



Research Article

YIELD STABILITY ANALYSIS OF DOLICHOS BEAN GENOTYPES USING AMMI MODEL AND GGL BIPLLOT

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Abstract- Land races are important sources of traits required for adaptation to low-input agricultural production systems. Hence, the *a priori* selected multiple-trait-specific germplasm accessions were evaluated over four locations to identify those with specific/wide adaptation to different locations using AMMI model and GGL biplot for use in breeding dolichos bean pure-line varieties adapted to target production environments. The AMMI analysis of variance showed that all eight productivity traits were significantly ($p < 0.01$) affected by genotype, location and GLI. The genotype, location and GLI, respectively contributing 43.02%, 36.42% and 18.20% of variation in fresh seed yield plant⁻¹. Proximate positioning of GKVK, Mandya and Chintamani locations together in the GGL biplot indicated their similarity with respect to the expression of days to 50% flowering, primary branches plant⁻¹, racemes plant⁻¹ and fresh pods plant⁻¹. The accessions, GL 250, GL 12 and GL 66 were regarded as widely adaptable based on the GGL bi-plot and lower estimates of IPC1 score, ASV and SI. The genotypes, KA, FPB 35, GL 12 and GL 250 with a fairly high fresh seed yield and reasonably good adaptability could be extensively used in breeding dolichos bean pure-line varieties with wide adaptability and high productivity.

Keywords- Lab, Stability, AMMI, Biplot, Yield.

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Introduction

Dolichos bean (*Lablab purpureus* L. Sweet) with $2n=22$ chromosomes [1,2] is one of the oldest legume crops grown in Asia, Africa, and Australia [3] and known for its food [3,4] and fodder value [5]. Dolichos bean is believed to have originated in India [6, 7]. Two botanical types of dolichos bean have been recognized [3,5]. These are (1) *Lablab purpureus* var. *typicus* and (2) *Lablab purpureus* var. *lignosus*. *Lablab purpureus* var. *typicus* produces pods that are flat, longer and more tapering with long axis of seeds parallel to the suture of the pod. It is predominantly grown for soft and fleshy whole pods for use as a vegetable. Due to its twinning habit it is trained on a pendal. *Lablab purpureus* var. *lignosus* is bushy type annual. It bears tough firm-walled parchmented pods which are relatively shorter and more abruptly truncated and long axis of the seeds is perpendicular to the suture of the pod. The pods of *Lablab purpureus* var. *lignosus* exude oily substances that emit characteristic fragrance, a highly preferred trait by farmers and consumers [3, 8].

In India, dolichos bean var. *lignosus* is primarily grown as a rainfed crop in Karnataka and adjoining districts of Tamil Nadu, Andhra Pradesh and Maharashtra both as an inter-crop and pure crop [8,9]. Karnataka alone contributing nearly 90 per cent of both area and production in India [10]. Despite its importance as a vegetable, pulse, forage, cover and green manure crop [11], dolichos bean has remained as an 'underutilized crop' as evidenced from limited area planted to this crop and efforts towards its genetic improvement [8]. However, underutilized crop like dolichos bean can contribute to food security and better nutrition, increased income to rural poor, ecosystem stability and cultural diversity associated with local food habits [12].

Broadening the genetic base and enhancing crop cultivar diversity is the key to attaining sustainable dolichos bean productivity and production, for which greater use of diverse plant genetic resources (PGR) is a prerequisite. Recognizing the importance of PGR, 648 dolichos bean accessions were collected and are being maintained at University of Agricultural Sciences (UAS), Bengaluru [13] in order to effectively utilize germplasm resources for dolichos bean improvement programmes, a core set which captures $\geq 90\%$ of variability of the whole collection was developed [14, 15]. Multi-year evaluation of core set resulted in identification of superior dolichos bean accessions for various productivity traits (Vijayanthi et al. 2016). The accessions, such as GL 142, GL 527, GL 110, GL 447, GL 576, KA, FPB-35, GL 441, GL 12 and GL 66, were promising for multiple quantitative traits and also for farmer- and consumer-preferred qualitative traits. Evaluation of these trait-specific accessions across target production environments and years help identify widely/specifically adapted most stable accessions for use in dolichos bean breeding.

Material and Methods

Experimental material: The material consisted of 11 multi trait-specific germplasm accessions of dolichos bean and two check varieties viz., Kadalav are (KA) and HA-4 identified from a core set of dolichos bean germplasm [28]. The 11 landraces are GL 6, GL 12, GL 66, GL 110, GL 142, GL 250, GL 441, GL 447, GL 527, GL 576 and KA, one advanced breeding line (FPB-35) and one high yielding released pure-line variety (HA-4). While all these 11 landraces and FPB-35 are photoperiod sensitive and exhibit indeterminate growth habit, HA-4 is photoperiod insensitive and display determinate growth habit.

