Table S2 List of primers for PCR and sequencing. In total 88 different barcodes (BC1-BC88) were used for PCR2 as described in Durán *et al.* (2018). An example was shown for reverse sequence with barcode number 1.

Region	Amplification step	Primer	Sense	Sequence 5'-3'	Size
Bacteria 16S V5/V7	PCR1	799F	forward	AACMGGATTAGATACCCKG	20
		1192R	reverse	ACGTCATCCCCACCTTCC	18
	PCR2	B5-F	forward	AATGATACGGCGACCACCGAGATCTACACGACTGCGACTGGCGAACMGGATTAGATACCCKG	62
		B5-1	reverse-Barcode1	CAAGCAGAAGACGGCATACGAGATTCCCTTGTCTCCCAGCCATTTAGTGTCACGTCATCCCCACCTTCC	69
	Sequencing	B5-R1	R1	ACGACTGCGACTGGCGAACMGGATTAGATACCC	33
		B5-R2	R2	CAGCCATTTAGTGTCACGTCATCCCCACCTTCC	33
		B5-Index	index	GGAAGGTGGGGATGACGTGACACTAAATGGCTG	33
Fungi ITS2	PCR1	fITS7	forward	GTGARTCATCGAATCTTTG	19
		ITS4	reverse	TCCTCCGCTTATTGATATGC	20
	PCR2	OF2-F	forward	AATGATACGGCGACCACCGAGATCTACACGTCACGCGTACTGCGTGARTCATCGAATCTTTG	62
		OF2-1	reverse-Barcode1	CAAGCAGAAGACGGCATACGAGATGTTATCGCATGGGCTACCGTGGTGCTCCTCCGCTTATTGATATGC	69
	Sequencing	OF2-R1	R1	GTCACGCGTACTGCGTGARTCATCGAATCTTTG	33
		OF2-R2	R2	GCTACCGTGGTGCTCCTCCGCTTATTGATATGC	33
		OF2-Index	index	GCATATCAATAAGCGGAGGAGCACCACGGTAGC	33
Oomycete ITS1	PCR1	ITS1-O	forward	CGGAAGGATCATTACCAC	18
		5.8s-O-Rev	reverse	AGCCTAGACATCCACTGCTG	20
	PCR2	Om-F	forward	AATGATACGGCGACCACCGAGATCTACACAGTTCCAGGCTCATGCGGAAGGATCATTACCAC	62
		Ot-1	reverse-Barcode1	CAAGCAGAAGACGGCATACGAGATTCGGAATTAGACGCCTGGAGTCATAGAGCCTAGACATCCACTGCTG	70
	Sequencing	Ot-R1	R1	AGTTCCAGGCTCATGCGGAAGGATCATTACCAC	33
		Ot-R2	R2	GCCTGGAGTCATAGAGCCTAGACATCCACTGCTG	34
		Ot-Index	index	CAGCAGTGGATGTCTAGGCTCTATGACTCCAGGC	34

Table S3 Explained variance of parameters affecting soil microbial diversity, based on beta-diversity. This includes all plant growth stages and managements (PERMANOVA), model ~ Management * Time * Location * Run * Plot was applied.

