

## Analysis of codon usage patterns of the chloroplast genomes in the Poaceae family

Yuerong Zhang<sup>A,B,E</sup>, Xiaojun Nie<sup>B,E</sup>, Xiaoou Jia<sup>B</sup>, Cunzhen Zhao<sup>D</sup>, Siddanagouda S. Biradar<sup>B</sup>, Le Wang<sup>B</sup>, Xianghong Du<sup>C</sup> and Song Weining<sup>A,B,C,F</sup>

<sup>A</sup>State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A&F University, Yangling 712100, Shaanxi, China.

<sup>B</sup>College of Agronomy, Northwest A&F University, Yangling 712100, Shaanxi, China.

<sup>C</sup>Yangling Branch of China Wheat Improvement Centre, Northwest A&F University, Yangling 712100, Shaanxi, China.

<sup>D</sup>College of Animal Science, Northwest A&F University, Yangling 712100, Shaanxi, China.

<sup>E</sup>These authors contributed equally to this work.

<sup>F</sup>Corresponding author. Email: [sweining2002@yahoo.com](mailto:sweining2002@yahoo.com)

### Supplementary material

**Table S1. Correlation analysis of gene length with ENc, GC<sub>3S</sub> and CAI.**

*Acidosasa purpurea*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.154	51.065±1.407	0.293±0.002
2	2000 ≤ and < 2999	4	0.166±0.022	50.053±2.933	0.282±0.040
3	1000 ≤ and < 1999	13	0.190±0.054	48.396±2.927	0.279±0.032

4	500 ≤ and < 999	17	0.166±0.020	50.046±3.731	0.277±0.037
5	< 500	15	0.155±0.025	49.163±7.186	0.267±0.053

*Agrostis stolonifera*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.154±0.000	50.875±1.054	0.286±0.001
2	2000 ≤ and < 2999	4	0.169±0.023	49.208±2.235	0.268±0.036
3	1000 ≤ and < 1999	13	0.193±0.057	47.378±2.993	0.268±0.026
4	500 ≤ and < 999	17	0.164±0.018	48.984±3.149	0.270±0.037
5	< 500	15	0.157±0.023	50.5000±6.291	0.268±0.048

*Anomochloa marantoidea*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.158±0.001	50.600±1.414	0.286±0.010
2	2000 ≤ and < 2999	4	0.168±0.023	49.838±2.537	0.279±0.044
3	1000 ≤ and < 1999	13	0.193±0.059	47.705±3.198	0.274±0.033
4	500 ≤ and < 999	16	0.163±0.020	51.111±5.145	0.274±0.039
5	< 500	17	0.160±0.025	48.308±5.272	0.272±0.049

*Bambusa emeiensis*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.155±0.001	50.940±1.853	0.288±0.013
2	2000 ≤ and < 2999	4	0.168±0.023	50.188±2.664	0.283±0.040
3	1000 ≤ and < 1999	13	0.191±0.054	48.241±2.699	0.280±0.035
4	500 ≤ and < 999	17	0.162±0.019	49.681±4.529	0.279±0.036
5	< 500	16	0.151±0.028	50.161±5.941	0.285±0.076

*Bambusa oldhamii*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.155±0.001	51.000±1.853	0.287±0.011
2	2000 ≤ and < 2999	4	0.168±0.023	50.063±2.683	0.283±0.040
3	1000 ≤ and < 1999	12	0.193±0.055	48.109±2.838	0.281±0.036
4	500 ≤ and < 999	17	0.162±0.019	49.691±4.493	0.281±0.037
5	< 500	15	0.155±0.025	49.740±6.123	0.269±0.050

*Coix lacryma-jobi*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s

1	≥3000	2	0.154±0.004	51.470±1.230	0.295±0.005
2	2000 ≤ and < 2999	4	0.167±0.025	48.978±3.757	0.270±0.044
3	1000 ≤ and < 1999	12	0.195±0.057	47.914±2.115	0.277±0.030
4	500 ≤ and < 999	18	0.165±0.022	49.974±3.621	0.284±0.064
5	< 500	16	0.155±0.027	48.811±6.221	0.263±0.052

