Legume Res., 24 (1) : 28 - 31, 2001

INHERITANCE OF PROTEIN CONTENT IN CHICKPEA*

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ABSTRACT

Chickpea is considered a source of quality protein in vegetarian diets. An experiment was carried out with three genotypes of chickpea P 9623, RS 11 and T 39-1 which differed significantly for their protein content. The experiment was conducted in deep vertisols under conserved soil moisture conditions. T 39-1, a high protein line was crossed with moderate and low protein parents P 9623 and RS 11. The crosses showed dominance of low protein over high protein content. Near normal frequency distribution was obtained for protein content in F_2 generations for both the crosses suggesting the role of atleast a few genes governing this character. Segregants with high protein content were recovered which could be used to enhance the nutritional value of chickpea.

INTRODUCTION

Grain legumes are important and rich sources of protein in human and animal nutrition. They contain 20-30% protein in their seed which is 2-3 times higher than that in cereals. The protein of pulses is nutritionally important and superior, as the amino acid lysine is found in larger quantity than in the cereal protein. Chickpea (*Cicer arietinum* L.) is an important pulse crop of India with protein content in the seed in the range of 12.6 - 30.5% (Singh, 1985), showing large variation for this character. Average protein concentration of chickpea is the smallest of all the pulses (Williams and Singh, 1987). Although genotypes with high protein content exist, reports on the development of high protein cultivars with a strong agronomic potential are not yet available. Such cultivars would pave the way to the harvest of more protein yield per unit area. Reports are available that the heritability of protein content of kabuli chickpea may be stronger and significant. Also higher protein content is an inherited characteristic with the possibility of selection for it (Williams and Singh, 1987). The improvement of protein content and quality are major considerations in chickpea breeding. T 39-1 is a blue flowered, high protein line found in the chickpea germplasm. A study was undertaken to investigate the inheritance of seed protein content in two crosses of chickpea involving this high protein line, T 39-1.

MATERIAL AND METHODS

The experiment was conducted during the *Rabi* (post-rainy season) 1997-98 at the International Crops Research Institute for the Semi Arid Tropics (ICRISAT). The experiment was conducted with three genotypes P 9623, RS 11 and T 39-1 involved in two crosses. T 39-1 is a high protein line used as a common male parent for moderate and low protein female parents, P 9623 and RS 11. F_1 and F_2 generations of the two crosses P 9623 x T 39-1 and RS 11 x T 39-1 along with the parents were studied. The crosses P 9623 x T 39-1 and RS 11 x T 39-1 were made in the *Rabi* season 1995 to get the F_1 generations. The F_1 seeds were grown during the *Rabi* season 1996 to get the F_2 seeds. These F_2 seeds were taken as the material for the present investigation. Fresh F_1 generations for the study were obtained from the glass house. The parental, F_1 and F_2 seeds of the two crosses were sown on 14 October 1997 on deep vertisols under conserved soil moisture conditions. They were sown on ridges 60 cm apart in an unreplicated block. The plot sizes were 10 rows, 4 m long, 60 cm apart for each F_2 and

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one row each for parents and F_1s. The seeds were planted at 20 cm within the row. Normal crop management practices were taken up.

Seed protein content estimation for individual plants was done in the Crop Quality Service Laboratory at ICRISAT. The seeds of each plant were ground in Udy cyclone grinding mill and passed through a 0.4 mm mesh to obtain the chickpea flour. Nitrogen content was determined using Technicon Autoanalyser (TAA) and the protein content was estimated by multiplying the total Nitrogen content in the seeds obtained with factor 6.25. Protein content was determined for 117 random competitive F_2 plants in the cross P 9623 x T 39-1, 90 F_2 plants in the cross RS 11 x T 39-1, 20 plants in each parent and 10 plants in each F_1.