Factors		Bacteria						Fungi						Oomycetes				
	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)
Management	3	5.328	1.77595	7.1457	10.58	0.001	3	8	2.66668	21.7014	25.42	0.001	3	7.834	2.61133	26.7789	26.31	0.001
Stage	2	5.085	2.54246	10.2298	10.10	0.001	2	2.2912	1.1456	9.3229	7.28	0.001	2	3.1886	1.59432	16.3496	10.71	0.001
Location	2	2.037	1.01855	4.0982	4.05	0.001	2	2.2345	1.11724	9.0921	7.10	0.001	2	2.3403	1.17016	11.9999	7.86	0.001
Run	2	0.855	0.42771	1.7209	1.70	0.001	2	0.6787	0.33935	2.7616	2.16	0.001	2	0.2766	0.1383	1.4183	0.93	0.117
Plot	1	0.475	0.47465	1.9098	0.94	0.003	1	0.4167	0.41669	3.391	1.32	0.001	1	0.2861	0.28607	2.9336	0.96	0.006
Management:Stage	6	3.088	0.51466	2.0708	6.13	0.001	6	1.8627	0.31044	2.5264	5.92	0.001	6	2.257	0.37616	3.8575	7.58	0.001
Management:Location	1	0.916	0.91591	3.6852	1.82	0.001	1	0.5611	0.56111	4.5663	1.78	0.001	1	1.2717	1.27171	13.0412	4.27	0.001
Stage:Location	4	1.568	0.3921	1.5776	3.12	0.001	4	0.7622	0.19056	1.5508	2.42	0.002	4	0.7304	0.18261	1.8726	2.45	0.004
Management:Run	6	1.599	0.26643	1.072	3.18	0.12	6	0.6358	0.10596	0.8623	2.02	0.893	6	0.4267	0.07112	0.7293	1.43	0.931
Location:Run	4	1.106	0.27657	1.1128	2.20	0.101	4	0.2884	0.0721	0.5867	0.92	1	4	0.2412	0.06031	0.6185	0.81	0.974
Stage:Plot	2	0.666	0.33315	1.3405	1.32	0.012	2	0.2958	0.1479	1.2036	0.94	0.156	2	0.2551	0.12757	1.3082	0.86	0.164
Run:Plot	2	0.516	0.2578	1.0373	1.02	0.346	2	0.1275	0.06373	0.5186	0.41	1	2	0.1201	0.06004	0.6157	0.40	0.912
Management:Stage:Location	2	0.723	0.36167	1.4552	1.44	0.008	2	0.395	0.19752	1.6075	1.26	0.019	2	0.2658	0.13289	1.3628	0.89	0.143
Management:Location:Run	2	0.535	0.26765	1.0769	1.06	0.224	2	0.1485	0.07425	0.6042	0.47	0.996	2	0.137	0.06851	0.7026	0.46	0.833
Residuals	104	25.848	0.24854		51.34		104	12.7796	0.12288		40.60		104	10.1415	0.09751		34.06	
Total	143	50.345			100.00		143	31.4777			100.00		143	29.7722			100.00	

Table S4 Taxonomy of 15 and 24 widespread bacterial and fungal OTUs in both root and rhizosphere compartments in the vegetative growth phase that persisted at the reproductive stage.

OTU	Composition ID	Kingdom	Phylum	Class	Order	Family	Genus
1	OTU_29	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinosynnemataceae	Lentzea
2	OTU_100	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	-
3	OTU_140	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter
4	OTU_7	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	-
5	OTU_75	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	-
6	OTU_53	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	-
7	OTU_32	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter
8	OTU_14	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	-
9	OTU_16	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	-
10	OTU_12	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium
11	OTU_8	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	-
12	OTU_3	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax
13	OTU_1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces mirabilis
14	OTU_4	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	-
15	OTU_88	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
1	OTUF_1	Fungi	Ascomycota	Leotiomycetes	Helotiales	-	-
2	OTUF_2	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces sayulitensis
3	OTUF_3	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium
4	OTUF_4	Fungi	Ascomycota	Dothideomycetes	Pleosporales	-	-
5	OTUF_5	Fungi	Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella minutissima
6	OTUF_6	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma terrestris
7	OTUF_7	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia
8	OTUF_8	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
9	OTUF_11	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium
10	OTUF_12	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	-
11	OTUF_15	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium
12	OTUF_20	Fungi	Ascomycota	Sordariomycetes	Xylariales	-	Fusidium
13	OTUF_28	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Melanommataceae	-
14	OTUF_29	Fungi	Ascomycota	Leotiomycetes	Helotiales	-	-
15	OTUF_30	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusariums culmorum
16	OTUF_39	Fungi	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tetracladium marchalianum
17	OTUF_48	Fungi	Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Microdochium colombiense
18	OTUF_54	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Lindgomycetaceae	Clohesyomyces aquaticus
19	OTUF_57	Fungi	Ascomycota	Sordariomycetes	Myrmecridiales	Myrmecridiaceae	Myrmecridium schulzeri
20	OTUF_70	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Lindgomycetaceae	Clohesyomyces aquaticus
21	OTUF_90	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metacordyceps chlamydosporia
22	OTUF_116	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium concentricum
23	OTUF_135	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	-
24	OTUF_8169	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Stagonosporopsis

