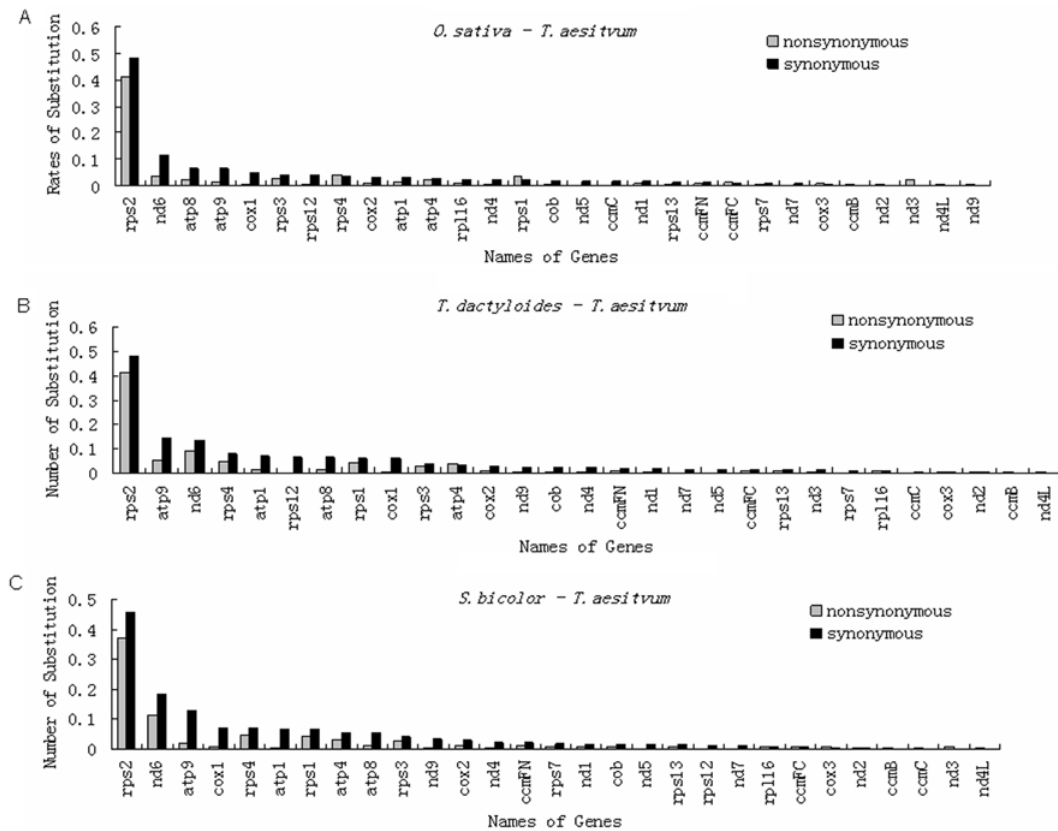


## Supplementary data:

# A complete mitochondrial genome of wheat (*Triticum aestivum* cv. Chinese Yumai), and fast evolving mitochondrial genes in higher plants

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**Figure 1.** The nonsynonymous and synonymous substitution rates among orthologous gene-pairs selected mitochondrial genomes of higher plants. A, the rates varied among gene-pairs from the rice–wheat clade; B, the rates varied among gene-pairs from the Triplacum–wheat clade; C, the rates varied among gene-pairs from the sorghant–wheat clade.

**Table 1.** The primers for DNA probes used for screening BAC clones.

Number	Sequence	Strand	Gene	Clone
1	5' AAAGCCCCAGGGATTATTGAA 3'	Forward	<i>atp1</i>	XB4 and ZG5
	5' GCCACCGCCTGTTTACTTAGAT 3'	Reverse		
2	5' TGCCTCAACAAAAATGGATGG 3'	Forward	<i>rps13</i>	XB4, XE5 and XC8
	5' GATAGGCGGGCGAAGTGAG 3'	Reverse		
3	5' TTCGGCCAATACAAAAGATGAGAC3'	Forward	<i>rpl5</i>	XE5, XC8

