Short Communication

Variability for grain protein content among germplasm accessions and advanced breeding lines in dolichos bean (*Lablab purpureus* L. Sweet var. Lignosus Prain)

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Abstract

Protein energy malnutrition (PEM) is prevalent in south-east Asian countries including India. Breeding and introduction of grain protein-rich varieties of legumes such as dolichos bean is considered as cost-effective approach to combat PEM. Exploitation of genetic variability within germplasm accessions (GAs) and/or breeding populations is the short-term strategy for identification and delivery of protein-rich dolichos bean cultivars to cater to the immediate needs of the farmers and target population. A set of 118 dolichos bean genotypes consisting of 96 GAs and 20 advanced breeding lines (ABLs) and two released varieties (RVs) was field evaluated in augmented deign for dry grain yield per plant and their grain protein contents were estimated. The grain protein content among the genotypes ranged from 18.82 to 24.5% with a mean of 21.73%. The magnitude of estimates of absolute range, standardized range, and phenotypic coefficient of variation (PCV) for grain protein content was higher among GAs than those among ABLs + RVs. However, average grain protein contents of GAs were comparable to those of ABLs + RVs. Nearly 50% of the genotypes (mostly GAs) had significantly higher grain protein content than those of RVs, HA 3 and HA 4. The grain protein contents of the genotypes were poorly correlated with grain yield per plant. These results are discussed in relation to strategies to breed grain protein-rich dolichos bean cultivars.

Keywords: correlation, dolichos bean, protein, variability

Introduction

Protein energy malnutrition (PEM), primarily the result of intake of diets poor in bio-available protein, can lead to reduced intellectual and physical abilities in pre-school children and irregular menstrual cycles among women of child-bearing age (Monica *et al.*, 2018). PEM is prevalent in south-east Asian countries including India. Grain legumes are the primary source of dietary protein and energy to human beings, especially to those depending on vegetarian diet (Welch and Graham, 2004). Dolichos bean is one of the most important grain legume crops cultivated and consumed by millions of people in large quantities on a daily basis in India (Ramesh and Byregowda, 2016). It can withstand drought better than cowpea (Ewansiha

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Table 1. Estimates of mean, absolute range, standardized range and phenotypic coefficient of variability among germplasm accessions advanced breeding lines for grain protein content in dolichos bean

	Number of genotypes	Mean	't'-Statistic	Probability	Absolute range		Standardized range	Phenotypic coefficient of variability
					Highest	Lowest		
Germplasm accessions (GAs)	96	21.69	−0.75	0.46	24.5	18.82	4.63	10.44
Advanced breeding lines (ABLs) + released varieties (RVs)	22	21.9			23.59	20.08	3.70	4.10
GAs + ABLs + RVs	118	21.73	–	–	24.5	18.82	4.82	6.32

and Singh, 2006), adapt to acidic soils (Mugwira and Haque, 1993) and saline soils (Murphy and Colucci, 1999) and produce higher green foliage and biomass (Magoon *et al*., 1974) better than other legumes. The introduction of dolichos bean pure-line varieties selected and/or bred for increased grain protein content through plant breeding approach is considered as most effective approach to combat PEM (Welch and Graham, 2004).

Exploitation of genetic variability within the natural populations such as germplasm accessions (GAs)/breeding populations is the short-term strategy for identification and delivery of protein-rich dolichos bean cultivars to cater to the immediate needs of the farmers for production and target population for consumption. It is expected to reduce PEM in target population at least by 50% through regular and large-scale intake of protein-rich diets based on the products of crops (Welch and Graham, 2004) such as dolichos bean. The objectives of the present investigation were to assess genetic variability for grain protein contents among GAs and advanced breeding lines (ABLs).

Experimental

A set of 118 genotypes which included 96 GAs and 20 ABLs and two released varieties (RVs) (HA 3 and HA 4, which are photoperiod insensitive and high yielding with determinate growth habit) constituted the genetic material for the study. These were evaluated in augmented design (Federer, 1956) at the experimental plots of Department of Genetics and Plant Breeding (GPB), College of Agriculture, Bengaluru, India during 2016 rainy season. The entries were sown in single rows of 3.0 m length with a row-to-row spacing of 0.45 and 0.3 m between plants within a row in five blocks, each containing 27 entries. Data were recorded on five randomly selected plants from each entry on grain yield per plant using descriptors (Byre gowda *et al*., 2015). The mean grain yield per plant of each genotype was adjusted for block effects.