*Dendrocalamus latiflorus*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.154±0.001	51.055±2.086	0.288±0.016
2	2000 ≤ and < 2999	4	0.168±0.023	50.080±2.997	0.281±0.043
3	1000 ≤ and < 1999	13	0.189±0.051	48.257±2.613	0.280±0.036
4	500 ≤ and < 999	17	0.162±0.017	50.079±4.282	0.282±0.036
5	< 500	15	0.156±0.026	49.805±6.310	0.269±0.049

*Ferocalamus rimosivaginus*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.153±0.001	50.860±0.990	0.289±0.005
2	2000 ≤ and < 2999	4	0.167±0.023	49.803±2.982	0.279±0.044
3	1000 ≤ and < 1999	13	0.190±0.054	48.403±2.922	0.279±0.034

4	500 ≤ and < 999	16	0.165±0.020	50.511±3.761	0.278±0.039
5	< 500	17	0.153±0.029	49.384±6.763	0.280±0.078

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*Festuca arundinacea*

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Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.153±0.003	51.970±1.485	0.290±0.006
2	2000 ≤ and < 2999	4	0.171±0.021	48.763±3.536	0.266±0.043
3	1000 ≤ and < 1999	13	0.190±0.052	47.546±2.397	0.268±0.031
4	500 ≤ and < 999	13	0.165±0.016	51.115±4.444	0.276±0.035
5	< 500	16	0.151±0.026	50.001±5.284	0.256±0.051

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*Hordeum vulgare subsp. Vulgare*

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Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.156±0.003	51.205±1.068	0.284±0.001
2	2000 ≤ and < 2999	4	0.168±0.023	48.618±3.092	0.263±0.043
3	1000 ≤ and < 1999	13	0.194±0.057	47.012±2.498	0.266±0.032
4	500 ≤ and < 999	17	0.161±0.018	49.256±3.004	0.269±0.034
5	< 500	15	0.154±0.022	49.499±5.615	0.269±0.051

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*Indocalamus longiauritus*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.155±0.002	51.185±1.450	0.294±0.004
2	2000 ≤ and < 2999	4	0.168±0.023	49.888±3.026	0.281±0.040
3	1000 ≤ and < 1999	13	0.189±0.054	48.368±2.864	0.280±0.034
4	500 ≤ and < 999	16	0.165±0.020	50.184±3.556	0.278±0.037
5	< 500	16	0.155±0.026	49.312±7.097	0.266±0.052

*Lolium perenne*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.155±0.004	51.470±0.721	0.289±0.000
2	2000 ≤ and < 2999	4	0.170±0.021	48.060±3.368	0.263±0.036
3	1000 ≤ and < 1999	13	0.191±0.055	47.355±2.531	0.265±0.031
4	500 ≤ and < 999	16	0.162±0.017	50.203±2.931	0.274±0.032
5	< 500	16	0.151±0.024	49.000±5.128	0.254±0.047

*Oryza nivara*

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s

1	≥3000	2	0.161±0.002	51.540±1.245	0.295±0.001
2	2000 ≤ and < 2999	4	0.169±0.024	49.975±2.502	0.272±0.045
3	1000 ≤ and < 1999	13	0.193±0.054	48.109±2.350	0.279±0.028
4	500 ≤ and < 999	17	0.165±0.020	49.919±3.958	0.287±0.053
5	< 500	22	0.162±0.029	50.552±6.520	0.306±0.082

*Oryza sativa* Indica Group

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.160±0.001	51.495±1.181	0.296±0.002
2	2000 ≤ and < 2999	4	0.169±0.024	49.980±2.505	0.272±0.045
3	1000 ≤ and < 1999	10	0.202±0.056	48.275±2.633	0.283±0.024
4	500 ≤ and < 999	11	0.165±0.018	49.265±2.733	0.272±0.039
5	< 500	16	0.160±0.023	49.878±7.834	0.275±0.053

