FASCIATION AND HETEROSIS IN PEA (III)

Loenning, W. E. Institute of Genetics, University of Bonn
Federal Republic of Germany

Another six thousand plants have been devoted to the problem of fasciation and heterosis, leading to definitive results.

I. Six fasciated lines, each with a different stem length, were crossed to a common line, 'Dippes Gelbe Viktoria' (non-fasciated):

a) 489 C x mother variety Dippes Gelbe Viktoria (DGV)
b) 251 A x DGV
c) R 710 x DGV
d) R 875 x DGV
e) Mutant 1/74 (of Vasileva's collection) x DGV
f) Mutant VI/10 (of Vasileva's collection) x DGV

Dominance for superior length was evidenced by 3:1 segregations in F3 and backcrosses of long, nonfasciated recombinants, derived from the heterotic hybrids, with Dippes Gelbe Viktoria (including segregations). Since the degree of hybrid vigor varied with the fasciated lines used, it can be concluded that the dominant genes for length were contributed by the fasciated parents. The following facts show that the fasciata genes themselves are responsible for the suppression of the dominant genes in the fasciated lines:

a) Originally long lines are shortened by fasciation. The original length can be regained by recombination. Example: F1 mutant 1/74 x R 46 C was as long as mutant's 1/74 mother variety 'Ramonski', the length of which could be regained by recombination.

b) The recessive fasciata genes cause growth anomalies, shortening several internodes but never elongating them in comparison with the long recombinants.

c) Heterozygotes segregating for only one fasciata gene are as long as the related nonfasciated homozygous lines but the fasciated lines are shorter.

d) Full length has only been regained in nonfasciated recombinants.

No heterotic stimulus of heterozygous fasciata genes could be found by the different methods applied (1).

II. Seed production, a polygenic trait, showed many interactions with genes for other characters, leading to a more complicated situation. There is no doubt, however, that seed production can also be affected strongly by fasciation. Three different cases can be cited at present, where the high seed production of the hybrids has been fixed in recombinants: R 710 x DGV, Mut 1/74 x DGV, and, in part, 478 C x DGV. For the latter, the results were contradictory during the last two years. In 1980 a recombinant was as productive as the hybrid; in 1981 the latter surpassed the former. Crossing highly reproductive recombinants (derived from the heterotic hybrids) with DGV has led to hybrids which compare favorably with the better parent.

All things considered, the investigation of some 15,500 plants (including more than 40 different hybrid stocks with replication of a

few outstanding cases and segregation and selection from F2 - F5, with backcrosses and their segregations) during the last three and a half years has clearly pointed to recessive epistasis and dominance as the main causes of the heterosis observed in crosses of fasciated with non-fasciated lines.

1. Loenning, W. E. 1982. Theor. Appl. Genet, (in press).

THE INHERITANCE OF THE ABILITY TO REGENERATE PLANTS FROM CELL CULTURES OF PISUM SATIVUM L. — A PRELIMINARY ANALYSIS

Malmberg, R. L. Cold Spring Harbor Lab, Cold Spring Harbor, NY USA

Previously we had reported that certain wild or primitive forms of peas had some ability to regenerate from callus cultures (1, 2). Specifically, two lines obtained from G. A. Marx (B77-259 and B77-276) were found to be able to give rise to whole plants when epicotyl derived callus was shifted to shoot inducing medium after as long as six months in culture; however, these lines showed an increasing difficulty in obtaining regeneration as a function of time, requiring progressively longer incubations on shoot medium to give rise to regeneration events. Also, because the pea callus grew very slowly, with doubling times on the order of three to four weeks, the six months regeneration window did not reflect very many cell divisions. Thus the ability to regenerate from cultures was very limited. In this note we report some preliminary results of crosses between one of the regenerating lines (B77-259) and a non-regenerating multiply marked line (A1078-234-0) also kindly provided by G. A. Marx. A partial genetic characterization of these lines is as follows:

B77-259: Le, A, D^{co}, Td Int or Ser, fr or fru or both, F Fs or (F fs f Fs), R, I, wild or primitive form, some regeneration ability.

A1078-234-0: A, D, wb, k, s, st, b, f, le, fa, gp, tl, cp, fs, wlo, te, i, r, non-regenerating.

By standard crossing methods we constructed F1, F2, and backeross generations. As previously described (1, 2) seeds to be tested for their callus/regeneration ability were surface sterilized and germinated on an agar medium. The epicotyls were dissected out two to three days later and cultured on callus medium for four to six months, after which they were transferred to shoot inducing medium. Successfully regenerated shoots were then rooted and transferred to soil and growth chamber conditions with a great deal of care at initially keeping the humidity high. Two problems with this experimental design seem unavoidable. First, the assay for regeneration potential can require as much as twelve months, e.g. six months in culture, four months to regenerate shoots, two months to obtain roots plus transplant to soil. This is before any linkage data could be obtained by monitoring the growth of the plants and scoring the markers. Second, non-regenerating calli cannot be scored at all for the whole plant markers, thus we lost a substantial portion of the linkage data that was present in the seeds. Initial data indicated that there was no maternal effect so subsequent data have been pooled.