Management	1	1.9601	1.96009	8.7601	0.13585	0.001	1	1.5182	1.51817	15.9874	0.13704	0.001
Stage	1	1.3906	1.39063	6.1961	0.09467	0.001	1	2.1440	2.14401	26.0036	0.25542	0.001
Genotype	1	0.4909	0.49085	2.1870	0.03342	0.005	1	0.2664	0.26637	3.2307	0.03173	0.015
Management:Stage	1	0.5839	0.58392	2.6017	0.03975	0.003	1	0.2118	0.21177	2.5685	0.02523	0.038
Management:Genotype	1	0.5097	0.50966	2.2708	0.03470	0.004	1	0.3999	0.39989	4.8500	0.04764	0.002
Stage:Genotype	1	0.3567	0.35666	1.5892	0.02428	0.046	1	0.2257	0.22566	2.7369	0.02688	0.030
Management:Stage:Genotype	1	0.4137	0.41375	1.8435	0.02817	0.015	1	0.5302	0.53020	6.4306	0.06316	0.001
Residuals	40	8.9774	0.22444	0.61117			40	3.2980	0.08245	0.39290		
Total	47	14.6890	1.00000				47	8.3941	1.00000			

Table S5 Taxonomy of the top 25 predictive bacterial and fungal OTUs for lipids.

OTU	Composition ID	Kingdom	Phylum	Class	Order	Family	Genus
1	OTU_67	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
2	OTU_21	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured
3	OTU_494	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured
4	OTU_109	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured
5	OTU_7	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured
6	OTU_93	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria	Incertae	Sedis
7	OTU_75	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Herbaspirillum
8	OTU_58	Bacteria	Actinobacteria	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Actinocorallia
9	OTU_51	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
10	OTU_52	Bacteria	Chloroflexi	TK10	uncultured	bacterium	uncultured
11	OTU_53	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium
12	OTU_30	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Ralstonia
13	OTU_34	Bacteria	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces
14	OTU_15	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
15	OTU_16	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Polaromonas
16	OTU_11	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
17	OTU_132	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured
18	OTU_12	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter
19	OTU_505	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured
20	OTU_8	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia
21	OTU_3	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Comamonas
22	OTU_1	Bacteria	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces
23	OTU_4	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
24	OTU_80	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured
25	OTU_89	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium
1	OTUF_1	Fungi	Ascomycota	Leotiomycetes	Helotiales	-	-
2	OTUF_4	Fungi	Ascomycota	Dothideomycetes	Pleosporales	-	-
3	OTUF_7	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia
4	OTUF_8	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala
5	OTUF_9	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium venenatum
6	OTUF_25	Fungi	-	-	-	-	-
7	OTUF_29	Fungi	Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	-
8	OTUF_43	Fungi	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Hymenoscyphus menthae
9	OTUF_50	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Drechslera
10	OTUF_54	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Lindgomycetaceae	Clohesyomyces aquaticus
11	OTUF_64	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Conocybe apala
12	OTUF_68	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Ophiosphaerella
13	OTUF_70	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Lindgomycetaceae	Clohesyomyces aquaticus
14	OTUF_83	Fungi	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Funneliformis mosseae
15	OTUF_90	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metacordyceps chlamydosporia
16	OTUF_112	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	Plenodomus biglobosus
17	OTUF_123	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia
18	OTUF_165	Fungi	Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella sarnyensis
19	OTUF_221	Fungi	Basidiomycota	-	-	-	-
20	OTUF_246	Fungi	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	-
21	OTUF_253	Fungi	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Funneliformis caledonium
22	OTUF_334	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	-
23	OTUF_343	Fungi	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Heteroconium
24	OTUF_529	Fungi	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Funneliformis mosseae
25	OTUF_2395	Fungi	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Schizothecium glutinans

Table S6 Explained variance root-associated microbial community diversity by each tested factor. Root samples from *pht1;6* and B73 plants at the vegetative and reproductive stages grown under NK and NPK soil managements were compared by PERMANOVA with formula ~ Management * Stage * Genotype.

