

Related characters of panicle density in a dwarf mutant with lax panicles and its parent cultivar, Fujiminori.^a

Year	Seeding time	Cultivar and strain	Culm length (cm)	Panicle length (cm)	Panicle density ^b	Spikelets (no.)	Fertility (%)	Primary branch (no.)	Primary branch length (cm)	Secondary branches (no.)	Rachis length (cm)
1992	Normal seeding	Fujiminori	88.0	24.1	1.58	158.4	96.0	10.8	8.0	32.8	18.7
		Dwarf mutant	74.8**	21.6*	1.11*	58.6**	66.2**	8.3**	7.3	16.5**	17.2
1994	Early seeding	Fujiminori	95.3	21.8	1.24	111.5	89.5	10.5	6.3	18.3	16.6
		Dwarf mutant	84.2**	18.8*	1.01**	68.1**	52.1**	7.2**	6.8	11.3**	12.7**
1994	Late seeding	Fujiminori	62.2	14.0	1.10	47.7	87.6	5.8	6.0	6.6	8.6
		Dwarf mutant	52.6**	12.8	1.09	39.9	34.5**	6.2	4.7*	5.1	8.7

^a* and ** = significant at the 1 and 0.1% level, respectively. ^b Panicle density = no. of spikelets/total length of rachis and primary branches (in cm) (Futsuhara et al 1979).

cultivar under all three conditions, was further reduced under late seeding condition (during an abnormally hot summer). Premature heading occurred in all the mutant plants grown under late seeding condition. Most of the panicles with premature heading showed malformed floral organs such as degenerated ovary,

multi-ovary, and long empty glumes. Late sowing also promoted premature heading. The results indicate that heat stress tolerance was depressed and premature heading was enhanced in the dwarf mutant.

Induced dwarf mutants with simultaneous changes in many traits are being used

in developmental genetic research to understand pleiotropic gene action.

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Genetic differentiation between Japanese lowland and upland rices

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Upland and lowland varieties are cultivated under different conditions in Japan. Lowland rice with useful agronomic traits is a major crop. In contrast, upland rice, useful as a genetic source of stress resistance to blast, is regarded as a minor crop. Thus, diagnostic genetic markers to evaluate upland rice will be useful to help improve resistance in modern rice varieties.

Isozyme genotypes were surveyed among Japanese lowland and upland traditional cultivars. Seventeen isozyme loci were monitored, and different genotypes were scored. A total of 27 genotypes were recognized, 16 for lowland rice and 13 for upland cultivars. Genotypic diversity for upland cultivars was 0.072, which is surprisingly higher than that of lowland cultivars (0.020). Such high genotypic diversity could not be seen from the data of Glaszmann (1987). Four hundred and fifty lowland and 200 upland cultivars were classified either as japonica or indica using discriminant score based on 11 loci (Ishikawa et al 1991, Sano and Morishima

1991). Except for five lowland and five upland cultivars classified as indicas, the rest of the cultivars were japonicas (Table 1). The 10 indicas were characterized with allele 3 for *Pgd1*, which is not common among other cultivars in Japan. Characteristics of the indica cultivars, such as short apiculus hair (APH) averaging 0.36 ± 0.11 mm, slender hull type represented by hull

Table 1. Genotypic variation for *Pgd* among Japanese lowland and upland rices.

Varietal type	<i>Pgd1-1</i>	<i>Pgd1-2</i>	<i>Pgd1-3</i>
Lowland			
Indica	0	0	5
Japonica	445	0	0
Upland			
Indica	1	0	4
Japonica	26	169	0

length-width ratio (L/W; av of 2.86 ± 0.14), and positive phenol reaction (Table 2), however, seemed to point to the cultivars' common origin.

Allele 2 for *Pgd1*, which is never observed in lowland rices, is also a remarkable diagnostic allele for specifying upland varietal groups. Upland cultivars can be classified into three groups based on *Pgd* and other trait combinations.

Group 1: characterized by the presence of allele 1 and represents longer APH (0.65 ± 0.12 mm) and round hull type (L/W; 2.14 ± 0.16) same as 445 lowland cultivars (APH; 0.72 ± 0.19 mm, L/W; 2.09 ± 0.34). However, only 19% of cultivars in this group showed positive phenol reaction.

Group 2: characterized by the presence of allele 2 and represents slightly shorter

Table 2. Morphological and physiological characteristics of Japanese lowland and upland varietal groups having different alleles for *Pgd*.

