S2 Table. Codon usage analysis. Comparison of codon usage and tRNAs for the 14 genes involved in oxidative phosphorylation and electron transport in the mitochondrial genomes of *Chrysoporthe austroafricana*, *C. cubensis*, *C. deuterocubensis* and *Cryphonectria parasitica*.

Amino acid	**Codon**	***C. austroafricana***		***C. cubensis***		***C. deuterocubensis***		***C. parasitica***	
		tRNA[a]	***% usage***[b]	**tRNA**[a]	***% usage***[b]	**tRNA**[a]	***% usage***[b]	**tRNA**[a]	***% usage***[b]
Ala	GCG		0.57		0.47		0.53		0.58
Ala	GCA	+	1.93	+	1.72	+	1.89	+	1.66
Ala	GCT		3.22		3.26		3.31		3.39
Ala	GCC		0.53		0.53		0.49		0.44
Cys	TGT		0.76		0.64		0.56		0.51
Cys	TGC	+	0.19	+	0.14	+	0.11	+	0.18
Asp	GAT		2.44		2.30		2.16		2.30
Asp	GAC	+	0.55	+	0.35	+	0.27	+	0.35
Glu	GAG		0.96		0.68		0.73		0.73
Glu	GAA	+	2.12	+	2.09	+	1.93	+	2.06
Phe	TTT		5.84		6.09		6.11		5.96
Phe	TTC	+	2.25	+	2.50	+	2.51	+	2.24
Gly	GGG		1.04		0.98		0.87		0.73
Gly	GGA	++	2.07	+	2.09	+	2.20	+	1.82
Gly	GGT		3.57		3.85		3.80		4.45
Gly	GGC		0.14		0.12		0.11		0.27
His	CAT		1.19		1.23		1.16		1.20
His	CAC	+	0.60	+	0.64	+	0.64	+	0.60
Ile	ATA		5.06		5.27		5.53	+	5.05
Ile	ATT		4.26		4.30		4.36		4.92
Ile	ATC	+	0.92	+	1.15	+	1.00	+	0.97
Lys	AAG		0.57		0.45		0.20		0.40
Lys	AAA	+	3.17	+	2.34	++	2.07	+	2.39
Leu	TTG		1.33		1.23		1.22		1.35
Leu	TTA	+	9.36	+	10.18	+	10.42	+	9.99

Leu	CTG		0.23		0.25		0.20		0.22
Leu	CTA	+	1.06	+	0.96	+	1.11	+	1.24
Leu	CTT		1.75		1.62		1.73		1.99
Leu	CTC		0.23		0.18		0.16		0.16
Met	ATG	++++	2.23	++++	2.46	++++	2.60	+++	2.37
Asn	AAT		4.07		4.00		3.96		4.30
Asn	AAC	+	0.92	+	0.94	+	0.89	+	0.60
Pro	CCG		0.11		0.08		0.20		0.18
Pro	CCA		1.08	+	1.05		0.98	+	0.75
Pro	CCT	+	2.03		2.19	+	2.04		2.17
Pro	CCC		0.16		0.20		0.22		0.20
Gln	CAG		0.27		0.18		0.24		0.18
Gln	CAA	+	1.84	+	1.74	+	1.71	+	1.68
Arg	AGG		0.18		0.14		0.09		0.09
Arg	AGA	++	1.65	++	1.68	+	1.64	+	1.37
Arg	CGG		0.12		0.08		0.09		0.09
Arg	CGA		0.11		0.14		0.16		0.16
Arg	CGT	+	0.41	+	0.37	+	0.24	+	0.33
Arg	CGC		0.04		0.04		0.00		0.02
Ser	AGT		3.27		3.36		3.49		3.46
Ser	AGC	+	0.46	+	0.53	+	0.51	+	0.49
Ser	TCG		0.16		0.20		0.18		0.31
Ser	TCA	+	2.02	+	2.07	+	1.98	+	1.64
Ser	TCT		2.60		2.38		2.38		2.64
Ser	TCC		0.39		0.25		0.27		0.16
Thr	ACG		0.21		0.27		0.27		0.22
Thr	ACA	+	2.02	+	1.84	+	1.91	+	2.15
Thr	ACT		2.53		2.68		2.73		2.48
Thr	ACC		0.28		0.29		0.33		0.22
Val	GTG		0.60		0.66		0.64		0.84
Val	GTA	+	2.94	+	2.77	+	2.91	+	2.66

Val	GTT		3.04		3.24		3.22		3.23
Val	GTC		0.18		0.16		0.18		0.42
Trp	TGG		0.09		0.08		0.07		0.07
Trp	TGA	+	1.20	+	1.29	+	1.31	+	1.28
Tyr	TAT		3.54		3.55		3.62		3.59
Tyr	TAC	+	1.13	+	1.19	+	1.22	+	1.22
End	TAG		0.07		0.04		0.07		0.09
End	TAA		0.18		0.25		0.24		0.22

a tRNA gene for specified amino acid,

b Percentage codon usage calculated from the total number of codons of standard mt genes.

+ Presence and number of *tRNA* genes. The number of plus signs corresponds to the frequency of the respective *tRNA* gene.