

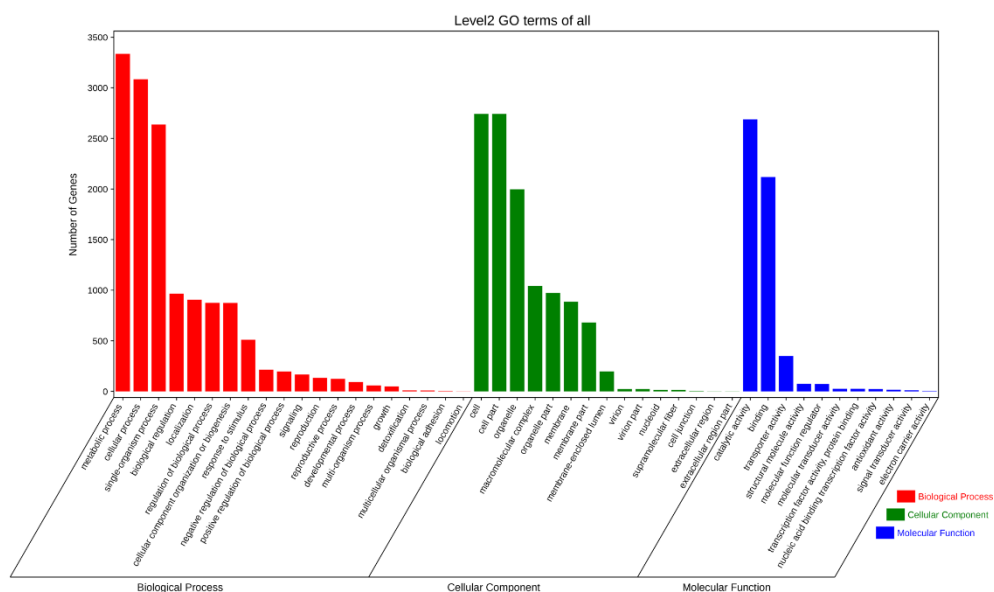


Figure S1 GO analyses of the *L. chartarum* and *C. trifolii* protein-coding genes

