

LIMITATIONS ON BREEDING HIGH-PROTEIN FIELD PEAS

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ABSTRACT

Peas (*Pisum sativum* L.) have been considered, along with other grain legumes, to provide increased production of plant protein for both animal and human use.

A study was undertaken to determine the factors affecting protein content in peas. In genotype x location and genotype x year trials, protein content varied with genotypes and location, but there was little variation over years. Protein content was not correlated with height or harvest index. It was, however, consistently negatively correlated with yield. This factor, coupled with only moderate broad-sense and narrow-sense heritability estimates for protein content, indicate that breeding for increased protein content in field peas would be a very marginal proposition.

Since yield of protein per unit area was greatest from high yielding rather than high protein genotypes, the suggestion that breeding for maximum protein production requires breeding for higher yield was investigated.

INTRODUCTION

Pisum sativum L. is a temperate-zone legume with edible seeds, rich in protein. As such, it has the potential to provide much-needed protein for both humans and animals in an increasingly protein-scarce world. For that potential to be realized, emphasis must be placed on improving the yield of protein as well as its quality, digestibility, and acceptability.

The work presented here was a contribution (Jermyn, 1976) to a large programme of research into all aspects of pea protein production and utilization, at the University of Saskatchewan in Canada (Slinkard, 1977).

Three major experiments were undertaken with field peas to assess the factors affecting variability of protein content, to study the relationship of protein content to other plant traits, and to obtain heritability estimates for protein content. This information should assist in devising the best strategy for improving protein concentration of New Zealand pea cultivars.

MATERIALS AND METHODS

Experiment One: Twenty-five cultivars, comprising commercial standards, advanced breeding lines from the Morden field pea programme, and introductions from the World Collection, were grown at three locations in one year; and 22 common genotypes were grown for three years at one location. They were planted in a 4-replicate randomised complete block design with 4-row plots 3 m long. No fertiliser was used. The plots were kept weed free from emergence to harvest. Yield and protein content were measured at all locations and in all years. In addition, at two of the three locations in one year, height and harvest index were measured.

Experiment Two: To gauge the extent of genetic variability of protein content in the World Pea Collection, 1071 genotypes from it were grown along with a standard, in 17 8x8, two-replicate, partially-balanced lattices, at Saskatoon in 1975. The 2-row plots were 3 m long. Yield, protein content, and seed weight were measured and yield of protein

was calculated.

Experiment Three: Narrow-sense heritability of protein content was estimated by F_2 mid-parent regression (Falconer, 1960) among 21 field pea crosses. Parents and F_2 populations were sown in a two-replicate randomised complete block design at Saskatoon in 1975. The two-row plots were 3 m long.

RESULTS AND DISCUSSION

Experiment One: Analysis of variance showed that there were differences among genotypes, locations, and years for both yield and protein content. There were also genotype by location interactions for both yield and protein content. However, genotype differences in protein content were consistent over the years. Thus there was considerable variation among genotypes, ranging from 22.4 to 28.9% protein, whilst location means varied from 22.6 to 27.1%. Protein content varied little over the three years at one location, averaging 24.0, 24.9 and 25%, despite conditions ranging from severe drought in 1973 to an abnormally cool, moist season in 1974.

Among relationships of protein content to other plant traits, there was a consistent and statistically significant negative correlation with yield (see Table 1). Between one third and two thirds of the observed variation in protein content was associated with

TABLE 1: Correlation coefficients of yield and protein content for 25 pea genotypes grown at three locations in 1974 and for 22 common pea genotypes grown in three consecutive years at Saskatoon.

| Location: | Saskatoon | Nipawin | Bellevue |
|-----------|-----------|---------|----------|
| r | -.811** | -.690** | -.759** |
| Year: | 1973 | 1974 | 1975 |
| r | -.582** | -.746** | -.603** |

** Significant at the 1% level.

variation in yield. Neither yield nor protein content was associated with height or harvest index (Table 2). This is in contrast to cereals where correlations between yield and harvest index have been reported, and harvest index is considered by some breeders a worthwhile breeding objective (Rosielle and Frey, 1975).

TABLE 2: Simple correlation coefficients among yield, protein content, harvest index, and height for 25 pea genotypes grown at Saskatoon and Nipawin in 1974.

| Traits | Location | Protein Content | Harvest Index | Height |
|-----------------|-----------|-----------------|---------------|---------|
| Yield | Saskatoon | -.811** | .009 | .103 |
| | Nipawin | -.690** | -.087 | -.009 |
| Protein content | Saskatoon | | -.177 | .034 |
| | Nipawin | | -.002 | .199 |
| Harvest Index | Saskatoon | | | -.744** |
| | Nipawin | | | -.799** |

