

## A6 Comparison of *indica-japonica* differentiation of cpDNA and mtDNA in cultivated, weedy, and wild species of rice (*O. sativa* complex)

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### Objectives

Phylogenetic analysis of chloroplast and mitochondrial genomes offers an effective way to study evolution of the rice species. This study was aimed to investigate *indica-japonica* differentiation of cpDNA and mtDNA and its evolutionary dynamics in cultivated, weedy, and wild rice.

### Materials and Methods

The study involved ten *Oryza* species consisting of a total of 96 accessions, in which the majority was *Oryza sativa* complex including various modern cultivars, landraces, weedy rice, and wild rice collected from worldwide.

PCR-RFLP approach as described by Chen et al. (2000) was employed to detect cpDNA and mtDNA marker specific to *indica* and *japonica*.

### Results and Discussion

1. Except *O. longistaminata*, all cultivated, weedy, and wild species of *O. sativa* complex appeared *indica-japonica* differentiation of cpDNA and mtDNA at regions of cp-ORF-100 and mt-*nad4*(2)-*nad4*(3), respectively (Table 1).
2. Progress of *indica-japonica* differentiation of cpDNA and mtDNA was variable from species to species.
3. In cultivated species (*O. sativa*.), all strain showed the identical specific marker in cpDNA and mtDNA, indicating that *indica-japonica* differentiation between cpDNA and mtDNA was highly synchronous in cultivated rice.
4. In weedy (*O. sativa*) and wild species (*O. rufipogon*), some of strains carried different specific markers in cpDNA and mtDNA, suggesting that *indica-japonica* differentiation between cpDNA and mtDNA was somewhat asynchronous in weedy and wild rice.

Table 1. Comparison genomic differentiation of chloroplast and mitochondria in *O. sativa* complex with various selected rice strains.

Strain Name	Accession Number	Isozyme group <sup>a</sup>	cpDNA <sup>b</sup> ORF100	mtDNA <sup>c</sup> <i>nad4(2)-nad4(3)</i>
<i>O. sativa</i> IR36	83430	I	D	A
<i>O. sativa</i> T65	83428	J	N	B
<i>O. sativa</i> Luzigu	86018	J	N	B
<i>O. sativa</i> Gangzhagu	86128	J	N	B
<i>O. sativa</i> Erlaiding	86119	J	N	B
<i>O. sativa</i> Lutao	61286	J	N	B
<i>O. sativa</i> Heidaogu	63399	I	N	A
<i>O. sativa</i> Ssalshare	64246	J	N	B
<i>O. sativa</i> W1714	63393	I	N	A
<i>O. sativa</i> US2	63395	I	D	A
<i>O. sativa</i> US1	63394	I	N	A
<i>O. rufipogon</i>	CYWR-1	J	D	A
<i>O. rufipogon</i>	CYWR-2	J	D	A
<i>O. rufipogon</i>	CBWR-1	I	N	C
<i>O. rufipogon</i>	W1944	M	N	B
<i>O. rufipogon</i>	W0120	M	N	A
<i>O. barthii</i>	WI 10	I	D	A
<i>O. barthii</i>	WI 13	I	N	-
<i>O. merid.</i>	WS 35	M	N	C
<i>O. merid.</i>	WS 37	I	D	C
<i>O. longistaminata?</i>	6209-3 (IRRI)	-	N	C

<sup>a</sup>I: indica, J: japonica, classified by the averaged D scores at 18 isozyme loci; M, off-type;

<sup>b</sup>D, N: chloroplast DNA of deletion (D) and non-deletion (N) types at ORF100;

<sup>c</sup>A, B, C: mitochondrial DNA specific to indica (A), japonica (B) and off-type (C) at *nad4(2)-nad4(3)*;

### Reference Cited

- Chen L.J., H.S. Suh, and D.S. Lee. 2000. PCR-RFLP analysis of cpDNA in the genus *Oryza* *Korean Journal of Crop Sciences*. 45(1):66-67.
- Chen L.J., H.S. Suh, and D.S. Lee. 2000. PCR-RFLP analysis of mtDNA in the genus *Oryza* *Korean Journal of Crop Sciences*. 45(1):67-68.