A GENE FOR STEM BIFURCATION WITH FULL PENETRANCE

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So far two polymeric genes, bif-1 and bif-2, are known to cause the stems of peas to become dichotomously branched. Both these genes exhibit an unstable penetrance depending on environmental factors as well as on the genetic background. This instability reduces the agronomic value of the two mutants which are of interest for pea breeding because of their favorable yield potential. The penetrance of bif-1 was fully stabilized by mutant genes responsible for small grains or long internodes. In both the recombinant types, however, the positive effect of gene bif-1 is offset by the negative effects of the other two genes.

After X-irradiation, mutant 37B was isolated and developed into a pure line. The plants are somewhat shorter than the mother variety. They are dichotomously branched in the upper part of the stem and have therefore an increased number of pods per plant. The internode below the point of stem bifurcation is fasciated. Seed size is normal. The mutant is morphologically identical with mutants 1201A and 157A homozygous for bif-1 and bif-2, respectively. The only difference is that 37B is fully penetrant for the new gene for stem bifurcation. In 1978, the following observations were made:

Mutant 1201A (bif-l/bif-1): penetrance = 62.8%
Mutant 157A Cbif-2/bif-2): penetrance = 39.2%
Mutant 37B : penetrance = 98.0%

Seed production of mutant 37B was about 15% better than that of the mother variety.

The genetic relations between 37B and the other two bifurcated mutants not yet clarified but the necessary crosses have been made.

EFFECT OF GENOTYPIC BACKGROUND AND ENVIRONMENT ON THE EXPRESSION OF THE dgl MUTANT

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Plants of the X-ray induced mutant 142B of our collection, homozygous for gene dgl, are small in stature (about 35 cm). Their small leaves develop brown spots and degenerate completely during ontogenetic development. Only the uppermost leaves are normal green and capable of photosynthesis. Seed production is very low, ranging between 10 and 35% of the control values of the initial variety over 9 generations of comparison at Bonn.

The mutant was crossed with some other mutants, and recombinants homozygous for dgl and the respective other genes were selected and propagated. A gene for stem fasciation, derived from mutant 489C, did not influence the action of dgl with regard to leaf degeneration. The seed production, however, was more than doubled due to an increase in the number of flowers which accompanies stem fasciation (recombinant R 142D).

Plant height of recombinant R 142C was the same as that of the initial variety. The leaves were severely damaged due to the presence of dg1 . A further increase in seed production over 142B was realized by combining a gene for very low degree of stem fasciation, likewise derived from 489C.

Gene dgl was also combined with genes for long internodes and lateness. In this combination, the effect of dgl was strongly reduced. The degeneration was limited to the lower leaves, the middle and upper leaves remaining normal (recombinant R 142F}. This led to a further increase in seed production up to about 700% of 142B.

These results show that the 5 mutant genes tested (2 different genes for stem fasciation, 2 genes for increased internode length, 1 gene for lateness) all influenced the selection value of dgl positively. One of them reduced the specific effect on leaf degeneration.

When mutant 142B is grown in a greenhouse, gene dgl does not express its action; all the leaves are normal green. The mutant also failed to manifest when grown in Egypt. The plants were vigorous and reached the height of the mother variety with full seed production. Thus, an environmental factor(s)—probably high temperature—suppresses the action of dgl. Seeds of these plants were sown in the field in Bonn and strongly damaged plants developed from them.

The influence of other genes and of environmental conditions on the action of gene dgl is schematically given in Fig. 1.

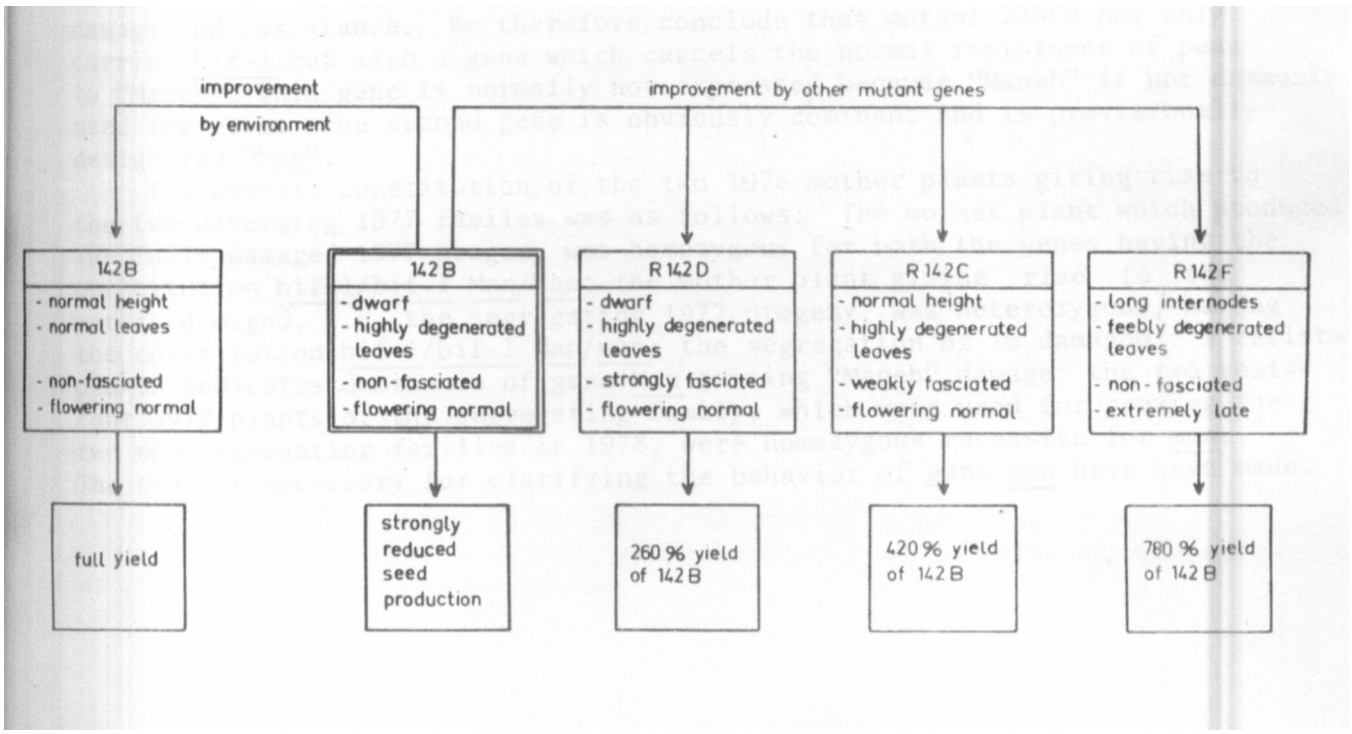

Fig. 1. The improvement of mutant 142B by changing the environmental conditions and the genotypic background.