Methodology

The seeds of 13 genotypes were sown in randomized complete block design (RCBD) with two replications at four locations viz., Gubbi-Tumkur, Gandhi Krishi Vignana Kendra (GKVK)-Bengaluru, Agricultural Research Stations (ARS)-Chintamani and Zonal Agricultural Research station (ZARS)-Mandya (representing central, southern and eastern dry zones of Karnataka) during late rainy season of 2015. Each accession was sown in a single row of 3m length with row-to-row spacing of 0.6m. Recommended crop management practices were followed during the crop growth period to raise a healthy crop.

Data were recorded on five randomly chosen plants in each replication on days to 50% flowering, primary branches plant⁻¹, racemes plant⁻¹, raceme length, nodes raceme⁻¹, pods plant⁻¹, fresh seed yield plant⁻¹ and 100-fresh seed weight following the descriptor [16].

Statistical analysis: The quantitative trait means of each germplasm accession and each check evaluated over four locations were used for pooled ANOVA [17]. The mean trait values of 13 genotypes evaluated in two replications were subjected to statistical analysis following Additive Main effects and Multiplicative Interaction (AMMI) model [18] to detect and characterize the patterns of interaction of accessions with production environments of four locations. The additive main effects of genotypes and locations were fitted by univariate ANOVA followed by fitting genotype × location interaction (GLI) by principal component (PC) analysis based on the following AMMI II model.

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where, Y_{ij} is the trait value of i^{th} genotype in the j^{th} location, μ is the experimental mean trait value, g_i and e_j are the i^{th} genotype and j^{th} location mean deviation from experimental mean trait value respectively. λ_k is the square root of eigen value of the k^{th} IPC axis, α_{ik} and γ_{jk} are the interaction IPC scores for k^{th} IPC of the i^{th} genotype and j^{th} location, respectively and ε_{ij} is the residual. The parameters of AMMI II model were estimated using least square principle implemented by GENSTAT software, version 14.

Visual and objective criteria were used to interpret GLI patterns of trait-specific germplasm accessions and their specific/wide adaptation. The visual criterion was based on Genotype + Genotype × location (GGL) biplot given by Yan et al [19]. The GGL biplot is based on the following model.

$$Y_{ij} - \bar{Y}_j = \lambda_1 \alpha_{i1} \gamma_{j2} + \lambda_2 \alpha_{i2} \gamma_{j1} + \varepsilon_{ij}$$

Where, Y_{ij} = trait mean of j^{th} genotype in the j^{th} location; \bar{Y}_j = trait mean of all the genotypes in the j^{th} location; λ_1 and λ_2 are the square root of eigen values of first and second IPC axes, respectively; α_{i1} and α_{i2} are the scores of the first and second IPC, respectively for the i^{th} accession, γ_{j1} and γ_{j2} are the first and second IPCs respectively for j^{th} location.

There are numerous ways to use a GGL biplot, but the polygon view of the biplot is most relevant [20]. Genotype and location interaction PC1 (IPC 1) scores were plotted against their IPC 2 scores to visually identify accessions with specific/wide adaptation and similarity between accessions and locations. The accessions that are more similar to each other in terms of their trait expression are closer to each other in the GGL bi-plot than those that are less similar. The accessions placed near the origin of IPC1 vs IPC 2 biplot are regarded as better adaptable across locations than those located far from the origin [21]. The accessions that are farther from bi-plot origin are connected with straight lines so that a polygon is formed with all other genotypes contained within the polygon. A set of lines were drawn from the biplot origin perpendicular to each side of the polygon. The perpendicular lines to the polygon sides divide the polygon into sectors, each having its own winning accession which is the vertex accession for that sector [19]. The areas between the two perpendicular axes cutting the polygon side are considered as mega environments. These mega environments in the present study are regarded as mega locations. The vertex accession for each sector is the one which is the best performer for the environments falling within that sector and mega locations.

