UTILIZATION OF THE HALF-SEED TECHNIC IN THE BREEDING OF HIGH PROTEIN VARIETIES OF PEA. I. GENETIC ANALYSIS OF LINES AND THEIR HYBRIDS WITH RESPECT TO CHOOSING CROSS COMBINATIONS FOR BREEDING

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Earlier investigations showed the potential of using the half seed method of estimating protein content (PNL 13:54-56). We intend to use this technic in genetic-breeding work towards developing lines of pea with high protein content. In practice it will involve selection of single seeds on the basis of the analysis of protein content in a half of a seed without the embryo.

On the basis of the earlier studies the following four lines were chosen for further investigation (with the average protein content): Mt 4042 - 29.2%, Wt 3527 - 24.4%, Wt 3026 - 29.2%, and L.X. - 25.6%. These lines were crossed in the following combinations: L.4042 x L.3527, L.4042 x L.3026, L.4042 x L.X, L.3527 x L.3026, L.3527 x L.X, L.3026 x L.X. For each cross combination, the protein content was analyzed (micro-Kjeldahl) in halves of seed without the embryo in the parental F1, F2, and backcross populations.

With such information it is possible to get general genetic-breeding information concerning the whole set of lines studied and their hybrids (diallel analysis of the F1 and generations) and more detailed genetic information concerning each of the cross combinations (analysis of the generations P1, P2, F1, F2, B1, B2). The estimation of general combining ability, obtained on the basis of the diallel analysis, were similar for both generations, F1 and F2. The high protein lines L.4042 and L.3026 had significant positive effects whereas lines L.3527 and L.X. showed significant negative effects.

The diallel analysis revealed an additive-dominant model of gene action for both F1 and F2. Thus, it was possible to obtain an estimation of genetic parameters according to Mather, i.e. D,F, h^2, H_1, H_2, and to estimate dominance and broad and narrow sense heritabilities (Table 1).

Table 1. Estimation of genetic parameters with their standard deviations and the functions of these parameters.

Parameters	Generation	
	F_1	F_2
D	5.95 ± 0.37	5.95 ± 0.38
F	2.19 ± 0.95	1.84 ± 0.98
h^2	21.33 ± 0.68	7.06 ± 0.69
H_1	14.19 ± 1.08	3.96 ± 1.10
H_2	13.14 ± 1.00	3.71 ± 1.02
$\left(\frac{H_1}{D}\right)^{\frac{1}{2}}$	1.54	0.82
H_{bs} (%)	98.10	96.41
H_{ns} (%)	41.44	67.57

The diallel analysis showed a significant dominance for low protein content, but the degree of dominance was different in different cross combinations. It varied from 1.06 (L.4042 x L.X.) to 8.47 (L.4042 x L.3026). The highest value was obtained in crosses involving two high protein lines, L.4042 and L.3026, indicating a genetic difference between them in spite of the similarity in protein content in the lines theemselves. On the basis of the results of diallel analysis and the analysis of particular cross combinations two hybrids, L.4042 x L.3026 and L.3026 x L.3527, were chosen for further breeding.

SUPPLEMENTARY EVIDENCE FOR THE LINKAGE OF afila WITH MUTANTS ON CHROMOSOME 1

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The afila (af) gene which converts leaflets into tendrils is now widely used in breeding programs around the world.

The data of Khangildin (1), Marx (2), and Snoad (3) place aX in chromosome 1 in the region of I.. My own findings confirm those presented by others.

The following lines were used:

— Induced afila mutant in cv. 'Wasata' (genotype: af Red I_)
— WL 1535 from Weibullsholm collection (genotype: Af red i)
— Variety 'Allround' (genotype: Af Red i)

The genetic analysis was carried out on F_ progeny derived from the following crosses: af Red *I* (Wasata) x Af Red i. (Allround) and af Red I (Wasata) x Af red i (WL 1535).

The crosses revealed the expected linkages, i.e. af-i and af-red. The Cro value for genes af -1 was 8.3 ± 2.9, and for genes af-red 3.1 + 1.3 (Table 1). This compares with 14.5 ± 1.6% between af-1 as determined by Snoad (3) and < 9% between af-red (1). It should be noted that my data, like those of Marx (1), show a deficiency of red segregants, thus evidently confirming the difficulty of scoring for red in an af background.

Table 1. Joint segregation of Af with I and with Red in two crosses.

Cross	Af I	Af i	af I	af i	Total
af I x Af i	572	280	292	1	1146
	Af Red	Af red	af Red	af red	
af Red x Af red	3125	118	1497	1	5741

1. Khangildin, W. V. 1966. Genetika (USSR) 6.
2. Marx, G. A. 1969. PNL 1:9-10.
3. Snoad, B. 1971. PNL 3:43.