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Research Article

GT biplot analysis for yield and drought related traits in mung bean (*Vigna radiata* L. Wilczek)

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Abstract

The present investigation was undertaken to evaluate thirty one mungbean genotypes for yield and drought related traits based on GT biplot analysis. The GT biplot analysis is a powerful statistical tool for studying relationship among traits, evaluating cultivars based on multiple traits and for identifying those that are superior in certain traits. GT biplot analysis showed positive relationship between yield and other traits *viz.*, number of pods per plant, number of clusters per plant, days to maturity, plant height, chlorophyll content and chlorophyll stability index are identified as important traits for yield as well as drought tolerance improvement. Hence, these traits could be considered as key components during the selection process aiming towards the breeding of mungbean genotypes for high yield and drought tolerance. The genotypes LGG 450, PUSA 9531, LGG 528, Asha, EC 396117 and MH 565 were identified as ideal cultivars which could serve as a good genetic raw material for development of better cultivars for high seed yield coupled with drought tolerance.

Key words

Genotype by Trait (GT) Biplot, Mungbean, Drought tolerance.

Introduction

Pulse crops play an important role in Indian economy. They have been integral part of Indian agriculture since time immemorial and are gaining more importance globally as they are the chief source of vegetable protein. Among the wide array of pulses cultivated in India, mungbean holds a key position and is considered as indigenous. Mungbean is utilized in various ways, where seeds and young pods are consumed as sources of protein, vitamins and minerals, while plant parts are used as fodder. Besides its rapid growth and early maturity, mungbean possesses an ability to improve soil fertility by fixing the atmospheric nitrogen (50-109Kg/ha) in symbiotic association with rhizobium bacteria. The crop also adapts well to various cropping systems in the tropics and subtropics. Though mungbean is considered to be an important pulse crop in India, our nation's production and productivity levels are low, which indirectly affect the nutritional status of people resulting in malnutrition. Among several reasons for low productivity, various abiotic and biotic factors play major role. Among the abiotic stresses, drought is a wide spread problem that seriously influences the mungbean productivity. Though various agronomic management practices help in mitigating the drought impact in greengram, drought tolerant varieties should be made more accessible to farmers than costly agronomic practices. Hence, there is an immediate need for plant breeders to develop drought tolerant varieties with higher yield.

In order to meet this objective an effective breeding programme requires a proper understanding of essential components of system and inter-relationship among them, since cultivar is more or less a complex biological system rather than simple collection of independent traits. Though various techniques like correlation and regression are most commonly used for assessment of association of characters, Genotype by Trait (GT) biplot analysis is better than the simple correlation coefficients and of late is gaining popularity among the breeders. GT biplot analysis graphically describes the interrelationships among all measured traits on the basis of overall pattern of the data, whereas simple correlation coefficients only describe the relationship between two traits (Yan and Rajcan, 2002). Further, the GT biplot analysis provides a tool for visual comparison among genotypes on the basis of multiple traits and it can be used in independent culling based on multiple traits and in comparing selection strategies, which are important for both cultivar evaluation and parental selection (Yan and Rajcan, 2002; Yan and Tinker, 2005).

Realizing the importance and need for such a comprehensive study in mungbean, the present study has been undertaken with an objective that to study the extent of association among different yield and drought related traits by using Genotype by Trait Biplot analysis. GT biplot is an excellent tool for visualizing genotype by trait data. First, it effectively reveals the interrelationships among the traits. Second, it provides a tool for visual comparison among genotypes on the basis of multiple traits such as yield, yield contributing traits and other related traits. Third, it can be used in independent culling based on multiple traits and in comparing selection strategies. Hence, the study was undertaken to identify ideal cultivars and traits that are suitable for improved grain yield and drought tolerance using genotype-by-trait approach.

