However, isozyme analysis indicated that this cultivar is more closely related to endive and escarole than to chicory (J. T. Puchalski and R. W. Robinson, unpublished). Thus, although 'San Pasquale' in appearance resembles chicory, and is listed as such in seed catalogs, it is evidently a form of *C. endivia* or a derivative of the interspecific cross.

Cichorium intybus × *C. endivia.* All F_1 plants of 'Catalogna' chicory crossed with 'Florida Deep Heart' escarole were resistant to TuMV. These plants exhibited greater vigor and wider leaf lamina than that of the maternal parent 'Catalogna'.

Discussion

This investigation has established that all the accessions of *C. intybus* that were tested are resistant to TuMV, whereas those of *C. endivia* are susceptible.

Rick (5) demonstrated that there is a high incidence of natural hybridization between *C. intybus* and *C. endivia.* We have taken advantage of this compatibility in crossing the 'Catalogna' chicory with the 'Florida Deep Heart' escarole for interspecific gene transfer. Preliminary genetic studies (6) have revealed that resistance to TuMV is dominant. Good seed production was obtained from this hybrid and research is in progress to elucidate the inheritance of resistance.

Chicory also represents a valuable source of resistance for other viral and mycoplasma diseases. Zitter and Guzman (7) recently reported that endive and escarole are susceptible to bidens mottle virus (BiMV), to which plant introductions of chicory are resistant. We have determined that 'Catalogna' chicory is resistant to broad bean wilt virus (BBWV), cucumber mosaic virus (CMV), and lettuce mosaic virus (LMV). These viruses also occur in endive and escarole grown in Oswego and Orange counties of New York State (R. Provvidenti, unpublished).

In 1977 in our experimental fields, a severe epiphytotic of aster yellows caused the total loss of lettuce, endive, and escarole, but 'Catalogna' and the F_1 plants of this chicory cultivar crossed with 'Florida Deep Heart' escarole remained symptomless. Thus, the role of chicory in breeding endive and escarole resistant to aster yellows, BBWV, BiMV, CMV, and LMV deserves attention since some of these pathogens have caused losses for many years (2, 3).

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Multivariate Analysis of Genetic Diversity for Yield and its Components in Mung Bean[1]

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Additional index words. Vigna radiata, cluster analysis, parent selection

Abstract. **Sixteen genotypes of mung bean (*Vigna radiata* (L.) Wilczek var. *radiata*) were subjected to 18 treatment combinations (environments) resulting from 3 levels of N, 3 planting densities, and 2 planting times. Measurements were made on yield and its components: pods per plant, seeds per pod, and seed weight. Cluster analysis was used to provide an index of similarity of the genotypes for each character. Genetic similarity of the genotypes, as indicated by a "one-trait-at-a-time" analysis, is reflected in their phenetic similarity in an 18 dimensional space corresponding to the 18 environments. No relationship between geographic distribution and genetic diversity was obtained for all characters. Information on the diversity of the components of yield would be useful in choosing parents that yield superior progenies. Pods per plant was the most important component followed by seeds per pod, and seed weight. Selection of parents for the component characters, with regard to high performance and genetic diversity, are expected to follow the same order.**

The studies on mung bean have been concerned primarily with the interrelationships among yield and its components (4, 6, 19, 21). The importance of divergent parents for successful hybridization has long been recognized both in self- and cross-pollinated crops. Singh and Jain (18) suggested that heterosis in F_1 generation of mung bean was due to genetic diversity of parents. Harrington (10) reported that genetic diversity of the parents in wheat was related to the superiority of crosses. Singh and Gupta (20) observed that divergent parents in cotton gave rise to superior progeneis. Moll et al. (13, 14) concluded that, within a restricted range, heterosis in corn was related to divergence. For the above reasons, introduction of exotic germplasms from different geographical regions has become a standard practice in most plant breeding programs. Several studies have indicated that geographical diversity does not necessarily correspond to genetic divergence (8, 17, 25). Harlan (9) stated that "many crop plants exhibit local areas of