**Table 1** (contd)

Number	Sequence	Strand	Gene	Clone
4	5' GGAGCCGGACGGTAATGGAC 3'	Reverse	<i>nad5c</i>	and XB7
	5'GCGGGCAGGAGGGCTTTGTTT3'	Forward		XE5, XH8
5	5'GGTCTCGCCGGTGTTCCTGTA3'	Reverse	<i>ccmFN</i>	and XB7
	5'TTCGCCTTCTCTCGCTCTGGACA3'	Forward		XE5 and
6	5'AAGCGCTACGGACGGGACGAAATC3'	Reverse	<i>cob</i>	XH4
	5'AGGGGGTAAAATAAGGGGGAAGA3'	Forward		XH8 and
7	5'AATGCGGCCAGATGAAGAAGAC3'	Reverse	<i>rpl16</i>	XA6
	5'TTGCGGGATTTCAGACCTAACCC3'	Forward		XA6
8	5'TCGCGAATGGAATGAGAAAG3'	Reverse	<i>ccmFCb</i>	XH6 and
	5'GGCGGGCGGCGTGAACCTCT3'	Forward		
9	5'AGCCTTCACTGCCCCCTTCTGTAA3'	Forward	<i>nad5d</i>	XH6 and
	5'TAGTAGTCCGTCGGCTGCTCTTG3'	Reverse		XG5
10	5'GGGGCCCCACTACTTCTTCATCA3'	Forward	<i>nad4a</i>	XG5 and
	5'AGCTTCGCGGGGACCTTTACTACT3'	Reverse		XC1
11	5'TGGCCGCAGGGGAAACACAG3'	Forward	<i>nad4d</i>	XC1
	5'AATACGCCGCGCCTAAAATCATCC3'	Reverse		
12	5'CACCCGCCGCTCTCAATA3'	Forward	<i>ccmC</i>	YE4
	5'GGCCCGTCCCCTCTTACCC3'	Reverse		
13	5'AGACGACCCGCCTCATTACAT3'	Forward	<i>nad2a</i>	YE4 and
	5'GCGCGGCAAAAGGATTAGGAC3'	Reverse		YG6
14	5' TTAGCTGGCGACGAAAAAGAG 3'	Forward	<i>atp4</i>	YG4 and
	5' AGCGTGCCGTTGGTAATGAT 3'	Reverse		YE6
15	5'GCCGGGCTCGATTCTTTCAA3'	Forward	<i>nad2d</i>	YE6 and
	5'CCGCTTCCATGTGGGCAGAGACC3'	Reverse		YF4
16	5'GATTTCAAGACGCAGCAACACC3'	Forward	<i>cox2</i>	YF4 and
	5'ACCCAATCCGCATAATCTTTCAA3'	Reverse		YH12
17	5'ATGCGTGGACCTGGAATGACTATG3'	Forward	<i>cox1</i>	YH12
	5'ATGCCCCGAAAGCCCTAAGAAATG3'	Reverse		
18	5' CGGTTTTTCTCCTTCCCTCTT 3'	Forward	<i>rps4</i>	YD7
	5' TTCCGGTTCGCTCCATTTTAG 3'	Reverse		
19	5'TGGGGGTGCCGGTGCTTAG3'	Forward	<i>rpl2-p</i>	YD7 and
	5'CCGGCCCTTTGTTCTCGTC3'	Reverse		YB1
20	5'CACCGCGGGGAGGATGGA3'	Forward	<i>nad5b</i>	YB1
	5'AAAGGCAGGGCGGCAGAGC3'	Reverse		
21	5'GGGCTTACAGGGCTAGGGCTCATA3'	Forward	<i>nad1a</i>	ZF5
	5'AAGGCTACGTACGCACCGACTC3'	Reverse		
22	5'ACATGGTTTACGCGTACTGGTT 3'	Forward	<i>mttB</i>	ZB10
	5'CCGGGGGTGTGGAAGAG 3'	Reverse		
23	5'TTCGCCTGCCTTTCTATCTGA 3'	Forward	<i>rps12</i>	ZB10
	5'AGCCCACATGCCCACTCTT 3'	Reverse		
24	5'CACCGCCTAGCTCGAACTGAACG3'	Forward	<i>rps7</i>	ZB6 and
	5'GCGGCATAGGGGAAAAAGCACA3'	Reverse		ZG5
25	5'AAGGGAGCCCCGACGGTGAAGA3'	Forward	<i>nad7a</i>	ZD10
	5'GGAGGAAGGGCGGGCAGCAGGTA3'	Reverse		
26	5'GCATCCCGGGAGCAGACC3'	Forward	<i>rps19-p</i>	ZD10
	5'AACGCGTTTGATTCCTTCCTT3'	Reverse		

**Table 2.** Genes in wheat mitochondrial genome.

Gene <sup>a</sup>	Size (bp)	Position		Strand <sup>b</sup>
		From	To	
Complex V				
<i>atp1</i>	1530	6832	8361	+
<i>atp4</i>	579	196581	197159	-
<i>atp6-1</i>	1161	19132	20292	-