Materials and methods

The experimental material for the present investigation consisted of thirty one mungbean genotypes obtained from Regional Agricultural Research Station, Lam, Guntur and Agricultural Research Station, Madira. The experiment was conducted in randomized block design (RBD) with three replications during *rabi*, 2013-14 at wet land farm, Sri Venkateswara Agricultural College, Tirupati. Each genotype was sown in three rows of 3m length and the inter and intra- row spacing adapted was 30 cm x 10 cm. The observations were recorded on five randomly selected plants from the centre row in each replication for characters *viz.*, plant height, number of clusters per plant, number of pods per plant, 100 seed weight, SPAD Chlorophyll Meter Reading (SCMR), Relative Water Content (RWC), Relative Injury (RI), Chlorophyll Stability Index (CSI), Specific Leaf Area (SLA), chlorophyll content and seed yield per plant. However, the data for days to maturity was recorded on plot basis. The data were subjected to analysis of variance (ANOVA) using a randomized block design. The Genotype by Trait (GT) biplot method was employed to display the genotype by trait two-way data. The biplot was generated using the standardized values of the trait means. The model equation for genotype by trait interaction biplot analysis is presented as follows:

$$\frac{\alpha_{ij} - \beta_j}{\sigma_j} = \sum_{n=1}^{2} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{2} \xi_{in}^{*} \eta_{jn}^{*} + \varepsilon_{ij}$$

Where,

α_{ij} = The mean value of genotype i for trait j

β_j = The mean value of all genotypes for trait j

σ_j = The standard deviation of trait j among genotype means

λ_n = The singular value for Principal Component (PCn)

ξ_{in} = The PCn score for genotype i

η_{jn} = The PCn score for trait j

ε_{ij} = The residual associated with genotype i in trait j

A Genotype by Trait (GT) biplot is constructed using ‘‘R’’ packages by plotting PC1 scores against PC2 scores for each genotype and each trait.

Result and discussion

The analysis of variance (ANOVA) showed significant differences among the genotypes for all the characters which revealed the presence of notable genetic variability among 31 mungbean genotypes and hence the data were subjected GT biplot analysis.

Performance of mungbean genotypes based on multiple traits: A genotype-by-trait (GT) biplot with a polygon view, which represents the data of thirty one mungbean genotypes for twelve characters, is presented in Fig 1. The traits were considered as the tester and the cultivars as entries. Among the traits high values for all the studied traits were considered as desirable except for the traits specific leaf area and relative injury, for which low values are desirable. The biplot accounted for 54.18% of the total variation among the varieties for the measured traits. Considering the genotypes from the biplot origin, a polygon was first drawn on genotypes so that all other genotypes are within the polygon (Fig. 1). Then perpendicular lines to each side of the polygon were drawn, starting from the biplot origin. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison (Yan and Tinker 2005). The equality lines divided the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. The genotype which occupied vertex position in the biplot is known as vertex genotype. The vertex genotypes in each sector were regarded as the genotype with the highest value of the traits within the sector. These vertex genotypes could be exploited in hybridization programme as potential parents in the development of varieties, hybrids and populations that are outstanding in those traits.

Based on the biplot presented in Fig. 1, the genotypes LGG 450, PUSA 9531, LGG 528, ASHA, EC 396117 and MH 565 were regarded as vertex genotypes which exhibited superior performance for the traits allocated within the sector. The genotype LGG 450 exhibited superior performance for the characters seed yield per plant, number of clusters per plant, days to maturity and plant height indicating that this genotype could be exploited in breeding programme for the development of variety or base populations that are outstanding in these traits. The genotypes PUSA 9531 and LGG 528 exhibited better performance for the trait chlorophyll content, while the genotype ASHA exhibited superior performance for SPAD chlorophyll meter reading (SCMR). For the characters relative water content and 100 seed weight the genotype EC 396117 showed better performance, whereas for the trait chlorophyll stability index the genotype MH 565 exhibited superior performance. Even though the genotypes PUSA 9531, LGG 528, ASHA, EC 396117 and MH 565 showed better performance for drought tolerant traits but they were not the best for grain yield. Whereas, for the traits specific leaf area and relative injury the genotypes PUSA 9531, LGG 528 and ASHA showed lower values indicating that these genotypes are better for improvement of specific leaf area and relative injury because for these traits low values are desirable.

