Legume Research, 40 (2) 2017 : 215-223
Print ISSN:0250-5371 / Online ISSN:0976-0571

AGRICULTURAL RESEARCH COMMUNICATION CENTRE
www.arccjournals.com/www.legumeresearch.in

Evaluation of morphological diversity of field pea [*Pisum sativum* subsp. *arvense* (L.)] germplasm under sub-tropical climate of Manipur

S. Bhuvaneswari*[1], Susheel Kumar Sharma[1], P. Punitha[1], K.S. Shashidhar[2], K.L. Naveenkumar[3] and Narendra Prakash[1]

ICAR-Research Complex for NEH region,
Manipur Centre, Imphal-795 004, India.

Received: 24-11-2015 Accepted: 14-03-2016 DOI:10.18805/lr.v0iOF.10756

ABSTRACT

An investigation was carried out to evaluate 51 diverse field pea genotypes at Langol Research farm, ICAR, RC, NEH Region, Manipur Centre for nine yield related quantitative traits and four morphological qualitative traits for practical field pea improvement in Manipur. The combined analysis of variance of genotypes for all the nine traits was found to be significant. The amount of variability in one variable as a linear function of another variable was also measured through phenotypic and genotypic correlation among nine quantitative traits. The pod number per plant, seed number per pod and 100 seed weight showed significant positive correlation with seed yield per plant both at phenotypic and genotypic levels. Multivariate analysis using principal component analysis (PCA) indicated that three principal components (PCs) accounted for > 75% of the total variation. The genotypes were grouped into seven clusters using distance based Agglomerative "Average linkage" method. Three genotypes IPF-5-19, EC-8495, HUDP-15 belonging to cluster II and DDR-30, early maturing variety belonging to Cluster VI were found promising in terms of seed yield for the region.

Key words: Agglomerative clustering, Combined ANOVA, Correlation, Field pea, PCA.

INTRODUCTION

Field pea is an important annual, cool-season pulse crop and dry pea seeds contain high levels of the essential amino acids like lysine and tryptophan, which are deficit in cereal grains (Ana Paula Rodino *et al.,* 2009). Being an important protein source, there is increase in demand for this pulse crop both for animal feed as well as for human consumption (Santalla *et al.,* 2001). In Manipur, a north eastern hill state of India, field pea is the major pulse crop grown in 26,000 ha area occupying about 85% of the total pulses area (Anonymous, 2015). There is huge deficit in production of pulses in Manipur state as against the requirement mainly due to lack of improved varieties with tolerance to acidity of soil, a characteristic feature of the soils of North East, in general. Also, the crop is mainly grown in marginal and sub marginal lands with residual moisture of soil during winter mostly under rice fallow condition. Due to high humidity of region, diseases like powdery mildew (*Erysiphe pisi*) and rust (*Uromyces fabae*) are the major yield limiting factors .

There are a number of high yielding varieties of field pea developed at the national level through coordinated research programme at ICAR-Indian Institute of Pulse Research, Kanpur for varied agro ecological regions of India. Under sub-tropical climate of Manipur, located between 92°58'E and 94°45'E longitude and 23°50'N and 25°42'N Latitudes (Economic Survey, 2013-14), it is imperative to evaluate these released varieties for their adaptability in the region in order to replace the old recommended varieties and also, quantifying the genetic variance at the target environment for practical crop improvement. The existence of genetic variability forms the basis of genetic improvement of a specific trait (Gatti *et al,* 2011).The present investigation was therefore undertaken for practical utility of field pea genotypes under Manipur conditions and the results discussed.

MATERIALS AND METHODS

The material used in the present study consisted of fifty one diverse field pea genotypes including released varieties, Exotic collections received from ICAR-Indian Institute of Pulses Research, Kanpur and two local genotypes of Manipur. The genotypes were evaluated for two consecutive years during winter 2013 and 2014 at ICAR RC NEH region, Manipur at Langol research farm on terraced land under protective irrigation in randomized complete block design replicated twice. Each genotype was planted in 3 rows of 2 meters length per replication with spacing of 30 cm between rows and 15 cm between plants. The recommended package of practices were adopted.

Observations were recorded on important quantitative traits like days to fifty percent flowering (DFF), days to first flower bud (FBN), days to 80% pod maturity (DTM) on population basis and plant height (cm), pod length

---

*Corresponding author's e-mail: bhuvana0284@gmail.com. ICAR-Research Complex for NEH region, Manipur Centre, Imphal-795 004, India. [2]Central Agricultural University, Imphal-795 004, India. [3]College of Post Graduate Studies, CAU, Umiam -793 103., India.

at maturity (cm), number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g) on five randomly selected plants per replication for both years. Also, morphological distinguishing qualitative traits like leaf type, flower color, seed coat color and nature of seed surface were recorded on population basis. The observations were recorded as per the DUS guidelines of peas (AICRP MULLaRP).