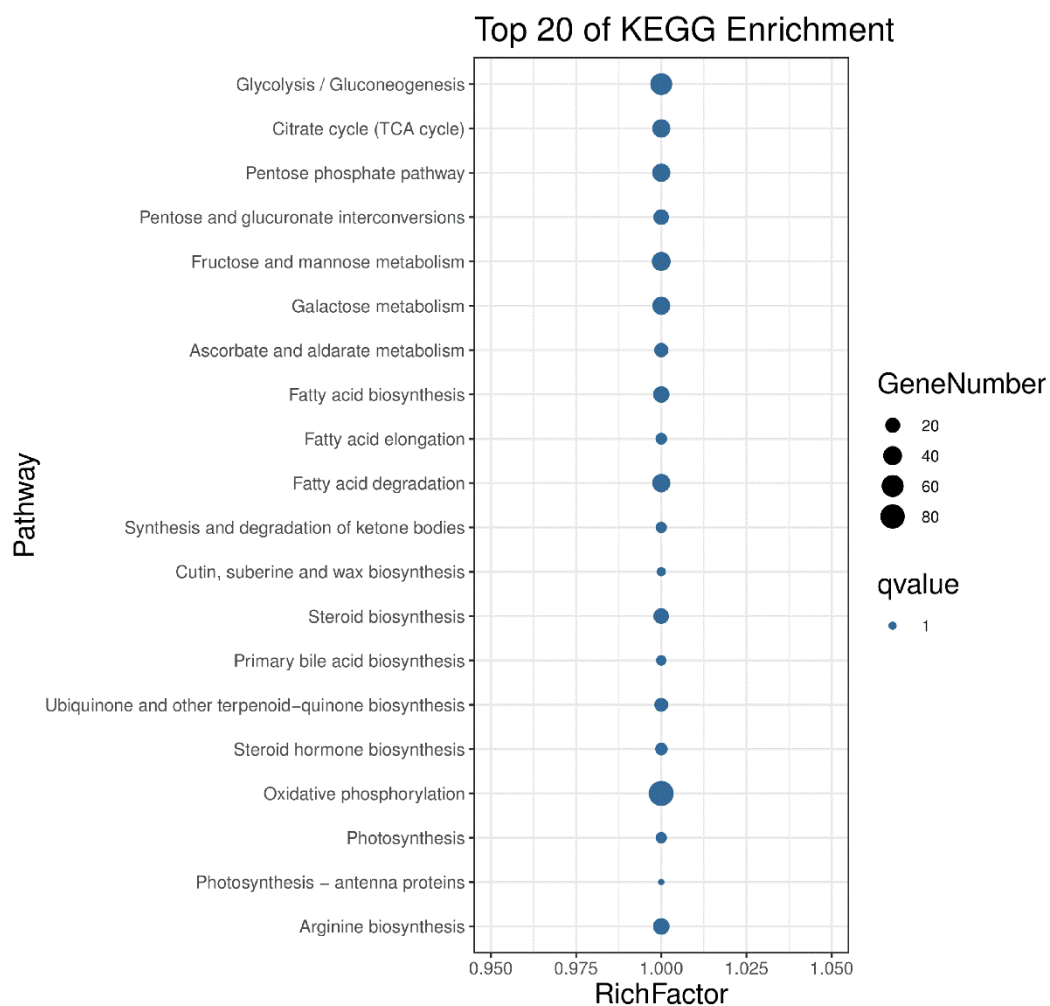


Figure S2 KEGG annotations in the *L. chartarum* genome

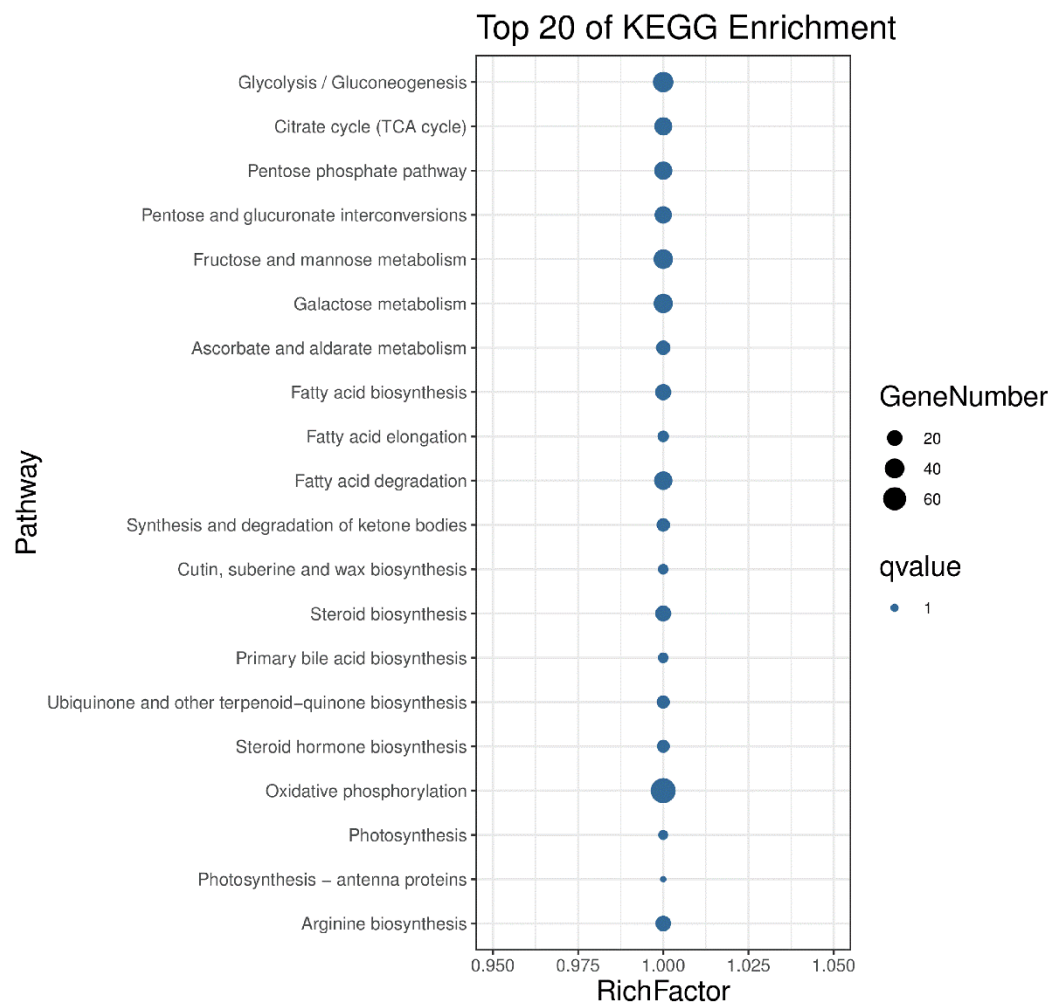


Figure S3 KEGG annotations in the *C. trifolii* genome