From Fig. 1 it was also realized that the vertex genotype LGG 450 showed superior performance for seed yield and morphological characters, whereas other vertex genotypes PUSA 9531, LGG 528, ASHA, EC 396117 and MH 565 showed better performance for drought tolerant traits. So the crosses *viz.*, LGG 450 X PUSA 9531, LGG 450 X LGG 528, LGG 450 X ASHA, LGG 450 X EC 396117 and LGG 450 X MH 565 may be suggested to incorporate seed yield and drought tolerant traits in single genotype.

Inter-relationship among traits: A vector view of GT biplot (Fig. 2) represented the interrelationship among all the measured traits. The lines connecting each trait marker to the origin of the biplot are called the trait vectors and the length of each trait vector approximates the standard deviation of each trait. The cosine of the angle between the vectors of any two traits approximates the correlation coefficient (degree of association) between the traits. On this premise, two traits are positively correlated if the angle between their vectors is an acute angle (< 90°) while they are negatively correlated if their vectors are an obtuse angle (> 90°). Trait vectors that are approximately at right angle (= 90°) are not closely related *i.e.* independent and traits that are at angle 180^o (directly opposite) are strongly negatively correlated.

From the present investigation, it is observed that the trait seed yield was highly positively correlated with number of pods per plant and number of clusters per plant and also positively correlated with remaining morphological traits, indicating that higher the values of these morphological traits, more the grain yield. The morphological traits were not redundant. They were mutually exclusive and each supplies useful and unique information about the cultivars. This was indicated by various angle sizes and vector lengths displayed in the biplot. These results were in agreement with Oladejo *et al.* (2011) in cowpea and Singh *et al.* (2014) in mungbean for morphological traits. For the physiological and drought related traits a strong positive correlation was observed between relative injury and chlorophyll stability index; between SCMR, chlorophyll content and relative water content and between relative injury, chlorophyll stability index and specific leaf area. The characters chlorophyll content, specific leaf area, relative injury and chlorophyll stability index showed a positive correlation with seed yield indicating the importance of these traits in manifestation of seed yield. Based on inter-relationships among the traits it could be suggested that the traits number of pods per plant, number of clusters per plant, days to maturity, plant height, chlorophyll content and chlorophyll stability index could be considered in the breeding programme aimed for the development of high yield and drought tolerance.

Ranking of genotypes: A vector view of genotype-by-trait biplot representing the ranking of thirty one mungbean genotypes on the basis of their mean performance across the selected traits is presented in Fig. 3. The biplot was based on trait-focused singular value partitioning (SVP = 1) and is therefore appropriate for visualizing the relationships among genotypes. The horizontal line passing through the biplot origin and the average tester, with an arrow pointing to the average tester, and its ordinate passing through the origin and perpendicular to the abscissa is called the average tester axis or ATC abscissa. Principal components for PC1 and PC2 explained 54.18 per cent of the variation among the traits.

The ideal entry (genotype) is described as the entry with the longest projection onto ATC abscissa and positioned closest to the ideal entry (innermost concentric circle with an arrow in Fig. 3). Based on the selected traits, LGG 450 was identified as the ideal genotype followed by MGG 350 and KM 122 as these two ranked close to the ideal genotype. Based on their performance, the genotypes may be ranked as follows; LGG 450 > MGG 350 ≈ KM 122 > GVIT 203 ≈ AKM 9904 > LGG 460 ≈ TM 96-2 ≈ WGG 37 ≈ LGG 407 > PUSA 9531 ≈ LGG 528 ≈ KM 8-657 ≈ ML 267 ≈ COGG 974 ≈ LGG 410 ≈ MH 3-18 ≈ ML 145 ≈ PUSA VISHAL ≈ RMG 492 ≈ PM 110 ≈ VG 6197A > WGG 2 ≈ MGG 295 ≈ MGG 347 > ASHA ≈ IPM-02-03 ≈ VG 7098A ≈ TLM 7 > IPM-02-19 > MH 565 > EC 396117.

