

Characterization and evaluation of pea germplasm in BangladeshMM Rahman¹ M.Shain-uz- Zaman² MS Iqbal³ N Naher⁴ and MM Hossain⁴**Present address**

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Abstract

Two hundred and twenty two genotypes of pea were evaluated to estimate the variation among the genotypes and to find out the short duration line for fitting rice based cropping system in between rice, fighting climate change in Bangladesh. All the genotypes were grouped into twelve clusters. The composition of various clusters varied from 1 to 40. Cluster V comprised of 40 genotypes followed by cluster XI, II, IX, IV and VII consisting of 30, 26, 24, 22 and 20 genotypes, respectively. There were 15 genotypes in clusters VI, 13 in cluster XII, 11 in cluster X, 9 in cluster I, 8 in cluster VIII while 1 genotype in cluster III. Cluster VII exhibited the lowest mean value for days to flower (28) and days to maturity both in fresh pod and seed harvest followed by cluster XII. The highest pod length and hundred seed weight also observed in cluster VIII but the highest yield per plant was recorded in cluster III followed by cluster VI. Cluster III also showed the highest number (6.7) of branch and pods (31.0) per plant whereas cluster I had genotypes with the highest plant height (152 cm) and highest number of seeds per pods.

Key words: Field Pea, *Pisum sativum*, Characterization, Evaluation, Cluster analysis

Introduction

Pea (*Pisum sativum* L.) is the fourth leading legume in terms of consumption in the world. It is rich in protein, used in rotation with cereals and oil seeds. Pea is an important winter pulse crop of west Europe, North America, India, Australia, Pakistan and South America. In Bangladesh it cultivated dispersedly under a wide range of different region; this is an important winter Pulse crop of India and was among the first crop cultivated by human being. This crop is highly productive, grown for food and forage. Field pea is extensively used as dry, whole or split pulse (dal). This crop plays an important role in nourishment because of a rich source of proteins, carbohydrates and vitamins for human nutrition. In the country this crop is grown in about 0.76 million hectare with annual production of 0.7 million tones. In Madhya Pradesh this crop covers 263.9 thousand hectare area with the production of 94.2 thousand tones. (Rabi Group Meet 2013 AICRP on MULLaRP). Utter Pradesh, Madhya Pradesh, Jharkhand, Bihar and Assam are the main leading states in terms of area and production. Dry seeds of field pea contain 22.9% protein, 60.7% carbohydrates, 1.45% fat, 1.4% crude fiber, 2.7% ash and 10.9% moisture with calorific value 343/100g (Duke1981). Field pea has high levels of

essential amino acids, lysine and tryptophan, which are usually low in cereal grains. The major production constraints in field pea have been found such as lack of improved high yielding varieties, on-availability of irrigation and use of poor quality seeds. The Genetic Resource and Seed Unit (GRSU) of the AVRDC aim to set up a core-collection (Holden and Williams, 1984) or a condensed, yet representative, assembly of accessions from this germplasm collection. To improve the genetic contents of any crops, genetic variability is a prerequisite for crop improvement programme. This collection has been acquired mainly through personal contact and exchange through different institution and individuals (Tey et al, 1989). Most of the reports on genetic variability showed a wide range of variability for plant height with moderate to high heritability and high genetic advance, based on studies varying number of genotypes and there were few reports based on the segregating material. A report showed moderate heritability and moderate genetic advance (Patil, 1986). Another report revealed that low heritability and low genetic advance for this trait (Apte et al., 1987) and Rangaiah and Nehru indicated low heritability (5.61%) with 6 % genetic advance. However, Selviet al. (1994) and Backiyarani and Nadarajan(1996) and Selvam et al.(2000) reported revealed that high heritability (99.89%) with

moderate GCV and PCV values. The nature and magnitude of genetic variability and extent to which the desirable traits are heritable important for exploitation of the desirable traits for enhancing the yield in field pea. The loss of genetic diversity has been dramatic for many cultivated species (Wikes, 1983).

