GENETIC DIVERGENCE AND REALISED HETEROSIS BASED ON DRY MATTER COMPONENTS IN MUNGBEAN (VIGNA RADIATA (L.) WILCZEK)

M. NATARAJAN* AND S. PALANISAMY

School of Genetics, Tamil Nadu Agricultural University, Coimbatore 641003

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ABSTRACT

Utilizing generalised distance and canonical analysis, the divergence in 8 genotypes of mungbean and their 15 hybrids were assessed for root weight, stem weight, petiole weight, leaf weight, pod weight, total dry matter production (TDMP), seed yield and harvest index. The 23 genotypes fell into five clusters. The clustering pattern did not conform to geographical distribution. Genotypes ML 65 and K 851 included in cluster II were the most divergent from the genotypes in cluster V, i.e. Co 4 and LM 222. The canonical analysis confirmed to a large extent, the clustering pattern obtained by multivariate analysis. Both measures of divergence identified the same characters, petiole weight, stem weight, root weight as the major sources of divergence. Canonical analysis identified harvest index as another source of divergence in the second vector. In general, there was fairly good correspondence between divergence between parents measured by generalised distance and the extent of superiority of F₁ over midparent in respect of pod weight and seed yield.

Key words: Vigna radiata, genetic divergence, canonical analysis, heterosis.

Examination of genetic diversity among the yield components in mungbean has been done by some workers [1–3]. The results of genetic divergence based on dry matter components are not available in mungbean. It was suggested that component characters that are important to adaptability and natural selection usually provide a good starting point and the functions of direct yield components may not increase the scope for a better classification [4]. The dry matter components which represent physiological and morphological complementation and balance required for high yield are the characters determining fitness may be a better choice for such study. The present study, therefore, examines genetic divergence in mungbean based on dry matter components by generalized distance and canonical analysis.

^{*}Present address: Agricultural Research Station, Kovilpatti, Tamil Nadu 627 701.

MATERIALS AND METHODS

The material for the present study consisted of five genetic stocks and three commercial varieties of mungbean differing in duration, total dry matter production, plant habit, seed size and seed yield, and their hybrids obtained by crossing in line x tester design. The 15 hybrids and their eight parents were raised under three NP levels: 13:25, 25:50 and 50:100 kg/ha (low, medium and high fertility levels) in three replications during summer season. Dry weight of roots, stems, petioles, leaves, pods, seeds and total dry matter yield was recorded on five competitive plants in each replication of the parents and hybrids. The harvest index was also calculated. Mahalanobis' D^2 and canonical analyses were carried out using the pooled data over the three environments as per the methods described by Rao [5]. Heterosis was measured as deviation of F_1 from midparent value in respect of mean fertility level.

RESULTS AND DISCUSSION

The 8 parents and their 15 hybrids were grouped in to five clusters. The parents were distributed over three clusters, I, II and V, while hybrids spread over clusters I, III and IV. Cluster I combined a few hybrids together with one or both of their parents. The clustering pattern did not conform to geographical distribution. Cluster III and IV consisting only of hybrids indicated that considerable variation was created by hybridisation and they were also widely dispersed from the parents (Table 1). The D values obtained between the 23 populations showed a wide range from 3.4 to 55.9 (Table 2). The intercluster distances observed indicated that the genotypes in cluster II, AC 300, ML 65 and K 851, were the most divergent from the genotypes in cluster V, Co 4 and LM 222. The cluster means between the most divergent clusters, clusters II and V, varied widely in respect of petiole weight, followed by stem weight, root weight, and leaf weight (Table 3), which also indicated the importance of these characters in total genetic divergence.

Table 1. Composition of clusters based on D² statistics in mungbean

| Cluste | er Parent/hybrid | Origin |
|--------|------------------|---------------|
| I | KM 2 | Tamil Nadu |
| | ADT 1 | Tamil Nadu |
| | COGG 236 | Tamil Nadu |
| | KM 2 x AC 300 | Hybrid |
| | KM 2 x ML 65 | Hybrid |
| | KM 2 x K 851 | Hybrid |
| | KM 2 x COGG 236 | Hybrid |
| | ADT 1 x AC 300 | Hybrid |
| | ADT 1 x ML 65 | Hybrid |
| | ADT 1 x COGG 236 | Hybrid |
| II | AC 300 | Punjab |
| | ML 65 | Punjab |
| | K 851 | Uttar Pradesh |
| III | KM 2 x LM 222 | Hybrid |
| | ADT 1 x K 851 | Hybrid |
| | Co 4 x AC 300 | Hybrid |
| | Co 4 x ML 65 | Hybrid |
| | Co 4 x K 851 | Hybrid |
| | Co 4 x COGG 236 | Hybrid |
| IV | ADT 1 x LM 222 | Hybrid |
| | Co 4 x LM 222 | Hybrid ' |
| v | Co4 | Tamii Nadu |
| | LM 222 | Punjab |

The canonical vectors corresponding to the two largest roots ($\lambda 1, \lambda 2$) supplied by the two best orthogonal vectors, Z₁ and Z₂, indicated that petiole weight followed by leaf weight, stem weight and root weight, were the most important primary sources of divergence, having recorded higher linear functions (0.58, 0.49, 0.44 and 0.39, respectively) in the first vector, while harvest index was a secondary source of divergence since it had the highest linear function (0.94) in the second vector. The first two vectors accounted for 97.1% of total variability. The canonical analysis more or less confirms the clustering pattern obtained by D² analysis [4, 5]. Both D² and canonical analyses identified

