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## INHERITANCE OF PROTEIN CONTENT IN PEA II. HERITABILITY OF PROTEIN CONTENT IN RANGER X STRAL AND PALOMA X STRAL CROSSES

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On the basis of breeding data obtained in the past, three varieties were chosen for studies, viz. 'Ranger', 'Stral' and 'Paloma'. The breeding data showed some strains with a higher protein content (WTD 4011 and WTD 4015), originating from crosses where one of the parents was the variety Ranger or Stral. Paloma lias a low protein content, but is among the highest yielding varieties in Poland. Crosses were made between varieties Ranger x StrSl and Paloma x Stral. The F1, F2, BC1, BC2, and parents were tested in each cross. Protein content was analyzed in single seeds by the Kjehldal method.

To assess the degree of genetic control over the protein content in the seeds, heritability coefficients were estimated in a narrow and a broad sense. The heritability coefficient estimate in the broad sense was calculated by a commonly used formula, i.e. by estimating the variance of the F2 and that of the parents. The value of this coefficient for the cross Ranger x Stral was 79.8% and that for Paloma x Stral 78.0%.

From the point of view of breeding it is far more interesting to know the heritability coefficient estimate in the narrow sense, expressed by the additive to phenotypic variance ratio (Mather and Jinks, 1971). It is possible to estimate this coefficient when gene action in a given cross is additivedominance (Kaczmarek, Surma, and Swiecicki, in press). The adequacy of the additive-dominance model of gene action was tested using the significance of differences between the observed and expected means for the analyzed generations (Chi square statistics). The results are presented in Table 1.

Cross	Generation	No. of obser- vations	Observed mean	Expected mean	Chi square
Ranger x Strål	P <sub>1</sub> Ranger	160	27.6	27.5	
	P <sub>2</sub> Strål	150	24.8	24.6	
	F <sub>1</sub>	170	24.6	24.6	
	$F_2$	850	24.5	25.3	0.57
	BČı	626	25.6	26.0	
	BC <sub>2</sub>	656	23.6	24.6	
Paloma x Strål	P <sub>1</sub> Strål	150	24.8	24.9	
	P <sub>2</sub> Paloma	134	21.1	21.7	
	F <sub>1</sub>	253	23.0	23.1	2.52
	F <sub>2</sub>	700	22.7	23.2	2.58
	BČ 1	1012	23.7	24.0	
	BC <sub>2</sub>	935	24.6	22.4	
Chi square <sub>3;</sub> 0.	05				7.82

Table 1. Observed and expected means for P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub>, and BC<sub>2</sub>

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Since in both crosses the calculated Chi square values were lower than the critical values of Chi squareg 05 there is no foundation to reject the hypothesis of the additive-dominance model of gene action.

Table 2 presents estimates of additive ([d]) and dominant ([fi]) gene action and of the mean (m), including standard errors as well as the heritability coefficients in the narrow sense  $(A_m)$ . The effects of additive gene action are similar in the two crosses. Marker differences, however, are noted for the effects of dominance.

	Genetic parameters				
Cross	m	[â]	[ĥ]	Ĥ <sub>ns</sub> %	
Ranger x Strål	26.0 + 0.64	$1.46 \pm 0.65$	-1.98 ± 1.08	29.2	
Paloma x Stral	23.3 ± 0.63	$1.60 \pm 0.63$	-0.24 ± 1.82	70.4	

Though dominance was well indicated in the lower protein content in both crosses, the cross Ranger x Stral, i.e. between high and medium protein varieties, showed a much greater effect of dominance than the cross Paloma x Stral. This is reflected in the narrow sense heritability coefficients. The results suggest that in breeding for high protein content the desired results may be better and easier to obtain when varieties with medium protein content are crossed.