Combined analysis of variance over two years (2013 and 2014) for quantitative traits was carried out after homogeneity of error variance was established through F-test as per procedure given by Gomez and Gomez (2010). The association between evaluated quantitative traits was quantified through genotypic and phenotypic linear correlation analysis using freeware Plant Breeding Tools (PB Tools) version 1.4 developed by IRRI, Philippines. Further, principal component analysis (PCA) and cluster analysis were carried out using freeware Statistical Tool for Agricultural Research (STAR) Version 2.0.1 by IRRI, Philippines. Agglomerative "Average linkage" method with the highest cophenetic correlation coefficient value 0.791 was chosen for clustering among other methods (Mohammadi and Prasanna, 2003).

RESULTS AND DISCUSSION

The combined analysis of variance (Table 1) depicted significant variance due to genotype for all the quantitative traits (P<0.01) except seed yield per plant being significant at P <0.05. This indicated the presence of sufficient genetic variability for the traits in order to select diverse parental lines for effective breeding programmes. Also, the genotypes showed significant interaction with years depicting varying performance across years with respect to all traits except seeds per pod. However, magnitude of genotypic variance in terms of F-value calculated was higher compared to G×E interaction for temporal traits, DFF and FBN. This indicated that performance of the genotypes remained stable across years with respect to DFF, FBN, and seeds per pod.

Mean comparison of genotypes for nine quantitative traits along with important qualitative traits is presented in Table 2. The simple measure of variations as measured by range for each trait depicted presence of wide variability in the evaluated traits. The available variability was large enough to undertake selection of diverse parents for improvement of traits in desired direction. On an average there was one week difference between days to first flower bud and days to fifty per cent flowering across genotypes. In terms of plant architecture, about 59 % of the genotypes were dwarf with plant height < 60 cm. The average number of pods per plant and other yield related traits were less as the genotypes were evaluated under moisture stress condition with life saving irrigation on slightly acidic soils, a representative soil of the region. These reiterate the importance of evaluating germplasm in the target environment for improvement of trait of interest. DDR 27, DDR-30, VRP-6 and VRP-7 were found to be early maturing in less than 110 days. For higher seed yield/plant(> 2.7 g), commercially released varieties, DDR-16, DDR 27, DMR 15,DMR 37,HUDP 15,IPF 5-19, TRCP-8 and germplasm lines, DDR 30, EC 209228,EC 8495, ET 5117 were also found to be promising. These were all leafy type except, HUDP -15 and IPF 5-29. However, Singh and Srivastava (2015) reported semileafless plant type to be significantly high yielding compared to normal foliaged types owing to their lodging resistance and better partitioning of photosynthates. Majority of the genotypes possessed white flowers and cream or green colour testa. Three genotypes *viz*., local *Makuchabi Ningtekpi*, P-1089 and P- 1459 with pink flower color produced non-cream colored seeds. Also, the local genotype *Makhyatmubi* seeds were cream colored with black funicle which was very distinguishable from other cream seeded genotypes.

The degree and nature of association between two metric traits in a population can be understood through measurement of amount of variability in one variable as a linear function of another variable (Gomez and Gomez, 2010). This further helps in bringing improvement of one trait through selection of another. Thus, simple linear correlation analysis will help in selecting yield attributing traits. The phenotypic and genotypic correlation coefficient

Table 1 : Combined Analysis of Variance of fieldpea genotypes

Source	df	DFF	FBN	PH	PL	PP	SP	DTM	100 SW	SYP
Year	1	772.59	796.12	22002.28	53.70	190.14	55.48	13556.71	9.46	206.49
Repl within Year	2	18.30	33.40	103.47	1.42	2.28	1.51	49.14	11.93	5.48
Variety	50	207.80** (10.01)	211.03** (1.59)	1396.10** (4.15)	1.22** (1.96)	5.44** (1.99)	1.87** (2.33)	108.21** (2.10)	25.80** (4.30)	2.14* (1.78)
Year*Variety	50	20.74** (4.52)	24.28** (1.47)	335.62** (5.26)	0.62** (2.37)	2.72** (4.83)	0.80^{NS} (1.29)	51.39** (17.29)	5.99** (8.42)	1.20** (7.86)
Pooled Error	100	4.59	5.80	63.81	0.26	0.56	0.62	2.97	0.71	0.15