*Oryza sativa* Japonica

Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.160±0.001	51.485±1.237	0.295±0.001
2	2000 ≤ and < 2999	4	0.168±0.024	50.065±2.311	0.273±0.042
3	1000 ≤ and < 1999	13	0.193±0.054	48.032±2.343	0.278±0.028

4	500 ≤ and < 999	17	0.166±0.020	49.964±4.068	0.286±0.053
5	< 500	21	0.160±0.032	50.168±6.584	0.293±0.073

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*Panicum virgatum*

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Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.156±0.001	50.915±0.969	0.288±0.003
2	2000 ≤ and < 2999	4	0.169±0.022	49.723±3.154	0.273±0.040
3	1000 ≤ and < 1999	13	0.192±0.056	47.939±2.826	0.274±0.041
4	500 ≤ and < 999	16	0.165±0.020	49.558±3.063	0.276±0.040
5	< 500	17	0.153±0.026	48.776±6.590	0.276±0.080

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*Phyllostachys edulis*

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Group	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	2	0.154±0.001	51.135±1.379	0.293±0.002
2	2000 ≤ and < 2999	4	0.168±0.023	49.900±3.039	0.281±0.040
3	1000 ≤ and < 1999	13	0.190±0.054	48.336±2.853	0.279±0.033
4	500 ≤ and < 999	16	0.165±0.020	50.132±3.733	0.277±0.037
5	< 500	17	0.152±0.028	49.683±6.691	0.281±0.077

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*Phyllostachys nigra* var. *henonis*



Group	Gene length(bp)	Number	$\bar{x} \pm SD^*$		
			CAI	NC	GC3s
1	$\geq 3000$	2	0.154 $\pm$ 0.001	51.135 $\pm$ 1.379	0.293 $\pm$ 0.002
2	2000 $\leq$ and $<$ 2999	4	0.168 $\pm$ 0.023	49.888 $\pm$ 3.026	0.281 $\pm$ 0.040
3	1000 $\leq$ and $<$ 1999	13	0.190 $\pm$ 0.054	48.387 $\pm$ 2.806	0.280 $\pm$ 0.033
4	500 $\leq$ and $<$ 999	16	0.165 $\pm$ 0.020	50.143 $\pm$ 3.737	0.277 $\pm$ 0.037
5	$<$ 500	17	0.152 $\pm$ 0.028	49.641 $\pm$ 6.691	0.281 $\pm$ 0.077

*Saccharum hybrid cultivar*

Group	Gene length(bp)	Number	$\bar{x} \pm SD^*$		
			CAI	NC	GC3s
1	$\geq 3000$	2	0.156 $\pm$ 0.005	51.530 $\pm$ 1.230	0.295 $\pm$ 0.001
2	2000 $\leq$ and $<$ 2999	4	0.168 $\pm$ 0.026	48.983 $\pm$ 3.912	0.271 $\pm$ 0.050
3	1000 $\leq$ and $<$ 1999	10	0.197 $\pm$ 0.064	47.219 $\pm$ 2.767	0.265 $\pm$ 0.043
4	500 $\leq$ and $<$ 999	14	0.170 $\pm$ 0.019	49.639 $\pm$ 2.758	0.275 $\pm$ 0.052
5	$<$ 500	19	0.152 $\pm$ 0.029	49.340 $\pm$ 6.625	0.284 $\pm$ 0.081

*Saccharum hybrid cultivar NCo 310*

Group	Gene length(bp)	Number	$x \pm SD^*$		
			CAI	NC	GC3s
1	$\geq 3000$	2	0.156 $\pm$ 0.005	51.530 $\pm$ 1.230	0.295 $\pm$ 0.001
2	2000 $\leq$ and $<$ 2999	4	0.168 $\pm$ 0.026	48.983 $\pm$ 3.912	0.271 $\pm$ 0.050
3	1000 $\leq$ and $<$ 1999	12	0.180 $\pm$ 0.044	47.660 $\pm$ 1.855	0.266 $\pm$ 0.042
4	500 $\leq$ and $<$ 999	19	0.165 $\pm$ 0.021	50.363 $\pm$ 3.451	0.290 $\pm$ 0.059
5	$<$ 500	21	0.150 $\pm$ 0.027	49.323 $\pm$ 6.405	0.284 $\pm$ 0.078