Dry pods from five randomly selected selfed plants from each genotype were harvested manually and hand-threshed. The grains were sun-dried and washed with double-distilled water to remove any surface contaminants and dried in hot-air oven at 70°C for 72 h. Washed and fine-powdered 1.0 g of grain samples divided into two replicates were used for estimating grain nitrogen content following Kjeldahl method (AOAC, 2005) and expressed in per cent. Per cent protein was calculated by multiplying per cent nitrogen with the factor 6.25 (AOAC, 2005). The data on grain protein contents averaged across two replicates were used for the statistical analysis. Absolute range (AR) = (highest–lowest) and standardized range (SR) = (AR/mean) × 100, and phenotypic coefficient of variability (PCV) (Fisher, 1950) of grain protein content were estimated. The significance of differences in grain protein content between GAs and (ABLs + RVs) was examined using two-sample *t*-test (Fisher, 1950). The genotypes were grouped into different clusters using model-based 'K-means' clustering algorithm (MacQueen, 1967) implemented using SPSS software. The statistical significance of mean and variances of grain protein contents of the genotypes grouped under different clusters were examined using 'F' (Fisher, 1950) and Levene's (Levene, 1960) tests, respectively. Correlation coefficients were estimated between grain protein content and adjusted mean grain yield per plant.

Discussion

A fairly high estimates of AR (24.5–18.82%) and SR (4.82) which indicate the occurrence of contrasting genotypes, and PCV (6.32%) which is a measure of average inter-genotypic differences in relation to the mean (21.73%) suggested adequate variability for grain protein content among 118 genotypes (Table 1). Ravelombola *et al*. (2016) and Weng *et al*. (2017) reported comparable range (23.7–27.4% and 21.03–29.69%) and average (25.4 and 25.53%) grain protein content, respectively, in cowpea.
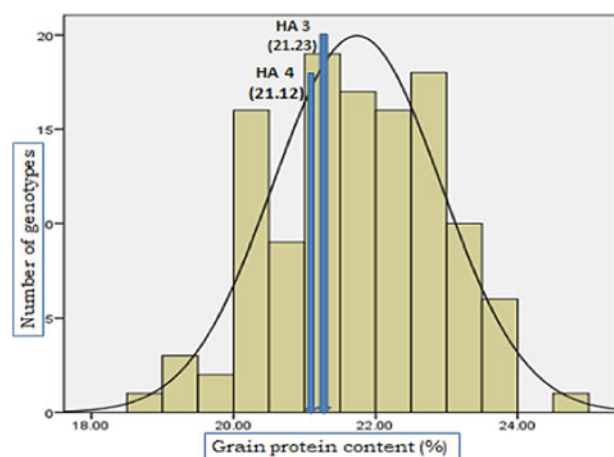
Fig. 1. Graph depicting frequency distribution for protein content in germplasm accessions and advanced breeding lines of dolichos bean.

The magnitude of estimates of AR, SR and PCV for grain protein content was higher among GAs than those among ABLs + RVs. However, mean grain protein content of GAs was comparable to those of ABLs + RVs (Table 1). Nearly 50% of the genotypes had significantly higher protein content than those of RVs, HA 3 and HA 4 (Fig. 1). Five genotypes, GL, 434, GL 444, GL 331 and GL 68 and FBP 15 had protein content more than twice of critical difference (online Supplementary Table S1). Grouping the genotypes into five different clusters with significant differences in the mean and comparable variances of the genotypes classified under different clusters further confirmed adequate variability for grain protein content (online Supplementary Table S2). Substantial variability among the genotypes could be attributed to the existence of differences in the expression of genes controlling protein synthesis and accumulation (Bliss, 1990). The genotypes grouped under clusters 4 and 5 were contrasting with highest and lowest estimates of grain protein contents. The genotypes from these two clusters could be selected for use in investigating genetic and physiological basis of accumulation of protein and as potential donors for breeding varieties rich in grain protein content.