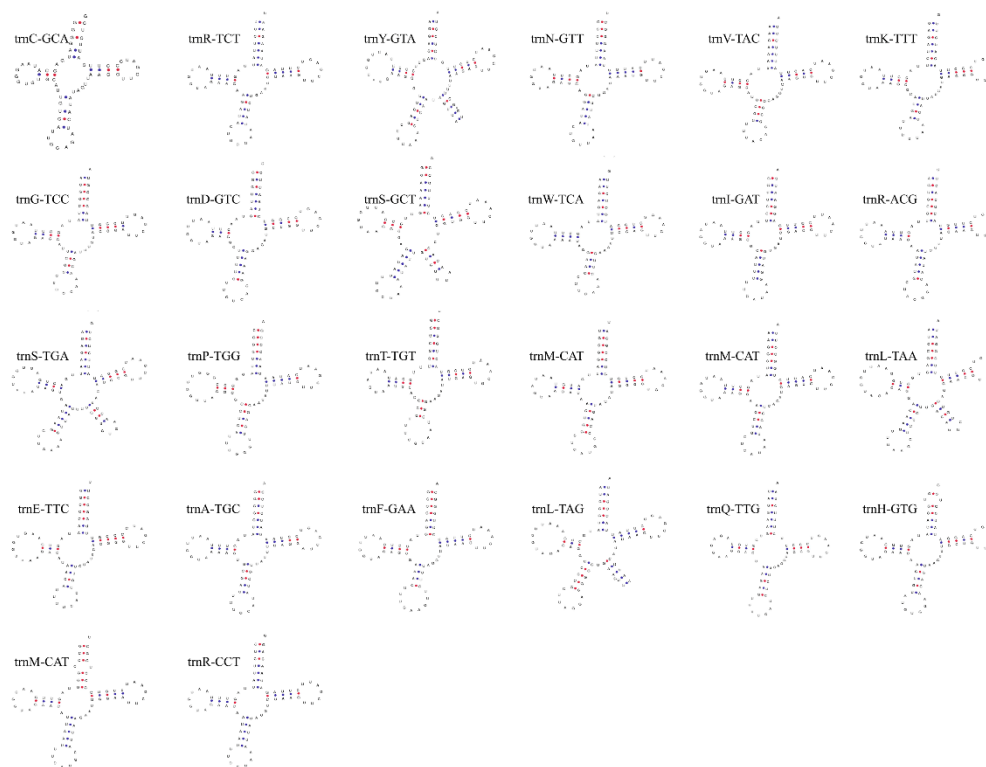


Figure S4 The predicted tRNA structures of *L. chartarum*

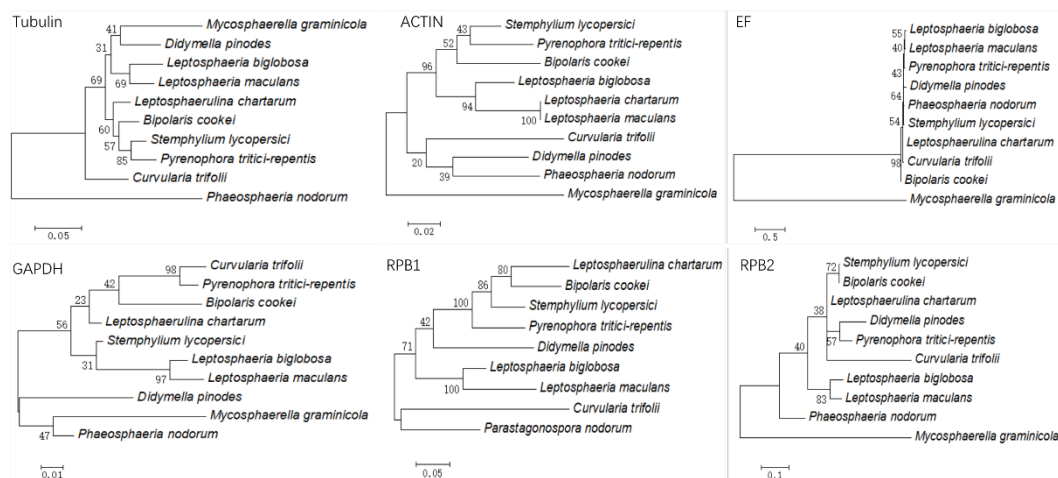


Figure S5 Phylogenetic analyses for individual genes from nuclear genome