		Lipid						Bacteria						Fungi				
Factors	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)
Management	1	61.1	61.1	4.158	0.01158	0.033	1	1.9661	1.96609	8.7601	0.13385	0.001	1	1.3182	1.31817	15.9874	0.15704	0.001
Stage	1	4259.4	4259.4	289.859	0.80714	0.001	1	1.3906	1.39063	6.1961	0.09467	0.001	1	2.1440	2.14401	26.0036	0.25542	0.001
Genotype	1	299.6	299.6	20.385	0.05677	0.001	1	0.4909	0.49085	2.1870	0.03342	0.005	1	0.2664	0.26637	3.2307	0.03173	0.015
Management:Stage	1	56.9	56.9	3.875	0.01079	0.048	1	0.5839	0.58392	2.6017	0.03975	0.003	1	0.2118	0.21177	2.5685	0.02523	0.038
Management:Genotype	1	27.0	27.0	1.836	0.00511	0.167	1	0.5097	0.50966	2.2708	0.03470	0.004	1	0.3999	0.39989	4.8500	0.04764	0.002
Stage:Genotype	1	57.7	57.7	3.929	0.01094	0.036	1	0.3567	0.35666	1.5892	0.02428	0.046	1	0.2257	0.22566	2.7369	0.02688	0.030
Management:Stage:Genotype	1	30.5	30.5	2.076	0.00578	0.145	1	0.4137	0.41375	1.8435	0.02817	0.015	1	0.5302	0.53020	6.4306	0.06316	0.001
Residuals	33	484.9	14.7		0.09189		40	8.9774	0.22444		0.61117		40	3.2980	0.08245		0.39290	
Total	40	5277.1			1.00000		47	14.6890			1.00000		47	8.3941			1.00000	

Table S7 Explained variance of parameters affecting root microbiota at vegetative and reproductive growth stages, based on beta-diversity. This includes all plant genotypes and managements (PERMANOVA), model ~ Management * Genotype * Location * Plot * Run was applied.

Vegetative stage

Factors		Bacteria						Fungi						Oomycetes				
	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)
Management	3	10.679	3.5597	16.7026	15.31	0.001	3	11.275	3.7582	27.7191	20.48	0.001	3	14.245	4.7482	31.73	18.89	0.001
Location	2	2.847	1.4236	6.6799	4.08	0.001	2	5.004	2.502	18.4539	9.09	0.001	2	5.442	2.7211	18.184	7.22	0.001
Genotype	4	2.159	0.5398	2.5327	3.10	0.001	4	2.728	0.6821	5.0309	4.96	0.001	4	3.082	0.7706	5.149	4.09	0.001
Run	5	2.506	0.5013	2.352	3.59	0.001	5	1.439	0.2878	2.1227	2.61	0.001	5	7.961	1.5923	10.64	10.56	0.001
Plot	1	0.318	0.3179	1.4915	0.46	0.026	1	0.427	0.4272	3.1507	0.78	0.001	1	1.703	1.7034	11.383	2.26	0.001
Management:Location	1	1.135	1.1352	5.3263	1.63	0.001	1	0.956	0.9555	7.0474	1.74	0.001	1	1.579	1.5792	10.553	2.09	0.001
Management:Genotype	**12**	**4.59**	**0.3825**	**1.7949**	**6.58**	**0.001**	**12**	**4.176**	**0.348**	**2.5665**	**7.59**	**0.001**	**12**	**5.454**	**0.4545**	**3.037**	**7.23**	**0.001**
Location:Genotype	8	2.368	0.2961	1.3891	3.40	0.001	8	1.926	0.2407	1.7755	3.50	0.001	8	1.869	0.2336	1.561	2.48	0.006
Management:Run	3	1.068	0.3559	1.6701	1.53	0.001	3	0.584	0.1947	1.436	1.06	0.024	3	1.079	0.3597	2.404	1.43	0.001
Location:Run	4	0.98	0.245	1.1497	1.41	0.095	4	0.624	0.156	1.1502	1.13	0.16	4	0.654	0.1636	1.093	0.87	0.317
Genotype:Run	17	4.13	0.2429	1.1399	5.92	0.013	17	2.518	0.1481	1.0924	4.57	0.153	13	2.597	0.1998	1.335	3.44	0.022
Management:Location:Genotype	4	1.097	0.2743	1.2869	1.57	0.009	4	0.917	0.2292	1.6906	1.67	0.001	4	0.673	0.1682	1.124	0.89	0.288
Management:Genotype:Run	11	2.656	0.2415	1.1331	3.81	0.038	11	1.281	0.1165	0.8589	2.33	0.918	11	3.124	0.284	1.898	4.14	0.001
Location:Genotype:Run	6	1.443	0.2405	1.1282	2.07	0.083	6	0.996	0.1661	1.2249	1.81	0.066	7	1.718	0.2454	1.64	2.28	0.005
Residuals	149	31.755	0.2131		45.54		149	20.202	0.1356		36.70		156	23.345	0.1496		30.96	
Total	230	69.733			100.00		230	55.052			100.00		238	75.408			100.00	

