

8. Allelism tests in three rice panicle genes, *Dn1*, *Ur1* and *Cl*, and the effects of genetic backgrounds

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Allelism tests were performed among semi-dominant mutants of *Dense panicle 1* (*Dn1*), *Undulated rachis 1* (*Ur1*) or *Clustered* (*Cl*) (Table 1) available on Oryzabase (<http://www.shigen.nig.ac.jp/rice/oryzabase/top/top.jsp>). These mutants were maintained in different laboratories for many years. Several mutants of each gene were regarded as alleles without allelism tests, since they were phenotypically alike and were mapped on the same chromosomal regions using a limited number of morphological markers (Iwata and Omura 1971, Nagao and Takahashi 1963).

Table 2 summarizes the allelism tests performed in the present study. Two mutations in HO576 and N53 were estimated to be derived from independent loci, because the segregation ratio of F₂ plants of HO576 x N53 fitted to 15 (*Dn*):1 (normal). Thus, a new gene name should be assigned for the causal gene of the mutation in N53. Two strains, FL197 and A32, were verified to be alleles of *Ur1*, since all F₂ plants of FL197 x A32 showed the *Ur1* phenotype and did not segregate normal plants. Similarly, HO797 and H339 were revealed to be allelic on the *CL* locus. For one strain showing the *Cl* phenotype, C5287, the allelism test was unsuccessful, because of the low seed fertility of F₁ plants when C5287 was crossed with japonica varieties/strains.

The expression of a mutant allele frequently depends on its genetic background. Complete penetrance, which means that the mutant allele is expressed equally in any genetic background, is desirable for mapping, but altered expression provides important clues about gene function (Freeling and Fowler 1989). We introduced alleles of *Dn*, *Cl* and *Ur1* into cvs Nipponbare and Koshihikari and established BC₄F₂ or BC₂F₂ plants (Table 1). The HO576 allele of *Dn1* and the HO797 allele of *Cl* showed severe phenotypes in both Nipponbare and Koshihikari. In contrast, the FL197 allele of *Ur1* showed a mild phenotype in the Koshihikari background, whereas a milder phenotype was observed in the Nipponbare background. Accordingly, the penetrance of *Ur1* depends on the genetic background.

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Table 1. Panicle mutants used in allelism test

Mutant	Strain (Acc. No.)	Stock Center	Year acquired	Original place /country	Year established	Generation backcrossed into Nipponbare & Koshihikari
<i>Dense panicle 1 (Dn1)</i>	HO576	K	1934	Kyoto Univ.	-	BC ₄ F ₂
	N53	H	-	-	1953	-
<i>Undulated rachis 1 (Ur1)</i>	FL197	K	-	-	1969	BC ₄ F ₂
	A32	H	1941	-	-	-
<i>Clustered (Cl)</i>	HO797	K	1956	USA	-	BC ₂ F ₂
	H339	H	-	-	1970	-
	C5287	NIG	1958	India	-	-

K: Kyushu University, H: Hokkaido University, NIG: National Institute of Genetics

Table 2. Allelism tests among strains of three panicle genes

Mutant	Segregation in F ₂			χ^2	Result
	Segregation	Expected			
Crosses	Mutant	Wild	ratio		
<i>Dense panicle 1 (Dn1)</i>					
HO576/ N53	76	4	15:1	0.213	non-allelic
<i>Undulated rachis 1 (Ur1)</i>					
FL197/A32	60	0	1:0	-	allelic
<i>Clustered (Cl)</i>					
HO797/ H339	60	0	1:0	-	allelic

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