PEA MUTATIONS OF PRACTICAL VALUE

Monti, L. M., University of Naples, Portici, Italy
F. Saccardo, and P. Vitale Center of Nuclear Studies, Rome, Italy

By comparing mutagenic treatments on seed and on pollen of the canning variety 'Sprinter', and by classifying all the mutations found in M2 for chlorophyll and morphological mutations (Table 1), a higher frequency of the latter types was found after pollen treatments (82.5%) than after seed treatments (less than 36.5%).

Table 1. Frequency of mutations induced in variety Sprinter after treatment of uollen and of seed with mutagenic agents.

Irradiation on	Mutagenic agent	Mi plant analyzed (no.)	Mutations per Mj plant (%)	Relative frequency of mutations Chlorophyll (%)	Morphological (%)
Pollen	X-rays	271	14.8	17.5	82.5
Seed	X-rays	1107	16.0	80.3	19.7
	DS	372	22.3	63.8	36.2

The progenies of the morphological mutants isolated in M2 after seed and pollen treatments were analyzed in succeeding generations, the same selection procedure being followed from M2 on. In M3, only mutations which could have a practical interest were considered, e.g. mutations for height, flowering time, fertility, pod length, and seed weight and size. From M4 on, only lines with agronomic merit were selected. In M8 only two lines, both derived from pollen-irradiated material, were superior to the control varieties in yield (Table 2).

Table 2. Number of the best lines selected in different generations after pollen- and seed-mutagenic treatments in the pea variety Sprinter.

Material coming from	Number of lines selected in M_3	M_5	M_6	M_8
Pollen treatments	40	19	6	2
Seed treatments	83	6	1	-

Comparative agronomic and technological trials, performed in different Italian districts, confirmed the improved nature of the two mutant lines, mainly for some qualities of the processed product, such as taste and color. The certification procedure has already been started to release the two lines as new varieties.

Comparison of the results between the two treatments seems to indicate that pollen treatment probably induces a higher rate of the so-called point mutations than seed treatments. This is substantiated 1) by the lower rate of chlorophyll mutations, which are mainly attributed to chromosomal mutations, and 2) by the higher number of high yielding lines selected from M5, on. The higher rate of point mutations induced by pollen treatments in comparison with seed treatments is probably due to the sieve action of the haplontic selection at the moment of the M1 zygote formation.

ISOLATION OF THE STORAGE PROTEINS OF PEA SEEDS

MUller, H. P. Institute of Genetics, University of Bonn, West Germany

Legume cotyledons accumulate during their development both albumins and globulins. The latter constitute a protein reserve deposition which serves the nutritional requirements of the developing embryo during germination. The incorporation of proteins into the cotyledon is governed by a genetically regulated protein-synthesizing system, the mechanism of which is unknown. The globulins are proteins with particular physical properties exhibiting heterogeneity with regard to their subunit composition. Since most of the cotyledon proteins are coded for by nuclear DNA of the embryo, the storage proteins constitute an especially valuable system for analyzing the control mechanism of the genome as well as the physiological influence of the seed-bearing plant.

For understanding the controlling mechanism responsible for the synthesis of specific proteins in the cotyledons we first must have an idea of the different protein species found within the seeds. Then it is important to isolate, purify, and finally to biochemically characterize those proteins in detail.

Using SDS-gel-electrophoresis for analyzing the purified globulin fraction of pea seeds, one obtains a genotype-specific polypeptide pattern.

Analyzing seeds of mutants of the same variety presents considerable difficulties witli regard to quantitative extraction of proteins. The:extraction methods commonly used for Phaseolus and Vicia are not well suited for extracting Pisum seed proteins. Therefore, it was necessary to develop an extraction method especially adapted for pea seed proteins: the proteins were first extracted at the isoelectric point (IEP) at low salt concentration (acid extraction), then under alkaline conditions. This procedure allowed 100% recovery. Sucrose gradient analysis of the two extracts resulted in two dilution profiles as demonstrated in Fig. 1.