Considering this biplot among all the genotypes tested, the genotypes LGG 450 was identified as the ideal cultivar followed by MGG 350, KM 122, GVIT 203 and AKM 9904. Hence these genotypes could be exploited for initiating the breeding programme aimed for high yield with drought tolerance.

Genotype by trait interaction biplot: The GT biplot can also be used to compare genotypes on the basis of multiple traits and to identify genotypes that are particularly good in certain aspects and therefore can be candidates for parents in mungbean breeding programmes. The relationship between traits by angle form between two or more variables for thirty one greengram genotypes was represented in Fig. 4. The genotypes LGG 450, KM 122, AKM 9904 and TM 96-2 showed superior performance for the traits seed yield per plant, number of pods per plant and number of clusters per plant indicating that these genotypes could be used as parents in the breeding programmes aimed towards high yielding genotypes in mungbean. For the characters days to maturity and plant height, the genotypes GVIT 203 and LGG 460 showed better performance indicating that these genotypes may be used to improve days to maturity and plant height. The genotypes, EC 396117 and IPM-02-19 exhibited superior performance for 100 seed weight. Hence, these genotypes could be used for the development of bold seeded types in mungbean.

The genotypes PUSA 9531, LGG 528, ASHA, MGG 347, IPM-02-03, KM-8-657, WGG 2, ML 267, COGG 974, LGG 410 and MH-3-18 showed superior performance for the traits SCMR and chlorophyll content and exhibited negative correlation with specific leaf area and relative injury. This means that these genotypes were having low values for specific leaf area and relative injury indicating that the above genotypes may serve as excellent drought tolerant genotypes and could be exploited in hybridization programme for the development of drought tolerant varieties.

The genotypes LGG 450, KM 122, AKM 9904 and TM 96-2 showed superior performance for seed yield as well as yield contributing traits. Whereas, the genotypes PUSA 9531, LGG 528, ASHA, MGG 347, IPM-02-03, KM-8-657, WGG 2, ML 267, COGG 974, LGG 410 and MH-3-18 showed superior performance for drought related traits. Hence, crosses involving these two categories of genotypes may result in the production of drought tolerant genotypes coupled with high seed yield and yield contributing traits.

Conclusion: By and large, based on genotype-by-trait biplot analysis it was concluded that the traits *viz.*, number of pods per plant, number of clusters per plant, days to maturity, plant height, chlorophyll content, specific leaf area, relative injury and chlorophyll stability index were identified as important traits for yield as well as drought tolerance improvement and these traits would be considered as key components during the selection. The genotypes LGG 450, KM 122, AKM 9904 and TM 96-2 showed superior performance for seed yield as well as yield contributing traits, whereas, the genotypes PUSA 9531, LGG 528, Asha, MGG 347, IPM-02-03, KM-8-657, WGG 2, ML 267, COGG 974, LGG 410 and MH-3-18 showed superior performance for drought related traits. Hence, crosses involving these two categories of genotypes may result in the production of drought tolerant genotypes coupled with high seed yield.

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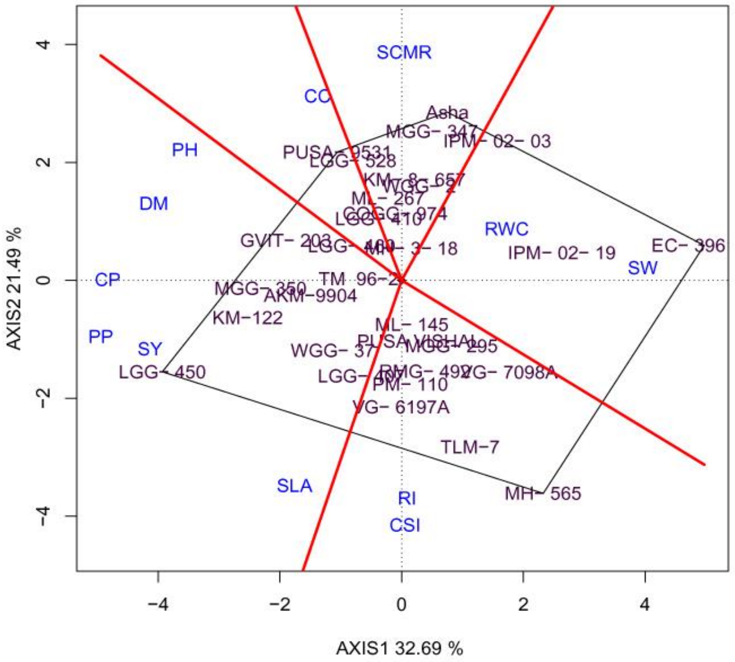

