COMPARISON OF PROTEIN AND ENZYME PATTERNS IN SEEDS FROM FIELD- AND PHYTOTRON-CULTIVATED PLANTS.

Muller, H. P. Institute of Genetics, University of Bonn
Federal Republic of Germany

Use of controlled environment facilities allows study of the genetic control of the photoperiodic and thermoperiodic reactions of various genotypes. Mature seeds from numerous genotypes with differing growth and flowering behavior were analyzed electrophoretically with regard to their protein and isozyme patterns. We used material from plants grown under 12 hr photoperiod at 25C day and 15C night, and compared the patterns with those obtained from field grown material. (The seed material was kindly provided by Dr. Gottschalk.) The results are shown in Figs. 1 and 2.

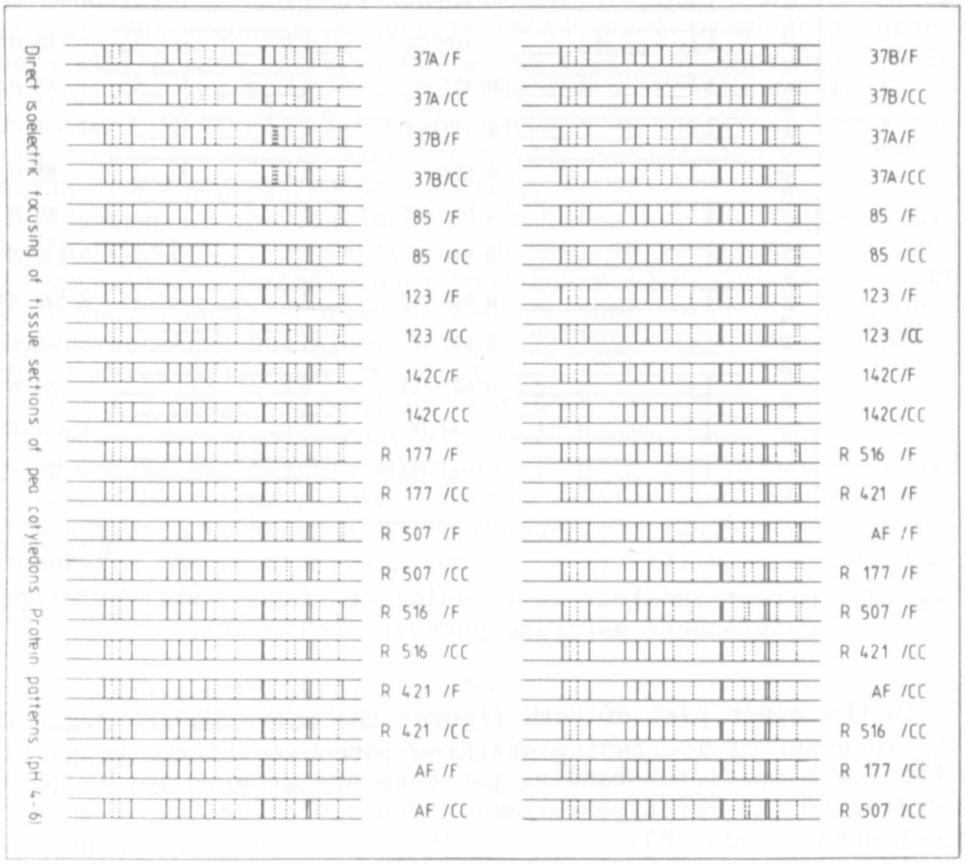

Fig. 1. Direct isoelectric focusing of tissue sections of pea cotyledons: protein patterns (pH gradient 4-6).