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extraordinary morphological diversity..." On the other hand, materials from different geographical regions may show little or no genetic diversity (8, 17, 25). Consequently, strong evidence as to the diversity of the introduced and local genotypes should be at hand before proceeding with their use as parents. In recent years, numerical taxonomy and its related multivariate methods have been used to assist in selection of parental combinations that would result in high yielding progenies (22, 26). These studies, based on numerous metrical characters, have been aimed to classify genotypes into divergent groups. However, such a classificatory approach has certain limitations. Classifications that are based on an overall combination of characters would result in groups within which genotypes are similar for some characters and dissimilar for others. Since plant breeders are interested in the improvement of more than one character, the limitations of such an approach in selection of parents with desirable divergent characters become evident. Grafius (7) proposed the use of a multidimensional phenetic concept for choosing parents. Muntgomery et al. (15) classified a large number of soybean lines for yield and seed protein percentage according to their responses under 4 locations and 2 years and found that within each group, lines responded similarly to environments and the magnitudes of genotype × environment interactions were low. Replication of genotypes in time and space, an expensive and time consuming procedure, is usually delayed to the later stages of breeding programs. As a result, faster and less expensive means of classification (to assess the genetic diversity of individual characters) are deemed necessary. Planting of local and introduced genotypes under a combination of cultural practices in the area, and their classifications for desirable characters would provide useful information as to the diversity of the genotypes for individual characters. The purpose of this study was to investigate divergence in yield and its components in 16 cultivars of mung bean. Since yield in mung bean is the result of the multiplicative effects of its components, such a study would be useful in selection of parental combinations that are diverse for all components.

Materials and Methods

The experimental material consisted of 10 Iranian and 6 introduced genotypes of mung bean (Table 1). The Iranian genotypes originated from 4 different localities, i.e., Karaj, Kerman, Varamin, and Zahedan. The introduced genotypes were from China, India, and the U.S.A. Eighteen treatment combinations (which will be referred to hereafter as environments) resulting from 3 levels of N, 3 planting densities, and 2 planting times were generated. The environments represented the range of cultural practices in the area. Nitrogen levels were, 0, 30, and 60 kg of N (in the form of urea) per ha. The planting densities were obtained by spacing plants 5, 10, and 15 cm apart on the rows. Planting dates were June 22 and July 22. All genotypes were subjected to all environments in 18 independent experiments at Safiabad Agricultural Research Center (150 km north of Ahvaz, Iran). Each experiment consisted of all genotypes planted in plots under one environment by using a randomized complete block design with 2 replications. Each plot was comprised of 4 rows 12 m long and 0.5 m apart. Before harvesting, 1 m from both ends of all rows were discarded. Eight plants from the 2 centered rows were randomly selected. For each plant number of seeds and number of pods were determined and the average number of seeds per pod was calculated by dividing the former by the latter. One hundred seed weight was also measured for each plant. The 2 centered rows of each plot were harvested and its yield was added to the yield of the 8 previously selected plants to obtain plot yield.

Table 1. Origin, yield, pods per plant, seeds per pod, and 100 seed weight of 16 genotypes of mung bean averaged over 18 environments.

Genotype no.	Origin	Yield (g/plot)	Pods per plant	Seeds per pod	Seed weight (g)
1	India	476.72	17.86	9.72	5.43
2	U.S.A.	499.35	17.91	9.46	4.62
3	Iran, Varamin	475.23	17.12	9.00	5.03
4	China	467.12	19.02	10.23	4.43
5	Iran, Varamin	563.88	17.66	9.80	4.09
6	Iran, Varamin	466.76	19.57	9.32	5.15
7	Iran, Zahedan	477.79	17.51	9.50	4.92
8	U.S.A.	508.61	16.40	8.43	5.41
9	Iran, Karaj	479.38	18.07	10.54	4.17
10	India	427.16	17.82	9.96	4.39
11	Iran, Zahedan	515.08	15.35	8.51	4.90
12	Iran, Zahedan	499.88	18.86	8.40	5.42
13	U.S.A.	473.09	17.84	8.77	5.43
14	Iran, Kerman	470.72	16.07	10.75	4.96
15	Iran, Karaj	487.26	16.53	8.95	4.98
16	Iran, Karaj	503.15	15.80	9.76	5.15
LSD 5%		39.47	2.29	1.06	0.26

