134	0.172	0.122	-0.077
ObsBac											0.041	-0.209	0.932	-0.165	0.049	-0.225	-0.251	-0.208
ShnBac												0.816	-0.150	-0.422	-0.224	-0.365	-0.361	-0.241
SimBac													-0.269	-0.144	-0.129	-0.157	-0.126	0.042
ChaoBac														-0.167	-0.028	-0.106	-0.102	-0.184
ObsFun															0.769	0.145	0.165	0.821
ReadFun																-0.210	-0.163	0.642
ShnFun																	0.979	-0.236
SimFun																		-0.201
ChaoFun																		

Pearson's correlation co-efficient (*R* value) was obtained between abiotic and environmental factors

Table. S6 Indicator bacterial OTUs in six regions and their characteristics on host plant.

OTU.ID	Probability		Indicator value index	P	UW	UE	North	Ash	BA	Vol	Characteristic	Reference	Host plant
	A	B											
Sporomusa_sp. OTU_B4896	0.9968	1.0000	0.998	0.002	**	**	**				Free living or unknown	[54]	
Burkholderia_sp. OTU_B40206	0.9739	1.0000	0.987	0.025	*	*	*	*			Both Endophyte and Pathogen	[96]	Rice and other plants
Pleomorphomonas_sp. OTU_B24241	0.9870	0.9167	0.951	0.027	*	*	*			*	Endophyte	[58]	rice
Amycolatopsis_sp. OTU_B44674	0.9946	1.0000	0.997	0.046	*	*	*	*	*		Endophyte	[97]	oil-seed plant
Dokdonella_sp. OTU_B57426	0.9913	1.0000	0.996	0.032	*	*	*	*	*		Free living or unknown	[98]	
Polyangiaceae. OTU_B60627	0.9968	1.0000	0.998	0.044	*	*		*	*	*	Free living or unknown	[99]	
Comamonadaceae. OTU_B48937	0.9934	1.0000	0.997	0.042	*	*		*	*	*	Free living or unknown	[100]	

Fungal Indicator OTUs in unique in Upper region (UW, UE, North) were revealed by indicator species analysis after removing low frequent OTUs (< 500 reads, 0.02 % total sequence) from both fungal OTU tables. Significance codes; 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05.

Table. S7 Indicator Fungal OTUs in six regions and their characteristics on host plant

OTU.ID	Probability		Indicator value index	<i>P</i>	UW	UW	North	Ash	BA	Vol	Characteristic	Reference	Host plant
	A	B											
Chaetomium. OTU_F4724	0.9272	1.0000	0.963	0.041	*						Endophyte	[72]	rice
Pezizacea. OTU_F11633	0.9993	1.0000	1.000	0.004		**					Endophyte	[75]	Quercus, Pinus, Populus
Thielavia_terrestris. OTU_F8307	0.9817	1.0000	0.991	0.012			**				Free living or unknow	[70]	
Bambusicolaceae. OTU_F3283	0.9476	1.0000	0.973	0.037	*		*				Endophyte	[67]	bamboo
Curvularia_prasadii. OTU_F6231	0.997	1.0000	0.998	0.002	**	**	**				Pathogen	[62]	Achyranthes aspera
Pleosporales. OTU_F4099	0.9966	1.0000	0.998	0.005	**	**	**				Both Endphyte and Pathogen	[61]	rice and other plants
Sebacinales. OTU_F1840	0.9648	1.0000	0.982	0.035	*	*	*				Endophyte	[63]	barley
Myrothecium_verrucaria. OTU_F7577	0.9997	0.8889	0.943	0.042	*	*	*				Pathogen	[66]	rice and other plants
Sordariomycetes. OTU_F2298	1.0000	0.7778	0.882	0.036	*	*	*				Both Endophyte and Pathogen	[71]	rice and other plants
Dothideomycetes. OTU_F7194	1.0000	0.6667	0.816	0.036	*	*	*				Both Endphyte and Pathogen	[73, 74]	lycopodium annotinum, wheat
Chaetomiaceae. OTU_F2865	0.9737	1.0000	0.987	0.019	*	*	*	*			Endophyte	[101, 102]	rice, frankincense tree
Stachybotryaceae. OTU_F3669	0.9957	1.0000	0.998	0.029	*	*	*			*	Endophyte	[64, 65]	black cottonwood, wild rice
Pleosporales. OTU_F3272	0.9986	1.0000	0.999	0.024	*	*	*	*	*		Both Endphyte and Pathogen	[61]	rice and other plants
Curvularia_lunata. OTU_F8146	0.9981	1.0000	0.999	0.028	*	*	*	*	*		Pathogen	[103]	rice, maize and other plants
Pseudophialophora_schizachyrii. OTU_F10789	0.9985	1.0000	0.999	0.049	*	*	*	*		*	Pathogen	[104]	Rice

Fungal Indicator OTUs in unique in Upper region (UW, UE, North) were revealed by indicator species analysis after removing low frequent OTUs (< 500 reads, 0.02 % total sequence) from both fungal OTU tables. Significance codes; 0 '****' 0.001 '**' 0.01 '*' 0.05.