** Significant at the 1% level.

Experiment Two: Lattice variances were heterogeneous and thus the lattices were not subjected to a combined analysis. There were significant differences among genotypes for percent protein and seed weight in all lattices, and significant differences among genotypes for seed yield and protein yield in all but two lattices. Experimental means were 747 g plot⁻¹, 26.1%, 194 g plot⁻¹, and 37.7 g 200⁻¹ seeds for seed yield, percent protein, protein yield, and seed weight, respectively. There was a considerable range in lattice means for seed yield and protein yield. To remove lattice effects, each line mean was converted to a percentage of the respective lattice mean and all lines were expressed as a percentage of the experimental mean. On a percentage basis, the ranges were 34.7 to 172.4% for seed yield, 85.1 to 118.7% for percent protein, 33.7 to 165.5% for protein yield, and 29.9 to 273.4% for seed weight. The actual range in percent protein was 22.6 to 30.9%. The distribution of all traits was close to normal, although seed yield and protein yield curves were negatively skewed and percent protein and seed weight curves were positively skewed.

Thus, the range in percent protein was narrow (0.4-fold from lowest to highest) in comparison to the range in seed yield (4-fold), protein yield (4-fold), and seed weight (8-fold). This narrow range in percent protein indicates that the U.S.D.A. World Pea Collection does not contain a large amount of genetic variability for percent protein. By extrapolation, it may be concluded that field peas do not contain much genetic variation for percent protein.

Simple correlation coefficients between percent protein, seed yield and protein yield were calculated for each lattice (Table 3). Seed yield and percent protein were negatively and significantly correlated in 15 of the 17 lattices and the significant coefficients ranged from $r = .24^*$ to $-.59^{**}$. Thus, up to 35% of

TABLE 3: Simple correlation coefficients between yield, protein content and protein yield in 17 random sub-sets from 1071 genotypes of the U.S.D.A. World Pea Collection. $n = 63$ plus a standard in each lattice.

| Lattice number | Yield-protein content | Yield-protein yield | Protein content-protein yield |
|----------------|-----------------------|---------------------|-------------------------------|
| 1 | -.59** | .97** | -.43** |
| 2 | -.47** | .96** | -.23 |
| 3 | -.43** | .93** | -.07 |
| 4 | -.36** | .97** | -.14 |
| 5 | -.09 | .95** | .21 |
| 6 | -.28* | .94** | -.04 |
| 7 | -.31* | .92** | -.06 |
| 8 | -.39** | .95** | -.10 |
| 9 | -.50** | .92** | .16 |
| 10 | -.53** | .95** | -.28* |
| 11 | -.42** | .95** | -.14 |
| 12 | -.24* | .94** | -.09 |
| 13 | -.29* | .94** | -.03 |
| 14 | -.53** | .88** | -.08 |
| 15 | -.52** | .96** | -.28* |
| 16 | -.04 | .95** | .25* |
| 17 | -.39** | .91** | -.00 |

* and ** Significant at the 5% and 1% level, respectively (d.f. = 62.)

the variation in percent protein was associated with variation in yield. Seed yield and protein yield were strongly positively correlated in all lattices, with correlation coefficients ranging from $r = +.88^{**}$ to $+.98^{**}$. This was inevitable because protein yield is protein percent (small range) multiplied by seed yield. Between 78 and 96% of the variation in protein yield was associated with variation in seed yield. However, percent protein and protein yield were not consistently related. The coefficients were significant in only 4 of the 17 lattices, and ranged from $r = -.43^{**}$ to $+.26^*$.

These findings, together with those described in Part 1, indicate that the negative relationship between seed yield and percent protein frequently found in cereals (Haunold *et al.* 1962; Spilde *et al.* 1974; Bhatia 1975; Gomez and DeDatta 1975) and in other legumes (Tandon *et al.* 1957; Furedi 1970; Leleji *et al.* 1972), occurred over a wide genetic base in peas and was of sufficient magnitude to interfere with the selection of productive high-protein genotypes. Further, the consistency of the relationship showed that percent protein data should not be considered in isolation from yield data in breeding or evaluation experiments. More important, the data reinforce the conclusions of Leleji *et al.* (1972) that high-protein yield would be obtained more easily from high-yielding rather than high-protein genotypes in beans.

Experiment Three: The heritability value obtained was 45%, which is low to moderate when compared with the high values of 80 and 97%, found for days to flower and seed weight respectively, in the same crosses. However, this value for protein content agrees with those of Pandey and Gritton (1976) and Shia (1976). Heritability estimates are always restricted in their validity to the material and conditions of each particular study and should thus be used with caution.

CONCLUSIONS

The limited genetic variation in protein content of peas, combined with a moderate heritability and a consistent negative relationship with yield, mitigate against successfully breeding for increased protein content.

These findings, together with others from the Saskatoon programme (Slinkard, 1977) have altered the direction of the field pea breeding programmes at Saskatoon and at Lincoln from emphasizing protein to emphasizing yield without sacrificing protein concentration.

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