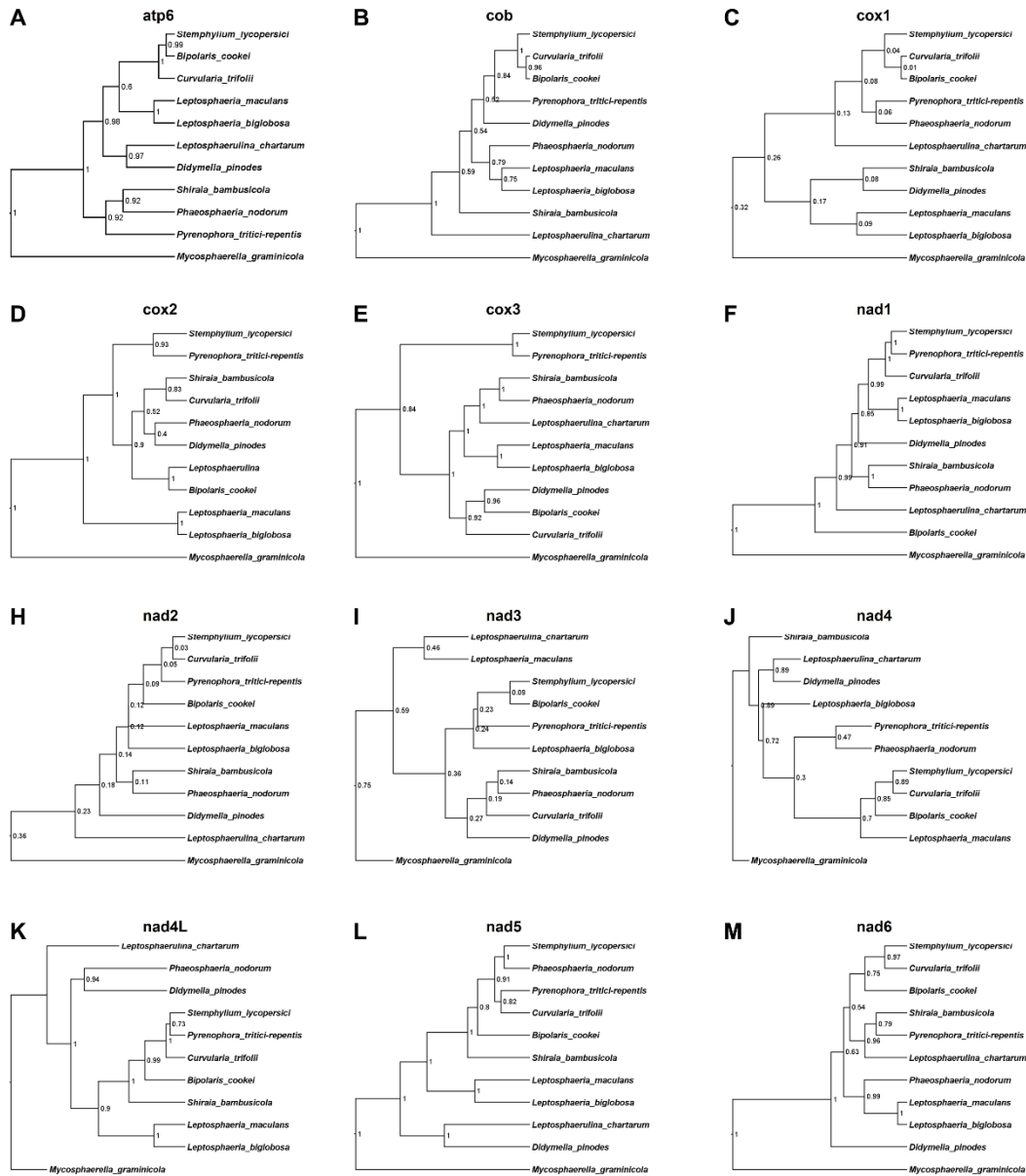


Figure S6 Phylogenetic analyses for individual genes from motichondrial genome

Table S1. Organization of the mitochondrial genome of *Leptosphaerulina chartarum*

