Short Communication



## Evaluation of seed protein content and quality of two Cajanus cajan $\times$ C. cajanifolius hybrids

J. Panigrahi, S. N. Patnaik and C. Kole<sup>1</sup>

Post Graduate Department of Botany, Utkal University, Bhubaneswar 751 004

(Received: March 2002; Accepted: November 2002)

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a rich source of dietary vegetable proteins that well compliment the cereals. The quality of its seeds is primarily expressed in terms of its protein content that ranges between 17.3 to 24.1% [1]. The quality of protein, in turn, is determined by the amount of sulphur containing amino acids and low content of protease inhibitors.

Pigeonpea seed proteins contain 54-60% globulin, 10-20% albumin, 10-20% glutelin and 2-5% prolamin [1], whereas globulins are deficient in sulphur containing amino acids, the enzymatic albumin fraction is a rich source of sulfur containing amino acids. Hence, higher proportion of albumin per unit protein or higher albumin to globulin ratio should reflect better protein quality [2, 3].

The wild species, *C. cajanifolius* (Haines) van der Maesen, is considered to be the putative progenitor of pigeonpea. It is a rich source of seed protein with minimal protease inhibitors and high albumin to globulin ratio [4, 5]. This species could be used as a donor for improvement of protein content and quality in pigeonpea. The present study, therefore, accentuated upon assessment of interspecific hybrids of *C. cajan* and *C. cajanifolius* with regard to a number of seed protein parameters.

Two F<sub>1</sub> hybrids were developed by crossing of two pigeonpea cultivars, AKT 9013 and AKPH 1156 with a common male parent of *C. cajanifolius* followed by embryo rescue. Total seed proteins from the seeds of the two pigeonpea cultivars, *C. cajanifolius* and the two hybrids were extracted by suspending seed flour in 50mM of phosphate buffer (pH 7.5) followed by centrifugation at 17000×g at 0°C for 10 min and then precipitation in 20% trichloro-acetate. The two major seed protein fractions, water soluble albumins and salt soluble globulins were extracted [6] and quantified [7] along with total protein content using the standard curve of BSA, fraction-V.

Protein content of C. cajanifolius was much higher than the two pigeonpea cultivars, AKT 9013 and AKPH 1156 (Table 1). The F1 hybrids from both the crosses had much higher protein content than the mid-parental values and were very close to the wild species C. cajanifolius evidencing for positive heterosis. These findings corroborated to those of Rangasamy et al. [5]. Similar were the results for albumin content. On the contrary, globulin content was lower in the wild species as compared to the cultivars. The F1 hybrids had globulin content much lower than the mid-parental values and even lower than the inferior parent C. cajanifolius in one cross evidencing for negative heterosis. The albumin to globulin ratio thus was much higher in the wild species than in the pigeonpea cultivars. In this regard, the F1 hybrids superseded the mid-paental values in both the crosses. In comparison to the wild species, one hybrid had slightly lower ratio while the

**Table 1.** Estimates of mean contents of total protein, albumin, globulin and albumin to globulin ratio in two *C. cajan*  $\times$  *C. cajanifolius* hybrids as compared to their parents<sup>1</sup>

Genotypes	Protein content (%)	Albumin (%)	Globulin (%)	Albumin to globulin ratio
Female parents (FP) : Cajanus cajan			_	
AKT9013 (FP1)	22.8	11.197	59.699	0.19
AKPH1156 (FP2)	21.6	10.916	59.697	0.18
Male parent (MP) : <i>C. cajanifolius</i>	30.8	14.298	54.899	0.26
Cross # 1: FP1 × MP	28.8	13.697	54.298	0.25
MPV <sup>2</sup> for Cross # 1	26.8	12.748	56.799	0.23
Cross # 2 : FP2 × MP	29.6	14.097	52.503	0.27
MPV for Cross # 2	26.2	12.607	56.798	0.22

 $^{1}$ Contents represent the mean values for randomly selected 20 seeds of parent genotypes and single seeds of the two hybrids  $^{2}$ MPV = Mid-parental value

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other hybrid surpassed the parental range suggesting positive heterosis for albumin to globulin ratio.

Higher albumin to globulin ratio is one of the desirable criteria for better protein quality in grain legumes [8]. It could then be possible to develop high yielding pigeonpea genotypes with higher seed protein content coupled with better seed protein quality through introgressive wide hybridization with *C. cajanifolius*. Further biometrical studies to delineate the precise nature of gene action for the protein parameters are now in progress.

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