To facilitate an objective method of identifying genotypes with specific/wide adaptation across locations, the AMMI stability value (ASV) was estimated [22].

$$ASV = \sqrt{\left[\frac{SSIPC1}{SSIPC2} (IPC1 \text{ score}) \right]^2 + (IPC2 \text{ score})^2}$$

Where, SS IPC1 and SS IPC2 are sum of squares attributable to first two IPC's. Conceptually, ASV is the distance from zero in a two-dimensional scatter gram of IPC 1 vs IPC 2 scores [22]. Since the IPC 1 score generally contributes proportionately more to GLI, it is weighted by the proportional difference between IPC 1 and IPC 2 scores in order to compensate for the relative contribution of IPC 1 and IPC 2 scores to total genotype × location sum of squares. Higher magnitude of estimates of ASV indicates specific adaptation, while lower magnitude of ASV indicates wide adaptation [22]. To facilitate simultaneous selection of genotypes for different quantitative traits and adaptability, stability index (SI) which incorporates both quantitative traits mean and stability in a single criterion was estimated as SI = RASV + RY (i.e., ranks of genotypes based on quantitative traits mean over locations added to ranks of genotypes based on ASV) [23]. The genotypes with low SI were regarded as those with high trait expression and wide adaptation.

Results and Discussion

Genotypes very often differ in their responses to production environments represented by temporal (year-to-year) and spatial (location-to location) variation resulting in significant crossover genotype × year and genotype × location interactions (GLI) [24]. From commercial crop production point of view, crop varieties should maintain consistent performance across years, referred to as stability and across locations referred to as adaptability [25]. However, cross-over genotype × environment interaction (GEI) leads to inconsistent performance of best yielding genotypes across environments and challenge plant breeders and complicates variety recommendations [24]. Nevertheless, GEI offer opportunities for selection of genotypes exhibiting favorable responses to only a few locations (exploitation of specific adaptation) or of genotypes with low frequency of poor yield across years in a location (exploitation of yield stability). However, it is widely acknowledged that only GLI could be exploited by selecting for specific adaptation or by growing specifically adapted genotypes [24]. This is because, from a farmer's point of view, location is a constant-not-variable factor and GLI effects are repeatable in time [24].

The genes controlling high economic product yield (EPY) in low-input agricultural production systems/ locations are at least partially different from those controlling EPY in high-input agricultural production systems/ locations [26]. Therefore, crop varieties bred under high yielding favorable conditions failed to have impact in low yielding unfavorable production systems [26]. The most effective way to enhance productivity of crops like dolichos bean which is normally grown in less favoured low-input rainfed production systems is to use land race varieties/ germplasm in breeding programmes and select advanced breeding material in target production environments. Land races are important sources of traits required for adaptation to low-input agricultural production systems [27]. Hence, the *a priori* selected multiple-trait-specific germplasm accessions [28] were evaluated over four locations to identify those with specific/wide adaptation to different locations for use in breeding dolichos bean pure-line varieties adapted to target production environments.

GEI largely affects selection process as it complicates superiority of genotype across environments and the selection of superior genotypes [29]. Another undesirable consequence of GEI includes low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance [30, 31]. In the present study, Bartlett's tests indicated homogeneity of error variance for each trait in the four locations and provided statistical justification for pooled analysis of variance. In pooled ANOVA, total variation was partitioned into sources attributable to genotypes, location, genotype × location and pooled error. Multilocation testing of thirteen genotypes has shown not only significant genotypic effects but also significant effects of the location and GLI for all the productivity traits [Table-1].

Table-1 Pooled ANOVA of dolichos bean core accessions evaluated over four locations for productivity traits

Sources of variation	Degrees of freedom	Mean sum of squares							
		Days to 50 % flowering	Primary branches plant ⁻¹	Racemes plant ⁻¹	Raceme length (cm)	Nodes raceme ⁻¹	Pods plant ⁻¹	Fresh seed yield plant ⁻¹ (g)	100 fresh seed weight (g)
Locations (l)	03	2833.37**	5.75**	45.19**	38.26**	8.26**	719.70**	16569.16**	3.45
Genotypes (g)	12	1110.15**	2.13**	29.59**	99.25**	6.59**	269.12**	4893.08**	641.61**
g × l	36	100.44**	0.57**	5.14**	4.21**	0.84**	31.82**	690.09**	10.06**
Pooled error (e)	48	0.22	0.16	0.82	2.31	0.39	5.40	61.68	3.76

*, **Significant at 5% and 1% probability level, respectively

The significance of GLI indicates the differential performance of genotypes in the four locations. This implies the necessity to examine patterns of adaptability of genotypes across locations. Several researchers have advocated numerous models and their associated parameters to assess the stability of genotypes [32, 25, 3]. However, no single model stability parameter can adequately explain cultivar performance across environments [34]. The Additive Main effect and Multiplicative Interaction Model (AMMI) effectively combines additive parameters of univariate ANOVA with multiplicative parameters of principle component analysis (PCA) and efficient in analyzing interaction patterns [35]. Gauch [36] also reported that AMMI model effectively captures a large portion of the genotype × environment interaction sum of squares clearly separating main and interaction effects, and the model often provides a meaningful interpretation of the data.