Gene	R/F	position		Length		Codon		Intergenic nucleotides
		From	To	nt	aa	Start	Stop	
atp6	R	836	1606	771	257	AAT	GTA	194
nad4	R	1849	3504	1656	552	AAT	GTA	242
orf297	R	5240	6133	894	298	GAT	GTA	1735
orf270	F	6871	7683	813	271	ATG	TAG	737
orf393	R	8667	9848	1182	394	AAT	GTA	983
cox1&2	R	9752	20506	1266	422	GAT	GTA	-97
orf374	R	11196	12320	1125	375	AAT	AAC	-9311
orf297	R	12640	13533	894	298	GAT	ACA	319
orf352	R	13880	14938	1059	353	GAT	AGT	346
orf363	R	15081	16172	1092	364	AAT	AAC	142
orf324	R	16344	17318	975	325	AAT	GCA	171
orf349	R	17553	18602	1050	350	AAT	AAA	234
orf328	R	19307	20293	987	329	AAT	AAG	704
trnC(gca)	R	20817	20887	71		TCT	GGG	523
orf156	F	22265	22735	471	157	ATG	TAG	1377
orf109	R	22708	23037	330	110	GAT	GTA	-28
orf329	F	23702	24691	990	330	ATG	TAG	664
trnR(tct)	F	25731	25801	71		TTC	AAT	1039
rns	F	25961	27638	1678	559	TTA	ATT	159
trnY(gta)	F	28148	28232	85		AGG	CTA	509
trnN(gtt)	F	28767	28837	71		GCC	GCT	534
nad6	F	29284	29958	675	225	ATG	TAA	446
trnV(tac)	F	29909	29981	73		AAG	TTA	-50
trnK(ttt)	F	30009	30080	72		GAG	TTG	27
trnG(tcc)	F	30090	30160	71		ACG	GTA	9
trnD(gtc)	F	30163	30235	73		GGG	TCG	2
trnS(gct)	F	30586	30665	80		GGA	CCG	350
trnW(tca)	F	30995	31066	72		AAG	TTG	329
trnI(gat)	F	31284	31355	72		GGT	TCA	217
trnR(acg)	F	31359	31430	72		AGT	CTT	3
trnS(tga)	F	31940	32024	85		AGA	CTG	509
trnP(tgg)	F	32240	32312	73		CGG	CGA	215
rnl	F	32353	36047	3695	1231	TAT	CTG	40
trnT(tgt)	F	36169	36239	71		GCT	GCT	121
trnM(cat)	F	36261	36331	71		TGC	CAT	21
trnM(cat)	F	36349	36421	73		AAG	TTA	17

trnL(taa)	F	36916	36998	83		ATC	ATA	494
trnE(ttc)	F	37317	37389	73		GGC	CTT	318
trnA(tgc)	F	37414	37485	72		GGG	CCA	24
trnF(gaa)	F	37868	37940	73		GCC	GCA	382
trnL(tag)	F	39268	39350	83		ATG	ATA	1327
trnQ(ttg)	F	39645	39716	72		TAT	TAG	294
trnH(gtg)	F	39731	39804	74		GGT	TCC	14
trnM(cat)	F	40128	40198	71		GCC	GCT	323
orf413	F	40936	42177	1242	414	ATG	TAA	737
nad2	F	43265	45013	1749	583	ATG	TAA	1087
nad3	F	45014	45436	423	141	ATG	TAG	0
orf224	F	45621	46295	675	225	ATG	TAA	184
orf152	F	47163	47621	459	153	ATG	TAG	867
orf240	F	47835	48557	723	241	ATG	TAA	213
nad1	F	48948	49940	993	331	ATG	TAA	390
orf143	R	52108	52539	432	144	GAT	GTA	2167
nad5	R	52687	58415	1272	1909	GAT	GTA	147
orf302	R	54083	54991	909	303	AAT	GTT	-4333
orf327	R	55431	56414	984	328	AAT	AAA	439
orf103	R	57780	58091	312	104	AAT	GGC	1365
nad4L	R	58415	58684	270	90	AAT	GTA	323
orf322	R	59200	60168	969	323	AAT	GTA	515
trnR(cct)	R	60278	60348	71		GGA	CTC	109
cob	R	60443	64134	677	1230	AAT	GTA	94
orf290	R	61449	62321	873	291	GAT	ACA	-2686
orf309	R	62812	63741	930	310	AAT	GTT	490
orf109	F	64266	64595	330	110	ATG	TAA	524
rnpB	R	64844	65014	171	57	TAT	GAC	248
orf331	R	65157	66152	996	332	GAT	GTA	142
cox3	R	67443	68731	179	429	AAT	GTA	1290

