ELECTROPHORETIC STUDY OF SEVERAL ENZYME SYSTEMS OF THE GENUS PISUM WITH REFERENCE TO ITS TAXONOMY

Przybylska, J., H. Parzysz, Institute of Plant Genetics, Poznan, Poland
and S. Blixt Weibullsholm Plant Breeding Institute, Landskrona, Sweden

In an investigation initiated recently, iso-enzyme analysis was used to explore the taxonomic relationship among diverse forms of Pisum. This report presents data on distribution of electrophoretic phenotypes of several enzyme systems: leucine aminopeptidase (LAP), glutamate oxaloacetate transaminase (GOT), and peroxidases (PX).

A total of 108 lines were examined, including P. elatius (4 lines), humile (3 lines), P. sativum (84 lines), P. abyssinicum (12 lines), and P. fulvum (5 lines). Most of the lines originated from the Weibullsholm Collection. Cotyledons of mature seeds (LAP), as well as leaves (GOT) and roots (PX) of 2-3-week-old seedlings were analyzed. An electrophoretic analysis of LAP and GOT systems was performed in starch gel, and that of the PX system in polyacrylamide gel.

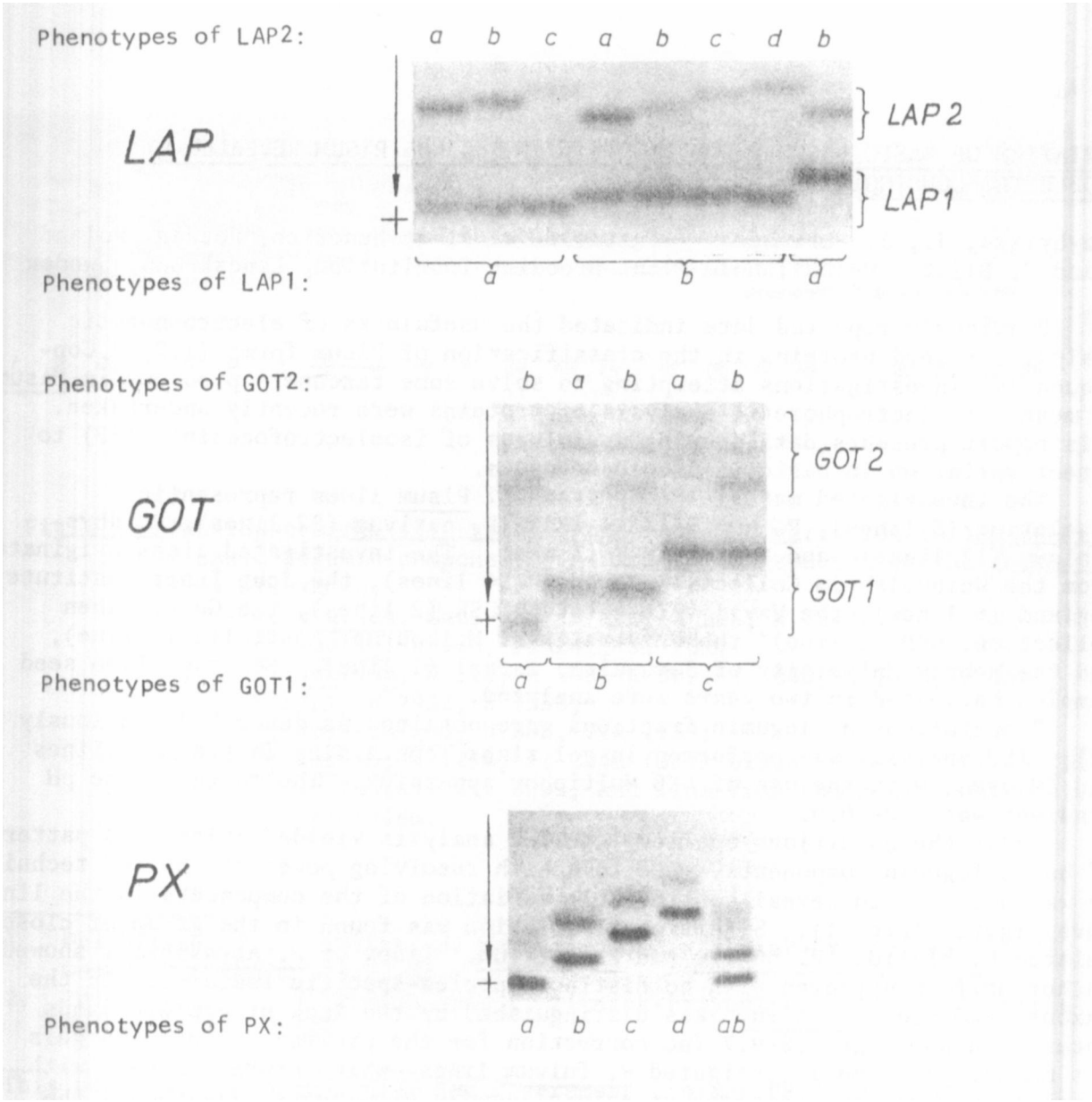
Zymograms showed the following variation in electrophoretic phenotypes: LAP - two zones of activity exhibiting independent variation, LAP1 and LAP2 with 3 and 4 phenotypes, respectively; GOT - two zones of activity exhibiting independent variation, G0T1 and G0T2 with 3 and 2 phenotypes, respectively; PX - one variant zone with 5 phenotypes (Fig. 1). In the 5 enzyme zones, representing probably at least 5 loci, 17 phenotypes were observed in total.

In considering the distribution of the different electrophoretic patterns that were found, two kinds of characters were taken into account: 1) Electrophoretic phenotypes of particular enzyme zones - assumed to be products of allelic genes at single loci, and 2) Combinations of electrophoretic phenotypes of different enzyme zones, i.e. combinations of phenotypes assumed to be controlled by various loci, named here Composite Electrophoretic Phenotypes (CEPHs).

The distribution of the electrophoretic phenotypes tentatively attributed to allelic genes at single loci, considered in terms of presence or absence in particular taxons, showed no species-specific characters. It can, however, be expected that when the investigated material is extended, differences between the examined taxons may be reflected in various frequencies of certain electrophoretic phenotypes.

As regards the distribution of the 29 CEPHs that were distinguished, the variation found in P. sativum (22 CEPHs) partly overlapped that found in P. elatius and P. humile. All the investigated P. abyssinicum lines showed the same CEPH, not observed in other taxons. Nor were three CEPHs found in P. fulvum observed in other forms. Grouping of Pisum forms on the basis of this enzyme analysis was similar to the classification based on electrophoretic patterns of seed albumins (3) and globulins (4). P. fulvum and P. abyssinicum appear to be different taxons, as distinguished from the group which showed greater similarity, viz. P. elatius, P. humile, and P. sativum.

Polymorphism of aminopeptidases (1,5), usually referred to as "leucine aminopeptidase", and that of peroxidases (2) in Pisum was reported earlier. The wide range of genetic variation presently analyzed revealed additional polymorphism of leucine aminopeptidase.



Fig, 1. Electrophoretic phenotypes of LAP, GOT, and PX systems revealed in Pisum. Remark: PXab phenotype, having a sum of bands of PXa and PXb phenotypes, was revealed in line W 809. The character is attributed to gene duplication effect; all thirty individuals of line W 809 examined had PXab phenotype.

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