*Sorghum bicolor*

Group	Gene length(bp)	Number	$x \pm SD^*$		
			CAI	NC	GC3s
1	$\geq 3000$	2	0.155 $\pm$ 0.004	51.430 $\pm$ 1.400	0.294 $\pm$ 0.001
2	2000 $\leq$ and $<$ 2999	4	0.168 $\pm$ 0.026	49.100 $\pm$ 3.859	0.274 $\pm$ 0.049
3	1000 $\leq$ and $<$ 1999	13	0.191 $\pm$ 0.057	47.350 $\pm$ 2.468	0.270 $\pm$ 0.038
4	500 $\leq$ and $<$ 999	16	0.164 $\pm$ 0.017	50.432 $\pm$ 3.172	0.273 $\pm$ 0.037
5	$<$ 500	17	0.157 $\pm$ 0.026	48.222 $\pm$ 6.192	0.263 $\pm$ 0.050

*Triticum aestivum*

Group	Gene length(bp)	Number	$x \pm SD^*$		
			CAI	NC	GC3s

p		r			
1	≥3000	2	0.158±0.001	51.195±1.266	0.284±0.000
2	2000 ≤ and < 2999	4	0.165±0.022	48.848±3.073	0.265±0.045
3	1000 ≤ and < 1999	13	0.194±0.057	47.218±2.557	0.268±0.029
4	500 ≤ and < 999	18	0.162±0.019	48.751±3.217	0.270±0.035
5	< 500	15	0.153±0.021	49.587±5.831	0.266±0.051

*Brachypodium distachyon*

Grou p	Gene length(bp)	Number	x ± SD*		
			CAI	NC	GC3s
1	≥3000	1	0.151	50.97	0.292
2	2000 ≤ and < 2999	4	0.167±0.020	49.063±2.369	0.271±0.035
3	1000 ≤ and < 1999	14	0.187±0.052	47.273±2.700	0.274±0.033
4	500 ≤ and < 999	17	0.163±0.016	50.212±2.887	0.279±0.038
5	< 500	18	0.155±0.022	49.616±6.396	0.265±0.053

**Table S2. Summary of correlation between the codon usage and amino acid usage indices in the chloroplast genomes of rest species**

