

Table S1. Bacterial community composition at genus level in soil

Genus	Soil 1	Soil 2	Soil 3	Soil 4	Soil 5	Soil 6
<i>Bacillus</i>	0.134176	0.116903	0.086166	0.156176	0.108563	0.097974
SC-I-84(f)	0.034790	0.04819	0.041810	0.044534	0.050242	0.043056
<i>Nocardioides</i>	0.022199	0.020587	0.020276	0.021427	0.069078	0.072689
<i>MND1</i>	0.032120	0.039929	0.039663	0.036208	0.027348	0.035585
67-14(f)	0.030474	0.029439	0.031288	0.032923	0.032155	0.036429
<i>Gaiella</i>	0.028517	0.026357	0.032546	0.027691	0.03247	0.032756
TK10(c)	0.038971	0.032061	0.032699	0.021618	0.007999	0.009835
<i>Ellin6067</i>	0.020598	0.022882	0.028896	0.022993	0.016708	0.019629
<i>Lapillicoccus</i>	0.006139	0.007212	0.005399	0.007142	0.063089	0.041072
<i>Candidatus_Solibacter</i>	0.015215	0.016981	0.021043	0.014743	0.015999	0.014141
MB-A2-108(c)	0.016550	0.017768	0.015951	0.016691	0.015486	0.017265
<i>Pseudolabrys</i>	0.014726	0.018227	0.018926	0.018753	0.013556	0.013508
<i>Fictibacillus</i>	0.016816	0.011474	0.008528	0.013368	0.021279	0.018236
Gaiellales(o)	0.012857	0.012261	0.014632	0.012719	0.016275	0.016294
<i>Sphingomonas</i>	0.013702	0.013310	0.014785	0.012910	0.011309	0.017096
Pedosphaeraceae(f)	0.012724	0.013572	0.012914	0.012680	0.012334	0.012073
Methyloligellaceae(f)	0.009609	0.009245	0.010767	0.010618	0.013556	0.012157
Gemmatumonadaceae(f)	0.012768	0.010490	0.011564	0.009510	0.009182	0.012748
TRA3-20(f)	0.010188	0.011998	0.013405	0.010121	0.007527	0.010595
Xanthobacteraceae(f)	0.008097	0.010425	0.010982	0.010198	0.012058	0.011650
<i>Ramlibacter</i>	0.011656	0.011474	0.010920	0.011611	0.006778	0.011524
<i>Pseudomonas</i>	0.015393	0.012130	0.014018	0.010847	0.001458	0.002068
<i>Anaeromyxobacter</i>	0.008586	0.009835	0.012423	0.010121	0.005596	0.007472
<i>Nitrospira</i>	0.009698	0.009900	0.010675	0.008823	0.006857	0.007345
mle1-7	0.007830	0.008130	0.010123	0.008326	0.007054	0.007260
Geobacteraceae(f)	0.008408	0.009441	0.011503	0.008632	0.003074	0.006796
S085(o)	0.009787	0.011736	0.011472	0.006187	0.002837	0.004812
<i>Terrabacter</i>	0.001913	0.002754	0.002577	0.002521	0.017417	0.013592
<i>Pseudarthrobacter</i>	0.000712	0.000262	0.000552	0.000573	0.024983	0.006965
<i>Arthrobacter</i>	0.000489	0.000852	0.000828	0.000649	0.016314	0.007260
others	0.434291	0.434173	0.442669	0.418685	0.351421	0.380118