Group	Allele	Cultivars (no.)	Apiculus hair length Mean ± SD (mm)		L/W Mean ± SD (mm)	Phenol reaction ^a	
						Cultivars (no.) +	-
Lowland							
Japonica	<i>Pgd1-1</i>	445	0.72 ± 0.19	2.09 ± 0.34	32	413	
Indica ^b	<i>Pgd1-3</i>	5	0.37 ± 0.12	2.79 ± 0.16	4	1	
Upland							
Japonica A	<i>Pgd1-1</i>	26	0.65 ± 0.12	2.14 ± 0.16	5	21	
Japonica B	<i>Pgd1-2</i>	169	0.44 ± 0.14	2.38 ± 0.21	131	38	
Indica ^b	<i>Pgd1-3</i>	5	0.34 ± 0.13	2.98 ± 0.19	4	1	

^a+ = hull of cultivars blackened. - = hull did not blacken. ^bTotal of 10 indica cultivars were found. Av APH and L-W ratios were 0.96 ± 0.11 and 2.8 ± 0.14, respectively.

APH (0.44 ± 0.14 mm) and more slender hull type (L/Wp ; 2.38 ± 0.21) than the first group.

Group 3: possesses mainly allele 3 belonging to the indica type mentioned earlier.

Pgd1 is located on chromosome 11 along with *la*, *v4*, and *Adh1* (Ishikawa et al 1991). Several key resistance genes have already been located on this chromosomal area (Goto 1970), which seemed to be a specific region for upland characters. Landmarks on chromosome 11 were used to obtain restriction fragment length polymorphism (RFLP) markers for constructing a detailed map around *Pgd1*. Sensho and Taichung 65 (Acc. 504) were used to ensure polymorphic regions on chromosome 11. Eleven probes and seven restriction enzymes were used; four of these probes showed polymorphism with some enzymes. Among the probes, *adh1*, G181, and G189 showed allelic band

trends specific to the upland group. The trend of RFLP patterns, however, was less specific than that of *Pgd*. These RFLP markers and *Pgd* are used to arrange several agronomic and stress resistance traits on the chromosome.

Recent plant breeding programs have failed to introduce upland-specific resistance genes into lowland modern varieties. This implies the presence of linkage blocks for useful stress resistance traits of upland cultivars, and also of existing undesirable agronomic traits in lowland varieties. Confirming the chromosomal region where upland-specific markers are located would increase understanding of the origin of Japanese upland rices. Also, detecting RFLP between upland and lowland cultivars will help rice breeders to introduce only useful genetic resources from upland rice into modern varieties.

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Evolutionary variations in the Gramineae: rearrangements of DNA fragments transferred from chloroplast genomes to mitochondrial genomes

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The transfer of DNA fragments from chloroplast to mitochondrial genomes is considered a general phenomenon in higher plants (Stem and Lonsdale 1982, Stern and Palmer 1984). For rice, Nakazono and Hirai (1993) have determined the entire set of transferred chloroplast sequences present in the mitochondrial genome. Total length of the transferred chloroplast sequences, whose lengths range from 32 bp to 6.8 kb, accounted for about 6% of the rice mitochondrial genome. Two of the 16 identified ct-derived fragments in rice mitochondrial genome, one comprising

rps 19 - trnH - rp12 - rp123 and the other comprising ψ rp123-rbcL-atpB-atpE-trnM-trnV, were found to be separated in the chloroplast genome but were joined in the mitochondrial genome, which might be the cause for homologous recombination between rp123 and rp123. Maize mitochondrial genome also contains these gene clusters (Lonsdale et al 1983).

Watanabe et al (1994) compared this region, which is homologous to chloroplast rps 19 in the mitochondrial genomes, among five gramineous plants (rice, maize, sorghum, Italian rye grass, and wheat) by Southern blot hybridization, polymerase chain reaction (PCR), and DNA sequencing techniques. In all the mitochondrial DNAs from the five gramineous plants — except for that from wheat — the ct-derived fragments of chloroplast DNA were found to be maintained and the same junctions of mitochondrion-specific and chloroplast-like sequences were found at one terminus (rps 19 side). Subsequent analysis revealed that the fragments had been variously rearranged among species with respect to the other terminus. For this region, however, rice rp123 includes a 135-bp deletion in both chloroplast and mitochondrial genomes. In contrast, neither gene in maize has such a deletion. This

suggests that this region must have been transferred separately in rice and maize after their divergence from one another, with subsequent homologous recombination between rp123 and Ψ rp123 in the mitochondrial genomes of rice and maize occurring independently (Fig. 1). These findings indicate that the transfer of the chloroplast sequence occurred in the distant past during the evolution of gramineous plants.

Maintenance of a common junction on one side (the rps19 side), despite the extensive rearrangements of mitochondrial genome, points to the possibility that these sequences might function in the mitochondria. For the result of reverse transcriptase(RT)-PCR and Northern blot hybridization in this study, the chloroplast-derived *trnH* gene was expressed in rice mitochondria (Fig. 2). Comparisons of such ct-derived fragments among or within species may provide some interesting information about the evolution of mitochondrial genomes.

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