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Identification of Selected Germplasm Accessions for Specific / Wide Adaptation Coupled with High Pod Productivity in Dolichos Bean ((*Lablab purpureus* L. Sweet)

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Abstract

An investigation was carried out to identify dolichos bean germplasm accessions with specific 8 wide adaptation to four locations representing central, eastern and southern dry zones of Karnataka.The Additive Main effects and Multiplicative Interaction (AMMI) analysis of variance showed that fresh pod yield was significantly ($p < 0.01$) affected by genotype, locations and genotype × location interaction(GLI) with 43.87, 36.2 and 19.20 per cent contribution, respectively. The first two interaction principal component (IPC) axes explained 76.74 and 22.62 per cent of the total GLI variance, respectively suggesting near perfect fit of AMMI II model to capture patterns of GLI for fresh pod yield with an R^2 value of 99.37 per cent. The accessions GL 250, FPB-35 and KA were identified as best genotypes with relatively better adaptability coupled with high productivity to all the locations.These genotypes are suggested for use in breeding dolichos bean pure-line varieties with specific / wide adaptation to tested locations.

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 cross over genotype × year and genotype × location interactions (GLI) (Annicchirarico, 1992). From commercial crop production point of view, crop varieties should maintain consistent performance across years, referred to as stability and across locations refered to as adaptability (Lin and Binns, 1998). 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 (Annicchirarico, 1992). Nevertheless, GEI offer opportunities for selection of genotypes exhibiting favourable 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 (Annicchirarico, 1992). This is because, from a farmer's point of view, location is a constant-not-variable factor and GLI effects are repeatable in time (Annicchirarico, 1992).

However, the genes controlling high economic product yield (EPY) in low-input agricultural production systems / locations are atleast partially different from those controlling EPY in high-input agricultural production systems / locations (Ceccarelli *et al.,* 1998). Therefore, crop varieties bred under high yielding favourable conditions failed to have impact in low yielding unfavourable production systems (Ceccarelli *et al.*, 1998). 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 lines (ABL) in target production environments. Land races are important sources of traits required for adaptation to low-input agricultural production systems (Zeven, 1998). Under these premises, the objective of the present study is to identify *apriori* selected high yielding land race varieties 8 germplasm accessions (Vaijayanthi *et al.,* 2016) with specific 8 wide adaptation to different locations for use in breeding dolichos bean pure-line varieties adapted to target production environments.

The material for the study comprised of 13 trait-specific germplasm accessions which included 11 landraces (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) identified from a core set of dolichos bean germplasm (Vaijayanthi *et al.*,2016). 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.

The seeds of 13 germplasm accessions were sown in randomized complete block design (RCBD) with two replications at four locations *viz.,* Gubbi-Tumkur; GKVK; Bengaluru; Agricultural Research Stations (ARS), Chintamani; and Zonal Agricultural Research Station (ZARS), Mandya (representing central, southern and eastern dry zones of Karnataka) during 2015 late rainy season. Each accession was sown in a single row of 3m length with row-to-row spacing of 0.6 m. Recommended 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 fresh pod yield plant^{-1}. The mean fresh yields of two replications were subjected to statistical analysis following Additive Main effects and Multiplicative Interaction (AMMI) model (Gouch and Zobel, 1988) to detect and characterize the patterns of interaction of germplasm accessions with four locations. The additive main effects of genotypes and locations were fitted by univariate analysis of variance (ANOVA) followed by fitting GLI by principal component (PC) analysis based on the following AMMI 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 fresh pod yield of ith genotype in the jth location, μ is the experimental mean fresh pod yield, g_i and e_j are the ith genotype and jth location mean deviation from experimental mean fresh pod yield, respectively. λ_k is the squre root of eigen value of the kth PC axis, α_{ik} and γ_{jk} are the interaction PC scores for kth PC of the ith genotype and jth location, respectively and ε_{ij} is the residual. The parameters of AMMI model were estimated using least square principle implemented by GENSAT software, version 12.

Genotype + Genotype × location (GGL) - biplot methodology which is a combination of AMMI biplot and GGE concepts (Yan *et al.,* 2000) was used for visual interpretation of patterns of GLI. Genotype and location interaction PC1 (IPC1) scores were plotted against their IPC2 scores to visually identify genotypes with specific 8 wide adaptation and similarity between genotypes and locations. Genotypes that are more similar to each other in terms of their trait expression are more close to each other in the GGL plot than those that are less similar. The genotypes placed near the origin of IPCA1 *vs* IPCA 2 biplot are regarded as adaptable across locations than those located far from the origin (Crossa *et al.,* 1990).

Criteria to identify genotypes with specific / wide adaptation : To facilitate an objective method of identifying genotypes with specific 8 wide adaptation across locations, the AMMI stability value (ASV) was estimated (Purchase *et al.,* 2000).

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

Where, SSIPC1 and SSIPC2 are sum of squres attributable to first two IPC's. Greater ASV indicates specific adaptation, while, lower ASV indicates wide adaptation (Purchase *et al.*, 2000). To facilitate simultaneous selection of genotypes for fresh pod yield and adaptability, yield stability index (YSI) which incorporates both mean fresh pod yield and stability in a single criterion (Farshadfar, 2011) was estimated as YSI= RASV+ RY (*ie.,* ranks of genotypes based on mean fresh pod yield over locations added to ranks of genotypes based on ASV). The genotypes with low YSI were regarded as high yielding and widely adapted.