Table S2. Fungal community composition at genus level in soil

OTU ID	Soil 1	Soil 2	Soil 3	Soil 4	Soil 5	Soil 6
<i>Coprinellus</i>	0.230134	0.114441	0.346799	0.134601	0.252542	0.456027
Sordariales(o)	0.092263	0.125837	0.059661	0.049287	0.195820	0.155501
<i>Emericellopsis</i>	0.026573	0.091599	0.033906	0.296464	0.035285	0.029920
<i>Preussia</i>	0.220604	0.024477	0.097961	0.059073	0.037355	0.056850
Sordariomycetes(c)	0.053733	0.048010	0.028770	0.094869	0.028744	0.033676
<i>Penicillium</i>	0.029818	0.126629	0.036435	0.030993	0.028923	0.013542
Fungi(k)	0.037968	0.077316	0.045455	0.025193	0.035643	0.018090
<i>Apiosordaria</i>	0.057770	0.005979	0.026573	0.010297	0.033625	0.100746
Branch03(o)	0.021079	0.141142	0.013593	0.019393	0.029792	0.009607
<i>Aspergillus</i>	0.040600	0.029766	0.031836	0.052072	0.032245	0.023277
<i>Talaromyces</i>	0.028821	0.017093	0.027901	0.032475	0.037176	0.010808
<i>Chaetomium</i>	0.035107	0.015739	0.018141	0.032781	0.037406	0.010987
<i>Zopfiella</i>	0.008406	0.014947	0.018805	0.008994	0.053605	0.010859
<i>Thielavia</i>	0.005468	0.007716	0.028974	0.015688	0.006924	0.007614
<i>Acrophialophora</i>	0.008406	0.009709	0.015100	0.012060	0.008483	0.002708
<i>Fusarium</i>	0.004855	0.004650	0.018652	0.010706	0.007512	0.004037
<i>Neocosmospora</i>	0.010092	0.003475	0.010271	0.005570	0.009454	0.004625
Alphamycetaceae(f)	0.004574	0.004395	0.029255	0.001226	0.001840	0.000945
Rozellomycota(p)	0.004165	0.013440	0.008023	0.006285	0.006950	0.003347
<i>Curvularia</i>	0.003756	0.004727	0.006260	0.006541	0.012418	0.002759
<i>Scedosporium</i>	0.004344	0.013210	0.001814	0.002095	0.002759	0.001175
<i>Acremonium</i>	0.000894	0.001022	0.000460	0.016403	0.002530	0.000818
<i>Cercophora</i>	0.000792	0.000869	0.000537	0.001686	0.013542	2.56E-05
others	0.069702	0.071593	0.094818	0.075247	0.076039	0.042056

Table S3. Fungi showed pathogenicity in barnyardgrass at genus level

Growth stages	genus
BBCH 17	<i>Curvularia, Acrophialophora, Gibellulopsis, Clonostachys, Ramichloridium, Ramichloridium, Podosphaera, Hawksworthiomyces, Hortaea, Gibellulopsis, Lectera, Curvularia</i>
BBCH 24	<i>Curvularia, Acrophialophora, Gibellulopsis, Clonostachys, Ramichloridium, Ramichloridium, Podosphaera, Hawksworthiomyces, Hortaea, Gibellulopsis, Lectera, Curvularia</i>
BBCH 37	<i>Curvularia, Gibellulopsis, Gibberella, Gibberella, Ramularia, Strelitziana, Exserohilum, Peroneutypa, Phaeophleospora, Ramularia</i>
BBCH 45	<i>Peroneutypa, Volutella, Veronaea, Exserohilum, Gibberella, Stagonospora, Moesziomyces, Cylindrocarpon</i>
BBCH 57	<i>Curvularia, Acrophialophora, Gibellulopsis, Gibberella, Ramularia, Clonostachys, Strelitziana, Pseudocercospora, Ramichloridium, Exserohilum, Stagonosporopsis, Erysiphe, Pestalotiopsis, Stagonospora, Passalora, Phlyctochytrium, Dirkmeia</i>

Table S4. The vital bacteria in rice groups

Node_Name	Degree Centrality	Closeness Centrality	Betweenness Centrality
<i>Schlegelella</i>	0.108696	0.386555	0.001612
<i>Phenylobacterium</i>	0.173913	0.429907	0.004738
<i>Bradyrhizobium</i>	0.173913	0.429907	0.004738
<i>Haliangium</i>	0.173913	0.429907	0.005048
Bacteroidales(o)	0.195652	0.438095	0.006291
<i>Ideonella</i>	0.195652	0.438095	0.006291
Rhizobiaceae(f)	0.043478	0.330935	0.008191
<i>Rhodococcus</i>	0.217391	0.446602	0.008332
<i>Ralstonia</i>	0.217391	0.446602	0.008332
Comamonadaceae(f)	0.217391	0.446602	0.008332
<i>Sideroxydans</i>	0.217391	0.446602	0.008332
<i>Stenotrophomonas</i>	0.217391	0.446602	0.008332
Xanthomonadaceae(f)	0.217391	0.446602	0.008332
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	0.043478	0.321678	0.010030
Pleomorphomonadaceae(f)	0.217391	0.455446	0.016766
Rhodocyclaceae(f)	0.217391	0.455446	0.016766
Rhodocyclaceae(f)	0.217391	0.455446	0.016766
<i>Delftia</i>	0.239130	0.464646	0.020241
<i>Pseudomonas</i>	0.239130	0.464646	0.020241
<i>Gallionella</i>	0.195652	0.429907	0.028086
Gallionellaceae(f)	0.239130	0.474227	0.047516
<i>Chthonobacter</i>	0.065217	0.422018	0.048066
possible_genus_04	0.195652	0.505495	0.218963

