International Journal of Plant Breeding ©2013 Global Science Books

Genetic Relationship and Diversity Based on Agro-Morphogenic Characters in Yard Long Bean (*Vigna sesquipedalis* L. Fruw) Germplasm

Mohammed K. Hossain[1] • Nazmul Alam[1] • Jaime A. Teixeira da Silva[2] • Bhabendra K. Biswas[3] • Gazi M. Mohsin[4*]

[1] Department of Botany, Jahangirnagar University, Savar, Dhaka, Bangladesh
[2] Faculty of Agriculture and School of Agriculture, Kagawa University, Ikenobe, Miki-cho, 761-0795 Japan
[3] Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh
[4] Lal Teer Seed Limited, Bangladesh

Corresponding author: * **professorbiswas@gmail.com**

ABSTRACT

Fifty six genotypes of yard long bean (*Vigna sesquipedalis* L. Fruw) were investigated to understand the extent of genetic diversity through 20 agro-morphogenic characters. Analysis of variance revealed significant differences for each character among all 56 genotypes. Mahalanobis' D^2 analysis established the presence of wide genetic diversity among these genotypes through the formation of nine clusters. Cluster V had the maximum number of genotypes (12) while none of the clusters were solitary. Genotypes of different sources fell into the same cluster, indicating that genetic diversity was not concurrent with geographical diversity. The genotypes in cluster I diverged genetically from the genotypes in cluster IX, thus, selection of parents from clusters I and IX would produce progeny which may show homeostasis over changing environments. The biggest cluster V had the highest intra-cluster distance (3.059) and the highest cluster mean for number of pods/plant (3.215), hence, hybridization between genotypes within cluster V could be used to increase the number of pods/plant. The highest cluster mean for yield/plant was recorded in cluster IX (920.050 g). Therefore, genotype BD-1564 from BARI and genotype YB-549 from China appeared as outstanding genotypes in terms of improved yield potential of yard long bean. Among the 20 characters, number of pods/plant contributed most (15.29%) to the total divergence followed by number of racemes/plant (13.13%). Therefore, these characters would respond better under selection. The character, 100-seed weight, contributed least (0.19%) and the contribution offered by yield/plant was also minimum (0.51%) to total divergence. Based on mean performance, genetic divergence and clustering pattern, few genotypes (BD-1595, Tender Green, BD-1564 and YB-549) were considered as potentially important for further breeding programs of yard long bean.

Keywords: D^2 statistics, hybridization, improvement, parental selection, segregants
Abbreviations: FAO, Food and Agriculture organization; **PCA**, principal component analysis; **USDA**, United States Department of Agriculture

INTRODUCTION

Yard long bean (*Vigna sesquipedalis* L. Fruw) was probably selected and developed in Southeast Asia from common cowpea, which is considered to have originated in Africa (Ng and Marechal 1985) while the center of genetic diversity of yard long bean is in Southeast Asia. The name yard long bean is well chosen because the bean is really long, although not exactly one yard while the French name "Haricot kilomètre" (kilometer bean) exaggerates the size even more. The Chinese refer to it as snake bean, which is closely related to the black-eyed pea. Some other common names also include asparagus bean, string bean and long-podded bean. Yard long bean is thought to have originated in Yunnan province of Southern China (Newman 2006) but it is now widely believed that the wild ancestors of domestic yard long species came from central Africa (Hansen 2013). Its immature, tender, edible pods are one of the most popular vegetables used in the Philippines and other East Asian cuisines. The bean is even grown on a small scale in the home gardens of the Southern United States, West Indies as well as Mediterranean regions, generally recognized by local names, including *bora* (West Indies), *dau gok* (China), *pole sitao* (Philippines), *kusasagemae* (Japan) (Power your diet 2013), *barboti* (Bangladesh) (Huque *et al.* 2012), etc.

Yard long bean is actually an annual food legume belonging to the *Fabaceae* family and the genus *Vigna*, which is comprised of about 80 species and occurs throughout the world. Besides, the tropical American species are likely to be placed in a separate genus in the near future, which would reduce the genus to 50-60 species (Rajerison 2006). However, *Vigna unguiculata* is extremely variable, both in wild and cultivated plants, and several subspecies (up to 10) have been distinguished, most of them comprising perennial wild types (Madamba *et al.* 2006). Verdcourt (1970) subdivided cultivated forms of *V. unguiculata* into three subspecies, *unguiculata*, *sesquipedalis* and *cylindrica*, including both annual wild and cultivated types. Marechal *et al.* (1978) then divided *V. unguiculata* into five cultivar groups viz. Unguiculata group (common cowpea), Sesquipedalis group (yard long bean and *Dolicos* bean), Biflora group (catjang cowpea), Melanophthalmus group (West African bean) and Textile group (Nigerian bean). Once again, cowpea was classified as belonging to the same group as yard long bean (Li *et al.* 2001; Phansak *et al.* 2005; Tantasawat *et al.* 2010). Therefore, the scientific identity of yard long bean either as a species or as a subspecies is still a controversy. Both yard long bean and cowpea are required by the world market, especially for developed countries (Earth Net Foundation 2006). Benchasri *et al.* (2012) reported that yard long bean is a common vegeta-

Received: 8 February, 2013. Accepted: 1 March, 2013.

Original Research Paper

ble in Asian markets. Because of its economic importance, agriculturalists try to increase production to meet consumers' high demand, particularly in Southeast Asian, Chinese, and Filipino cultures. Along with yard long bean, other legumes are an important component in the diets of humans and animals throughout the world and are cultivated under a wide range of environmental conditions. Total world production exceeds 17 million tons, with China, Indonesia, India and Turkey among the largest producers and consumers of this crop (FAOSTAT 2010).