Values in paranthesis correspond to calculated F-values

*Significant at 5% probability level ** significant at 1% probability level

DFF: Days to 50% flowering
DFB: Days to First flower
PH: plant height (cm)
PL: Pod length (cm)
PP: Pods per plant
SP: Seeds per pod
DTM: days to maturity
100 SW: 100 seed weight (g)
SYP: Seed yield per plant (g)

Table 2: Mean comparison for quantitative and morphological qualitative traits among 51 Fieldpea genotypes

Genotype	DFF	FBN	PH	PL	PP	SP	DTM	100SW	SYP	FC	SCC	Seed surface	Leaf type
Azad P-2	86	78	75	5.78	3	4	116	16.70	1.65	White	cream	wrinkled	Leafy
Azad P-4	87	80	51.90	5.70	4	3	116	18.13	1.71	white	cream	wrinkled	Leafy
DDR 16	84	78	49.55	5.49	6	4	115	17.75	3.11	white	cream	smooth	Leafy
DDR 17	80	72	50.50	6.62	4	4	116	18.38	2.32	White	cream	smooth	Leafy
DDR 27	62	54	35.10	5.51	3	4	106	21.12	3.01	white	green	smooth	Leafy
DDR 30	65	58	37.10	7.05	3	5	105	27.32	3.25	white	cream	smooth	Leafy
DDR 7	79	74	89.85	5.93	6	4	112	17.87	2.58	White	cream	smooth	Leafy
DMR 11	80	72	78.70	5.64	3	5	114	15.53	1.86	white	cream	smooth	Leafy
DMR 15	85	76	46.20	6.12	5	4	114	19.36	3.35	white	cream	smooth	Leafy
DMR 34	88	80	72.70	5.30	4	3	112	18.14	2.08	White	cream	smooth	Leafy
DMR 37	85	76	77.05	5.76	5	4	113	20.12	3.68	white	cream	smooth	Leafy
EC 507770	77	74	76.45	5.46	4	4	114	19.94	2.49	white	green	smooth	Leafy
EC-209228	85	78	59.90	5.50	6	4	121	17.97	3.06	White	cream	smooth	Leafy
EC-499761	84	75	49.55	6.10	3	5	118	20.56	2.58	white	green	smooth	Leafy
EC-499762	85	77	51.15	4.73	4	3	121	17.18	2.36	white	green	smooth	Leafy
EC-538004	81	69	59.45	4.74	3	4	110	11.07	0.64	White	cream	smooth	Semileafless
EC-564802	81	74	45.00	6.18	2	5	115	17.21	1.64	white	cream	smooth	Leafy
EC-8495	88	80	88.25	6.16	6	6	118	20.07	3.21	white	cream	smooth	Leafy
ET-5117	82	73	81.10	5.63	4	5	119	20.18	3.20	White	cream	smooth	Leafy
HFP 4	96	89	31.55	5.55	3	4	126	17.16	1.56	white	cream	smooth	Semileafless
HFP 8712	92	84	34.75	5.65	3	5	124	20.49	2.10	white	cream	wrinkled	Semileafless
HFP 8909	91	84	30.35	5.31	2	4	123	18.75	2.16	White	cream	smooth	Semileafless
HFP 9426	88	80	46.40	5.12	1	3	116	14.04	1.06	white	green	smooth	Leafy
HUDP 15	90	84	46.03	5.80	5	5	118	15.03	3.18	white	green	smooth	Semileafless
HUDP 16	97	90	51.15	5.60	2	4	126	17.39	1.19	White	cream	wrinkled	Semileafless
HUDP 8	85	77	38.80	5.91	2	4	117	16.12	1.38	white	cream	smooth	Leafy
HUDP6	85	77	38.85	6.32	2	5	117	18.88	2.03	white	cream	wrinkled	Semileafless
IM-9102	86	75	61.45	5.46	3	4	119	17.78	2.58	White	cream	smooth	Leafy
IPF-5-19	91	83	80.60	5.76	5	6	118	16.56	3.55	white	Green	smooth	Semileafless
IPF-99-25	87	78	93.65	5.49	5	4	118	17.65	2.63	white	Cream	smooth	Leafy
IPFD-1-10	86	79	44.35	6.17	3	5	117	18.39	2.78	White	Green	smooth	Leafy
IPFD-6-3	91	84	51.40	5.81	3	4	122	18.87	2.45	white	Green	smooth	Semileafless
JP-868	82	73	86.35	5.63	4	4	120	20.21	2.64	white	Green	smooth	Leafy
KFP 103	85	74	79.45	5.41	4	4	116	18.48	2.03	White	Cream	smooth	Leafy
KPMR -11-1	88	80	75.70	5.72	3	3	120	21.01	1.82	white	Cream	smooth	Semileafless
KPMR 144-1	98	84	37.60	5.73	4	5	124	16.88	2.30	white	Cream	smooth	Leafy
KPMR 516	97	93	45.30	5.59	3	6	127	18.58	2.39	White	Cream	smooth	Semileafless
KPMR-385	90	84	41.25	6.10	4	4	125	19.92	2.45	white	Cream	smooth	Semileafless
Makhyatmubi	82	75	82.55	6.03	3	4	120	19.03	1.62	white	Cream (black funiculus)	smooth	Leafy
Makuchabi Ningtekpi	82	74	68.85	4.97	2	4	109	15.19	1.29	pink	Dark brown	smooth	Leafy