Table S5. The vital fungi in rice groups

Node Name	Degree Centrality	Closeness Centrality	Betweenness Centrality
Sordariales(o)	0.108696	0.389831	0.071670
<i>Cladosporium</i>	0.152174	0.396552	0.042995
<i>Acrophialophora</i>	0.217391	0.418182	0.267963
<i>Vishniacozyma</i>	0.282609	0.460000	0.028120
Pleosporaceae(f)	0.347826	0.425926	0.017526
<i>Tetracladium</i>	0.347826	0.425926	0.022430
<i>Alternaria</i>	0.413043	0.522727	0.047928
<i>Solicoccozyma</i>	0.413043	0.522727	0.047928
<i>Tausonia</i>	0.413043	0.522727	0.047928
<i>Fusarium</i>	0.434783	0.534884	0.056858
Glomerellales(o)	0.434783	0.534884	0.147014
<i>Filobasidium</i>	0.456522	0.547619	0.077631
<i>Thermomyces</i>	0.478261	0.560976	0.121110

Table S6. The vital bacteria in barnyardgrass groups

Node Name	Degree Centrality	Closeness Centrality	Betweenness Centrality
<i>Geobacter</i>	0.032258	0.302439	0.000121
Rhizobiales_Incertae_Sedis(f)	0.032258	0.291080	0.000193
<i>Trepomema</i>	0.032258	0.314721	0.000737
<i>Dechloromonas</i>	0.080645	0.311558	0.001082
Micromonosporaceae(f)	0.064516	0.321244	0.001455
Hungateiclostridiaceae(f)	0.080645	0.324607	0.001724
<i>Pseudactinotalea</i>	0.096774	0.328042	0.003042
<i>Ralstonia</i>	0.064516	0.314721	0.003141
<i>Clostridium_sensu_stricto_1</i>	0.129032	0.335135	0.006212
Fibrobacteraceae(f)	0.032258	0.358382	0.006872
Paludibacteraceae(f)	0.048387	0.400000	0.013035
<i>Massilia</i>	0.145161	0.380368	0.018088
Methylophilaceae(f)	0.177419	0.366864	0.020010
<i>Streptomyces</i>	0.048387	0.405229	0.023338
<i>Gallionella</i>	0.096774	0.416107	0.032187
<i>Sideroxydans</i>	0.096774	0.416107	0.032187
Gallionellaceae(f)	0.096774	0.416107	0.032187
Rhodocyclaceae(f)	0.048387	0.394904	0.044992
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	0.225806	0.405229	0.047708
<i>Rhodococcus</i>	0.306452	0.433566	0.089451
<i>Bacillus</i>	0.306452	0.433566	0.089451
<i>Methylcystis</i>	0.177419	0.459259	0.116417
<i>Pseudomonas</i>	0.161290	0.452555	0.150900

Table S7. The vital fungi in barnyardgrass groups

Node Name	Degree Centrality	Closeness Centrality	Betweenness Centrality
<i>Scolecobasidium</i>	0.048387	0.378049	0.001084
<i>Exserohilum</i>	0.032258	0.316327	0.002862
<i>Phaeosphaeriopsis</i>	0.080645	0.387500	0.004240
Helotiales(o)	0.080645	0.387500	0.005239
<i>Ascobolus</i>	0.064516	0.397436	0.006515
Tremellaceae(f)	0.080645	0.387500	0.006737
<i>Thielavia</i>	0.064516	0.397436	0.014272
<i>Albifimbria</i>	0.112903	0.413333	0.016282
<i>Aspergillus</i>	0.145161	0.407895	0.019798
Fungi(k)	0.145161	0.407895	0.019798
Didymellaceae(f)	0.096774	0.392405	0.026070
Ascomycota(p)	0.161290	0.413333	0.029296
Glomerellales(o)	0.161290	0.430556	0.033501
Chytridiomycota(p)	0.161290	0.430556	0.033501
<i>Penicillium</i>	0.161290	0.413333	0.034316
<i>Phoma</i>	0.161290	0.413333	0.037049
<i>Epicoccum</i>	0.161290	0.430556	0.038152
<i>Acremonium</i>	0.177419	0.418919	0.043604
<i>Pseudopithomyces</i>	0.129032	0.402597	0.063354
<i>Apodus</i>	0.193548	0.424658	0.068320
<i>Acrophialophora</i>	0.403226	0.543860	0.509230

