

Locus designations for temperature-sensitive mutants

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Abstract

Locus designations for temperature-sensitive mutants

Perkins, D. D. and T. Ishikawa. Locus designations

for irreparable temperature-sensitive mutants.

genes as shown in Table 1. "n-7 and -8 originated in experiments of Inoue and Ishikawa (1970 Japan. J. Genet. 45:357) at survivors of filtration enrichment of UV-treated conidia from wild type 74A. The original "n-8 isolate contained reciprocal translocation T(I;V)T27M9 from which it has been separated. T53M50 was originally called un(31) and T27M9 was coined "n(I) by Inoue and Ishikawa.

Irreparable temperature-sensitive mutants have been mopped at two new loci, bringing to eight the number of mopped conditional lethals of this type. It is proposed to call the new loci "n-7 and "n-8, and to redesignate the six previously mopped irreparable temperature-sensitive

Table 1. loci of irreparable temperature-sensitive genes.

Proposed locus symbol	Isolation No.	Former locus symbol	Linkage group and arm	Reference for location
<u>un-1</u>	44409	<u>un (44409)</u>	IR	Perkins et al. 1969 <i>Genetica</i> 40:247.
<u>un-2</u>	46006	<u>un (46006)</u>	IC	Perkins et al. 1969
<u>un-3</u>	55701	<u>un (55701)</u>	IL	Howe 1962 <i>Microb. Genet. Bull.</i> 18:12.
<u>un-4</u>	66204	<u>un (66204)</u>	VIL	Stadler 1956 <i>Genetics</i> 41:528.
<u>un-5</u>	b39	<u>un (b39)</u>	IL	Kuwana 1960 <i>Japan. J. Gene.</i> 35:49. Perkins et al. 1969.
"n-6	83106	"n (83106)	IIIR	Perkins et al. 1969
"n-7	T53M50		IR	
<u>un-8</u>	T27M9		IVR	

The newly proposed symbols in Table 1 have the advantage of brevity and of consistency with other series of "mimic" loci that share a common phenotype. When precise information becomes available regarding the characteristic defect of a particular "n mutant, a decision can be made whether to replace the present symbol with one that is more explicit.

Table 2. Mop locations of new un mutants.

Mutant	Sequence and % recombination	Parental	Numbers		
			Singles 1	Singles 2	Doubles 1,2
<u>"n-7 (T53M50)</u>	<u>un-7</u> (4) <u>aur</u> (22) <u>os-1</u>	44	2	13	0
	<u>act-1</u> (12) <u>al-1</u> (1) <u>un-7</u>	74	10	1	0
<u>"n-8 (T27M9)</u>	<u>cys-10</u> (47) <u>"n-8</u> (5) <u>col-4</u>	39	38	4	0
	<u>"n-8</u> (0) <u>pyr-1</u> centromere <u>IVR→VIR</u> ALS159 "n-8 (by duplication-coverage)	47	0		

Linkage relations of the new mutants are summarized in Table 2. The isolation number for the al-1 allele is ALS4. "n-8 is known to be right of the centromere in IV because it is heterozygous in duplications from T(IVR→VIR)ALS159. • ~ • Department of Biological Sciences, Stanford University, Stanford, California 94305 and Institute of Applied Microbiology, University of Tokyo, Bunkyo-ku, Tokyo 113, Japan.