The leaves of yard long bean are somewhat shiny and flower color is either purple or white. Usually, flower size is larger than that of cowpea. Seed color ranges from black, brown, and various types of mottled color. Pods attach downward to the peduncles. Young pods are used as vegetables and the pods are used much like traditional field beans (FAO 2013). The pods hang in pairs that should be picked for vegetable use before maturity (Van Horn and Myers 2003; Coker *et al.* 2007). Yard long bean is a significant source of nutrition, particularly vitamins A and C, providing 17 and 31%, respectively of the recommended daily allowance USDA (2005). It is an important source of protein in many tropical and subtropical countries. The health benefits of yard long bean are mentioned below (*verbatim*):

- "Yard long beans are one of the ancient cultivated crops. Young, immature pods are one of very high calorie vegetables; 100 g beans contain about 47 calories.
- The pods contain large quantities of soluble and insoluble fibers. Since the entire green pod is eaten as in French beans; sufficient amount of dietary fiber is obtained in the diet. Dietary fiber helps to protect the mucous membrane of the colon by decreasing its exposure time to toxic substances as well as by binding to cancer causing chemicals in the colon. Fiber rich food also found to reduce LDL-cholesterol levels by decreasing re-absorption of cholesterol binding bile acids in the colon.
- Fresh yard long beans are one of the finest sources of folates; 100 g beans provide 62 µg or 15% of daily requirement of folates. Folate along with vitamin B-12 is one of the essential components of DNA synthesis and cell division. Adequate folate in the diet around conception and during pregnancy may help to prevent neural tube defects in the newborn baby.
- Fresh beans contain a good amount of vitamin C; 100g yard long beans provide 18.8 mg or 31% of vitamin C. Vitamin C is a powerful water-soluble antioxidant and when adequately provided in the diet, it helps to build immunity against infections, maintains blood vessel elasticity and offers some protection from cancers.
- Furthermore, the long beans are excellent sources of vitamin A; at 865 IU/ 100g. The beans have more of this vitamin than that of the other same family legumes such as lima beans, fava beans, green beans etc. Vitamin A is one of the essential vitamins for the body provided through our diet. Vitamin A maintains mucus membrane integrity, enhances skin complexion and improves night vision.
- In addition, yard long beans provide average amounts of minerals such as iron, copper, manganese, calcium and magnesium. Manganese is used by the body as a cofactor for the powerful antioxidant enzyme, superoxide dismutase" (Power your diet 2013).

According to the Oregon State University Commercial Vegetable Production Guide, the world production of yard long bean is about 13,450 kg/ha whereas, its production is only 3640 kg/ha in Bangladesh (Huque *et al*. 2012). Therefore, high-yielding yard long bean varieties need to be developed through utilization of valuable local and overseas germplasm collections.

Genetic relationships and diversity prevailing among genotypes decide species characteristics such as the degree of inbreeding versus outbreeding, or the relative contributions from asexual or sexual reproduction. The key message is that flowering plants show remarkable ecological and evolutionary lability in their sexual systems (Barrett 2002). Such studies can also provide insight into the evolutionary history of a species. Genetic distance and proximity of genotypes within a population for different characters of any crop are very important to determine their phylogenetic relationship and their evolutionary pattern (Hoque and Rahman 2007). Moreover, genetic diversity plays an important role in the survival and adaptability of a genotype. When a habitat changes, the populations of a genotype may have to adapt to survive, and the ability of populations to cope with this challenge depends on their capacity to adapt to their changing environment (Andrew 2002). The D^2 statistical technique is applied based on multivariate analysis developed by Mahalanobis (1936). It gauges similarity of an unknown sample set to a known one. It takes into account the correlations of the data set and is scale invariant. In other words, it refers to a generalized distance, clustering of genotypes, intra- and inter-cluster distances and to the contribution of individual characters to the total genetic divergence among genotypes.

The D^2 analysis is the most effective method for quantifying the degree of genetic diversity among genotypes, and helps in the selection of parents for hybridization. It is generally accepted that genetically divergent parents, when crossed, will show maximum heterosis and offer the maximum chance of isolating transgressive segregrants (Makanur 2010). Moreover, genetic diversity is the basic requirement for a successful breeding program with the objective of obtaining high-yielding varieties (Rahman and Munsur 2009) while collection and evaluation of genotypes of any crop are prerequisites for any program, providing a greater scope for exploiting genetic diversity. The quantitative assessment of genetic divergence among germplasm collections and the relative contribution of different characters towards genetic divergence create essential and effective information for breeders in a hybridization program and thereby genetic improvement of yield. The need to identify genetic divergence among genotypes is more pronounced for two reasons: i) genetically divergent parents, if included in a hybridization program, are likely to produce a high heterotic effect; ii) a wide spectrum of variability is expected in the segregating generation of crosses involving distantly related parents (Nagalakshmi *et al.* 2010).

Understanding genetic relationships and diversity would facilitate the transfer of useful genes among genotypes and maximize the use of available germplasm resources in plant breeding and characterized genotypes would provide clues to plant breeders on how to select accessions for use in a hybridization program (Ghafoor *et al*. 2002). Based on this theoretical background, the present study aimed to 1) evaluate the genetic relationship and diversity in 56 long yard bean genotypes collected from different origins/sources, 2) relate genetic diversity patterns to geographical regions and 3) select desirable parental lines for initiating hybridization programs to evolve new genetic recombinants.

MATERIALS AND METHODS

A total of 52 genotypes were collected from different sources of Bangladesh, 3 from China and 1 from India (**Table 1**). Among the domestic sources, 39 genotypes were received from BARI (Bangladesh Agricultural Research Institute), 10 from different national seed companies, one from BADC (Bangladesh Agricultural Development Corporation), one from a farmer's field of Chittagong district and one from a local market of Sylhet, Bangladesh. The experiment was conducted at a research field under the Department of Botany, Jahangirnagar Unversity, Savar, Dhaka, Bangladesh during March to June, 2010. The experimental site was located in the Young Brahmaputra and Jamuna Floodplains (FAO 1988; UNDP 1988) characterized by shallow, permeable sandy loams and silty loams on the ridge crests. The experiment was laid out in a randomized block design with three replications. Each genotype was assigned to three row plots 3 m in length with

Table 1 List of the collected yard long bean genotypes.