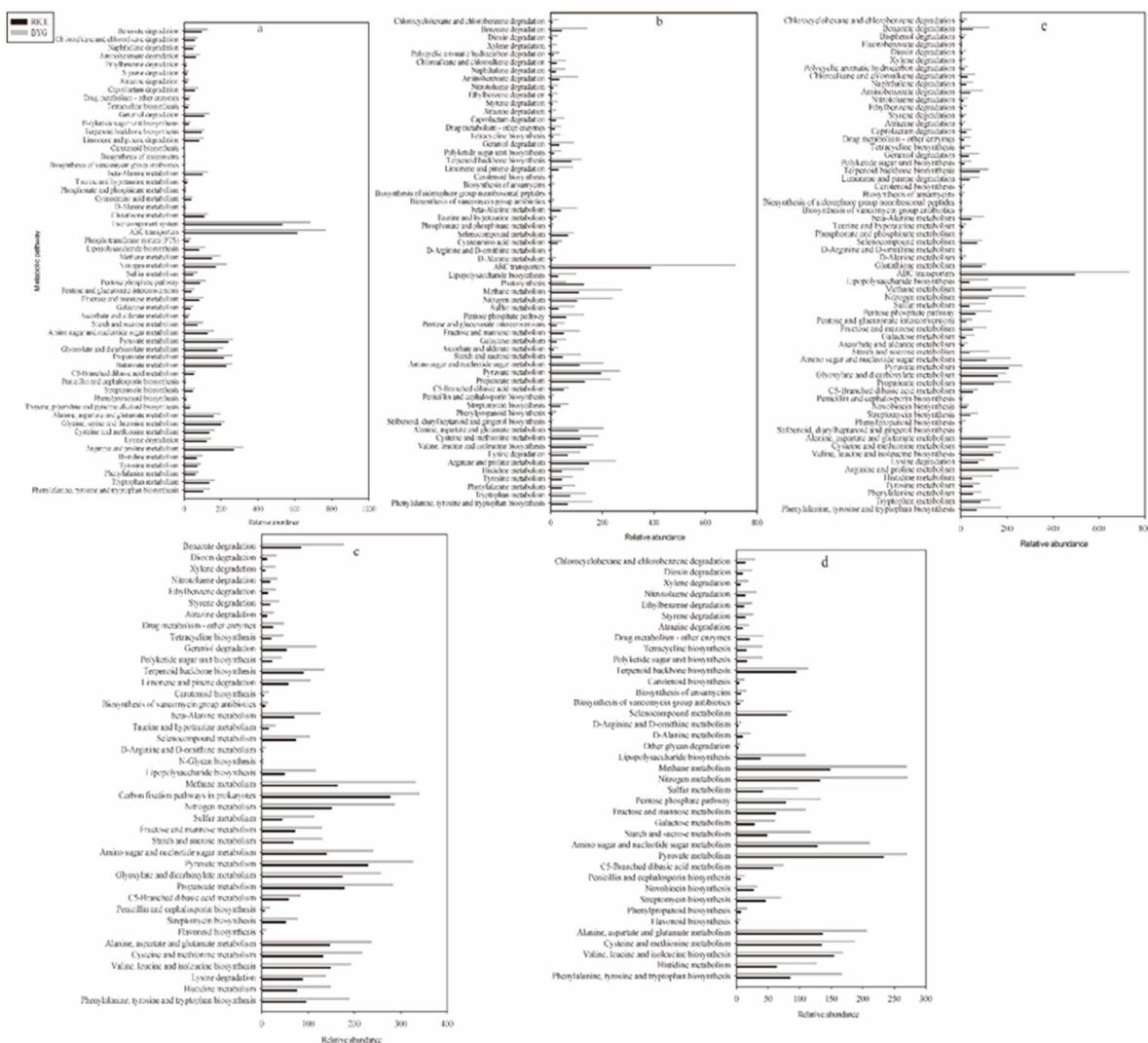


Figure S1. The significant microbial functional features in barnyardgrass at different growth stages.