Mean plot yield of each genotype under each environment was obtained by averaging over 2 replications. However, mean performances for the yield components were obtained by averaging over 8 plants and 2 replications. Before proceeding with cluster analysis, the differences among environments and genotypes for all characters were tested by a combined analysis of variance procedure. Cluster analysis, a method of grouping operational taxonomic units as defined by Sneath and Sokal (23) and Sokal (24), was used to provide an index of similarity of the genotypes in their responses across the environments. Each character was subjected to the analysis independently. In such an analysis, the 18 environments create an 18 dimensional hyperspace. Each genotype is represented by a point in this hyperspace, the coordinates of which correspond to its mean performance in each of the 18 environments. Similarity of the genotypes for their responses across the environments is reflected in their contiguity in the hyperspace or phenetic similarity. A hierarcial, agglomerative, and polythetic algorithm (12) employed by the Statistical Analysis System (SAS 76) of North Carolina State University (2) was used. The analysis begins with forming one cluster for each genotype and proceeds to form one final cluster containing all genotypes. In the present study, the number of clusters was arbitrarily chosen as 5 and further fusion of genotypes and clusters was ignored. The metric used in the calculation of distances among genotypes was unstandardized Euclidean. A stepwise regression procedure was used to determine the order of importance of the yield components.

Results and Discussion

Differences in genotypes and environments for yield and its components were highly significant (Table 2). Clusters II and III possess almost the same mean values for yield, 479 and 480 g/plot respectively (Table 3). A similar pattern also exists for

Table 2. Combined analysis of variance for yield and its components.

		Mean squares			
Source	df	Yield	Pods per plant	Seeds per pod	Seed weight
Genotypes (G)	15	23793**	50.61**	19.33**	7.22**
Environments (E)	17	650508**	199.03**	58.91**	1.70**
G x E	255	7300	24.76	5.34	0.34

**Significant at 1% level.

Table 3. Composition of clusters and their means for yield and its components in 16 genotypes of mung bean.

Trait	Cluster	Cluster composition	Cluster mean
Yield (g/plot)	I	1, 16, 3, 8, 12, 2, 7, 14	488.93
	II	9	479.37
	III	13, 15	480.17
	IV	6	466.76
	V	4, 11, 5, 10	493.31
Pods per plant	I	1, 3, 12, 13	17.92
	II	8, 16, 11, 14	15.90
	III	2, 7, 10, 5, 15	17.49
	IV	9	18.07
	V	4, 6	19.29
Seeds per pod	I	1	9.72
	II	3, 15, 11, 13, 8, 12	8.68
	III	2, 4, 9, 5, 16, 7, 10	9.89
	IV	6	9.32
	V	14	10.75
100 seed weight (g)	I	1, 13, 12, 8	5.42
	II	3, 14, 6, 16, 15, 7, 11	5.01
	III	2	4.62
	IV	4, 10, 5	4.30
	V	9	4.17

the component characters. Such a pattern implies that even though the genotypes belonging to different clusters were similar in their means (resulting from contrasting values in most of the environments), they occupied different regions of the hyperspace. Location of a genotype in the hyperspace does not depend on its mean, rather it depends on its performance in each of the environments. As a result, genotypes with a similar response to most of the environments comprise a single more or less homogenous cloud of points in the hyperspace.

Composition of clusters for the individual characters shows that there is no relationship between geographic distribution and phenetic similarity (Table 1 and 3). Gupta and Singh (8) reached the same conclusion by using D^2 analysis on a combination of 9 characters of mung bean. For all characters the Iranian genotypes fell into different clusters. The Iranian materials had been sampled from 4 localities with diverse climatic and cultural conditions. Rezai (16) working on a large population of wild oats (*Avena sterilis* L.) concluded that within countries, primitive cultivars could be grouped into different clusters due to ecological niches. As a result, collection of germplasms should include such ecological niches within national boundaries. Genotypes from the same localities were also grouped into different clusters for all characters. Polygenic nature of variations in local populations make them sensitive to minor environmental fluctuations and results in numerous locally adapted populations (16). Mode of pollination could have a pronounced effect on local genetic divergence. In the areas where land varieties predominate, occasional outcrossing, in a self pollinated crop such as mung bean, followed by inbreeding could lead to further heterogenity of the local populations. Overall similarity of genotypes within clusters does not necessarily imply genetic relationship (23). But it is an indication of extensive similarity in their responses to the environments. To the extent that phenetic similarity is a reflection of genetic similarity, grouping of genotypes within clusters could be due to common heritage and/or similar forces of selection (natural and artificial), mutation, migration, and genetic drift. Sachan and Sharma (17) emphasized that for selection of divergent parents in tomato only component characters of yield should be taken into consideration. Crosses involving genetically divergent parents with high performances, such as (6 × 14) × (1), should result in superior progenies. The stepwise regression analysis showed that pods per plant is the most important component followed by seeds per pod and seed weight. As a result selection of parents for the component characters with regard to high performance and genetic diversity should follow the same order.