Total entries	Genotypes	Origin/ Source
39	BD-1516, BD-1518, BD-1528, BD-1532, BD-1532, BD-1533, BD-1537, BD-1548, BD-1549, BD-1560, BD-1561, BD-1562, BD-1563, BD-1564, BD-1569, BD-1575, BD-1577, BD-1578, BD-1579, BD-1583, BD-1591, BD-1594, BD-1595, BD-1598, BD-1599, BD-3064, BD-3067, BD-3074, BD-3078, BD-10071, BD-10073, BD-10075, BD-10078, BD-10080, BD-10081, BD-10082, BD-10084, BD-10086 and BARI-1 (released variety)	BARI, Gazipur, Bangladesh
1	Kegarnatki	BADC, Dhaka, Bangladesh
5	Toki, Lal Beni, Saba, Banalata and 1070	Lal Teer Seed Industry Ltd., Dhaka, Bangladesh
1	Green Long	Masud Seed Company, Dhaka, Bangladesh
1	White Bean	Ripa Seed Company, Dhaka, Bangladesh
1	Sada Sundori	Namdhari Seed Company, Dhaka, Bangladesh
1	Kashem King	Kashem Seed Company, Dhaka, Bangladesh
1	Tender Green	Techspark Seed Company, Dhaka, Bangladesh
1	Sobuj Sathi	Local market, Sylhet, Bangladesh
1	YB-465	Chittagang, Bangladesh
1	YB-501	Chengdu, China
2	YB-549 and YB-550	Anhui, China
1	YB-490	India

Table 2 Clustering pattern and distribution of 56 genotypes of yard long bean.

Cluster	No. of genotypes	Name of the genotypes
I	11	BD-1518, BD-1533, BD-1548, BD-1549, BD-1560, BD-1575, BD-1577, BD-1578, BD-10073, BD-10075, BD-10086
II	4	BD-1532, BD-10071, BD-10082, BD-10087
III	3	BD-1528, BD-1537, White Bean
IV	10	BD-1516, BD-1561, BD-1569, BD-1595, BD-1598, BD-1599, Green Long, Kegarnatki, Lal Beni, YB-465
V	12	BD-3074, BD-3078, BD-10080, Sobuj Sathi, Toki, Saba, YB-490, YB-501, YB-550, 1070, BARI-1, Kashem King
VI	9	BD-1562, BD-1563, BD-1583, BD-1591, BD-3064, BD-3067, BD-10078, BD-10081, BD-10084
VII	2	Bd-1595, Tender Green
VIII	3	BD-1579, Banalata, Sada Sundori
IX	2	BD-1564, YB-549

inter and intra-row spacing of 30 cm and 20 cm, respectively. Recommended agronomic practices were followed to obtain the best possible harvest. Out of 45 plants per plot, data was recorded from 10 randomly selected competitive plants for several characters: MVL = main vine length (cm), PB/P = primary branches/plant, L/P = leaves/plant, TLL = terminal leaf length (cm), TLB = terminal leaf breadth (cm), DFF = days to first flowering, R/P = racemes/plant, DNF = days to 95% flowering, P/R = pods/raceme, P/P = pods/plant, PL = pod length (cm), PG = pod girth (cm), DPM = days to pod maturity, IPP = infected pod percentage, PAP = pod abortion percentage, S/P = seeds/pod, HSW = 100-seed weight (g), FW/P fresh weight/pod (g), LHT = length of harvesting time and Y/P = yield/plant (g). Mean data for each character were subjected to both univariate and multivariate analysis. For univariate analysis, ANOVA (analysis of variance) was calculated for individual characters and tested by the F-test.

Principal component analysis (PCA), as well as principal coordinate analysis (PCoA) analysis, was also performed. At first, the data were subjected to PCA (Rao 1964) to group the genotypes into different clusters using a non-hierarchical classification based on maximum variance and the principal succeeding components with latent roots greater than unity (Jeger *et al*. 1983). Genetic divergence based on the 20 characters was computed using GENSTAT 5.5 software program and then the genotypes were clustered by using on hierarchical classification through covariance matrix. The intra- and inter-cluster distances were measured following the D^2 statistics proposed by Mahalanobis (1936).

$$P^{D^2} = Wij(\bar{x}^1 i - \bar{x}^2 i)(\bar{x}^1 j - \bar{x}^2 j)$$

where

P^{D^2} = Genetic divergence between two cultivars;

Wij = The inverse of estimated variance and covariance matrix;

xi and xj = The multiple measurements available for each of the genotypes.