Characterization and evaluation of field pea genotypes for yield and quality attributing traits are one of the important activities of the breeders deputed in field pea improvement programme. Development of cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pests has significantly increased the yield and cultivated area (Ehlers and Hall, 1997). Knowledge about the genetic characteristics of a population is fundamental in breeding programs and it involves the local farmers. This strategy allows improving and also necessary to conservation of the genetic reliability of landrace genetic resources (Kahraman and Onder, 2009). To select the better genotypes for the improvement of the genetic constitutions of the field pea is required now to fulfill the future increasing demand. Grain yield, grain quality and resistance are three important objectives of field pea breeding programmes in developing countries. Environment has high impact on yield trait therefore direct selection for yield alone constraints the selection efficiency. Yield is a complex character and is associated with some yield contributing characters. The understanding of association of characters is of prime importance in developing an efficient breeding programme. Principal Component Analysis is a multivariate statistical analysis to reduce the data with large number of correlated variables into a substantially.

But it has enough opportunity in rice based cropping system where the farmers remain their land fallow about 80- 90 days between aman and boro rice. If the farmers get extra early (60-80 days) or early (80- 100 days) pea variety they will be able to grow pea in between rice either as sole or relay cropping. The overall effect of plant breeding on genetic diversity has been a long standing concern in the evolutionary biology of crop plants (Simmonds, 1962). Considering the above points it is clear that screening and identification of desired genotypes having major yield and quality attributing traits is an important

activity for the crop improvement programmes related to this crop. The present study is undertaken in order to find out the genetic variability, inter relationships among different characters and the direct and indirect contributions of these characters towards yield and quality traits. To achieve such goals the present investigation "Characterization and Evaluation of Field Pea Genotypes for Yield and Quality Attributing Traits" will be conducted with the following objectives which ultimately the pea growing area will be increased by the utilization of fallow land. Considering the importance of pea crop and the importance of its genetic diversity, the available germplasm was evaluated, to find out the short duration lines with economically important traits for releasing as a variety, to characterized the field pea genotypes as per the DUS guidelines, to estimate the genetic parameters of variability for yield and its attributing traits, to screen out characters based on the direct and indirect effect towards yield, to identify suitable genotypes for yield and quality attributing traits and also their further utilization in the breeding programs.

Materials and Methods

A total of 220 germplasms from exotic and local sources collected earlier were evaluated at PRC Ishurdi. Each entry was planted on 13 November, 2011 in one/ two rows plot of 2 m length with plant spacing of 40 cm x about 5 cm. Data was recorded on quantitative traits from five randomly selected plants where as rust and powdery mildew disease score was recorded from whole plot. Selection emphasis was given on short duration (early/extra early) and disease reaction (Powdery mildew and Rust) to fit them in between Aman and Boro rice (project objective). Some were also selected for their high yield and disease reaction so that they can be grown as relay crop or sole crop. The screening of rust and powdery mildew diseases were done just in natural environment. At maturity best individual lines were selected on the basis of earliness, disease reaction, insect susceptibility (against pod borer) and higher yield. The traits were included Days to flower, Days to maturity, plant height, Pods per plant, Pods per cluster, Cluster per plant, Pod length (cm), Seeds per pod, 100 SW (gm) and Grain yield/plant (gm). The genetic diversity was studied following the

generalized distance (D^2) of Mahalanobis extended by Rao. The accessions were grouped into clusters using canonical variate analysis. The statistical analysis was done using Genstat 5 computer software.

Results and Discussion

The quantitative traits of all the genotypes differed from each other with respect to yield and yield contributing characters. The ward's and the average linkage clustering methods are both hierarchical clustering techniques. Starting with each object as a separate cluster, clusters are fused one at a time at each generation based on a defined "distance" as a measure of similarity between clusters until, at the final generation, only one cluster of all the objectives is obtained. Both result in a tree-like presentation of a stage-wise grouping of the objects referred to as a dendrogram (Sneath and Sokal; Clifford and Stephenson; Marriott and Solomon, 1977). Through multivariate analysis, two hundred and twenty two genotypes were grouped into twelve

clusters based on D^2 values (Table 1). The composition of different clusters varied from 1 to 40 genotypes. Cluster V comprised of 40 genotypes followed by cluster XI, II, IX, IV and VII consisting of 30, 26, 24, 22 and 20 genotypes respectively. There were 15 genotypes in clusters VI, 13 in cluster XII, 11 in cluster X, 9 in cluster I, 8 in cluster VIII while 1 genotype in cluster III.