RESULTS AND DISCUSSION

The mean seed protein content of P 9623, RS 11 and T 39-1 was 24.32%, 22.47% and 30.24% respectively which were significantly different from each other (Table 1). The ranges were 23.10 - 26.30%, 20.40 - 24.90% and 27.10 - 31.80% respectively for P 9623, RS 11 and T 39-1. The F_1 mean value of the cross P 9623 x T 39-1 was 23.51% + 0.640, while in the cross RS 11 x T 39-1 it was 21.72% ± 0.650. In both the crosses, the F_1 mean was almost equal to the low protein parent indicating dominance for low protein content. This varies with Singh *et al.* (1992) who reported partial and over dominance for protein content. But Garcia *et al.* (1985) showed that the segregation pattern for protein content varied with the crosses, the genetic system being heterogeneous. In the F_2 generation, mean protein content was 25.94% ± 0.182 and range was 21.0 - 30.50% in the cross P 9623 x T 39-1 and mean was 24.32% ± 0.224 and range was 20.50 - 30.10% in the cross RS 11 x T 39-1. In both the crosses, F_2 mean was lower than the mid parental value and nearing the low protein parent.

Table 1. Seed protein content for the parental, F_1 and F_2 generations for two crosses of chickpea, *Rabi* 1997-98.

Cross	Parent / Generation	Seed protein content (%)	Range
P 9623 x T 39-1	P 9623	24.32 ± 0.554	23.10 - 26.30
	T 39-1	30.24 ± 0.440	27.70 - 31.80
	F_1	23.51 ± 0.640	22.60 - 24.90
	F_2	25.94 ± 0.182	21.40 - 30.50
RS 11 x T 39-1	RS 11	22.47 ± 0.520	20.40 - 24.90
	T 39-1	30.24 ± 0.440	27.70 - 31.80
	F_1	21.72 ± 0.650	20.20 - 23.10
	F_2	24.32 ± 0.224	20.50 - 30.10

The frequency distributions for seed protein content for the parents and F_1 and F_2 generations for the crosses P 9623 x T 39-1 and RS 11 x T 39-1 are presented in Fig 1 and 2. Near normal frequency distribution was observed in the F_2 generations of both the crosses which suggested multigenic control of this trait. It was slightly skewed towards the low protein parent in the cross RS 11 x T 39-1 cross suggesting the dominance of low protein over high protein content. The presence of multigenic interactions for this trait was also indicated by Rang *et al.* (1986). Tyagi and Singh (1988) found that the differences did not have extrachromosomal or cytoplasmic basis. Singh *et al.* (1990) reported that protein content followed normal distribution pattern. The cross P 9623 x T 39-1 showed transgressive segregation towards low protein parent. This indicated the presence of some genes for low protein content in the high protein parent apart from the genes for high protein

content resulting in non-isodirectional distribution of genes for protein content. The other cross RS 11 x T 39-1 did not show transgressive segregation which could be due to isodirectional distribution of genes for protein content.

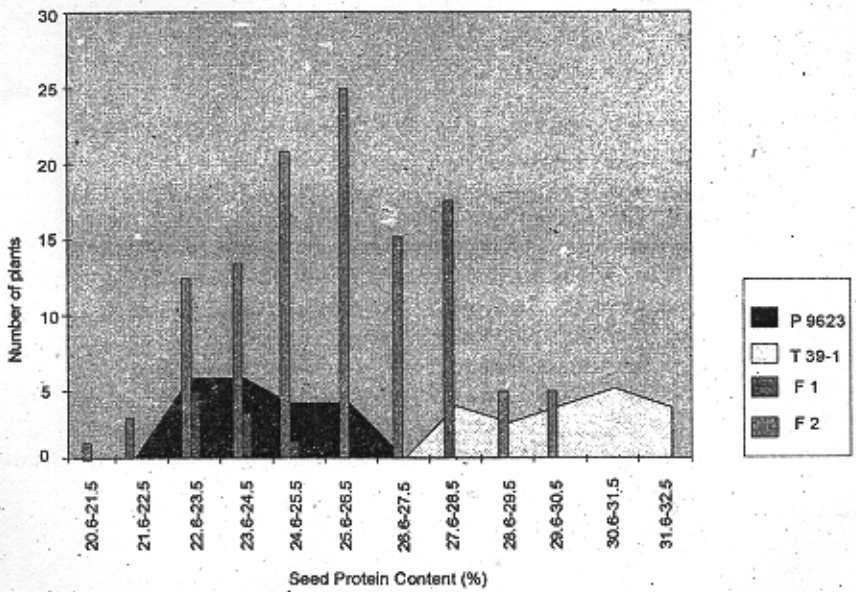

Fig.1 Frequency distribution for seed protein content in Parental, F_1 and F_2 generations for the cross P 9623 x T 39-1, *Rabi*, 1997/98