RESULTS AND DISCUSSION

The ANOVA exhibited significant differences among the 56 yard long bean genotypes for all 20 characters studied. Therefore, the observations on all 20 quantitative characters in the 56 genotypes were analyzed for genetic diversity. The coefficient of variation (CV) is in general high in legumes: Adewale *et al.* (2010) estimated a wide range of CVs (1.80-34.10%) for yield and its related characters in combined analysis over two years in cowpea. The CVs along with standard errors for 20 characters are presented in **Fig. 1**. CVs ranged from 5.28-15.30%. The D^2 values, corresponding to all possible combinations among the 56 genotypes, were computed. The distribution pattern of the genotypes into different clusters indicated that cluster V was the largest, containing 12 genotypes followed by cluster I with 11 genotypes; cluster IV with 10 genotypes, cluster VI with 9 genotypes, clusters III and VIII with 3 genotypes each and two clusters (VII and IX) which had 2 genotypes each (**Table 2**). The clustering pattern of the 56 genotypes were also confirmed by PCA, in which PCA score 1 and PCA score 2 were geometrically distributed into four quadrants, following which the D^2 values were superimposed to develop nine different clusters (**Fig. 2**). The pattern of distribution of genotypes in various clusters showed the existence of considerable genetic diversity (Upadhyay and Mehta 2007). Nine genotypes of the largest cluster III (12) were collected from different Bangladeshi organizations, two genotypes (YB-501 and YB-550) from China and another one (YB-490) from India. Resmi *et al*. (2005) determined the magnitude of genetic divergence among 30 diverse genotypes of yard long bean using Mahalanobis D^2 statistics and grouped them into four clusters. The inter-cluster distance was maximum between clusters I and III. Heterotic combinations are expected between the selected parents of the diverged groups (Resmi *et al.* 2005). Besides, the extensive use of closely related genotypes by breeders could result in vulnerability to pests and diseases. Therefore, determination of genetic diversity of any given crop species is a suitable indicator for improvement of that crop because it generates baseline data to guide the selection of parental

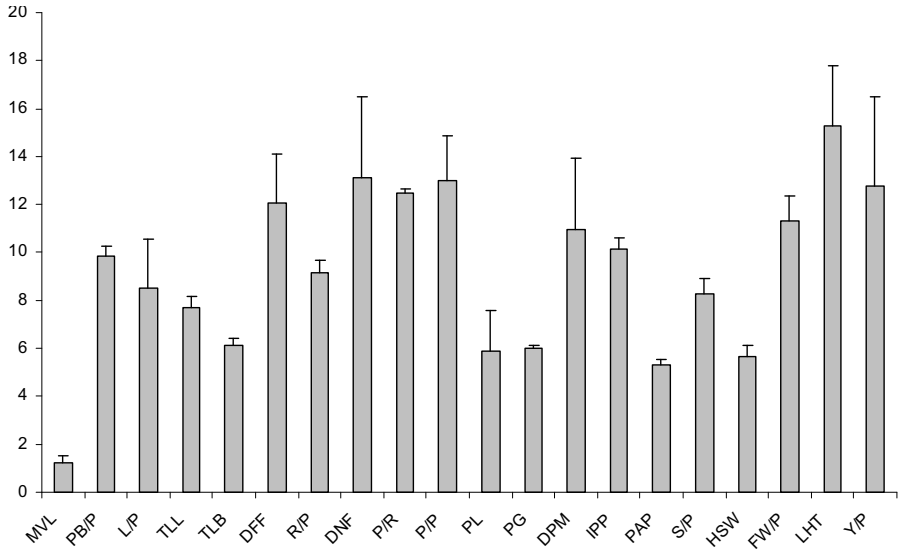

Fig. 1 Coefficient of variation with standard errors for 20 characters.

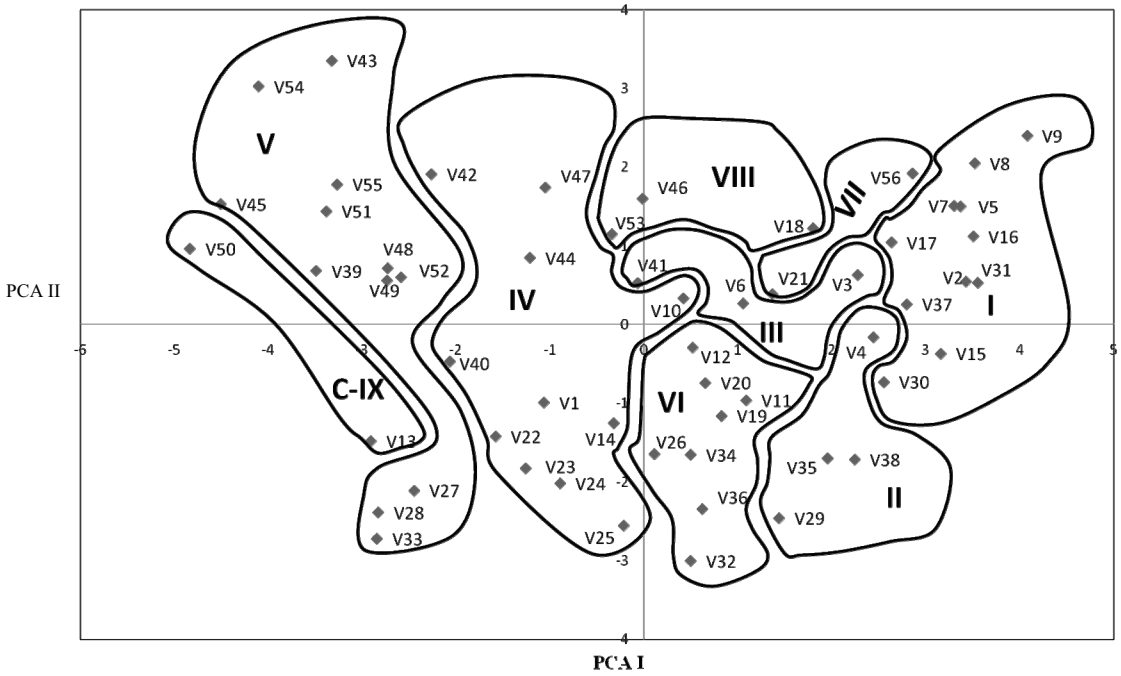

Fig. 2 Clustering pattern of 56 yard long bean genotypes where D^2 values have been superimposed on PCA values.

lines and design a breeding scheme (Ahmad *et al.* 2010).

