PROBLEMS OF MUTATION RESEARCH IN AUTOGAMOUS PLANTS WITH LOW RATES OF CROSS FERTILIZATION

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Autogamous plants have distinct advantages over allogamous species for mutation research. However, virtually any incidence of cross fertilization can critically affect the results of studies of the rates and kinds of spontaneous and induced mutations (including para-, back-, and suppressor-mutations), research on transposons, and intragenic recombination, etc. The following example illustrates how unwanted cross pollination may affect the interpretation of such studies.

Table 1 shows the M2 of our recombinant 650 A, which has tendrils instead of leaflets (gene af, 'afila') and a fasciated stem instead of a normal one (gene fa). This recombinant was originally chosen to study back- and/or suppressor-mutations in higher plants. The seeds were treated with ethylenimine (14 hours in a 0.03% ethylenimine solution). As a pilot test, 33 M2 families were investigated in 1983. Excluding family No. 33 (24 seeds were sown, but the exact number of plants grown from them was not ascertained) the 32 families were composed of 878 plants. Twenty (=2.3%) of the latter bore the dominant alleles Fa and/or Af. These 20 plants were distributed among 10 (=31.2%) of the 32 families. In the case of back- or suppressor-mutations this would be an exceptionally high rate. The data are, however, in full agreement with the rates of cross fertilizations obtained for other pea lines (compare the preceding research report).

Apart from the cases where marker genes of lines growing in the same field and at the same time as the M1 could be identified in the M2 (red flower color among others), suppressor mutations could be distinguished from cross fertilizations only by a crossing program with the other genotypes which were grown in the same experimental field. By recombination, not closely linked supressor gene loci would segregate from the fa and/or af loci and the original recessive phenotype would be regained. This method is, however, ineffective in the case of close linkage between the suppressor locus and the recessive gene and is useless in the case of true back mutations.

Further problems involved may be shown by the following example: As no fa plants with afila leaves were In the field together with the M1, the only explanation for a Fa~af phenotype (one was among them) would have been a back or suppressor mutation [or impenetrant fa - Ed.]. In the field there were, however, two control groups of R 380, which has a normal stem and pleiofila Leaves - one group stood adjacent to R 650 A. Because the pleiofila leaves result from a specific interaction between the two recessive genes af and tl (acacia) and R 650 A has af and the dominant allele Tl, a cross fertilization between these two lines would result in plants with afila leaves and normal stems. So at present none of the plants can be proved to bear a suppressor or back mutation.

Table 1. M2 of the recombinant R 650 A.

Family No.	R 650 A (homozygous for **fa** and **af**)	No. of plants with the dominant alleles **Fa** and/or **Af** among them
1	40	2
2	25	–
3	41	1
4	42	–
5	13	–
6	41	–
7	31	–
8	41	–
9	33	–
10	39	–
11	36	–
12	33	3
13	29	–
14	23	–
15	18	–
16	21	1
17	36	1
18	51	–
19	31	–
20	35	4
21	35	–
22	29	–
23	28	–
24	26	5
25	19	1
26	20	1
27	13	–
28	9	–
29	7	–
30	7	1
31	5	–
32	1	–
(33)	(24)	(1)
	858	20

The extent of the whole problem may be Illustrated as follows: Assuming that 10,000 seeds be treated with a mutagenic agent and 5,000 M1 plants be grown: 1-2% cross fertilizations result in 50 to 100 plants being already heterozygous for different genes without a mutation having taken place. As nearly one third of all the plants will again be subject to cross fertilizations, some 1,500 plants could bear one or more heterozygous seeds, from which a whole array of descendents could be confused with mutants. To avoid such disturbances, which is also important for gene localization studies, special precautions may be required, such as closed greenhouses or isolation plots containing a single line.