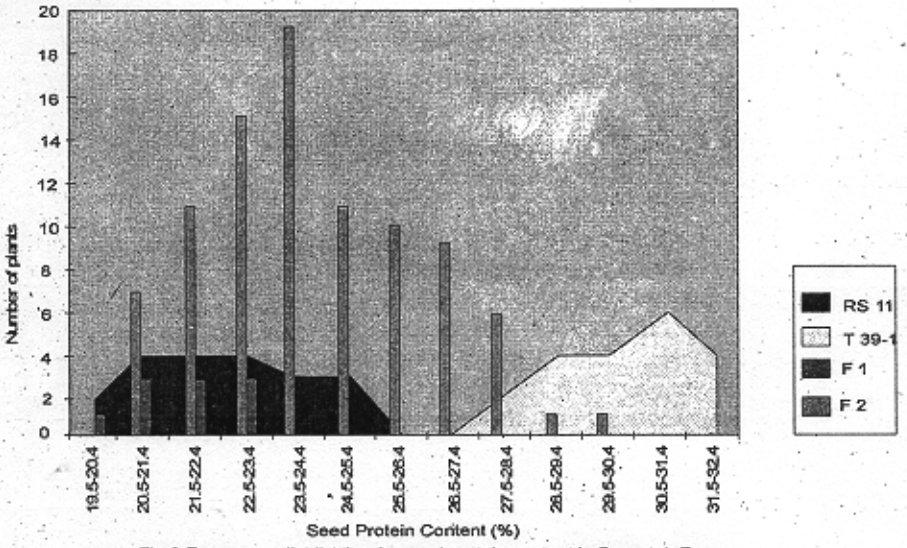

Fig.2 Frequency distribution for seed protein content in Parental, F_1 and F_2 generations for the cross Rs11 x T 39-1, *Rabi*, 1997/98

The multigenic control suggests significant influence of environment on seed protein content. Substantial genotype x environment interaction has been reported for this character (Sengupta *et al.*, 1986 and Singh *et al.*, 1990). Location had the greatest influence on seed protein content in chickpea more than growing season (Singh *et al.*, 1990). However, high heritability for protein content was also observed by Sandhu *et al.* (1989) which indicates that relatively quick progress in breeding for this character should be possible. In the F_2 generation of both the crosses, segregants with high protein content were recovered which could be stabilised in later generations. Thus, T 39-1, which is a high protein genotype, may be used as parent with existing genotypes. Subsequent selection for high protein content and high seed yield may be done to recover cultivars with high yield as well as high protein content.

ACKNOWLEDGEMENTS

We thank B. V. Rao and M. Aziz for their technical assistance during this study.

REFERENCES

Garcia, J. A. G. *et al.* (1985). *Int Chickpea Newslett.*, **13** : 3-6.
Rang, A. *et al.* (1986). *PAU J. Res.*, **23** : 375-379.
Sandhu, T. S. *et al.* (1989). *PAU J. Res.*, **26** : 1-9.
Sengupta, K. *et al.* (1986). *Indian Agriculturist.*, **30** : 63-66.
Singh, K. B. *et al.* (1990). *J Sci Food Agric.*, **53** : 429-441.
Singh, U. (1985). *Qual P.Foods Hum Nutr.*, **35** : 339-351.
Singh, V. P. *et al.* (1992). Program and abstracts. Second International Food Legume Research Conference, Cairo, Egypt, 12-16 April 1992, pp 71
Tyagi, P. S. and. Singh, B. D. (1988). *Ann. Biol.*, **4**: 54-58.
Williams, P. C. and Singh, U. (1987). In: The Chickpea, C. A. B. International, London U. K .pp 329-356.