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 2). Cluster VII exhibited the lowest mean value for days to flower (28) and days to maturity both in fresh pod and seed harvest followed by cluster XII. The highest pod length and hundred seed weight also observed in cluster VIII but the highest yield per plant was recorded in cluster III followed by cluster VI. Cluster III also showed the highest number (6.7) of branch and pods (31.0) per plant whereas cluster I had genotypes with the highest plant height (152 cm) and highest number of seeds per pods.

Table 1. Distribution of 220 genotypes/ lines of pea in different clusters based on quantitative characters

Cluster	No. of genotypes	Name of Genotypes
I	9	244191, 244187, 347471, 331413, 118408, E-15, E-16, , BD-4219
II	26	379505, BD-4163, BD-9039, BD-4164, BD-4174, BD-4141, BD-7217, BD-4138, BD-4194, BD-7207, BD-4179, BD-4142, BD-4139, BD-4193, BD-9042, BD-4156, BD-4186, BD-4151, BD-4192, BD-6945, BD-4173, BD-4180, BD-4191, BD-4191, BD-4146, 210550
III	1	BD-9047
IV	22	BD-4152, BD-4183, BD-4190, BD-4148, BD-4158, 357036, BD-4160, BD-4147, BD-4135, BD-4177, BD-7213, BD-4147, BD-4187, BD-4166, BD-4162, BD-4189, BD-6946, BD-4137, E-1(RYT)
V	40	BD-4149, 210618, 347529, 208846, 274584, 356977, 357017, 347460, 347452, 272181, 194344, 143686, 261672, 269789, E-23, E-9, E-3, 272166, 193581, BD-4496, BD-4228, BD-4161, BD-9052, BD-6944, BD-8881, BFP-07009, BD-9040, BD-9032, BD-4223, BD-9040, BD-4160, BD-7210, BD-9037, BD-9054, BD-4222, BD-4181, BD-9049, BD-4144, BD-9038 and BD-BAGHE
VI	15	BD-4210, 356952, 124478, 269770, 347440, BFP-07007, BD-4218, BD-4232, BD-4143, BD-9032, BD-4220, BD-4212, BD-4209, BD-7209 and 195253
VII	20	BFP-4153, EARLY-97, EARLY-94, EARLY-92, EARLY-98, PEA-99, PEA-86, PEA-88, PEA-98, PEA-92, 34223, 210655, BD-4245, 269820, 244105, ISD-01, 244181, 343223, BD-9056, BD-4223
VIII	8	BD-4495, BD-9059, BD-9035, 349510, 244238, 279827, 244223, E-13
IX	24	244227, BD-7219, BD-7208, 251625, 356949, 376987, 347428, 343293, 294241, 285713, 344088, 347478, 347461, 288022, 183336, 244156, BD-4154, BD-4176, BD-8882, BD-4208, BD-4184, 206842, Early-99 and 206822
X	11	BFP-07002, 384504, 183416, 288030, 24414, 347501, 210615, 206824, 210670, BD-4153 and BD-4195
XI	30	BD-4171, BD-4182, BD-4492, BD-7210, BD-7214, BD-4143, BD-4140, BD-4493, Pabna local, BD-4157, BD-4227, BD-7215, BD-4185, BD-9041, BFP-07006, BD-4182, BFP-07003, ISD-02, 210588, 347516, 316586, 166142, 261632, BD-4150, 210706, BD-9033, BD-4136, BD-9050, BD-9060, BD-4230
XII	13	210592, BD-4494, BD-4165, Narail, BD-7216, BD-7211, BD-4226, BD-9053, BD-9045, 206841, E-7, 250428 and BD-9058