The AMMI analysis of variance showed that all eight productivity traits were significantly ($p < 0.01$) affected by genotype, location and GLI. For example, days to 50% flowering of the test genotypes was significantly affected by genotype, location and GLI with 52.35%, 33.40 % and 14.21% contribution, respectively [Table-2]. The genotype, location and GLI, respectively contributing 43.02%, 36.42% and 18.20% of variation in fresh seed yield plant⁻¹. Significant mean squares attributable to locations indicated differences in the influence of locations on the productivity of genotypes. The substantial contribution of GLI towards traits variation suggested differential responses of genotypes to locations. Significant GLI reduces responses to selection of superior genotypes [37]. Hence, it is appropriate to assess yield stability under different production environments and identify genotypes with specific/wide adaptation (Kang, 1993). Further, the GLI was partitioned into two IPC axes by the Gollob's F-test [38] which together explained $\geq 90\%$ of the total GLI variance for all the traits [Fig-1] indicating a good fit of AMMI model to the data. These results suggested a good approximation of bi-plot for inferring patterns of GLI and good predictability of genotype performance across four locations. Abeya [39] in common bean and Girma[40] in field pea also reported near complete capture of GEI by first two IPC for most traits.

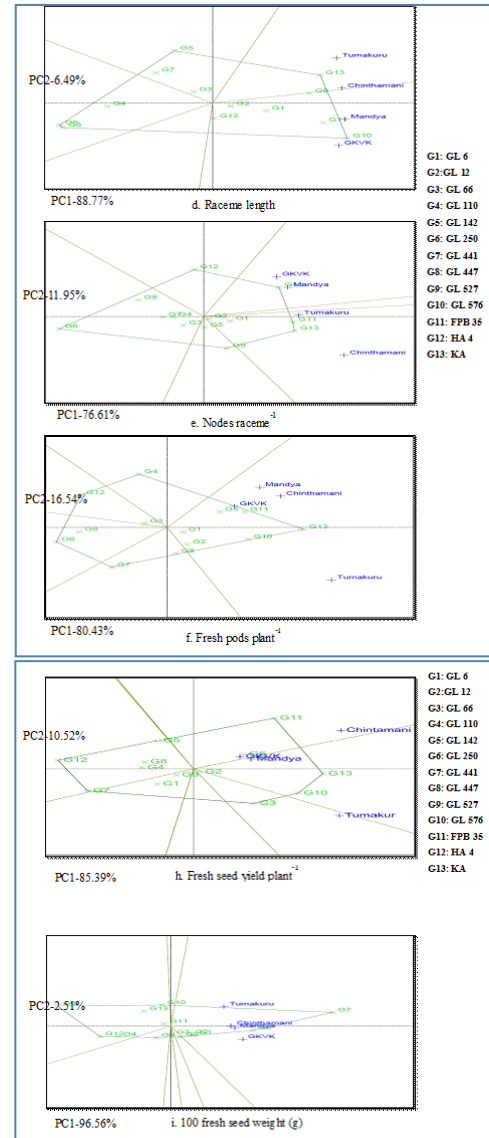
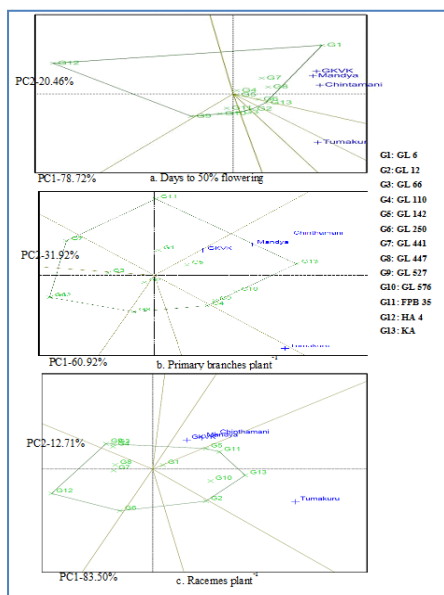


Fig 1- GGL bi-plot showing patterns of interaction of dolichos bean germplasm accessions with locations.