This revealed that the genotypes collected or released from different countries were invariably placed in the same cluster. The clustering pattern of the varieties in the present study clearly indicated that there was no parallelism between genetic and geographic diversity. The major clusters contained genotypes of heterogeneous origin and/or regions which suggested that the pattern of clustering of genotypes was independent of their geographic origin/place of release and hence, that there is no parallelism between genetic and geographic diversity. These findings are in general agreement with those of Resmi *et al.* (2005). The D^2 statistics, when employed for various crops, suggests that genetic diversity is not always associated with geographical diversity, as shown by Prakash (2006) in chickpea (*Cicer arietinum* L.), by Golani *et al.* (2006) in Indian bean (*Catalpa bignonioides*. L.), by Singh and Singh (2006) in field pea (*Pisum sativum* L.), and by Pandey (2007), Suganthi *et al.* (2007), Sulnathi *et al.* (2007) and Nagalakshmi *et al.* (2010) in cowpea [*Vigna unguiculata* (L) Walp.]. In contrast, Das *et al*. (2001) reported that the grouping pattern of divergent genotypes suggested no parallelism between genetic divergence and geographical distribution of soybean genotypes. The clustering pattern of chickpea genotypes did not necessarily follow their geographic distribution (Syed *et al.* 2012). The logical explanation for observing genotypes from different geographic regions falling into one cluster may be that there is a free exchange of genetic material from one place to another or due to the fact that unidirectional selection practiced in different places might have had a similar effect and therefore, varieties evolved under similar selection pressure might have clustered together, irrespective of their geographic origin. Murty and Arunanchalam (1996) reported that genetic drift and selection in different environments could cause greater diversity than geographic distance. The average intra- and inter-cluster distances are presented in **Table 3**. The intra-cluster distance ranged from 0.282 (VII) to 3.059 (V) and the highest intra-cluster distance did transgress the limits of some inter-cluster distances. The highest inter-cluster distance (12.453) was recorded between cluster I and cluster IX, revealing that genotypes under these two clusters were most diverged,

Table 3 Average intra- (**bold**) and inter-cluster distances (D^2 values) in yard long bean.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**1.911**								
II	1.758	**0.890**							
III	3.023	1.108	**1.022**						
IV	6.003	2.143	1.700	**1.863**					
V	9.433	4.393	3.447	0.994	**3.059**				
VI	4.257	1.307	0.701	0.829	2.081	**2.271**			
VII	0.693	0.948	2.083	4.133	6.773	2.786	**0.282**		
VIII	4.425	1.450	0.774	0.720	1.912	0.562	2.906	**0.374**	
IX	12.453	6.673	5.055	1.803	0.728	3.288	8.872	3.285	**0.353**

Table 4 Cluster means for twenty agro-morphogenic characters in yard long bean.

Characters	I	II	III	IV	V	VI	VII	VIII	IX
Main vine length (cm)	311.627	383.775	332.200	361.540	332.975	387.256	294.800	315.367	344.750
Primary branches/plant	7.142	7.473	7.963	8.290	7.917	8.592	8.665	8.371	8.888
Leaves/plant	45.081	44.918	41.333	41.525	40.688	42.137	39.775	40.370	45.890
Terminal leaf length (cm)	12.192	11.778	11.860	12.240	11.763	11.706	11.985	11.317	12.240
Terminal leaf breadth (cm)	3.312	3.303	3.517	3.859	3.805	3.390	3.390	3.837	3.414
Days to first flowering	37.547	37.638	38.407	38.722	38.630	37.407	37.665	38.627	37.445
Racemes/plant	6.260	6.568	5.927	7.598	10.481	6.645	6.065	6.321	11.575
Days to 95% flowering	45.263	45.083	45.853	45.479	45.628	45.520	43.610	44.443	45.330
Pods/raceme	2.413	2.529	2.220	2.877	2.713	2.543	2.885	2.369	3.169
Pods/plant	15.083	16.625	13.173	21.371	28.068	16.707	17.655	14.983	36.250
Pod length (cm)	11.360	23.138	35.607	49.577	63.764	42.610	12.475	44.353	70.580
Pod girth (cm)	2.299	1.938	2.577	2.802	3.215	2.538	2.280	2.547	3.170
Days to pod maturity	49.870	49.638	50.297	50.424	50.168	50.382	49.330	49.777	48.610
Infected pod (%)	10.341	6.940	10.037	7.874	7.896	8.108	8.050	8.517	7.940
Pod abortion (%)	8.997	9.220	10.183	9.554	9.683	9.342	9.275	9.629	8.940
Seeds/pod	15.242	15.835	15.257	16.155	15.508	14.531	15.610	15.407	15.055
100-seed weight (g)	11.361	13.625	15.990	16.367	17.967	13.893	11.730	14.220	18.000
Fresh weight/pod (g)	5.981	10.596	14.703	18.763	23.140	16.344	8.179	18.433	25.440
Length of harvesting time	27.525	27.223	27.630	28.090	28.213	27.593	28.780	28.110	27.945
Yield/plant (g)	89.658	172.025	190.900	394.140	638.292	269.789	138.350	276.867	920.050

followed by clusters I and V (9.433). Hence, intercrossing between genotypes from different clusters may give a high heterotic response and better segregants (Suganthi *et al.* 2007). On the contrary, the lowest inter-cluster distance (0.562) was estimated between clusters VI and VIII, indicating that the genotypes included in these two clusters were more closely related than to other genotypes. The data on the cluster means of all 20 characters are presented in **Table 4**. It is evident that different clusters exhibited distinct mean values for almost all 20 characters. A wide range of CVs was observed among different clusters for all cluster means and for all 20 characters. Cluster VI had the highest mean value for MVL (387.256 cm). DFF was very close among the nine clusters and ranged from 37.407-38.722. Cluster VII had the minimum mean value for DPM (43.610) but had the highest FW/P (28.780 g). The P/P was recorded maximum (36.250) in cluster IX and cluster II had the minimum (6.940%) IPP. Cluster I had the highest mean value for PL (10.341 cm). Moreover, cluster IX had the maximum value for IPP (48.610%) but had the highest means for S/P (18.000), HSW (25.440 g) and Y/P (920.050 g).