**Table 2 (contd)**

Gene <sup>a</sup>	Size (bp)	Position		Strand <sup>b</sup>
		From	To	
<i>atp6-2</i>	1161	85008	86168	–
<i>atp8-2</i>	471	233390	233860	–
<i>atp8-1</i>	471	338881	339351	–
<i>atp9</i>	243	8824	9066	+
Cytochrome c biogenesis				
<i>ccmB</i>	621	185575	186195	–
<i>ccmC</i>	723	156955	157677	+
<i>ccmFCa</i>	755	99514	100268	+
<i>ccmFCb</i>	559	101280	101838	+
<i>ccmFN</i>	1770	50112	51881	–
Complex III & IV				
<i>cob</i>	1197	63122	64318	–
<i>cox1</i>	1575	245282	246856	+
<i>cox2a</i>	390	224809	225198	–
<i>cox2b</i>	393	223197	223589	–
<i>cox3</i>	798	28053	28850	–
Others				
<i>matR</i>	2037	44172	46208	–
<i>mttB</i>	816	314989	315804	+
Complex I				
<i>nad1a</i>	386	306342	306727	+
<i>nad1b</i>	82	17602	17683	–
<i>nad1c</i>	192	15988	16179	–
<i>nad1d</i>	59	282280	282338	–
<i>nad1e</i>	259	43394	43652	–
<i>nad2a</i>	153	182358	182510	–
<i>nad2b</i>	392	181152	181543	–
<i>nad2c</i>	161	210080	210240	–
<i>nad2d</i>	573	207090	207662	–
<i>nad2e</i>	188	205499	205686	–
<i>nad3</i>	357	341096	341452	–
<i>nad4a</i>	461	135541	136001	+
<i>nad4b</i>	515	137026	137540	+
<i>nad4c</i>	423	140981	141403	+
<i>nad4d</i>	89	143059	143147	+
<i>nad4L</i>	303	421630	421932	–
<i>nad5a</i>	231	295839	296069	–
<i>nad5b</i>	1216	293761	294976	–
<i>nad5c</i>	21	43010	43030	–
<i>nad5d</i>	395	111614	112008	+
<i>nad5e</i>	150	112942	113091	+
<i>nad6</i>	744	280546	281289	–
<i>nad7a</i>	143	409837	409979	+
<i>nad7b</i>	69	410793	410861	+
<i>nad7c</i>	467	412174	412640	+
<i>nad7d</i>	244	413639	413882	+
<i>nad7e</i>	262	415582	415843	+
<i>nad9</i>	864	211707	212570	–
Ribosomal proteins				
<i>rps13</i>	351	18628	18978	–
<i>rpl16</i>	558	90168	90725	–
<i>rpl5</i>	570	29778	30347	–
<i>rps1</i>	525	49341	49865	–
<i>rps12</i>	378	340674	341051	–

**Table 2** (contd)

Gene <sup>a</sup>	Size (bp)	Position		Strand <sup>b</sup>
		From	To	
<i>rps19-p</i>	198	422831	423028	–
<i>rps2</i>	1083	215088	216170	+
<i>rps3a</i>	74	93925	93998	–
<i>rps3b</i>	1612	90574	92185	–
<i>rps4</i>	1074	273583	274656	–
<i>rps7</i>	447	379577	380023	–
<i>rpl2-p</i>	169	283447	283615	–
<i>rRNAs</i>				
<i>rrn18-1</i>	1955	300877	302831	+
<i>rrn18-2</i>	1955	393727	395681	–
<i>rrn18-3</i>	1955	56762	58716	–
<i>rrn26-1</i>	3467	371219	374685	–
<i>rrn26-2</i>	3467	259481	262947	–
<i>rrn26-p</i>	422	170630	171051	–
<i>rrn5-1</i>	122	302946	303067	+
<i>rrn5-2</i>	122	393491	393612	–
<i>rrn5-3</i>	122	56526	56647	–
<i>tRNAs</i>				
<i>Ala-tRNA 5' ex*</i>	38	74738	74775	+
<i>Ala-tRNA 3' ex*</i>	35	75581	75615	+
<i>Ala-tRNA*</i>	73			
<i>Cys-tRNA*</i>	71	97420	97490	+
<i>Asp-tRNA</i>	74	222077	222150	–
<i>Asp-tRNA</i>	74	429341	429414	–
<i>Asn-tRNA*</i>	72	428634	428705	+
<i>Ile-tRNA</i>	73	430118	430191	–
<i>Gln-tRNA</i>	72	174907	174978	+
<i>Gln-tRNA</i>	72	193279	193350	+
<i>Gln-tRNA</i>	72	266803	266874	+
<i>Glu-tRNA</i>	72	27050	27121	–
<i>Phe-tRNA*</i>	73	382953	383025	–
<i>Lys-tRNA</i>	73	178637	178709	+
<i>Lys-tRNA</i>	73	270533	270605	+
<i>Lys-tRNA</i>	73	442700	442772	+
<i>Met-tRNA</i>	74	58718	58791	–
<i>Met-tRNA</i>	74	300802	300875	+
<i>Met-tRNA</i>	74	395683	395756	–
<i>Met-tRNA</i>	73	436154	436226	–
<i>Pro-tRNA</i>	75	117692	117766	+
<i>Pro-tRNA</i>	75	305092	305166	+
<i>Ser-tRNA*</i>	87	383441	383527	–
<i>Ser-tRNA</i>	87	408502	408588	+
<i>Ser-tRNA</i>	88	341965	342052	–
<i>Trp-tRNA*</i>	74	445612	445685	+
<i>Tyr-tRNA</i>	83	210877	210959	–