No. of axis		CAI														
		AM	CL	SH1	SH2	SB	ZM	AS	BD	FA	LP	ON	OI	BE	BO	DL
Axis1		0.16	-0.09	0	0.04	0.23	0.17	-0.21	0.12	0.24	-0.01	-0.07	-0.03	0.27	0.02	0.01
Axis2		-0.50**	0.1	-0.08	0.18	0.53**	0.16	-0.49**	-0.25	-0.34*	0.50**	0.1	0.25	-0.42**	-0.62**	0.58**
Axis3		0.41**	0.72**	-0.13	0.16	-0.1	-0.65**	0.1	0.26	-0.30*	0.11	0.42**	0.12	0.51**	0.08	0.07
Axis4		0.29*	0.13	0.22	0.56**	0.23	0.26*	-0.09	0.55**	0.30*	-0.25	0.25	0.39**	-0.26	-0.38**	0.12
No. of axis		NC														
		AM	CL	SH1	SH2	SB	ZM	AS	BD	FA	LP	ON	OI	BE	BO	DL
Axis1		0.2	-0.1	-0.62**	0.55**	-0.05	-0.54**	0.34*	-0.41**	-0.23	-0.23	0.52**	0.43**	-0.24	-0.16	0.11
Axis2		0.34*	0.54**	0.03	-0.23	0.11	-0.17	0.04	0.09	0.40**	-0.13	-0.24	0.11	0.16	0.14	-0.05
Axis3		0.01	-0.01	-0.19	-0.16	0.50**	-0.08	0.27	0.02	-0.03	0.08	0.09	0.18	-0.06	0.34*	0.33*
Axis4		-0.29*	0.12	-0.21	-0.15	0.2	0.08	0.40**	-0.06	0.34*	0.42**	0.07	0.53**	-0.44**	-0.1	0.24
No. of axis		GC3s														
		AM	CL	SH1	SH2	SB	ZM	AS	BD	FA	LP	ON	OI	BE	BO	DL
Axis1		-0.05	-0.12	-0.81**	0.81**	0.12	-0.79**	0.2	-0.39**	-0.03	-0.06	0.79**	0.2	-0.2	-0.01	0.04
Axis2		0.25	0.68**	0.16	-0.18	0.25	-0.11	-0.21	0.09	0.25	0.27	0.23	0.06	-0.03	-0.04	0.1
Axis3		0.18	0.23	-0.26*	-0.17	0.35**	-0.07	0.14	0.02	-0.18	0.01	0.11	0.45**	0.11	0.40**	0.33*
Axis4		-0.19	0.09	-0.2	0.01	0.34**	0.12	0.25	0.28*	0.56**	0.28*	0.25	0.47**	-0.57**	-0.11	0.36**
No. of axis		GC														
		AM	CL	SH1	SH2	SB	ZM	AS	BD	FA	LP	ON	OI	BE	BO	DL
Axis1		-0.04	-0.02	-0.40**	0.48**	-0.06	-0.44**	0.16	-0.06	-0.03	0.06	0.45**	0.2	0.26	-0.16	0.16
Axis2		0.08	0.29*	0.09	-0.12	0.15	-0.1	-0.14	-0.23	0.08	0.25	0.09	0	0.02	-0.19	0.18
Axis3		0.22	0.11	-0.18	-0.03	0.15	-0.17	0.16	-0.1	-0.25	-0.09	-0.05	0.22	0.14	0.1	0.09
Axis4		0.02	-0.06	0.1	0.2	0.28*	0.11	-0.29*	0.22	0.12	0.21	0.21	0.05	0.02	-0.05	-0.08

Note: AM: *Anomochloa marantoidea*; CL: *Coix lacryma-jobi*; SH1: *Saccharum* hybrid cultivar NCo310; SH2: *Saccharum officinarum* hybrid SP-80-3280; SB: *Sorghum bicolor*; ZM: *Zea mays*; AS: *Agrostis stolonifera*; BD: *Brachypodium distachyon*; FA: *Festuca arundinacea*; ON: *Oryza nivara*; OI: *Oryza sativa* cv. 93-11; BE: *Bambusa emeiensis*; DL: *Dendrocalamus latiflorus*; ON: *Oryza sativa* cv Nipponbare; TA: *Triticum aestivum*; HV: *Hordeum vulgare* ssp. *vulgare*.