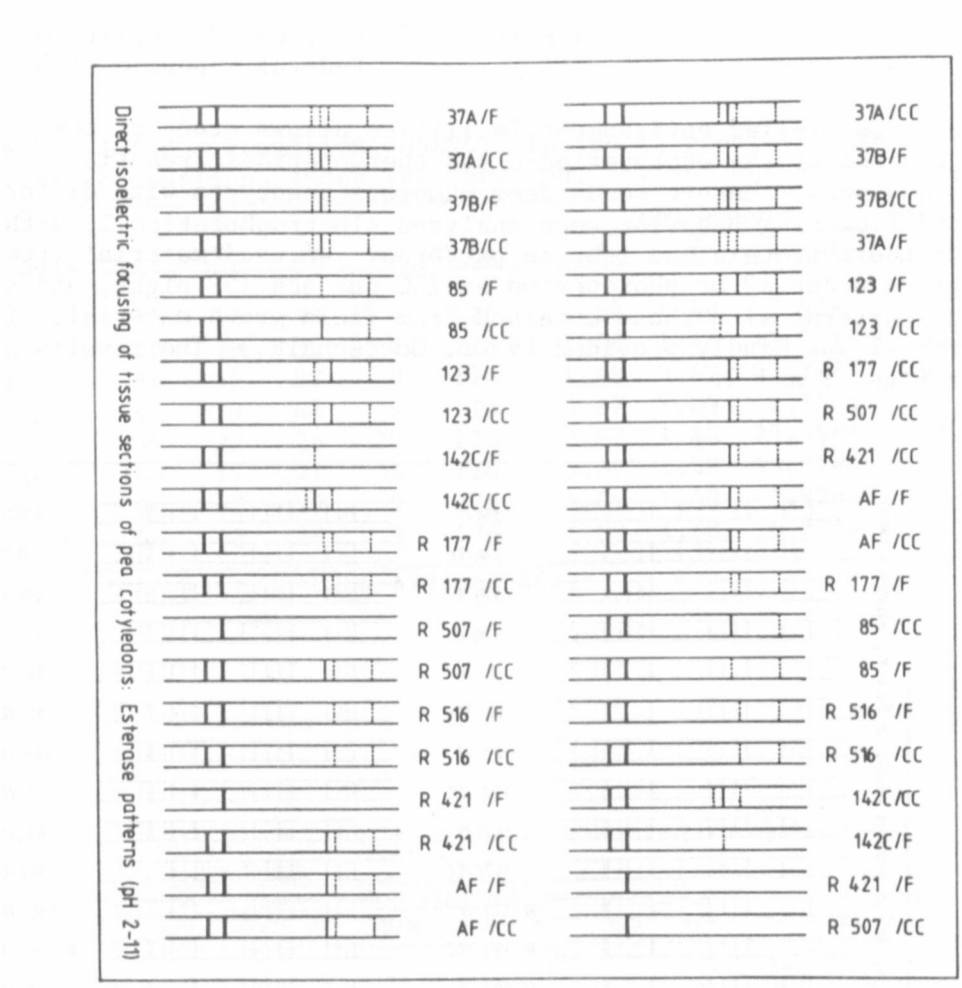

Fig. 2. Direct isoelectric focusing of tissue sections of pea cotyledons: esterase patterns (pH 2-11).

In the upper part of both figures the patterns are drawn schematically in order of increasing staining intensity of the respective bands; in the lower parts the banding patterns are grouped for comparison according to the genotypes grown in the phytotron (CC) and in the experimental field (F).

It can be seen that, although all genotypes were uniform for many seed protein characters, distinct quantitative differences are discernible. The comparison of the protein and isozyme patterns from seeds deriving from the experimental field and the phytotron also reveals distinct quantitative differences among numerous bands, indicating a different expression of the respective genes which code for them. This provides a way to analyze the influence of environmental factors on the regulation of protein incorporation into seeds. Of great interest are genotypes which show qualitative differences, indicating substantial changes in gene expression. Such changes may be seen in the esterase patterns of genotypes 142, 507, and 421. This provides a "selection filter" for the rapid selection of mutant genotypes which can be analyzed in detail for the understanding of regulatory processes.