Biplot scatters the genotypes according to their interaction principal component (IPC) scores [41] and qualitatively demonstrates differences in genotype stability and adaptability. Yan [19] proposed a standard biplot of genotype (G) + Genotype × environment (GE) based on a SREG (sites regression) model referred to GGE biplot. It is a multivariate analytical tool that graphically displays interaction between each genotype and each environment in a two-dimensional biplot [42] and allows visualization of the inter-relationship among environments, and the inter-relationship between genotypes and environments. GGE bi-plot is useful in displaying which-won-where pattern of the data that helps to identify high-yielding and stable cultivars and discriminating representative test environments [19]. The model with first IPC axes capturing most of the GEI variation is considered as the best one for extracting patterns and rejecting noise from the data [19]. The partitioning of the G + GE sum of squares through GGE biplot showed that two

Table-2 AMMI ANOVA of dolichos bean core accessions for productivity traits

Source of Variation	Degrees of freedom	Days to 50% flowering				Primary branches plant ⁻¹				Racemes plant ⁻¹			
		MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation
Genotypes	12	1110.21	5019.83	0.00	52.35	2.13	13.18	0.00	35.88	29.59	36.21	0.00	49.12
Location	03	2833.43	8185.30	0.00	33.40	5.76	99.78	0.00	24.20	45.19	23.27	0.00	18.76
G x L	36	100.47	454.20	0.00	14.21	0.57	3.51	0.00	28.70	5.14	6.29	0.00	25.62
IPCA 1	14	247.70	1119.81	0.00	95.88	1.07	6.59	0.00	72.95	11.70	14.32	0.00	88.44
IPCA 2	12	9.71	44.04	0.00	3.24	0.33	2.02	0.04	19.19	0.95	1.16	0.34	6.16
Residual	10	3.20	14.55	0.00		0.16	1.00	0.46		1.00	1.22	0.30	
Error	48	0.21				0.16				0.82			

Source of Variation	Degrees of freedom	Raceme length (cm)				Nodes raceme ⁻¹				Fresh pods plant ⁻¹			
		MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation
Genotypes	12	99.25	43.04	0.00	75.79	6.596	16.6	0.00	50.89	269.10	49.80	0.00	46.96
Location	03	38.27	43.92	0.00	7.31	8.266	13.65	0.00	15.95	719.70	35.06	0.00	31.40
G x L	36	4.21	1.83	0.03	9.65	0.835	2.10	0.01	19.34	31.80	5.89	0.00	16.67
IPCA 1	14	6.23	2.70	0.01	57.52	1.25	3.15	0.00	58.21	66.90	12.39	0.00	81.76
IPCA 2	12	4.56	1.98	0.05	62.84	0.878	2.21	0.03	35.04	13.80	2.56	0.01	14.49
Residual	10	0.96	0.42	0.93		0.203	0.51	0.87		4.30	0.79	0.64	
Error	48	2.31				0.397				5.40			

Table-2 contd...

Source of Variation	Degrees of freedom	Fresh seed yield plant ⁻¹ (g)				100 fresh seed weight (g)			
		MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation
Genotypes	12	4893.00	79.32	0.00	43.02	641.61	170.72	0.00	93.19
Location	03	16569.00	268.51	0.00	36.42	3.45	1.59	0.20	0.12
G x L	36	690.00	11.19	0.00	18.20	10.06	2.68	0.00	4.38
IPCA 1	14	1165.00	18.89	0.00	65.68	20.30	5.40	0.00	78.45
IPCA 2	12	685.00	11.10	0.00	50.36	5.62	1.50	0.16	18.51
Residual	10	31.00	0.51	0.88		1.05	0.28	0.98	
Error	48	62.00				3.76			

significant IPCs explained > 90% of G + GE sum of squares for all the traits.

Among different GGL bi-plots, polygon view of the bi-plot is the best way to visualize GLI patterns and help identify possible existence of different mega-environments [19]. Proximate positioning of GKVK, Mandya and Chintamani locations together in the GGL biplot [Fig-1] indicated their similarity with respect to the expression of days to 50% flowering, primary branches plant⁻¹, racemes plant⁻¹ and fresh pods plant⁻¹. The near origin positioning of the genotypes GL 110 and GL 142 in the bi-plot suggested their wide adaptation to all the four locations for days to 50 % flowering. The accessions KA and GL 576 were winners in Tumkur for fresh seed yield plant⁻¹, while the ABL FPB 35 was the winner in Chintamani for fresh seed yield plant⁻¹ [Fig-1]. The genotype KA was specifically adapted to Tumkur location for most of the traits. The proximate positioning near to the origin in GGL bi-plot indicated wider adaptability of GL 12 and GL 527 for most of the traits.

