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Short Communication

Seed protein studies in common bean (*Phaseolus vulgaris* L.) germplasm grown at high altitude

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The dry bean or common bean (*Phaseolus vulgaris* L.), a native to the Western hemisphere, is an important dietary component for many people worldwide. It is a major source of protein in the Americas and in parts of Asia and Africa where animal products are either scarce or too expensive for widespread consumption. Among the crops grown in hills in general and high altitude in particular, common bean is one of the most important legume. Some of the pockets in central Himalaya located in higher elevation like Auli, 2903 meter, above mean sea level (amsl)), Harsil (3225 m), Munsiyari (2100 m) etc. are very promising sites as common bean produced in the areas are of good cooking quality and taste probably due to interactive factor of climate and genotype.

Among the commercially grown common bean varieties, limited genetic variability (2-3%) for seed protein has been found [1]. However, a wide range of protein content (17-35%) has been reported for common bean based on assessment of additional germplasm [2-3]. Central Himalaya where the present investigation was carried out contains wide array of common bean germplasm due to its traditional cultivation and adaptation from foothills to higher Himalayan regions under different agro-climatic conditions. The different types of common bean grown are based on farmers preference, taste and cooking quality. However, information on one of the important parameters i.e. seed protein content is scanty. Keeping the protein aspect in view, the present investigation was carried out to assess the variation in seed protein content of 88 common bean germplasm in order to identify the potential genotype(s) which can be used as genetic resource for improvement of seed protein in common bean.

A set of 88 accessions of common bean was evaluated during 1999 at Defence Agricultural Research Laboratory, Field Station, Auli (Uttaranchal) located at 2903 m (amsl) in the central Himalaya. Seeds for the present investigation were obtained from the trial conducted at Auli and analyzed for seed protein during 2000-2001 in the Plant Molecular Biology Laboratory, Defence Agricultural Research Laboratory, Pithoragarh in Completely Randomized Design (CRD) with three replications. Fully matured randomly chosen healthy seeds of each genotype were soaked in distilled water in triplicate for 3-4 hours to facilitate the removal of seed coat. After removing the seed coat, cotyledon meal was homogenized in 2 ml of 0.1 M Tris-HCl buffer (pH 7.5). The homogenized mixture was centrifuged at 17600 g at 4°C for 20 minutes and the supernatant was collected. Quantification of protein was done following the method of Lowery *et al.*, [4]. Bovine Serum Albumin (BSA) was used as standard. The absorbance at 660 nm wave length was recorded using double beam spectrophotometer. Seed protein data obtained from 88 genotypes were analyzed statistically in CRD.

Analysis of variance for seed protein of 88 common bean germplasm revealed statistically significant variance ratio for protein percentage among 88 accessions. The results, therefore, indicated that the difference in seed protein content among common bean germplasm studied so far might be due to genetic cause and not due to environmental or error factors.

The range of variation for seed protein content was found to be 17.45% in Auliphas-75 to 24.67% in Auliphas-04 with a mean seed protein of 20.90%. Previous studies on common bean have also revealed seed protein of similar ranges, such as, 18.57 to 20.06% [5]; 13.30 to 20.75% [6] and 19.80 to 24.90% [7] among common bean germplasm from different geographical regions.

Perusal of mean over repetitions revealed that highest seed protein was associated with Auliphas-04 (24.67%), which is a genotype with pole type of growth habit, small seed size and yellowish brown in colour, collected from a village located at higher elevation.

Auliphas-91, another pole type genotype touched the protein content level of 24.10%, which was statistically *at par* in seed protein content with Auliphas-04. However, Auliphas-04 exhibited significantly higher seed protein content over all other accessions presently investigated. Other genotypes having remarkably higher seed protein level were Auliphas-84 (23.95%), Auliphas-39 (23.89%), Contender (23.82%), Auliphas-74 (23.70%), Auliphas-12 (23.60%), Auliphas-21 (23.53%), Auliphas-34 (23.40%) and Auliphas-17 (23.13%).

Based on the seed protein content, 88 accessions were classified in three groups. Group I contained 42 genotypes with seed protein content less than μ ± Sem (20.901±0.174). Group II included 9 genotypes, which were at par with mean (μ±Sem), in seed protein content whereas 37 genotypes with seed protein per cent more than the mean (μ±Sem) formed group III (Table 1). Thirty-four genotypes were noted to be of pole type and 8 were of bush type plant growth habit among the genotypes containing seed protein less than the mean seed protein content. Genotypes of group II, which were *at par* with mean value in seed protein, consisted of 8 pole type and 1 bush type of plant growth habit. The III group composed of 34 pole type and 3 bush type of plants. Thus, out of 88 accessions, 76 were of pole type whereas 12 were with bush type of plant growth habit.