Table S2. Organization of the mitochondrial genome of *Curvularia trifolii*

Gene	R/F	position		Length		Codon		Intergenic nucleotides
		From	To	nt	aa	Start	Stop	
trnR(acg)	F	59	130	72		AGT	CTT	117
trnS(tga)	F	248	332	85		AGA	CTG	230
trnP(tgg)	F	563	635	73		CAG	TGA	99
rnl	F	735	4181	3447	1149	TAT	TTA	99
trnT(tgt)	F	4281	4351	71		GCC	GCT	323
trnM(cat)	F	4675	4745	71		TGC	CAT	5
trnM(cat)	F	4751	4823	73		AAG	TTA	752
trnE(ttc)	F	5576	5648	73		GGC	CTT	32
trnA(tgc)	F	5681	5752	72		GGG	CCA	516
trnF(gaa)	F	6269	6341	73		GCC	GCA	378
trnL(tag)	F	6720	6802	83		ATG	ATA	77
trnQ(ttg)	F	6880	6951	72		TAT	TAA	4
trnH(gtg)	F	6956	7029	74		GGT	TCC	196
trnM(cat)	F	7226	7297	72		GCC	GCT	788
trnL(tag)	F	8086	8158	73		CGG	TGA	311
atp6	F	8470	12281	341	113	ATG	TAG	-3470
orf333	F	8812	9813	1002	334	AAA	TAA	1349
orf259	F	11163	11942	780	260	ATG	TAG	496
trnC(gca)	F	12439	12510	72		GGG	CCT	246
nad2	F	12757	14487	1731	577	ATG	TAA	0
nad3	F	14488	14925	438	146	ATG	TAA	1536
cox3	F	16462	17271	810	270	ATG	TAA	463
orf490	F	17735	19207	1473	491	ATG	TAA	1323
nad1	R	20531	24611	480	160	AAT	GTA	-1554
orf469	R	23058	24467	1410	470	AAT	TGT	699
nad5	R	25167	27509	2343	781	AAT	GTA	402
nad4L	R	27912	29189	1278	426	GAT	GTA	826
nad4	R	30016	31485	1470	490	AAT	GTT	204
trnM(cat)	R	31690	31760	71		TAA	CTT	576
cob	R	32337	36050	668	222	GAT	GTA	-2702
orf296	R	33349	34239	891	297	AAT	AAA	486
orf257	R	34726	35499	774	258	GAT	GTA	895
trnN(gtt)	R	36395	36465	71		TCG	CCG	508
orf996	R	36974	39964	2991	997	AAT	GTA	270
trnN(gtt)	R	40235	40305	71		TCG	CCG	260
trnN(gtt)	R	40566	40636	71		TCG	CCG	395