Thus, it is evident that GGL biplot provided an effective means for visual interpretation of GLI patterns and identification of adaptable genotypes. However,

it does not provide an objective means to identify genotypes with specific/wide adaptation. The parameters, AMMI stability value (ASV) [22] and Stability index (SI) [23] are considered as parameters for objective assessment of stability/adaptability of genotypes and identification of specifically/widely adapted accessions. The ASV is the distance from the coordinate point to the origin in a two dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model [22]. ASV aids selection of relatively stable high yielding genotypes. An ideal genotype should have high mean grain yield and low magnitude of ASV. Based on these criteria, the genotypes GL 142, GL 110, GL 250 with low ASV for days to 50 % flowering; KA, GL 110 and GL 66 for primary branches plant⁻¹; GL 12, GL 250 and GL 6 for racemes plant⁻¹; GL 142, GL 66 and GL 527 for raceme length; GL 66, GL 142 and GL 6 for nodes raceme⁻¹; FPB 35, GL 250 and GL 12 for fresh pods plant⁻¹; GL 527, GL 250 and GL 12 for fresh seed yield plant⁻¹ and HA-4, FPB 35 and GL 6 for 100 fresh seed weight [Table-3] were identified as widely adaptable across the four locations.

Table-3 Estimates of IPC scores and stability parameters to assess adaptability of 13 dolichos bean genotypes

Genotypes	Days to 50% flowering								Primary branches plant ⁻¹							
	Mean	Rank	IPC 1	IPC2	ASV	Rank	SI	Rank	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank
GL 6	92.62	01	-4.22	0.60	8.96	13	14	01	4.13	11	0.61	0.08	2.32	12	23	13
GL12	79.12	06	1.34	0.99	3.01	07	13	2.5	4.75	07	0.36	-0.28	1.41	08	15	7.5
GL66	76.62	07	1.62	0.37	3.45	09	16	2.5	4.63	08	-0.09	0.08	0.36	03	11	04
GL110	76.38	08	-0.29	-0.60	0.86	02	10	4.5	4.38	10	0.09	0.05	0.33	02	12	5.5
GL142	76.25	09	0.09	0.31	0.36	01	10	4.5	5.00	04	-0.52	-0.26	1.99	11	15	7.5
GL250	80.38	05	0.48	0.77	1.28	03	08	06	4.88	06	0.10	-0.54	0.66	04	10	03
GL441	81.12	04	-1.37	-1.13	3.11	08	12	07	4.00	13	-0.19	0.63	0.97	06	19	10.5
GL447	82.25	02	-0.58	0.78	1.46	04	06	08	4.50	09	-0.52	-0.02	1.98	10	19	10.5
GL527	67.62	12	1.94	0.40	4.13	11	23	9.5	5.13	03	-0.44	0.02	1.66	09	12	5.5
GL576	73.13	11	1.73	-1.64	4.02	10	21	9.5	5.25	02	-0.34	-0.29	1.32	07	09	02
FPB 35	74.38	10	1.25	0.01	2.66	06	16	11	4.88	05	1.13	0.11	4.31	13	18	10
*HA 4	41.62	13	-2.80	-0.48	5.95	12	25	12	4.00	12	-0.19	0.63	0.97	05	17	09
**KA	81.75	03	0.81	-0.39	1.75	05	08	13	5.75	01	0.00	-0.23	0.23	01	02	01
SEm±	4.59								0.26							
CD @p=0.05	13.46								0.76							

*Determinate check; ** Indeterminate check

Table-3 contd...

Genotypes	Racemes plant ⁻¹								Raceme length (cm)							
	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank
GL 6	8.38	11	0.43	0.13	6.11	03	14	06	20.88	10	-0.91	0.88	1.70	11	21	12
GL12	10.25	06	0.04	-0.85	1.02	01	07	03	24.76	05	0.25	-1.35	1.41	10	15	09
GL66	10.75	05	-1.36	-0.14	19.59	13	18	11	23.52	06	0.09	0.43	0.45	02	08	02
GL110	8.88	07	1.01	0.38	14.51	10	17	9.5	22.18	08	-0.33	-0.55	0.76	04	12	6.5
GL142	8.75	08	0.91	0.39	13.12	08	16	08	19.10	11	0.07	-0.36	0.38	01	12	6.5
GL250	11.75	03	-0.22	0.80	3.19	02	05	01	21.54	09	-1.54	0.45	2.50	13	22	13
GL441	7.88	12	-0.49	-0.22	7.03	05	17	9.5	17.39	13	0.61	0.21	1.00	06	19	10.5
GL447	8.63	09	0.59	-0.67	8.55	06	15	07	17.51	12	0.68	0.20	1.10	07	19	10.5
GL527	8.63	10	1.09	0.10	15.67	11	21	13	26.33	04	-0.26	-0.59	0.72	03	07	01
GL576	11.25	04	-1.00	0.20	14.41	09	13	4.5	27.69	01	1.07	0.61	1.81	12	10	3.5
FPB 35	12.13	02	-0.44	-0.18	6.38	04	06	02	26.84	02	0.60	0.84	1.27	08	10	3.5
*HA 4	6.00	13	0.72	-0.20	10.28	07	20	12	22.91	07	0.45	-0.43	0.84	05	12	6.5
**KA	12.50	01	-1.27	0.26	18.28	12	13	4.5	26.71	03	-0.78	-0.33	1.29	09	12	6.5
SEm±	0.79								1.36							
CD @p=0.05	2.30								3.96							