The usefulness of the present study depends on the stability of groupings and the composition of clusters under other sets of environments. Since the number of environments used was large it is reasonable to assume that further experimentation *in the area,* but under different sets or artificially generated environments, should result in the same clustering patterns. Janoria et al. (11) studied phenetic similarity of rice cultivars under 2 levels of high and low fertility and concluded that fertility had a minor effect on clustering pattern. Somayajulu et al. (25) observed some stability in the number of clusters and their compositions for wheat strains planted under 3 fertility levels. They further concluded that widely divergent clusters were not affected by the levels of fertility. Investigations on the stability of D^2 over time and space have also provided evidence as to the consistency of clustering patterns. Murty et al. (in Somayajulu et al. (25)] working on linseed found that the number of clusters and their compositions were similar over 2 seasons at the same location. Bhatt (3) in an experiment involving 12 cultivars of wheat found reasonable consistency of the estimates of divergence obtained over 4 sites and years.

In conclusion, multivariate analysis of individual characters, as performed in the present study, provides useful information as to their genetic diversities. Such a numerical approach should be superior to the use of ecological and geographic diversity as an index of genetic diversity. We do not suggest that the procedure described in this article for identification of superior diverse parental genotypes, be used as a sole criteria for selection of parents in making crosses. However, it could be used as an adjunct to other procedures (such as a test of general combining ability) for evaluation of parental genotypes. Moreover, crosses involving divergent parents with superior performance for the component characters may not produce progenies with high yields. The negative associations among components of yield, arising from competitive forces for a limited input of metabolites lead to yield homeostasis rather than yield improvement (1). Denis and Adams (5) suggested that high yields in dry beans should be based on plants with physiological and morphological attributes that facilitate higher levels of net photosynthesis, effective translocation of photosynthate to the sinks, more reproductive sites, and more uniform interception of solar energy throughout the canopy.

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Water Relations and Yields of Three Rabbiteye Blueberry Cultivars with and without Drip Irrigation[1]

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Additional index words. blueberry, irrigation, epicuticular, wax, SEM

Abstract. **Drip irrigation applied to cultivars of rabbiteye blueberry (*Vaccinium ashei* Reade) maintained soil moisture at 25 to 35%, (volume basis), –0.07 bars soil-water potential while no irrigation resulted in 12.5% soil moisture, –2 to –3 bars. Irrigation reduced leaf diffusive resistance (r_L) by 50% and increased transpiration (T) by 70% but had no significant effect on midday stem xylem pressure potentials (ψ_x). Both yield and berry weight from irrigated plots were increased from 20 to 25% over those on nonirrigated plots. Seasonal changes in ψ_x, r_L, and T of nonirrigated bushes suggested this species has some characteristic adaptations to drought conditions, one such adaptation being wax rodlets observed in and adjacent to stomatal pores. These may have contributed to a favorable water balance under stress by increasing leaf diffusive resistance.**

Rabbiteye blueberry bushes are shallow rooted yet capable of surviving substantial drought periods (9). Yearly precipitation in Florida is 140 cm but seasonal distribution is not suitable for highest yields, since rabbiteye blueberries develop from March to June, the usual dry season in north Florida.

Irrigation is an important means of increasing crop productivity (5, 11, 15, 19, 20, 24, 26, 28). Prior work demonstrating the benefits of irrigation on rabbiteye blueberries has not been found. The objective of this study was to determine if drip irrigation would increase yield and fruit size enough to be of value to commercial blueberry growers. Plant moisture status was monitored as were environmental variables in order to relate yield data with water stress.

Materials and Methods

The experimental site was a 0.8 ha planting of 5-year-old rabbiteye blueberries at the IFAS Horticultural Unit 12 km northwest of Gainesville Florida. The soil was Kanapaha fine sand with pine bark mulch and a clay hardpan at 25 to 35 cm depth. 'Woodard', 'Bluegem', and 'Tifblue' plants were spaced 2 m within and 4 m between rows. Zero, 10.8 (a dripper) and 21.6 (2 drippers) liters per day per bush were applied through a drip irrigation system.

Yield, berry weight and percentage total soluble solids were measured on 108 plants. The experimental design was randomized block with 4 bush plots and 3 replications per cultivar.

Soil moisture was monitored weekly at a depth of 20 cm with a Troxler neutron probe meter from bloom in March to the

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