Table 1. Seed protein based grouping of common bean germplasm from Central Himalaya

Group	Range of protein (%)	Number of genotype	Growth habit	
			Pole type (No.)	Bush type (No.)
I	< 20.90 ± 0.174 (μ ± SEm)	42	34	8
II	= 20.90 ± 0.174 (μ ± SEm)	09	08	1
III	> 20.90 ± 0.174 (μ ± SEm)	37	34	3
	Total	88	76	12

The genotype with highest protein content (24.67%) i.e. Auliphas-04 and the one with lowest protein content (17.45%) i.e. Auliphas-75 were of pole type in growth habit. Among the pole types, around 45% genotypes were with protein content more than the mean seed protein content whereas among the bush type common bean only 25% of the accessions were with seed protein surpassing the mean seed protein value. Thus pole type of common beans contained high frequency of high protein genotypes in comparison to bush type of genotypes. However, looking at the protein content ranking, it is obvious that 2 bush type genotypes having protein content more than the mean value were under 5 best seed protein genotypes group. Although the top seed protein ranking pole type genotype Auliphas-04 had significantly higher seed protein (24.67%) in comparison to bush type of genotypes namely Auliphas-39 (23.89%) and Contender (23.82%), yet in general, no clear cut evidence appeared to support that pole type of genotypes are superior than bush types of genotypes in terms of seed protein content. 88 accessions studied were ranked according to their seed protein content and out of these, 10 high ranking genotypes were chosen and are depicted along with some morphological parameters in Table 2. These genotypes seem to be promising and potential genetic resource for seed protein content in common bean and may be utilized in improvement programme aimed to protein enhancement in common bean.

Table 2. Common bean genotypes as potential genetic resource for seed protein

Genotype	Protein (%)	Growth habit	Pod shape	Grain colour	Grain size
Auliphas-04	24.67	Pole	Straight	Yellowish brown	Small
Auliphas-91	24.10	Pole	Curve	Violet	Medium
Auliphas-84	23.95	Pole	Straight	Light brown	Medium
Auliphas-39	23.89	Bush	Straight	Light red spotted	Medium
Contender	23.82	Bush	Curve	Light brown	Medium
Auliphas-74	23.70	Pole	Straight	Light violet	Bold
Auliphas-12	23.60	Pole	Straight	Grey with black spotted	Small
Auliphas-21	23.53	Pole	Straight	Off-white with red spotted	Medium
Auliphas-34	23.40	Pole	Straight	White spotted	Bold
Auliphas-17	23.13	Pole	Straight	Yellow	Small
CD at 1%	**0.64**				

References

1. **Silbernagel M. J.** 1970. Protein improvement work by USDA- Bean and Pea Investigations. *In*: Report of 10th Dry Bean Research. Conference. Davis, California, U.S.A: 70-83.

2. **Meiners J. P. and Litzenberger.** 1975. Breeding for nutritional improvement. *In*: M. Milner (Ed) Nutritional improvement of food legumes through breeding. Wiley, New York, USA: 131-141.

3. **Evans A. M. and Gridley H. E.** 1979. Prospects for the improvement of protein and yield in food legumes. Curr. Adv. Pl. Sci., **3**: 1-17.

4. **Lowry O. H., Rosebrough N. J., Farr A. L. and Randal R. J.** 1951. Protein measurement with the folin phenol reagent. J. Biol. Chem., **193**: 265-275.

5. **Hu M. L., Hung T. T. and Chion R. Y. Y.** 1997. Agronomic Characteristics of various cultivars of common bean (*Phaseolus vulgaris* L.) and analysis of their seed compositions. J. Chinese Agric., **35**: 9-17.

6. **Guzman-Maldonado S. H., Castellanos J. Z. and Conzalez de M. E.** 1997. Relationship between the physical chemical and sensory properties of 16 common bean genotypes. Agrociencia, **31**: 405-409.

7. **Milve G. and Nankova M.** 1998. Seed protein content of common bean cultivars (*Phaseolus vulgaris* L) depending on biotic and abiotic factors. Bulgarian J. Agric. Sci., **4**: 633-639.