*Determinate check; ** Indeterminate check

Table-3 contd...

Genotypes	Nodes raceme ⁻¹								Fresh pods plant ⁻¹							
	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank
GL 6	8.63	11	0.19	-0.28	0.42	03	14	8.5	24.00	10	-1.33	-0.05	7.50	09	19	11
GL12	9.50	04	-0.29	0.77	0.90	08	12	4.5	30.88	05	-0.32	0.40	1.83	03	08	03
GL66	9.25	07	-0.05	-0.19	0.20	01	08	1.5	30.50	06	-1.04	-0.50	5.89	07	13	5.5
GL110	8.88	09	-0.05	-0.47	0.48	04	13	6.5	28.12	09	0.45	0.80	2.68	04	13	5.5
GL142	8.75	10	0.10	0.20	0.26	02	12	4.5	28.88	08	2.63	-1.08	14.90	13	21	12
GL250	9.13	08	-0.29	0.48	0.68	06	14	8.5	34.12	04	0.16	-0.86	1.25	02	06	02
GL441	7.13	13	0.33	0.11	0.56	05	18	11	20.75	13	0.49	1.35	3.07	05	18	9.5
GL447	8.38	12	0.66	-0.47	1.19	11	23	13	22.88	12	0.74	1.18	4.36	06	18	9.5
GL527	9.38	05	-0.70	-0.46	1.25	12	17	10	29.62	07	-1.24	0.55	7.01	08	15	08
GL576	10.38	01	0.33	-0.47	0.72	07	08	1.5	35.38	03	-1.42	-1.19	8.08	11	14	07
FPB 35	10.38	02	-0.52	0.29	0.91	09	11	03	36.00	02	-0.10	-1.02	1.18	01	03	01
*HA 4	9.25	06	0.95	0.59	1.68	13	19	12	23.88	11	2.32	0.02	13.08	12	23	13
**KA	10.38	03	-0.66	-0.09	1.11	10	13	6.5	40.38	01	-1.35	0.40	7.65	10	11	04
SEm±	0.39								2.29							
CD @p=0.05	1.14								6.72							

*Determinate check; ** Indeterminate check

Table-3 contd...

Genotypes	Fresh seed yield plant ⁻¹ (g)								100 fresh seed weight (g)							
	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank	Mean	Rank	IPC 1	IPC 2	ASV	Rank	SI	Rank
GL 6	85.77	09	1.72	2.30	4.12	07	16	10	81.88	01	0.39	0.29	1.30	03	4	01
GL12	98.05	06	0.36	0.63	0.95	02	08	2.5	63.36	03	0.73	-0.62	2.45	08	11	4.5
GL66	110.17	05	-3.55	2.63	7.53	10	15	7.5	62.85	04	0.67	-0.12	2.19	06	10	03
GL110	79.53	10	1.77	0.28	3.53	05	15	7.5	60.38	06	0.54	-0.16	1.77	05	11	4.5
GL142	88.16	08	3.26	-1.80	6.73	09	17	11	53.38	11	0.20	-1.18	1.34	04	15	09
GL250	113.89	04	0.27	-0.95	1.09	03	07	01	58.36	09	0.67	0.63	2.28	07	16	10
GL441	59.53	12	1.69	2.29	4.07	06	18	12	45.75	13	-2.18	0.81	7.18	13	26	13
GL447	76.74	11	0.26	-1.20	1.31	04	15	7.5	71.15	02	0.99	1.13	3.41	10	12	06
GL527	88.30	07	-0.10	0.44	0.49	01	08	2.5	61.51	05	0.79	0.25	2.59	09	14	08
GL576	124.02	02	-4.65	1.36	9.33	13	15	7.5	59.50	08	-1.49	-0.69	4.90	12	20	11
FPB 35	118.09	03	-2.27	-6.20	7.67	11	14	05	59.59	07	-0.24	-0.92	1.21	02	9	02
*HA4	54.06	13	4.51	0.03	8.95	12	25	13	50.97	12	0.12	0.16	0.41	01	13	07
**KA	136.04	01	-3.27	0.19	6.50	08	09	04	57.08	10	-1.17	0.41	3.85	11	21	12
SEm±	9.64								2.81							
CD @p=0.05	18.74								8.22							