The AMMI analysis of variance showed that fresh pod yield of the test genotypes was significantly ($p < 0.01$) affected by genotype, location and GLI with 43.87, 36.2 and 19.20 per cent contribution, respectively (Table I). Significant GLI suggested substantial differences inresponses of genotypes to locations. An important implication of GLI is increased cost of testing genotypes across multiple locations.

TABLE I

AMMI ANOVA of dolichos bean genotypes for fresh pod yield (g) plant^{-1}

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	F Ratio	P ≥F
Genotypes (G)	12	220974	18414	274.15	0.00
Location (L)	03	182441	60814	1073.20	0.00
G × L	36	96741	2687	40.01	0.00
IPCA 1	14	74241	5303	78.95	0.00
IPCA 2	12	21891	1824	27.16	0.00
Residual	10	609	61	00.91	0.53
Error	48	3224	67	-	-

Significant GLI preludes the use of main effects of overall genotype means across locations and also increases the prospects of establishing regional breeding programme (Kang, 1998). The first two IPC axes explained 76.74 and 22.62 per cent, respectively of the total GLI variance suggesting that the observed variation in fresh pod yield is adequately captured by AMMI II model with an R^2 value of 99.37 per cent.

Near perfect fit of IPC1 and IPC2 (99.37%) to the total GLI variation (Fig.1) suggested a good approximation of the bi-plot regarding patterns of GLI and good predictability of genotype performance across four locations. Proximate positioning of GL 250 with Mandya and GKVK in GGL bi-plot (Fig. 1) suggested

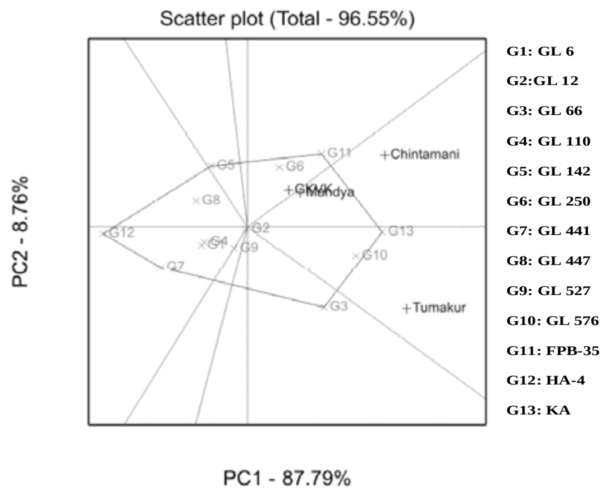

Fig 1. GGL bi-plot showing patterns of interaction of dolichos bean germplasm accessions with locations.

its specific adaptation to these locations. The germplasm accessions GL 6, GL12, GL 110, GL 447 and GL 527 were identified as widely adapted as indicated by their near-origin position inGGL bi-plot. In addition to these, GL 250 were regarded as widely adaptable based on the lower estimates of IPC1 score and ASV (Table II). However, these genotypes were not the best performers for fresh pod yield. On the contrary and as expected, the good performers such as KA, GL 576, FPB-35 and GL 66 exhibited poor adaptability. Keerthi *et al*. (2014) 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 8 adaptability could be attributed to involvement of different sets of genes controlling *per se* performance and stability (Caligari and Mather, 1975) and trade-offs between performance and stability (Ludlow and Muchow, 1990). However, in the present study, when the estimate of YSI was considered as the criteria, which take into account both level of performance and adaptability, KA and FPB-35 were adjudged as the best genotypes. Thus, KA, FPB-35 and GL 250 with a fairly high fresh pod 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

TABLE II

Estimates of IPC scores and parameters to assess adaptability of 13 dolichos bean genotypes

Genotypes	Mean	IPC 1	IPC 2	AMMI stability value (ASV)	Yield stability index (YSI)
GL 06	163.30	1.77	1.83	6.26	11
GL 12	194.70	1.22	1.71	4.48	8
GL 66	224.40	-6.78	3.11	23.21	8
GL 110	167.70	2.34	2.39	8.29	17
GL 142	177.70	4.24	-2.43	14.56	16
GL 250	218.80	1.38	-2.62	5.37	14
GL 441	134.50	2.27	2.71	8.16	16
GL 447	156.90	1.63	-3.01	6.28	18
GL 527	180.10	-0.32	1.08	1.54	24
GL 576	248.60	-6.48	-0.11	21.95	14
FPB-35	234.10	-2.63	-7.05	11.36	11
HA-4	104.40	6.11	1.40	20.77	17
KA	275.20	-4.75	0.98	16.13	8
SEm ±	2.00	-	-	-	-
CD@ 5%	8.19	-	-	-	-

and hence maintain competitiveness of dolichos bean with other crops. Further, GKVK and Mandya locations were similar (as indicated by their proximate positions in GGL bi-plot) in their influence on the expression of genotypes for fresh pod yield potential suggesting breeding varieties in either of the locations for adaptation to both the locations. On the contrary, highly variable (as indicated by their farther positions in GGL bi-plot) influence of Chintamani and Gubbi-Tumkur locations on the expression of genotypes suggested the need for shuttle breeding programmes to develop varieties specific to these locations.

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