In the present investigation, the percentage contribution of different important characters towards genetic divergence are calculated (**Table 5**). The study indicated that P/P contributed maximum (15.29%) to total divergence followed by R/P (13.13%). The least contribution to total genetic divergence was by HSW (0.19%). The minimum contribution by this character revealed that this character was least affected in the course of evolution. Genetic diversity is the basis for survival and adaptation and allows individuals to continue to advance adaptive processes on which evolutionary success depends (Rao 2002). Nevertheless, species diversity of a community and genetic diversity of a species may covary positively within and between sites due to the possible effects of drift, selection and species turnover (Odat *et al.* 2004; Vellend and Geber 2005; Gugerli *et al.* 2008). The contribution of MVL towards total genetic diversity was 2.05%. The final product, Y/P also exerted minimum load (0.51%) to total genetic divergence. Venkatesan *et al.* (2004) reported that FC/P (flower clusters/plant), P/C (pods/cluster), P/P and SY/P (seed yield/plant) had the maximum contribution towards total divergence. Kumawat and Raje (2005) also showed that SY/P contributed the most to total genetic divergence followed by S/P, DFF, plant height and reproductive period. Sulnathi *et al.* (2007) assessed genetic divergence in 56 genotypes of cowpea using D^2 statistics for 13 yield-contributing characters and showed that genotypes could be grouped into nine clusters

Table 5 Contribution of twenty characters to the total genetic divergence in yard long bean.

Characters	Mean range	Contribution towards genetic divergence (%)
Main vine length (cm)	287.90 – 411.70	2.05
Primary branches/plant	5.89 – 9.44	2.23
Leaves/plant	34.11 – 50.33	4.61
Terminal leaf length (cm)	8.67 – 12.34	1.14
Terminal leaf breadth (cm)	2.78 – 4.64	0.85
Days to first flowering	36.11 – 41.67	7.90
Racemes/plant	5.46 – 12.94	13.13
Days to 95% flowering	41.11 – 48.11	7.38
Pods/raceme	2.11 – 3.56	4.27
Pods/plant	12.22 – 37.35	15.29
Pod length (cm)	9.32 – 91.87	12.15
Pod girth (cm)	1.52 – 3.68	0.28
Days to pod maturity	44.33 – 51.89	10.27
Infected pod (%)	5.00 – 12.89	3.00
Pod abortion (%)	7.11 – 11.55	3.49
Seeds/pod	8.33 – 19.33	2.96
100-seed weight (g)	8.50 – 22.33	0.19
Fresh weight/pod (g)	5.28 – 27.64	2.15
Length of harvesting time	26.33 – 30.33	6.15
Yield/plant (g)	66.78 – 957.60	0.51

in which cluster I had the maximum number of genotypes and in which the characters DM (days to maturity), HSW and DF (days to flowering) were the highest contributors to D^2 values. Pandey (2007) evaluated the genetic diversity among 13 characters of 44 grain cowpea genotypes using Mahalanobis D^2 statistics. The genotypes fell into nine clusters. Cluster strength varied from a single genotype (Cluster IV to IX) to 31 genotypes in Cluster I. Cluster III had minimum days to first flower opening and SY/P in addition to maximum P/P and PB/P. Cluster II had maximum Y/P and HSW, cluster V had maximum PL, cluster VII had maximum number of S/P along, cluster II had minimum DM, while cluster VII showed maximum DM. Suganthi and Murugan (2007) evaluated the genetic diversity of 10 characters of 30 cowpea genotypes using Mahalanobis D^2 statistics, grouping them into 11 clusters. Cluster strength varied from a single genotype (Clusters VI, IX and XI) to 7 genotypes (Cluster III). Cluster VI had maximum SY/P, P/C, PL, S/P and P/P. The contribution of a particular character mainly depended upon the genotypes included in the study and on the environment influence over the character. Among the 13 quantitative characters studied, the most important character contributing to divergence was seed size followed by PL, HSW and clusters/branch (Backiyarani *et al*. 2000). Oliveira *et al.* (2003) studied the importance of several characters for divergence in cowpea and indicated that PL (36.87%), HSW (19.21%) and S/P (9.62%) were the most important contributors to total genetic divergence. On the other hand, Passos *et al.* (2007) showed that, for semi-upright cowpea genotypes, the characters of greatest magnitude for divergence were PY (pod yield) (43.91%) for genotypes of prostrate growth and PY (35.92%), PL (28.56%) and weight of grains/pod (28.14%) for upright genotypes. The number of P/P contributed the most to divergence followed by pod weight and yield (Baswana *et al.* 1980).

Any success through hybridization followed by selection depends primarily on the selection of parents having high genetic variability for different characters. While choosing the genotypes as parents for hybridization for heterosis breeding, the *per se* performance of the genotypes with higher D^2 values should be taken into consideration, in addition to maximum inter-cluster distance between clusters. If the mean *per se* performance of two genotypes is too low with less genetic divergence, such a pair is not likely to produce very high-yielding segregants or heterotic effects, therefore, has no practical value. Hence, the effective method of identifying ideal parental combinations, or genotypes with high-yielding ability along with other desirable characters would be selected and also all possible D^2 values among the clusters would be observed (Shimoya *et al.* 2002).

