GENETICS OF EARLY FLOWERING PEA MUTANTS

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Early flowering pea mutants (Table 1), which differ from the initial variety in a low node of the first flower, date of flowering, and length of the vegetative period, were induced by gamma rays (mutant 2), EMS (398, 400, 418, 578), NEU (319, 320, 320/1, 326), or NMU (629). In all mutants except 319, 320, and 326 a low node of flower initiation correlates with early flowering as well as early ripening. Two mutants (2 and 400) have a shorter vegetative period but higher seed productivity than their initial varieties. Further details are given elsewhere (4,5).

Table 1. Initial variety and early flowering pea mutants.

Initial variety	Node of 1st flower	Mutant number	
		1st flower at nodes 5-7 (Group I)	1st flower at nodes 8-9 (Group II)
Torsdag	11-13	2, 578	319, 320, 320/1, 326
Falensky 42	12-15	398	400
Parvus	11-13	629	
Saratovsky mestniy 231	12-15	418	

In crosses with initial varieties and between themselves, in order to determine their allelism, all mutants appeared to be monogenic recessive mutations and to result from the mutation of different alleles of one locus (5). The Lf locus is indicated since Murfet (3) has identtified cultivar 'Torsdag' as Lf and mutants 2 and 519 as $\underline{1f}^a$ and lf, respectively. This conclusion was confirmed by several crosses. A cross between mutant 2 and marker line NGB1238 segregated in a monohybrid ratio for node of the first flower and the flowering gene showed linkage with marker A on chromosome 1. The Lf locus shows close Linkage with the A locus (1,6). In addition, the mutants were crossed with the type lines for lf^a (Hobart line 7) and lf (Hobart line 58 = Nordic Gone Bank line 1792). The mutants were also crossed with Hobart lines 59 (lf) and 64 (lf), Vasileva's mutant XVIII/17 (obtained from the variety 'Wesna'), Wellensiek's M and E mutants (obtained from the variety 'Dominant', and Gottschalk's mutant 46C obtained from the variety 'Dippes Gelbe Viktoria'). The last three mutant lines were formed by mutatiions of the type Lf^d to Lf, Lf^d to lf, and Lf to lf^a, respectively (2). The results of the crosses indicated that all the mutants and lines studied are allelic and appear to be the result of mutations at the Lf locus; Group I mutants (2, 578, 398, 629, 418) have genotype lf^a and Group II mutants (319, 320, 320/1, 326, 400) have genotype lf. Under Siberian conditions mutants XVIII/17, 46C, and Hobart line 7 formed their first flower at nodes 5-7, mutant E and Hobart lines 58 (NGB1792), 59, and 64 flowered at nodes 8-9, and mutant M at nodes 11—14. All node counts commenced from the first foliage leaf as node 1. Thus under Siberian conditions the four alleles lf^d, $\underline{Lf}$, $\underline{lf}$, and $\underline{lf}^a$ lead to the first flower forming at nodes 18-20, 11-14, 8-9, and 5-7, respectively.

We thank Dr. S. Blixt, Professor W. Gottschalk, Dr. I. C. Murfet, Dr. M. Vasileva, and Professor S. J. Wellensiek for providing mutants and lines.

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