Table 2 continue.........

Table 2 continue......

P-1089	89	77	57.55	4.49	3	4	115	12.29	1.18	pink	Green	smooth	Leafy
P-1459	83	75	65.90	5.57	2	4	112	14.02	1.27	pink	Green(mottled)	wrinkled	Leafy
P-489	88	82	78.40	5.50	3	4	121	19.02	1.99	white	cream	smooth	Leafy
P-725	77	69	62.90	4.38	3	3	113	16.62	1.51	white	cream	smooth	Leafy
Pant P 14	82	73	41.20	6.65	2	5	119	17.12	2.06	white	cream	wrinkled	Leafy
Pant P 25	82	74	33.45	5.47	2	5	118	18.02	2.37	white	cream	wrinkled	Leafy
Rachna	87	79	34.38	5.70	3	5	111	15.29	1.48	white	cream	smooth	Leafy
TRCP-8	77	71	81.65	5.32	5	4	115	19.47	2.93	white	Cream	smooth	Leafy
VL-45	83	74	65.80	5.73	3	4	110	15.53	1.92	white	cream	smooth	Leafy
VRP-6	63	56	34.25	6.42	2	5	108	16.66	1.43	white	Green	wrinkled	Leafy
VRP-7	84	76	37.25	7.27	2	6	108	15.52	1.08	white	Green	wrinkled	Leafy
Range	62-97	54-90	30.4-86.4	4.4-7.3	1-6	3-6	105-127	11.07-27.32	0.64-3.68				
Mean ± SE	84.29	76.44	57.52	5.70	3.37	4.35	116	17.85	2.20-1.14				
	+2.98	+3.14	+ 13.79	+ 0.64	+ 1.26	+0.68	+ 8.88	+ 1.23					
LSD (5%)	3.0	3.4	11.2	0.7	1.1	1.1	2.4	1.2	0.5				

Table 3: Phenotypic (above) and Genotypic (below) Correlation coefficients between different quantitative traits in fieldpea

Days to first flower	Plant height	Pod Length	Pods/Plant	Seeds/Pod	Days to Maturity	100SeedWeight	Seed Yield/Plant	Days to50%Flowering
	0.97**	-0.03	-0.20	0.02	0.00	0.76**	-0.25	-0.09
	1.00**	-0.07	-0.28*	-0.05	0.03	1.00**	-0.24	-0.15
Days to first flower		-0.03	-0.15	0.03	0.03	0.78**	-0.18	-0.05
		- 0.01	-0.21	-0.07	0.08	1.00 **	-0.16	-0.14
Plant height			-0.25	0.49**	-0.22	-0.06	0.03	0.19
			-0.69**	0.39 **	-0.51**	-0.31*	0.03	-0.04
Pod length				-0.04	0.46**	-0.13	0.42**	0.21
				-0.49**	0.29*	-0.42**	0.73**	0.06
Pods/plant					0.05	0.06	0.28*	0.76**
					-0.14	-0.23	0.48**	0.74 **
Seeds/pod						-0.04	0.06	0.32*
						-0.18	0.13	0.41**
Days to Maturity							0.11	0.10
							0.28*	-0.06
100Seed Weight								0.62**
								1.00**

between nine quantitative traits is presented in Table 3. In general, the genotypic correlation coefficient was higher than the phenotypic value indicating strong inherent association between traits under study (Chaudhary and Sharma, 2003; Necat *et al.,* 2008; Espósito *et al.*, 2009, Ghobary, 2010 and Gatti *et al.,* 2011).