Fig. 1. Genotype-by-trait biplot of twelve yield and drought related traits of 31mungbean genotypes

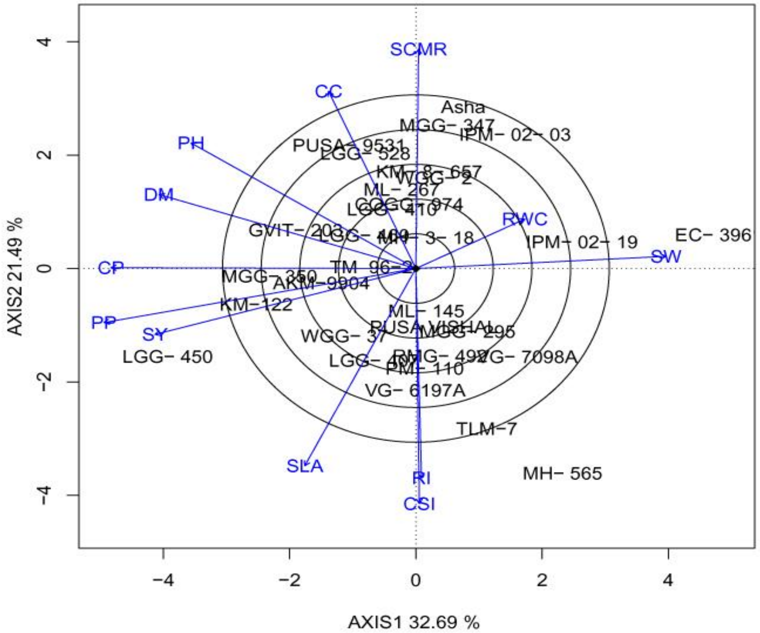

Fig. 2. Vector view of the genotype-by-trait biplot showing inter-relationships among various yield and drought related traits of 31 mungbean genotypes.

PH = Plant height
CP = Clusters per plant
SW = 100 seed weight
RWC = Relative water content
RI = Relative Injury
SLA = Specific leaf area
SCMR = SPAD Chlorophyll meter reading
DM = Days to maturity
PP = Pods per plant
SY = Seed yield
CC = Chlorophyll content
CSI = Chlorophyll stability index