\*Represents significance at  $P < 0.05$ ; \*\*at  $P < 0.01$

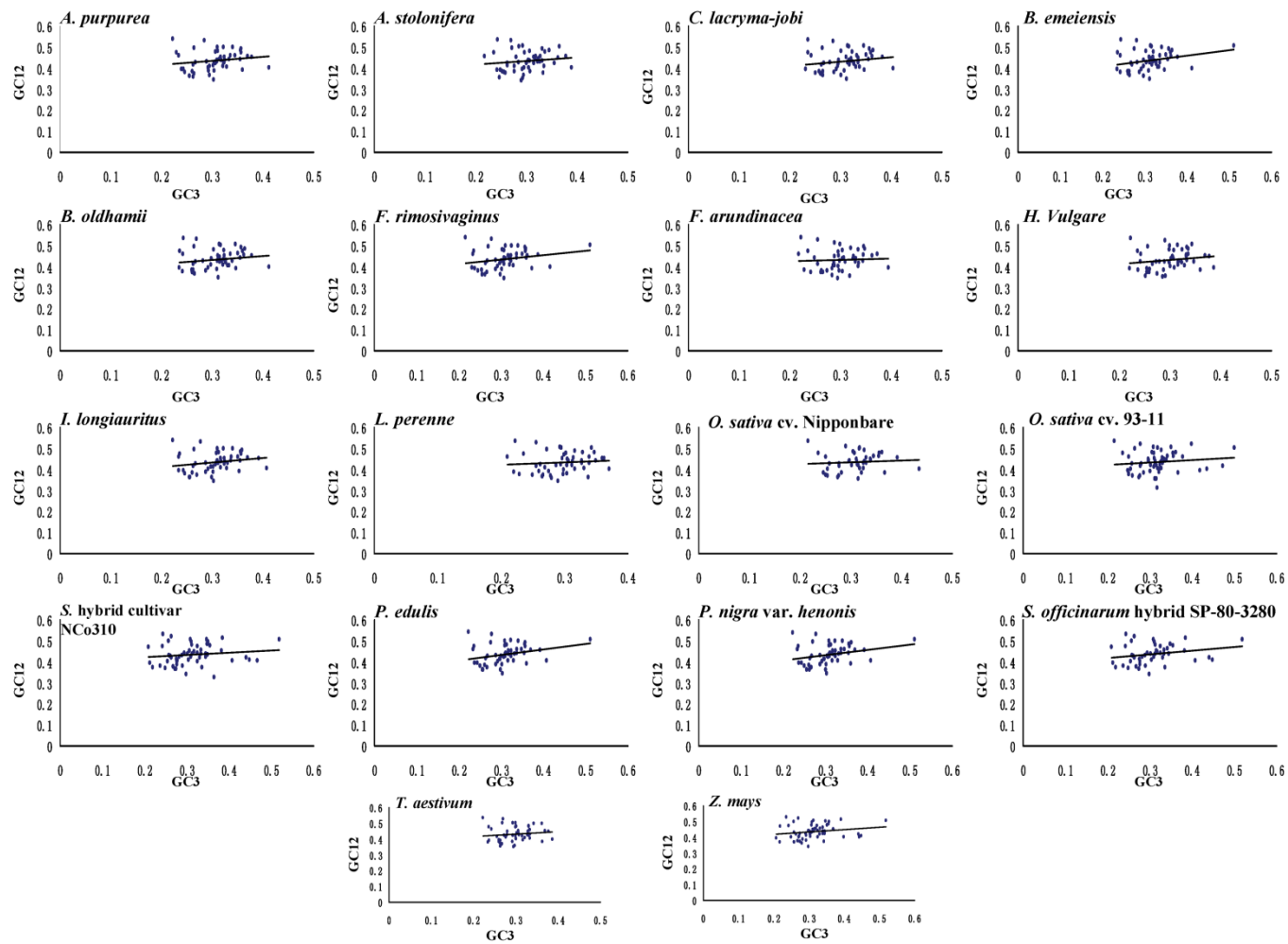