Table 2. Cluster means for yield and yield contributing characters of 220 pea genotypes

Cluster	Days to flower	1 st DPH	2 nd DPH	DSM	Pod leng. (cm)	100 SW (g)	Plant ht. (cm)	Branch/Plant	Pods/Plant	Sees/Pod	Yield/plant (g)
I	60	94	104	114	5.0	12.9	152	2.7	16.4	9.0	5.5
II	55	92	101	112	3.9	6.2	82	3.9	14.2	4.8	3.7
III	70	95	106	114	3.5	4.5	75	6.7	31.0	4.0	14.2
IV	62	95	105	115	4.0	6.1	96	5.4	24.8	5.1	4.1
V	55	91	101	113	4.7	12.2	118	3.4	19.1	4.9	7.2
VI	72	97	107	116	5.5	18.5	108	3.8	17.7	4.4	8.1
VII	28	61	68	81	5.7	21.7	44	0.4	4.1	4.3	5.1
VIII	69	97	108	117	5.9	15.8	25	3.0	11.8	6.9	3.9
IX	70	95	106	116	4.8	8.9	76	3.9	15.8	5.2	3.9
X	57	88	99	111	5.0	15.3	51	2.7	14.3	4.6	5.1
XI	56	88	98	111	4.5	11.0	99	3.4	14.7	4.7	6.2
XII	47	76	86	100	4.6	12.5	95	2.6	10.8	5.0	3.7

N. B. DPH =Days of pod harvest and DSM= Days of seed maturity

Table 3. Different characters of selected 7 extra early and 15 seed purpose pea genotypes from evaluation of existing germplasm at PRC, Ishurdi, Pabna

Entry Name	Days to flower	1 st DPH	2 nd DPH	DSM	Pod Length(cm)	100 Sw (g)	Plant ht. (cm)	Branch / Plant	Pods /Plant	Seeds /Pod	Yield /plant (g)	P	R
Extra early													
244105	24	60	65	85	5.84	18.95	58	1.2	3.6	3.6	5.36	0	1
EARLY-97	24	52	60	70	5.40	19.48	47	1.4	3.0	4.2	7.52	0	1
BD-4223	25	58	66	75	5.90	21.48	25	2.1	4.0	4.0	4.23	0	1
34223	27	54	62	70	6.00	23.12	42	1.5	3.0	4.8	6.32	0	1
EARLY-94	27	52	63	75	6.02	23.70	68	2.4	3.8	5.2	6.54	0	1
PEA-88	27	62	66	77	5.80	24.64	37	1.6	4.2	4.0	6.78	0	1
BD-4245	41	63	70	90	5.80	22.11	40	1.6	5.0	4.8	4.81	3	5
Seed purpose													
250428	42	70	80	95	5.40	17.79	110	2.6	15.2	5.6	8.93	1	1
BD-7216	44	76	83	95	4.20	13.09	83	2.8	10.2	4.2	2.97	1	1
BD-7211	44	76	90	95	4.60	13.67	104	1.2	8.6	5.6	4.05	1	1
BD-9053	44	77	83	98	4.40	11.25	110	2.6	11.6	4.8	3.53	1	1
BD-9045	43	78	83	95	4.20	11.82	87	1.6	6.0	5.2	2.39	3	1
BD-9047	70	95	106	114	3.48	4.54	75	6.7	31.0	4.0	14.2	2	3
BD-4228	50	86	95	110	4.92	18.09	114	3.6	23.6	5.4	13.8	2	5
BD-4209	71	93	107	112	5.38	27.43	119	2.2	9.4	4.6	13.8	1	5
BD-9052	58	93	103	112	4.14	10.66	113	3.6	22.4	5.6	9.82	3	3
BD-9041	57	88	95	113	5.04	14.68	100	2.8	8.8	4.2	8.23	3	3
BD-4222	56	88	95	113	5.12	12.62	118	2.6	13.8	6.8	9.79	2	5
BD-4493	58	89	97	113	4.30	18.10	105	2.0	10.4	4.2	10.7	3	3
210618	54	83	96	113	4.34	12.20	121	3.8	24.0	4.8	12.9	2	3
244227	70	89	96	112	4.70	16.20	79	2.3	11.3	5.2	14.8	4	3
347516	57	83	94	110	4.74	12.39	96	3.2	17.1	4.2	11.7	3	5

