CHARACTERS OF THE BIFURCATED MUTANT 157 OF GOTTSCHALK'S PISUM COLLECTION

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Mutant 157 exhibits stem bifurcation but because it is incompletely penetrant the yield of this genotype varies in relation to the number of bifurcated plants in the population (bifurcated plants produce more seed than monopodial plants). Mutant 157 is reported to be a single-gene mutant, designated bif-2 (1).

This genotype was analyzed for seed protein content after being grown under relatively similar conditions in 1975 and 1976. We could show that in both years the seed protein content of the mutant was statistically significantly higher than that of the initial line (DGV): 1975 - 113% of the initial line; 1976 - 111% (2). The same tendency was evident in subsequent years though significant differences were not found. A possible explanation for this was that the growing conditions were not precisely comparable.

Investigations on the composition of the seed proteins showed that the increased protein content of the mutant was mainly due to a 16% increase in the albumin fraction over that of the initial line. The electrophoretic separation of the albumins revealed a similar banding pattern for both genotypes. Since no quantitative deviations in the subfractions could be identified, it was proposed that in the mutant the albumin fraction as a whole was increased (Fig. 1).

The enzymes catalase, alcohol dehydrogenase, ribonuclease, fructose-1,6-biphosphatase, amylase, esterase, and certain glycoproteins exhibited Identical phenotypes in both parental and mutant lines when extracts were subjected to electrophoresis.

Pisum seeds also contain the enzyme leucine-amino-peptidase (LAP). The pattern on the gel shows two bands (A and B) in the region of Rf-values of about 0.55, a broad one and a faint one below. Both bands are unchanged in the mutant. In the lower part of the gel (Rf-values between 0.75 and 0.95) is a group of nine bands. Some differences between the genotypes are evident (Fig. 3a, b). Band 7 of the initial line is very prominent, whereas in the mutant it is reduced, and instead hand 8 is prominent. There may be other differences as well but the interpretation of these may not be reliable given the lack of clarity of the gel.

We have crossed both of these genotypes. The middle column of Fig. 1 a and b shows the pattern of the heterozygote genotype. The upper bands (A and B) are identical to those of the parents while the lowet part seems to show a heterozygous pattern. Bands 1 to 4 correspond to those of the control genotype.

Possibly, gene bif-2 regulates the amount of a special subtraction or component of the LAP in the mutant, reducing the quantity of the substance in position 7 while that in position 8 is increased. This character is co-dominantly inherited in the **F«j** both alleles are expressed. In fractions 1 to 6, on the other hand, the dominant, influence of the initial line is expressed.

To what extent, if any, the deviations in LAP are connected with earlier findings that the leucine composition in the seed proteins is altered (7% in the mutant and 8% in the initial line) remains unknown.

If the variation in LAP is causally connected to the bif phenotype then it is questionable whether really only one gene in this mutant is responsible for all the variation found. Perhaps further investigations will show that a series of genes is mutated in this genotype, or that a

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1. Gottschalk, W. 1978. Genetica 49:21-29.
2. Quednau, H.-D. and G. Wolff. 1978. Theor. Appl. Genet. 53:181-190.

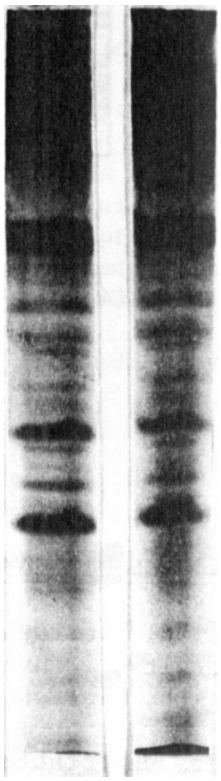


Fig. 1.

Electrophoretic banding pattern of the seed albumin fraction of Pisum sativum 'Dippes Gelbe Viktoria' (DGV) Left: DGV; Right: Mutant 157

