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THE RELATIONSHIP BETWEEN THE MUTANT ALLELES AT THE na LOCUS IN LINE L81 AND WL1766

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The recessive mutation na (type line WL1766) causes extremely short internodes and a phenotype known as nana (6). The na locus is on chromosome 6 (3,7) near wlo (2). The na allele blocks a step early In the gibberellin biosynthetic pathway and shoots of these nana plants do not contain detectable levels of C ^-gibberellins (1,4). Two additional independently isolated mutations have been traced to this locus, one occurring in a Geneva progeny (2) and the other in a line from Bulgaria known as Hobart L81 (5). The internodes of L81 are about 75% longer than those of the nana type line WL1766 (Table 1). Nevertheless, the phenotype is still regarded as nana since L81 is considerably shorter than members of the dwarf class. The question arises therefore as to whether alleles na^{81} and na^{1766} do really differ in their ability to shorten internode length, i.e. is the length difference between L81 and WL1/66 due to an allelic difference at the na locus or to a difference in the remaining genetic background?

Lines 81 and 1766 differ at another chromosome 6 locus, pl, which shows a recombination value of about 24% with na (2). Thus segregation for Pl/pl may be used as a moderately effective marker to compare the action of na^{81} and na^{1766} in a segregating progeny. The results in Table 1 show no sign of any significant difference in internode length between the PI- and plpl segregates in either the F2 or F3 of cross 81 (pl) x 1766 (Pl). Indeed, the pl segregates, which should contain an above random proportion of na^{81} types, are on average slightly shorter in both generations. The genetic evidence therefore suggests that alleles na^{81} and na^{1766} are equivalent and equally effective in shortening internode length.

Table 1. Stem length between nodes 1 and 9 for parental lines L81 (pl) and WL1766 (Pl) and Pl- and plpl segregates In the F2 and segregating F3 progenies of cross 81x1 766. The parental data come from plants grown with the F2.

Genotype	Generation	Stem length between nodes 1 and 9		
		Mean	SE	n
P1	WL1766	3.08	0.13	5
pl	L81	5.38	0.10	6
P1	F_2	4.49	0.20	27
pl	F_2	4.28	0.41	5
P1	F_3	5.38	0.34	26
pl	F_3	5.13	0.45	11

Difference between the genotype means not significant in either F2 or F3 (t value = 0.43 in each case).

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