cox2	R	41032	42968	522	174	GAT	TAG	-1170
orf324	R	41799	42773	975	325	AAT	TTA	195
cox1	R	42969	49330	391	130	TGT	GTA	-5770
orf274	R	43561	44385	825	275	AAT	GGA	406
orf318	R	44792	45748	957	319	AAT	AAA	405
orf350	R	46154	47206	1053	351	AAT	AAA	333
orf431	R	47540	49935	1296	432	AAT	ATG	-27
orf198	R	49909	50505	597	199	AAT	GTA	1701
orf182	F	52207	52755	549	183	ATG	TAG	570
trnR(tct)	F	53326	53396	71		TTC	AAT	64
trnR(cct)	F	53461	53531	71		TTC	AAA	95
rns	F	53627	55255	1629	543	TTT	ATT	445
trnL(taa)	F	55701	55783	83		ATC	ATA	16
trnY(gta)	F	55800	55884	85		AGG	CTA	81
trnN(gtt)	F	55966	56036	71		GTT	GCT	304
nad6	F	56341	56916	576	192	ATG	TAA	81
trnV(tac)	F	56998	57070	73		AAG	TTA	32
trnK(ttt)	F	57103	57174	72		GAG	TTA	690
trnG(tcc)	F	57865	57936	72		GCG	GTA	2
trnD(gtc)	F	57939	58010	72		GGG	TCG	317
trnS(gct)	F	58328	58407	80		GGA	CCG	364
trnW(tca)	F	58772	58843	72		AAG	TTG	-58844

Table S3. AT-content, AT-skew and GC-skew for mitochondrial genes of *Leptosphaerulina chartarum*

Feature	A%	C%	G%	T%	(A+T)%	AT skew	GC skew
Whole genome	35.99	14.19	14.43	35.39	71.38	0.01	0.01
Protein-coding genes	35.33	14.65	15.14	34.89	70.22	0.01	0.02
<i>cox1&2</i>	36.73	16.43	16.19	30.65	67.38	0.09	-0.01
<i>cox3</i>	41.34	17.32	12.29	29.05	70.39	0.17	-0.17
<i>cob</i>	40.92	15.36	14.62	29.10	70.01	0.17	-0.02
<i>nad1</i>	28.50	12.99	15.21	43.30	71.80	-0.21	0.08
<i>nad2</i>	34.71	12.98	12.81	39.51	74.21	-0.06	-0.01
<i>nad4</i>	32.86	12.77	13.24	41.13	74.00	-0.11	0.02
<i>nad4L</i>	40.70	15.28	13.41	30.62	71.32	0.14	-0.07
<i>nad5</i>	40.57	15.71	10.00	33.71	74.29	0.09	-0.22
<i>nad6</i>	38.99	14.47	14.62	31.92	70.91	0.10	0.01
<i>atp6</i>	40.34	12.71	14.27	32.68	73.02	0.10	0.06
<i>orf103</i>	27.56	20.83	13.78	37.82	65.38	-0.16	-0.20
<i>orf109</i>	43.33	12.12	11.21	33.33	76.67	0.13	-0.04
<i>orf109</i>	36.06	8.48	12.73	42.73	78.79	-0.08	0.20
<i>orf143</i>	34.03	15.97	13.89	36.11	70.14	-0.03	-0.07
<i>orf152</i>	35.08	12.42	13.94	38.56	73.64	-0.05	0.06
<i>orf156</i>	44.16	13.16	11.25	31.42	75.58	0.17	-0.08
<i>orf224</i>	34.37	15.41	16.59	33.63	68.00	0.01	0.04
<i>orf240</i>	41.49	8.58	15.08	34.85	76.35	0.09	0.27
<i>orf270</i>	30.01	20.79	22.39	26.81	56.83	0.06	0.04
<i>orf290</i>	37.92	12.71	12.60	36.77	74.68	0.02	0.00
<i>orf297</i>	24.05	23.27	19.35	33.33	57.38	-0.16	-0.09
<i>orf297</i>	32.89	17.79	13.31	36.02	68.90	-0.05	-0.14
<i>orf302</i>	34.43	13.75	12.54	39.27	73.71	-0.07	-0.05
<i>orf309</i>	33.44	14.62	12.90	39.03	72.47	-0.08	-0.06
<i>orf322</i>	36.12	17.75	16.31	29.82	65.94	0.10	-0.04
<i>orf324</i>	31.79	15.08	12.41	40.72	72.51	-0.12	-0.10
<i>orf327</i>	33.54	16.06	12.60	37.80	71.34	-0.06	-0.12
<i>orf328</i>	32.22	15.50	12.46	39.82	72.04	-0.11	-0.11
<i>orf329</i>	40.30	9.49	15.66	34.55	74.85	0.08	0.24
<i>orf331</i>	37.55	12.95	14.06	35.44	72.99	0.03	0.04
<i>orf349</i>	33.52	14.95	13.05	38.48	72.00	-0.07	-0.07
<i>orf352</i>	32.58	17.85	16.81	32.77	65.34	0.00	-0.03
<i>orf363</i>	34.43	15.11	11.54	38.92	73.35	-0.06	-0.13
<i>orf374</i>	35.02	13.51	11.38	40.09	75.11	-0.07	-0.09