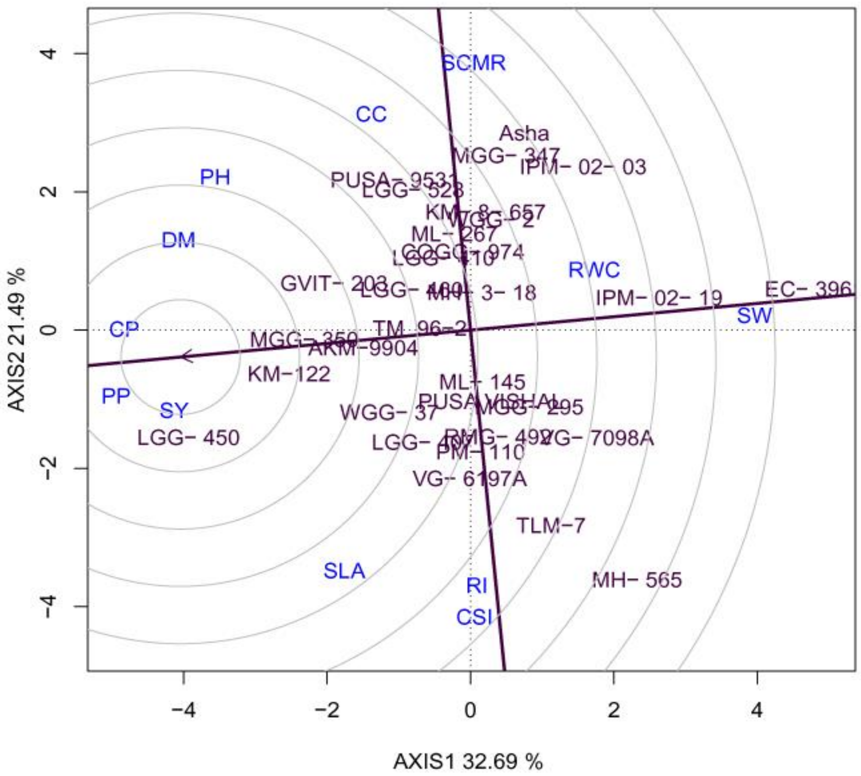

Fig. 3. A vector view of genotype-by-trait biplot showing the ranking of thirty one mungbean genotypes for various yield and drought related traits

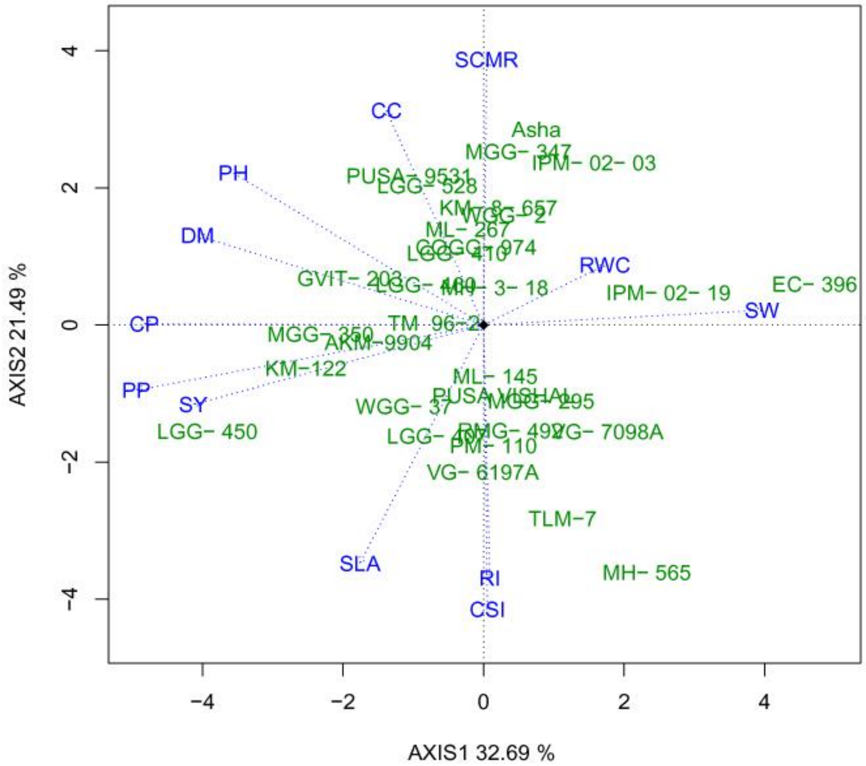

Fig. 4. Genotype-by-trait interaction biplot for various yield and drought related traits in mungbean

PH = Plant height
CP = Clusters per plant
SW = 100 seed weight
RWC = Relative water content
RI = Relative Injury
SLA = Specific leaf area
SCMR = SPAD Chlorophyll meter reading
DM = Days to maturity
PP = Pods per plant
SY = Seed yield
CC = Chlorophyll content
CSI = Chlorophyll stability index