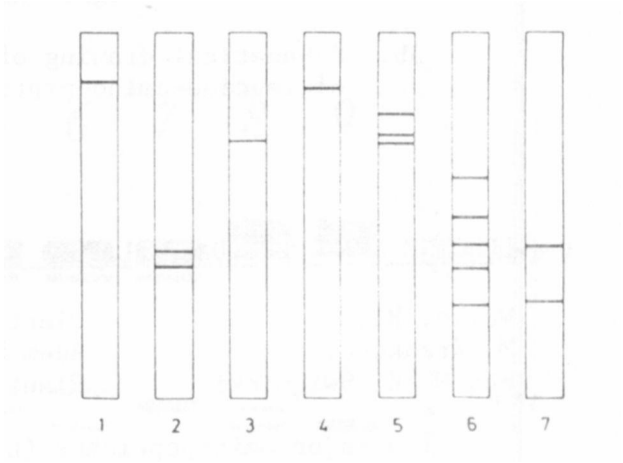
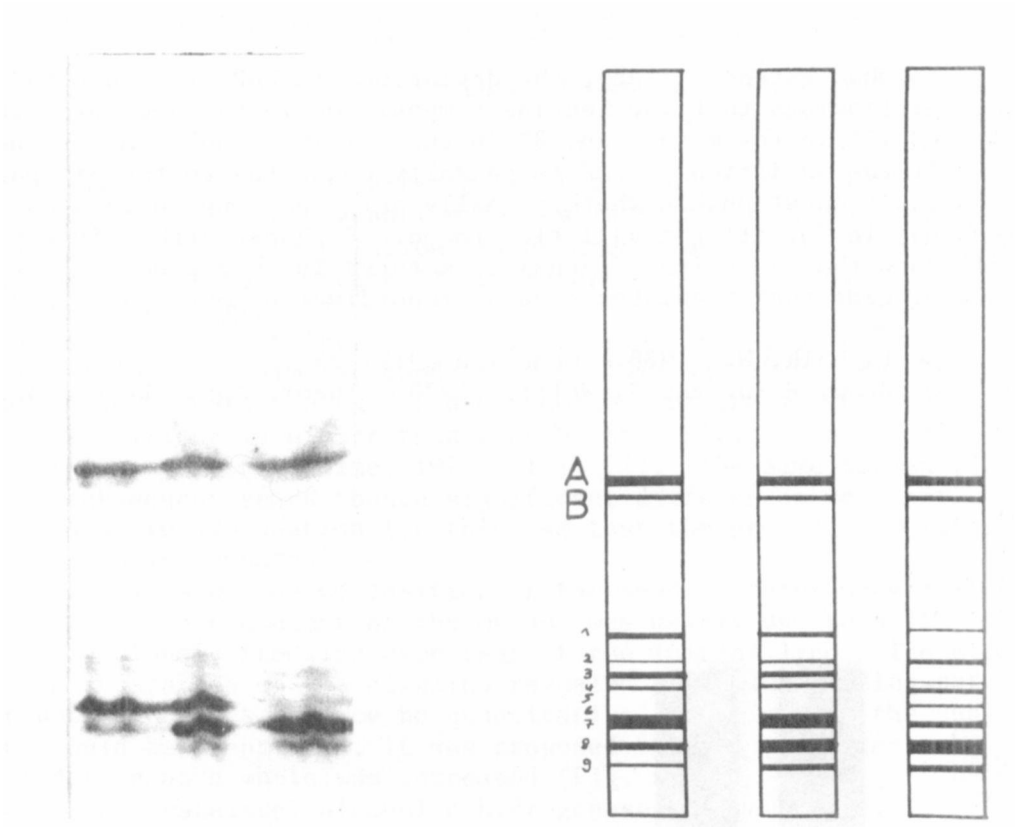


Fig. 2.
Electrophoretic banding pattern of several enzymes of the pea seed (DGV); schematical drawing. 1-catalase, 2-alcohol-dehydrogenase, 3-ribonuclease 4-fructose-1,6-diphosphatase, 5-amylase 6-esterase, 7-glycoproteins.



a b

Fig. 3a. Electrophoretic banding pattern of leucine-amino-peptidase.
Left: DGV Right: Mutant 157 Middle: DGV x 157

3b. Schematical drawing of the electrophoretic banding pattern of leucine-amino-peptidase.

LEUCINE AMINOPEPTIDASE (LAP-2) VARIABILITY IN THE GENUS PISUM

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Two major aminopeptidase (LAP) activity zones detectable after electrophoresis can be observed in many tissues and developmental stages of Pisum sativum. The two forms were described for the firs) time by Scandalios and Espiritu (6) as AmP-1 and AmP-2. Later investigations I, Scandalios and Campeau (7) showed that the faster migrating polymorphic locus LAP-1 is composed of two alleles AmP-lF and AmP-lS. Appropriate crosses made between LAP-1 pea lines differing with respect to the mobility of the two LAP-1 forms demonstrated that the LAP-1 locus in Pisum is controlled by two alleles exhibiting codominant expression.