The results suggested ample scope for selecting and/or breeding protein-rich dolichos bean varieties. However, it is necessary to develop protein-rich varieties in high yielding genetic background for acceptance and adoption by farmers. A rather poor correlation (−0.052) between grain protein content and grain yield per plant (online Supplementary Fig. S1) suggested their independent genetic control and hence possibility of developing protein-rich dolichos bean varieties without compromise in grain yield. Our results and inferences draw strong support from the studies of Singh *et al.* (2017) in faba bean and Hussan *et al.* (2018) in lentil, who reported non-significant correlation between grain protein content and yield among GAs.

Supplementary material

The supplementary material for this article can be found at https://doi.org/10.1017/S1479262118000424

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References

AOAC (2005) *Official Method of Analysis*, 18th edn. Washington, DC, USA: Association of Officiating Analytical Chemists, Method 935. 14 and 992.24.

Bliss FA (1990) Genetic alteration of legume seed proteins. *HortScience* 25: 1517–1520.

Byre Gowda M, Girish G, Ramesh S, Mahadevu P and Keerthi CM (2015) Descriptors of dolichos bean (*Lablab purpureus* L.). *Journal of Food Legumes* 28: 203–214.

Ewansiha SS and Singh BB (2006) Relative drought tolerance of important herbaceous legumes and cereals in the moist and semi-arid regions of West Africa. *Journal of Food, Agriculture and Environment* 4: 188–190.

Federer WT (1956) Augmented (or hoonuiaku) designs. Hawaii. *Plant Research* 2: 191–208.

Fisher RA (1950) *Statistical Methods for Research Workers*, 11th edn. London, UK: Oliver and Boyd.

Hussan S, Khuroo NS, Lone AA, Dar ZA, Dar SA and Dar MS (2018) Study of variability and association analysis for various agro-morphological traits in lentil (*Lens culinaris* L.). *Journal of Pharmacognosy and Phytochemistry* 7: 2172–2175.

Levene H (1960) Robust test for equality of variances. In: Olkin *et al.* (eds) *Contributions to Probability and Statistics: Essays in Honour of Harold Hotteling*. Stanford: Stanford University Press, pp. 278–292.

MacQueen J (1967) Some methods for classification and analysis of multivariate observations. Fifth Berkeley Symposium on Mathematics, Statistics and Probability. University of California Press, pp. 281–297.

Magoon ML, Amar Singh and Mehra KL (1974) Improved field bean for dryland forage. *Indian Farming* 24: 5–7.

Monika G, Natasha S, Saloni S, Payal K, Aman K, Venkatesh C and Priya A (2018) Biofortified crops generated by breeding, agronomy, and transgenic approaches are improving lives of millions of people around the world. *Frontiers of Nutrition* 5: 1–33.

Mugwira LM and Haque I (1993) Screening forage and browse legumes germplasm to nutrient stress: II. Tolerance of *Lablab purpureus* L. to acidity and low prosperous in two acid soils. *Journal of Plant Nutrition* 16: 37–50.

Murphy AM and Colucci PE (1999) A tropical forage solution to poor quality ruminant diets: a review of *Lablab purpureus*. *Livestock Research and Rural Development* 11: 96–113.

Ramesh S and Byregowda M (2016) Dolichos bean (*Lablab pur-pureus* L. Sweet var. Lignosus) genetics and breeding – present status and future prospects. *Mysore Journal of Agricultural Sciences* 50: 481–500.

Ravelombola WS, Shi A, Weng Y, Motes D, Chen P, Srivastava V and Wingfield C (2016) Evaluation of total seed protein content in eleven arkansa cowpea (*Vigna unguiculata* (L.) Walp) lines. *American Journal of Plant Sciences* 7: 2288–2296.

Singh Y, Sharma S, Sekhon BS, Sharma S, Verma A and Vishalakshi A (2017) Association studies for seed yield and related morpho-physiological traits in faba bean (*Vicia faba* L.) under mid hill conditions of north western Himalayas, India. *International Journal of Current Microbiology and Applied Science* 6: 2417–2422.

Welch RM and Graham RD (2004) Breeding for micronutrients in staple food crops from a human nutrition perspective. *Journal of Experimental Botany* 55: 353–364.

Weng Y, Shi A, Revelomba WS, Yang W, Qin J, Motes D, Moseley DC and Chen P (2017) A rapid method for measuring seed protein content in cowpea (*Vigna unguiculata* (L.) Walp). *American Journal of Plant Sciences* 8: 2387–2396.