<sup>a</sup> Lower-case letters, exons of a protein-coding gene.<sup>b</sup> Plus and minus, coded by the forward and reverse strand.

\*Probable chloroplast origin.

**Table 3.**  $K_a/K_s$  ratio of all orthologous gene-pairs.

Gene	Intra-monocotyledon <sup>b</sup>				Intra-dicotyledon <sup>c</sup>		
	<i>Zea</i>	Rice	Sorghum	<i>Tripsacum</i>	Brass	Sugar beet	Tabacum
<i>atpl</i>	0.15	0.34	0.08	0.20	0.35	0.27	0.31

**Table 3** (contd)

Gene	Intra-monocotyledon <sup>b</sup>				Intra-dicotyledon <sup>c</sup>		
	<i>Zea</i>	Rice	Sorghum	<i>Tripsacum</i>	Brass	Sugar beet	Tabacum
<i>atp4</i>	1.11	0.79	0.52	1.05	2.69	1.18	1.62
<i>atp8</i>	0.33	0.41	0.22	0.19	0.16	0.50	0.84
<i>atp9</i>	0.13	0.20	0.14	0.34	0.00	0.10	0.41
<i>ccmB</i>	∞ <sup>a</sup>	∞	∞	∞	0.74	1.15	0.98
<i>ccmC</i>	∞	0.00	∞	0.34	∞	0.41	0.56
<i>ccmFC</i>	0.74	1.05	1.09	0.74	0.46	0.66	0.57
<i>ccmFN</i>	0.62	0.65	0.42	0.46	0.97	0.66	0.48
<i>cob</i>	0.36	0.18	0.45	0.28	0.00	0.24	0.10
<i>cox1</i>	0.11	0.09	0.10	0.12	0.06	0.04	0.24
<i>cox2</i>	0.22	0.25	0.37	0.31	∞	0.54	0.60
<i>cox3</i>	1.31	1.31	1.31	1.31	0.21	0.24	0.42
<i>nd1</i>	0.35	0.52	0.35	0.26	0.11	0.37	0.53
<i>nd2</i>	1.71	∞	1.71	1.71	0.34	0.52	0.67
<i>nd3</i>	0.30	∞	∞	0.30	0.00	0.37	0.45
<i>nd4</i>	0.12	0.12	0.08	0.12	0.13	0.49	0.54
<i>nd4L</i>	0.28	∞	∞	∞	0.28	0.38	0.21
<i>nd5</i>	0.14	0.00	0.09	0.14	0.25	0.36	0.50
<i>nd6</i>	0.67	0.30	0.63	0.69	0.00	0.44	0.45
<i>nd7</i>	0.18	0.15	0.10	0.07	∞	0.62	0.73
<i>nd9</i>	0.20	∞	0.13	0.18	0.19	0.52	0.67
<i>rpl5</i>	–	–	–	–	0.08	0.52	0.35
<i>rpl16</i>	1.20	0.39	0.89	1.19	–	–	–
<i>rps1</i>	0.73	1.56	0.62	0.66	–	–	–
<i>rps12</i>	0.00	0.09	0.00	0.00	–	–	–
<i>rps13</i>	0.53	0.27	0.53	0.53	–	–	–
<i>rps2</i>	0.79	0.85	0.81	0.86	–	–	–
<i>rps3</i>	0.57	0.63	0.61	0.70	0.55	0.53	0.61
<i>rps4</i>	0.65	1.20	0.69	0.58	0.46	1.12	0.56
<i>rps7</i>	0.00	0.31	0.30	0.00	–	–	–

<sup>a</sup> The value of  $K_a/K_s$  shows infinite because of  $K_s$  was estimated to be zero.

<sup>b</sup> In the monocotyledon, the genes of wheat are used as outgroup.

<sup>c</sup> In the dicotyledon, the genes of *Arabidopsis* are used as outgroup. The genes of NADH dehydrogenase are abridged as *nd*.