CONCLUSION

All 20 characters studied contributed to diversity, in which the highest contribution was recorded by pods/plant. Based on D^2 values, 56 genotypes were grouped into nine clusters. Cluster V was the biggest with 12 genotypes followed by cluster I (11) and IV (10). There was no solitary cluster. Intra-cluster D^2 values ranged from 0.282 to 3.059 and inter-cluster D^2 values exhibited a range of 0.562-12.45. Fresh weight/pod was maximum (28.780 g) in cluster VII and the highest yield/pod (920.050 g) was in cluster IX, revealing the superiority of genotypes in clusters VII and IX to obtain segregants with high fresh weight as well as high yield after hybridization. It is essential to determine how influential characters lead to the improvement of yard long bean genotypes. As hybridization between closely related genotypes results in depressed vigor and fertility, hence, future breeding program utilizing the studied genotypes should be based on the genetic analysis of various characters and hybridization carried out among clusters rather than within clusters. The present investigation showed significant variation between genotypes for the 20 characters considered. Improvement in yield could be achieved through hybridization followed by selection for high-yielding segregants. The intercrossing among genotypes showed that greater genetic divergence should result in superior heterotic effects and also generate valuable segregants in later generations. It is expected that better performing varieties could be developed from this study which ultimately increases sustainable productivity in yard long bean.

REFERENCES

Adewale BD, Okonji C, Oyekanmi AA, Akintobi1 DAC, Aremu CO (2010) Genotypic variability and stability of some grain yield components of cowpea. *African Journal of Agricultural Research* **5**, 874-880

Ahmad G, Mudasir, Kudesia R, Shikha, Srivastava MK (2010) Evaluation of genetic diversity in pea (*Pisum sativum* L.) using RAPD analysis. *Genetic Engineering and Biotechnology Journal* **16**, 1-5

Andrew PS (2002) *Conservation Biology* (1st Edn), Cambridge University Press, Cambridge, 345 pp

Backiyarani S, Nadarajan N, Rajendran C, Shanthi S (2000) Genetic divergence for physiological traits in cowpea (*Vigna unguiculata*. (L.) Walp). *Legume Research* **23**, 114-117

Barrett SCH (2002) The evolution of plant sexual diversity. *Natural Reviews on Genetics* **3**, 274-284

Baswana KS, Pandita ML, Partap PS, Dhankhar BS (1980) Genetic divergence for yield and its components in Indian bean (*Dolichos lablab* var. *lignosus* L.). *Haryana Journal of Horticultural Sciences* **9**, 184-187

Benchasri S, Bairaman C, Nualsri C (2012) Evaluation of yard long bean and cowpea for resistance to *Aphis craccivora* Koch in southern part of Thailand. *The Journal of Animal and Plant Sciences* **22**, 1024-1029

Coker C, Ely M, Freeman T (2007) Evaluation of yard long bean as a potential new crop for growers in the Southeastern United States. *HortTechnology* **17**, 592-594

Das SP, Harer PN, Biradar AB (2001) Genetic divergence and selection of genotypes in soybean. *Journal of Maharasta Agricultural University* **25**, 250-25

Earth Net Foundation (2006) Organic vegetable: eating safety. TCG Printing Ltd., Bangkok, pp 289-296

FAO (Food and Agriculture Organization) (1988) Agroecological Regions of Bangladesh, Report 2, pp 195-211

FAO (2013) Yard long bean [*Vigna unguiculata* (L.) Walpers cv-gr. Sesquipedalis E. Westphal]. Source: Yard long bean- NIAS Genebank

Ghafoor A, Zahoor A, Qureshi AS, Bashir M (2002) Genetic relationship in *Vigna mungo* (L.) Hepper and *V. radiata* (L.) R. Wilczek based on morphological traits and SDS-PAGE. *Euphytica* **123**, 367-370

Golani IJ, Naliyadhara MV, Mehta DR, Purohit VL, Pandya HM (2006) *Legume Research* **29**, 286-288. Cited from Nagalakshmi RM, Usha Kumari R, Boranayaka MB (2010) Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electronic Journal of Plant Breeding* **1**, 453-461

Gugerlia F, Englisch T, Niklfeld H, Tribsch A, Mirek Z, Ronikier M, Zimmermann NE, Holderegger R, Taberlet P (2008) Relationships among levels of bio-diversity and the relevance of intraspecific diversity in conservation - a project synopsis. *Perspectives in Plant Ecology, Evolution and Systematics* **210**, 259-281

Hansen V (2013) Snake (yard long) Beans, Black Book Cooking. Available online: http://www.blackbookcooking.com/snake-beans-or-yard-long-beans

Hoque MN, Rahman L (2007) Estimation of Euclidean distance for different morpho-physiological characters in some wild and cultivated rice genotypes (*Oryza sativa* L.). *Journal of Biological Science* **7**, 86-88

Huque AKMU, Hossain MK, Alam N, Hasanuzzaman M, Biswas BK (2012) Genetic divergence in yard long bean [*Vigna unguiculata* (L.) Walp. ssp. *sesquipedalis* Verdc.]. *Bangladesh Journal of Botany* **41**, 61-69

Jeger MI, Gerethrojones D, Griffiths E (1983) Components of partial resistance of wheat seedlings to *Septoria nodorium. Euphytica* **32**, 558-575

Kumawat KC, Raje RS (2005) Association analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Journal of Arid Legumes* **2**, 47-49

Li CD, Fatokun CA, Benjamin U, Singh BB, Scoles GJ (2001) Determining genetic similarities and relationships among cowpea breeding lines and cultivars by microsatellite markers. *Crop Science* **41**, 189-197

Madamba R, Grubben GJH, Asante IK, Akromah R (2006) *Vigna unguiculata* (L.) Walp. In: Brink M, Belay G (Eds), *PROTA 1: Cereals and pulses/ Céréales et légumes secs*. [CD-Rom]. PROTA, Wageningen, Netherlands, 1 p

Mahalanobis PC (1936) On generalized distance in statistics. *Proceedings of the National Academy of Science of India* **2**, 49-55

Makanur B (2010) Phenotypic characterization, assessment of genetic diversity, screening for protein content and bruchid infestation in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes, MS thesis. University of Agricultural Sciences, 100 pp