<i>orf393</i>	31.05	18.87	14.21	35.87	66.92	-0.07	-0.14
<i>orf413</i>	42.35	9.58	13.61	34.46	76.81	0.10	0.17
<i>rnpB</i>	28.65	14.62	14.04	42.69	71.35	-0.20	-0.02
<i>tRNAs</i>	41.53	24.88	33.51	48.61	90.14	-0.08	0.15
<i>rns</i>	33.08	15.49	22.11	29.32	62.40	0.06	0.18
<i>rnl</i>	35.53	13.75	20.73	29.99	65.52	0.08	0.20
NCR	37.63	12.44	12.95	36.98	74.61	0.01	0.02

Table S4. AT-content, AT-skew and GC-skew for mitochondrial genes of *Curvularia trifolii*

Feature	A%	C%	G%	T%	(A+T)%	AT skew	GC skew
Whole genome	35.15	14.55	14.75	35.54	70.69	-0.01	0.01
Protein-coding genes	35.86	14.59	13.53	36.02	71.88	0.00	-0.04
<i>cox1</i>	38.36	14.58	17.65	29.41	67.77	0.13	0.10
<i>cox2</i>	36.40	16.48	15.71	31.42	67.82	0.07	-0.02
<i>cox3</i>	29.26	15.43	16.79	38.52	67.78	-0.14	0.04
<i>cob</i>	39.37	15.27	16.02	29.34	68.71	0.15	0.02
<i>nad1</i>	41.88	15.00	13.13	30.00	71.88	0.17	-0.07
<i>nad2</i>	33.28	14.38	13.29	39.05	72.33	-0.08	-0.04
<i>nad3</i>	33.11	12.33	14.16	40.41	73.52	-0.10	0.07
<i>nad4</i>	42.31	13.54	13.67	30.48	72.79	0.16	0.01
<i>nad4L</i>	35.37	15.18	12.52	36.93	72.30	-0.02	-0.10
<i>nad5</i>	37.99	17.63	13.53	30.86	68.84	0.10	-0.13
<i>nad6</i>	34.72	9.72	13.19	42.36	77.08	-0.10	0.15
<i>atp6</i>	38.42	15.84	10.56	35.19	73.61	0.04	-0.20
<i>orf182</i>	35.34	12.02	15.48	37.16	72.50	-0.03	0.13
<i>orf198</i>	28.48	16.92	15.24	39.36	67.84	-0.16	-0.05
<i>orf257</i>	31.52	16.67	10.21	41.60	73.13	-0.14	-0.24
<i>orf259</i>	37.56	13.33	17.56	31.54	69.10	0.09	0.14
<i>orf274</i>	31.15	16.85	11.27	40.73	71.88	-0.13	-0.20
<i>orf296</i>	35.47	14.03	13.47	37.04	72.50	-0.02	-0.02
<i>orf318</i>	33.44	15.26	12.75	38.56	72.00	-0.07	-0.09
<i>orf324</i>	30.26	16.82	14.36	38.56	68.82	-0.12	-0.08
<i>orf333</i>	40.92	12.28	14.07	32.73	73.65	0.11	0.07
<i>orf350</i>	32.67	14.53	13.68	39.13	71.79	-0.09	-0.03
<i>orf431</i>	32.48	15.51	13.66	38.35	70.83	-0.08	-0.06
<i>orf469</i>	36.17	14.04	10.57	39.22	75.39	-0.04	-0.14
<i>orf490</i>	43.31	10.86	12.90	32.93	76.24	0.14	0.09
<i>orf996</i>	36.04	13.81	13.24	36.91	72.95	-0.01	-0.02
tRNAs	29.02	16.92	21.34	32.72	61.73	-0.06	0.12
<i>rns</i>	35.28	14.22	20.37	30.14	65.42	0.08	0.18
<i>rnl</i>	32.11	15.04	22.59	30.26	62.37	0.03	0.20
NCR	35.08	13.38	14.06	37.48	72.56	-0.03	0.02