

CHARACTERIZATION OF TISSUE-SPECIFIC SEED PROTEINS IN PISUM

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A realistic estimation of an expected increase in protein quantity and quality of crop plants depends on an understanding of the genetic control of protein structures as well as of the regulatory processes during the incorporation of functional units involved in the synthesis, processing, and deposition of seed proteins.

A study for elucidating some of the problems indicated involves detailed biochemical and physiochemical analysis and characterization of the proteins available in seeds. This implies that not only the total nitrogen content of seeds but also the enzymatically active proteins as well as the storage proteins have to be analyzed.

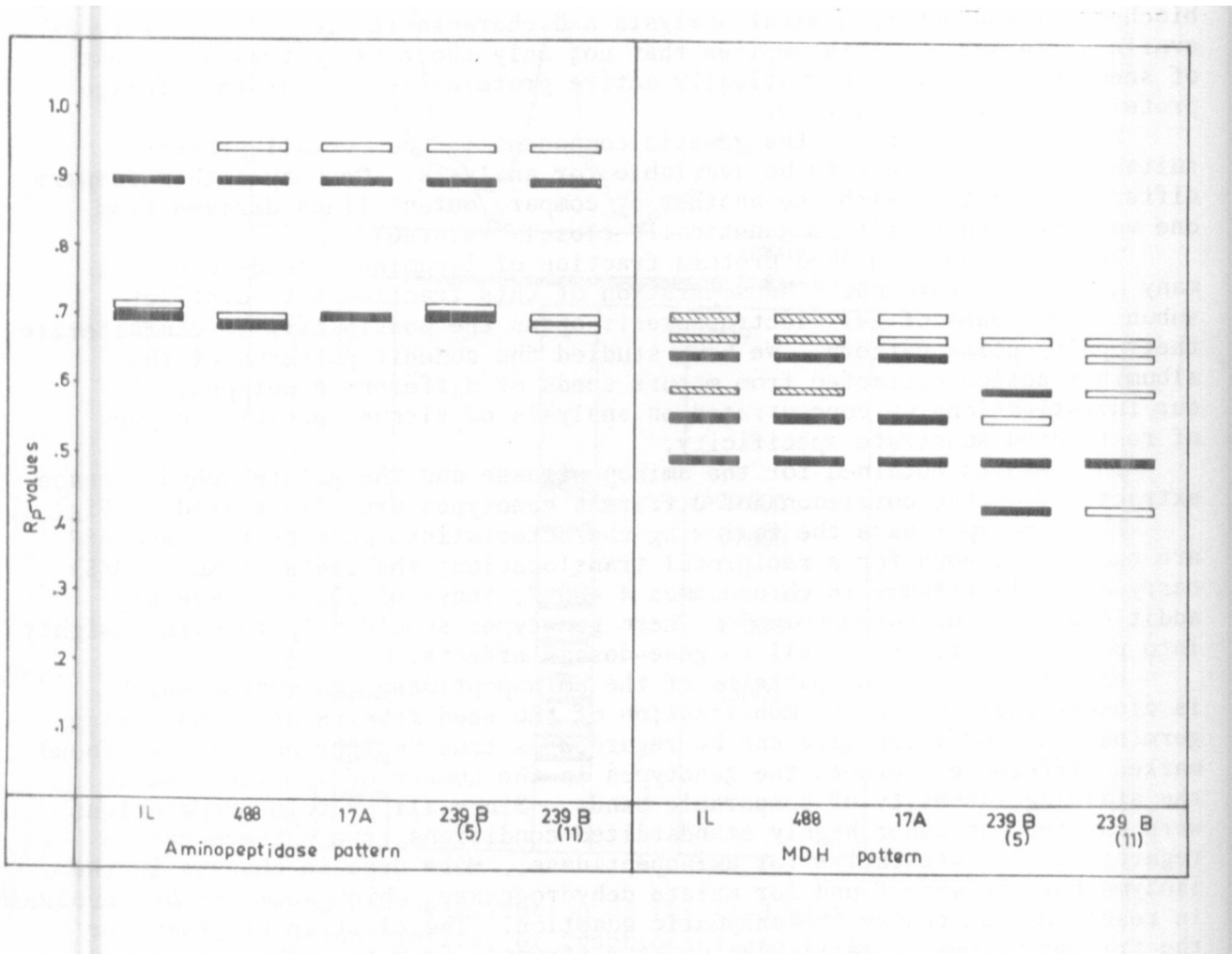
For an assessment of the genetic component in the overall process, suitable genotypes have to be available for analysis. One may either compare different varieties with one another or compare mutant lines derived from one variety (and therefore genetically closely related).

The water soluble seed protein fraction of leguminous seeds contains many different proteins. The separation of this fraction into distinct subunits by means of gel-electrophoresis opens the possibility to characterize their polypeptide pattern. We have studied the subunit patterns of the albumin fraction extracted from mature seeds of different genotypes. In our investigations we concentrated on analysis of tissue-specific enzymes of restricted substrate specificity.

The results obtained for the aminopeptidase and the malate dehydrogenase extracted from the cotyledons of different genotypes are illustrated in Fig. 1.

The genotypes have the following characteristics: mutants 17 A and 488 are each homozygous for a reciprocal translocation; the seeds of No. 239(5) carry a double trisomy in chromosomes 4 and 7; those of 239(11) have an additional copy of chromosome 7. These genotypes should help to gain insights into position effects as well as gene-dosage effects.

With respect to the patterns of the aminopeptidase, an enzyme which is closely involved in the mobilization of the seed reserve proteins during germination, and which also can be regarded as true "marker enzyme", we found marked differences between the genotypes in the number of isozymes and in the staining intensity of comparable bands. Since all protein preparations were carried out under highly standardized conditions, the pattern can be regarded as representative for aminopeptidase. More drastic changes in the isozyme pattern were found for malate dehydrogenase, which seems to be involved in reactions concerning the enzymatic adaptation. The electropherograms for the trisomic lines in particular deviate strongly from the other genotypes. There are some common bands, but others are lacking or are additionally detectable. The results show that considerable heterogeneity of aminopeptidase and MDH-isozymes, as judged by variance in the polypeptide patterns, is produced by or associated with the genetic differences. There are some indications of structural modifications of enzymes. Polymorphic forms of enzymes seem to have adaptive significance. Furthermore, the knowledge of the presence of enzymatically active proteins found in seeds should constitute a useful basis for studying the metabolic events during seed germination.



Tg. 1. Aminopectidase and malate dehydrogenase banding patterns in seeds of different pea genotypes.