Marechal R, Mascherpa JM, Stainer F (1978) Etude taxonomique d'un groupe complexe d'speces des genres *Phaseolus* et *Vigna* (Papilionaceae) sur la base de donnees morphologiques et polliniques, traitees par l'analyse informatique. *Boissiera* **28**, 191-193

Murty BR, Arunachalam V (1996) The nature of divergence in relation to breeding system in some crop plants. *Indian Journal of Genetics and Plant Breeding* **26**, 188-198

Nagalakshmi RM, Kumari RU, Boranayaka MB (2010) Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electronic Journal of Plant Breeding* **1**, 453-461

Newman JM (2006) Long beans are twins. Flavor and fortune, dedicated to the art and science of Chinese cuisine. *Vegetables and Vegetarian Foods* **13**, 25-28

Ng NQ, Marechal R (1985) Cowpea taxonomy, origin and germplasm. In: Singh SR, Rachie KO (Eds) *Cowpea Research, Production and Utilization*, John Wiley & Sons Ltd. London, pp 11-21

Odat N, Jetschke G, Hellwig FH (2004) Genetic diversity of *Ranunculus acris* L. (Ranunculaceae) in relation to species diversity and habitat type in grassland communities. *Molecular Ecology* **13**, 1251-257

Oliveira FJ, Filho ACJ, Bastos GQ, Reis OV (2003) Divergencia genetica entre cultivares de caupi. *Pesquisa Agropecuária Brasileira* **5**, 605-611

Pandey I (2007) Genetic diversity in grain cowpea. *Legume Research* **30**, 92-97

Passos AR, Silva AS, Cruz PJ, Rocha MM, Cruz EMO, Rocha MAC, Bahia HF, Saldanha RB (2007) Divergência genetic em feijão-caupi. *Bragantia* **4**, 579-586

Phansak P, Taylor PWJ, Mongkolporn O (2005) Genetic diversity in yard long bean (*Vigna unguiculata* ssp. *sesquipedalis*) and related *Vigna* species using sequence tagged microsatellite site analysis. *Scientia Horticulturae* **106**, 137-146

Power your diet (2013) Yard long beans nutrition facts, © 2009-13. Available online: www.nutrition-and-you.com/yard-long-beans.html

Prakash V (2006) Divergence analysis in Kabuli chickpea (*Cicer arietinum* L.). *Indian Journal of Genetics* **66**, 241-242

Rahman MM, Munsur MAZ (2009) Genetic divergence analysis of lime. *Journal of Bangladesh Agricultural University* **7**, 33-37

Rajerison R (2006) *Vigna umbellata* (Thunb.) Ohwi & H.Ohashi In: Brink M, Belay G (Eds), *PROTA 1: Cereals and pulses/Céréales et légumes secs.* [CD-Rom]. PROTA, Wageningen, Netherlands, 1 p

Rao CR (1964) The use and interception of principal component analysis in applied research. *Sankhya Series A* **22**, 317-318

Rao VR, Toby Hodgkin T (2002) Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell, Tissue and Organ Culture* **68**, 1-19

Resmi PS, Celine VA, Vijayaraghavakumar (2005) Genetic divergence analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* L. Verdcourt). *Legume Research* **28**, 77-78

Shimoya A, Cruz CD, Ferreira RP, Pereira AV, Carneiro PCS (2002) Divergencia genetica entre acessos de um banco de germoplasma de capim-elefante. *Pesquisa Agropecuária Brasileira* **37**, 971-980

Singh JD, Singh IP (2006) Genetic divergence in advanced genotypes for grain yield in field pea (*Pisum sativum* L.). *Legume Research* **29**, 301-303

Suganthi S, Murugan S (2007) Variability studies in cowpea [*Vigna unguiculata* (L) Walp.]. *Crop Research* **33**, 195-197

Suganthi S, Murugan S, Venkatesan M (2007) D^2 analysis in cowpea [*Vigna ungiculata* (L.) Walp]. *Legume Research* **30**, 145-147

Sulnathi G, Prasnthi L, Sekhar MR (2007) Character contribution to diversity in cowpea. *Legume Research* **30**, 70-72

Syed MA, Islam MR, Hossain MS, Alam MM, Amin MN (2012) Genetic divergence in chickpea (*Cicer arietinum* L.). *Bangladesh Journal of Agricultural Research* **37**, 129-136

Tantasawat P, Trongchuen J, Prajongjai T, Seehalak W, Jittayasothorn Y (2010) Variety identification and comparative analysis of genetic diversity in yard long bean (*Vigna unguiculata* spp. *sesquipedalis*) using morphological characters, SSR and ISSR analysis. *Scientia Horticulturae* **124**, 204-216

UNDP (United Nations Development Program) (1988) Agroecological Regions of Bangladesh, Report 2, pp 195-211

Upadhyay D, Mehta N (2007) Biometrical studies in Dolichos bean (*Dolichos lablab* L.) for Chhattisgarh Plains. *Research Journal of Agricultural Sciences* **1**, 441-447

USDA (United States Department of Agriculture) (2005) National nutrient database for standard reference, release 18. Available online: horttech.ashspublications.org/content/17/4/592

Van Horn M, Myers C (2003) Chinese long bean, yard-long bean, asparagus bean. 7 Apr. 2003. Available online: http://www.rain.org/greennet/docs/exoticveggie html/chineselongbeans.html

Vellend M, Geber MA (2005) Connections between species diversity and genetic diversity. *Ecology Letters* **8**, 767-781

Venkatesan M, Veeramani P, Thangavel L, Ganeshan J (2004) Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research* **27**, 223-227

Verdcourt B (1970) Studies in the Leguminosae - Papilionoideae for the "Flora of Tropical East Africa": IV. Kew Bulletin 24, pp 542-544