N. B. DPH =Days of pod harvest and DSM= Days of seed maturity, P =Powdery mildew disease score (0-5 scale) and R=Rust disease (1-9 scale)

A total of 22 genotypes were selected based on different characters (Table-3). Seven early maturing lines viz. 244105, EARLY-97, BD-4223, 34223, EARLY-94, PEA-88 and BD-4245 were

selected whose pods can be harvested completely within 70 days and these can be fitted in between two rice as a sole crop. All the lines showed resistance against rust and powdery mildew

(may escape the diseases due to earliness) except BD4245 and are short in height (25-68 cm). These also have long pods (5.4-6.0 cm) with bold seeds (19.5- 24.6 g) and these are also good criteria for higher price.

Another 15 lines were selected for seed purpose. These got maturity within 95-114 days, intensive branching, podding and obtain higher yield per plant. These lines can be grown in between aman and T-aus rice for vegetable or seed purpose as relay or sole crop. All of these lines will be tested on station under replicated trials next year to select the desired genotype(s). The selected lines may also be used in our breeding programme for the development of high yielding variety.

Conclusion

There are 7 genotypes 244105, EARLY-97, BD-4223, 34223, EARLY-94, PEA-88 and BD-4245 were selected for extra early and 15 genotypes 250428, BD-7216, BD-7211, BD-9053, BD-9045, BD-9047, BD-4228, BD-4209, BD-9052, BD-9041, BD-4222, BD-4493, 210618, 347516 and 244227 were selected for seed purpose pea genotypes for next multiplication trial to find out the desired lines of pea as per utilized in crop improvement program

References

- Apte UB, Chavan SA and Jadhav BB. 1987. Genetic variability and heritability in cowpea. *Indian Journal of Agricultural Sciences*, 57: 596 - 598.
- Backiyarani S and Nadarajan N. 1996. Variability studies in Cowpea. *Legume Research*, 19: 59 - 61.
- Ehlers JD and Hall AE. 1997. Cowpea (*Vigna unguiculata* L. Walp.) *Field Crops research*, 53: 187- 204.
- Holden JHW and Williams eds JT. 1984. *Crop Genetic Resources: conservation and evaluation*. George Allen and unwin, Ltd.
- Kahraman A and Onder M. 2009. Genetic Diversity in the Dwarf Dry Bean (*Phaseolus vulgaris* L.) Populations Grown in Konya. 1st International Symposium on Sustainable Development, Sarajevo-Bosnia 3: 13-19.
- Selvam YA, Manivannan N, Murugan S, Thangavelu P and Ganeshan J. 2000. Variability studies in cowpea (*Vigna unguiculata*(L.) alp.). *Legume Research*, 23: 279-280.
- Simmonds N. 1962. Variability in crop plants, its use and conservation. *Biol. Rev.* 26: 422- 462.
- Selvi B, Rangaswamy P, Nadrajan N, Ramalingam J and Vannirajan C. 1994. Genetic variability in cowpea. *Annals of Agricultural Research*, 15: 248-249.
- Solomon H. 1977. Data-dependent Clustering Techniques, in classification and clustering, ed. J.V. Ryzin. New York: Academic Press.
- Tey David C, Yung-kuang Huang S and Yuh-ling Chen. 1989. Germplasm Catalog of Mungbean(*Vigna radiata* (L.) Wilczek) and other vigna species, AVRDC, Taipei.
- Wikes G. 1983. Current status of crop plant germplasm. *CRC Crit. Rev. Plant Science* 1:133- 181.