Fig. S1

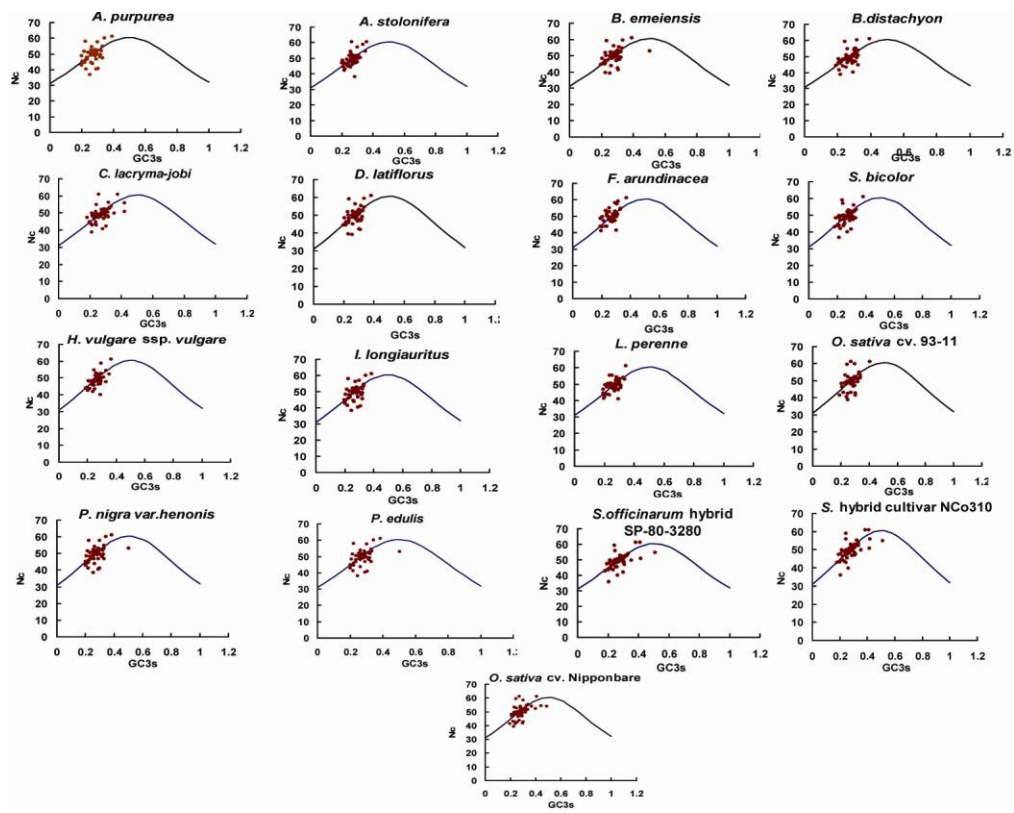


Fig. S2

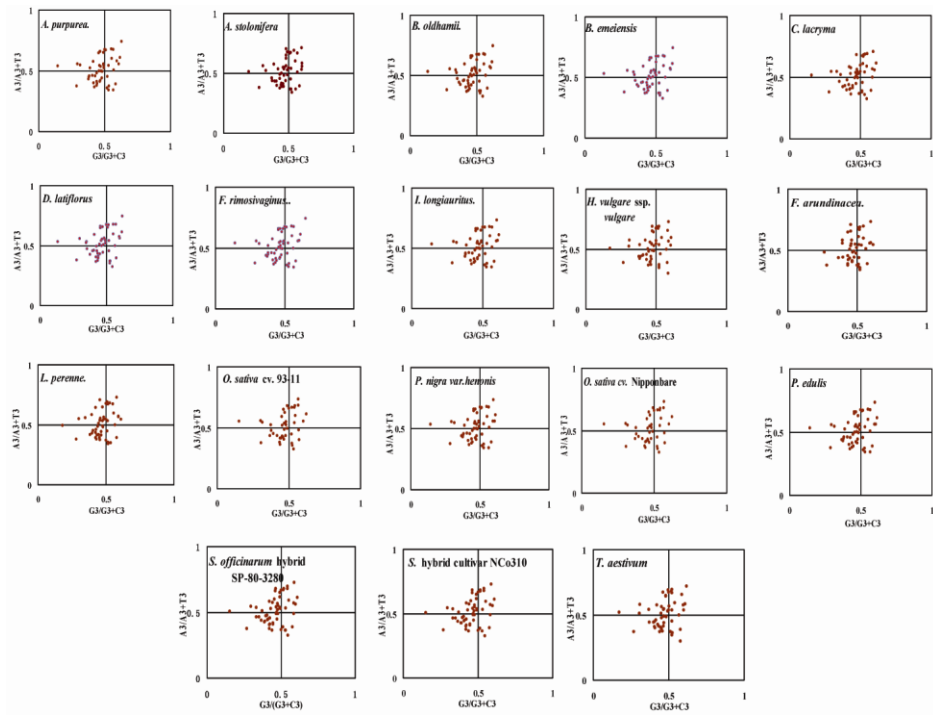


Fig. S3