*Determinate check; ** Indeterminate check

Cotes [43] reported that breeding for stable mean yields has overshadowed the goal for increased yield. The SI is a useful parameter to identify stable genotypes based on both mean yield and stability. Low magnitude of SI indicates wide adaptability. Based on this criterion the genotypes GL 6, GL 12 and GL 66 with low SI for days to 50% flowering; KA, GL 576 and GL 250 for primary branches plant⁻¹; GL 250, FPB 35 and GL 12 for racemes plant⁻¹; GL 527 and GL 66 for raceme length; GL 66, GL 576 and FPB 35 for nodes raceme⁻¹; FPB 35, GL 250 and GL 12 for fresh pods plant⁻¹; GL 12, GL 250 and GL 527 fresh seed yield

plant⁻¹ and GL 6, FPB 35 and GL 66 for 100 fresh seed weight [Table-3] were identified as widely adapted to four locations.

Negative environmental indices for days to 50 % flowering for all locations except Tumkur [Table-4] suggested tendency of advancing days to 50% flowering at GKVK, Mandya and Chintamani relative to that of Tumkur. Similarly, negative indices for most of the productivity traits suggested production environments at Chintamani and Tumkur are less favorable for trait expression. Further, positive indices indicated that GKVK and Mandya locations were similar (also indicated by

their proximate positions in GGL bi-plots) in their influence on the expression of genotypes for fresh pod yield potential suggesting breeding varieties in either of the locations for adaptation to these locations. On the contrary, highly variable (also indicated by their farther positions in GGL bi-plots) influence of Chinthamani and Tumkur locations on the expression of genotypes for fresh pod yield plant⁻¹, fresh seed yield plant⁻¹ and 100 fresh seed weights suggested the need for shuttle breeding programmes to develop varieties specific to these locations.

Table-4 Estimates of environmental indices for nine quantitative traits in dolichos bean

Trait	GKVK	ZARS-Mandya	ARS-Chinthamani	Gubbi-Tumkur
Days to 50% flowering	-2.53	-2.01	-0.96	5.50
Primary branches plant ⁻¹	0.44	0.45	0.53	-1.43
Racemes plant ⁻¹	1.19	0.83	0.55	-2.58
Raceme length (cm)	1.67	0.65	-0.56	-1.76
Nodes raceme ⁻¹	0.86	0.53	-1.39	0.04
Fresh pods plant ⁻¹	1.45	1.73	0.81	-3.99
Fresh pod yield plant ⁻¹ (g)	7.32	5.96	-3.86	-9.42
Fresh seed yield plant ⁻¹ (g)	5.26	4.11	-3.69	-5.67
100 fresh seed weight (g)	2.25	0.43	-0.09	-2.58

Thus, it is evident from the discussion that the accessions, GL 250, GL 12 and GL 66 were regarded as widely adaptable based on the GGL bi-plot and lower estimates of IPC1 score, ASV and SI [Table-3]. However, these genotypes were not the best performers for fresh pod yield plant⁻¹. On the contrary, and as expected, the good performers such as KA, GL 576, and GL 142 and FPB 35 exhibited poor adaptability. Keerthi [44] have also reported that best yielders were not stable across different sowing date environments in dolichos bean. Such negative relationship between performance levels and stability/ adaptability could be attributed to involvement of different sets of genes controlling *per se* performance and stability [45] and trade-offs between performance and stability [46].

Conclusion

The genotypes, KA, FPB 35, GL 12 and GL 250 with a fairly high fresh seed yield and reasonably good adaptability could be extensively used in breeding dolichos bean pure-line varieties with wide adaptability and high productivity. Such widely adaptable varieties are expected to contribute to sustainable dolichos bean production. Also, breeding varieties with high yield and wide adaptability is essential to increase economic returns to the farmers and hence maintain competitiveness of dolichos bean with other crops.

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Application of research: The study has applicability in identifying genotypes with wide/specific adaptability.

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