Table 2. Inter and intracluster divergence (D²) and D
(in parentheses) in mungbean

| Clusters I | | II | Ш | IV | V | |
|------------|-------|--------|--------|--------|--------|--|
| <u> </u> | 37.3 | 215.9 | 190.3 | 598.4 | 2154.9 | |
| | (6.1) | (14.7) | (13.8) | (24.5) | (46.4) | |
| II | | 28.0 | 667.2 | 1244.3 | 3124.4 | |
| | | (5.3) | (25.8) | (35.3) | (55.9) | |
| III | | | 43.9 | 203.0 | 1285.1 | |
| | | | (6.6) | (14.3) | (35.9) | |
| IV | | | | 11.4 | 536.6 | |
| | | | | (3.4) | (23.2) | |
| V | | | | | 89.5 | |
| | | | | | (9.5) | |

the same characters, petiole weight, stem weight, root weight and leaf weight, as the major sources of divergence. The canonical analysis identified harvest index as a secondary source of divergence, which indicated that in the course of evolution, divergence had taken place for petiole, leaf, stem and root characters in the first instance, as can be seen in the native mungbean types with profuse vegetative growth. As a result of conscious selection, the plant type with increased source: sink ratio might have resulted later, as can be seen in the cultivated types.

An examination of MP heterosis in respect of four important characters i.e., pod weight, TDMP, seed yield and harvest index between the parental clusters in respect of 15 hybrids revealed that, in general, there is fair agreement between the degree of heterosis and the distance between the parental clusters (Table 4). For pod weight and seed yield, crosses between divergent parenets have recorded higher magnitude of heterosis, mostly in positive direction. The findings are in agreement with those of [5] in mungbean and [6] in soybean.

Table 3. Cluster means for different characters

| Cluster | Root weight (g) | Stem weight (g) | Petiole weight (g) | Leaf weight (g) | Pod weight (g) | TDMP (g) | Yield per plant (g) | Harvest index % |
|---------|-----------------------|-----------------------|--------------------------|-----------------------|----------------------|-------------|---------------------------|-----------------------|
| I | 1.80 | 4.63 | 1.46 | 7.59 | 11.23 | 26.71 | 6.40 | 23.96 |
| II | 1.02 | 2.39 | 0.77 | 4.38 | 8.48 | 17.04 | 5.32 | 31.22 |
| III | 2.56 | 6.91 | 2.39 | 10.51 | 15.84 | 38.21 | 8.74 | 22.87 |
| IV | 3.61 | 8.84 | 3.11 | 14.66 | 12.22 | 42.44 | 6.31 | 14.87 |
| v | 4.90 | 12:32 | 5.1 7 | 18.79 | 12.54 | 53.72 | 6.67 | 12.42 |

Table 4. Relationship between genetic diversity and realised heterosis for four important characters at medium fertility level

| Cross | Divergence (D) | Heterosis over midparent, % | | | | |
|------------------|---------------------------|-----------------------------|--------------------|---------------|---------------------|--|
| | between parental clusters | pod weight | TDMP | seed yield | harvest index | |
| Co 4 x ML 65 | 55.9 | 85.3** | 6.6* | 83.5** | 30.2** | |
| Co 4 x AC 300 | 55.9 | 51.8** | 4.3 | 53.0** | 14.9* | |
| Co 4 x K 851 | 55.9 | 67.1 ^{**} | 15. 7** | 51.0** | -2.0 | |
| Co 4 x COGG 236 | 46.4 | 76.2** | 4.8 | 64.0** | 33.3** | |
| KM 2 x LM 222 | 46.4 | 9.2 | -6.6 * | 17.0 * | 10.5 | |
| ADT 1 x LM 222 | 46.4 | -11.9 | 1.1 | -0.2 | -8.1 | |
| KM 2 x K 851 | 14.7 | 39.9** | 44.4** | 38.2** | -6.6 | |
| ADT 1 x AC 300 | 14.7 | 11.3 | 16.5** | 12.2 | -2.1 | |
| KM 2 x ML 65 | 14.7 | 13.4 | 14.2** | 8.5 | -6.8 | |
| KM 2 x AC 300 | 14.7 | -2.6 | 8.9 | 3.5 | -6.0 | |
| ADT 1 x K 851 | 14.7 | 6.6 | 38.7 ^{**} | 2.7 | -29.8 ^{**} | |
| ADT 1 x ML 65 | 14.7 | 0.7 | 18.0** | 0.5 | -19.2** | |
| Co 4 x LM 222 | 9.5 | -7.4 | -25.2** | -6.0 | 25.3* | |
| KM 2 x COGG 236 | 6.1 | 34.4** | 23.1** | 33.8** | 8.6 | |
| ADT 1 x COGG 236 | 6.1 | 6.9 | 18. 7** | -0.8 | -17.1** | |

[&]quot;," Significant at 5% and 1% levels, respectively.

In general, comparatively higher heterosis in positive direction was realised between less divergent crosses in respect of TDMP, and such crosses showed negative heterosis for harvest index (HI) which, in turn, resulted in poor heterosis for seed yield.

An examination of the cluster means (Table 3) reveals that mean TDMP was low and mean HI high in clusters I and II and vice versa in cluster V. The hybrids between genotypes of these clusters were included in cluster III, recording high mean seed yield but moderate TDMP and HI. Thus, the diversity estimated by generalized distance showed a good measure of heterosis for seed yield.

The cluster means of parents and hybrids obtained from D² analysis of seed yield, TDMP and HI as well as by the heterosis actually realized showed that the crosses between the parents with high TDMP and low HI and those with low TDMP and high HI resulted in

maximum seed yield. This was also confirmed by the high seed yield recorded in the F4 and F5 progenies of the crosses among genotypes belonging to clusters I, V and II, V, e.g. ADT 1 x LM 222 and Co 4 x ML 65, respectively, in a separate study.

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