Reproductive stage

Factors		Bacteria						Fungi						Oomycetes				
	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)	Df	SumsOfSqs	MeanSqs	F.Model	R2 (%)	Pr (>F)
Management	3	12.62	4.2068	23.154	18.55	0.001	3	7.6893	2.5631	49.364	24.36	0.001	3	19.379	6.4597	62.48	30.93	0.001
Genotype	4	3.272	0.8181	4.5026	4.81	0.001	4	1.8821	0.47054	9.062	5.96	0.001	4	7.608	1.902	18.397	12.14	0.001
Location	2	2.972	1.4858	8.1778	4.37	0.001	2	4.694	2.34701	45.202	14.87	0.001	2	2.366	1.1832	11.444	3.78	0.001
Run	5	2.918	0.5836	3.212	4.29	0.001	5	0.707	0.14141	2.723	2.24	0.001	5	0.884	0.1768	1.71	1.41	0.027
Plot	1	0.452	0.4523	2.4894	0.67	0.002	1	0.7343	0.73435	14.143	2.33	0.001	1	0.547	0.5475	5.295	0.87	0.001
Management:Genotype	**12**	**4.457**	**0.3714**	**2.044**	**6.55**	**0.001**	**12**	**2.1442**	**0.17869**	**3.441**	**6.79**	**0.001**	**12**	**3.8**	**0.3167**	**3.063**	**6.06**	**0.001**
Management:Location	1	0.861	0.8608	4.7378	1.27	0.001	1	0.4355	0.43545	8.387	1.38	0.001	1	1.016	1.0155	9.823	1.62	0.001
Genotype:Location	8	2.227	0.2784	1.5323	3.27	0.001	8	1.5294	0.19117	3.682	4.85	0.001	8	3.026	0.3783	3.659	4.83	0.001
Management:Run	3	1.013	0.3376	1.8583	1.49	0.001	3	0.3072	0.10241	1.972	0.97	0.006	3	0.251	0.0836	0.808	0.40	0.639
Genotype:Run	16	3.39	0.2118	1.166	4.98	0.01	12	0.8074	0.06729	1.296	2.56	0.036	12	1.669	0.1391	1.345	2.66	0.064
Location:Run	4	0.817	0.2041	1.1235	1.20	0.133	4	0.3328	0.08321	1.603	1.06	0.03	4	0.696	0.1739	1.682	1.11	0.058
Management:Genotype:Location	3	0.748	0.2493	1.3723	1.10	0.012	3	0.2128	0.07093	1.366	0.67	0.108	3	1.004	0.3345	3.235	1.60	0.001
Management:Genotype:Run	12	2.518	0.2098	1.155	3.70	0.017	12	1.0838	0.09032	1.74	3.43	0.001	12	1.638	0.1365	1.32	2.61	0.063
Genotype:Location:Run	7	1.419	0.2027	1.1158	2.09	0.089	7	0.5056	0.07223	1.391	1.60	0.029	7	1.416	0.2023	1.957	2.26	0.004
Residuals	156	28.343	0.1817		41.67		158	8.2037	0.05192		25.99		158	16.336	0.1034		26.07	
Total	237	68.027			1		239	31.5598			1		239	62.665			100.00	