Among temporal traits *viz*., days to fifty per cent flowering (DFF), days to first flower bud (FBN) and days to 80% pod maturity (DTM) showed positive and significant ($P<0.01$) correlation at both phenotypic and genotypic levels. Genotypic Association of DFF and DTM with pod length and plant height was significant and negative ($P<0.05$). Similar result reported for days to flowering with pod length by Javaid *et al.,*(2002). Plant height, an important plant architecture indicative trait was strongly associated with number of pods per plant in the positive direction. The linear association of temporal traits and Plant height with seed yield per plant was negative but non-significant indicating presence of nonlinear relationship. The results obtained agree with reports of Joshi *et al.,* (1992); Kumar et *al.,* (2003) and Sardana *et al.,* (2007). Correlation of pod length with number of seeds per pod and 100 seed weight was positive and significant ($P< 0.01$) at both genotypic and phenotypic levels suggesting longer pods contain more number of seeds and also, bolder seeds. The number of pods per plant, number of seeds per pod and 100 seed weight showed significant positive correlation($P<0.01$) with seed yield per plant both at phenotypic and genotypic levels. This suggested that these three traits can be advantageously used as a selection criterion to improve yield. Singh and Srivastava (2015) also reported significant correlation between 100 seed weight and seed yield per plant among tall as well as dwarf pea genotypes.

The pattern of variations among genotypes was studied by Multivariate analysis using Principal component analysis (PCA) by considering all nine quantitative traits simultaneously (Table 4). Principal component analysis helps to reduce the number of traits analyzed for characterizing the genotypes to be used as parents based on strength of contribution to principal component (Gatti *et al.,* 2011). The optimal number of principal components (PCs) that explain the maximum amount of original data variation was determined by considering PCs with Eigen value > 1.0 (Jeffers,1967 and Lezzoni and Pritts, 1991). In the present investigation, first three PCs showed Eigen value >1.0 and accounted for > 75% of the total variation observed. The first principal component which accounted for 31 % of total variation was positively influenced by temporal traits such as DFF, FBN and DTM. The second PC which contributed to 25.9 % of total variation was influenced negatively by all the nine traits with larger influence by yield traits such as number of pods per plant, 100 seed weight and seed yield per plant. Third principal component accounted for 19.2 % of total variation, was positively influenced by pod length and seeds per pod and almost equally negatively influenced by plant height and pods per plant. The characters influencing each of above three principal components are significantly correlated with each other as observed in Table 3 of correlation matrix. The Scatter plot of Individual genotypes drawn with important Principal components gives a 2- or 3-dimensional view so as to understand the genetic relatedness of genotypes since geometrical distances reveals genetic distances (Mohammadi and Prasanna, 2003). Thus, in the present study, Scatter plot of PC1 and PC2 (Figure 2), clearly revealed the outlayers VRP-6, DDR 27,DDR 30 from other genotypes horizontally with maximum distance from HUDP 16, HFP 4 and KPMR 516 mainly due to large difference in flowering and maturity duration, traits which influenced PC1. On vertical axis,EC 8495, IPF 5-19, DMR 37 were placed with maximum distance from EC 538004, HFP 9426 due to difference in seed yield correlated traits influencing PC2.

Further the pattern of genetic diversity was studied using cluster analysis based on similarity index by "Average linkage" method. The 51 genotypes were grouped into seven clusters (Figure 1 and Table 5) with members within cluster

Table 4: Principal component analysis of nine Quantitative traits of Fieldpea

Statistics	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Standard deviation	1.675	1.528	1.315	0.948	0.755	0.596	0.428	0.298	0.165
Proportion of Variance	0.311	0.259	0.192	0.100	0.063	0.039	0.020	0.009	0.003
Cumulative Proportion	0.311	0.571	0.764	0.864	0.927	0.966	0.987	0.997	1.000
Eigen Values	2.805	2.337	1.731	0.899	0.570	0.355	0.183	0.089	0.027
Eigen vectors									
Days to 50% flowering	0.558	-0.163	0.073	-0.089	0.089	-0.149	-0.349	-0.066	-0.701
First blossom node	0.547	-0.196	0.102	-0.057	0.122	-0.099	-0.350	0.046	0.705
Plant height	-0.041	-0.197	-0.568	-0.217	0.673	0.347	0.024	-0.120	-0.006
Pod length	-0.236	-0.162	0.531	0.027	0.602	-0.464	0.189	-0.143	-0.003
Pods per plant	-0.098	-0.505	-0.338	-0.223	-0.173	-0.487	0.172	0.521	-0.020
Seeds per pod	-0.101	-0.197	0.483	-0.656	-0.069	0.472	0.003	0.238	-0.034
Days to Maturity	0.464	-0.275	0.107	0.285	-0.031	0.260	0.739	-0.000	-0.019
100 Seed weight	-0.242	-0.405	0.137	0.614	0.093	0.320	-0.365	0.361	-0.070
Seed yield per plant	-0.192	-0.578	-0.027	-0.035	-0.341	0.004	-0.091	-0.706	0.050

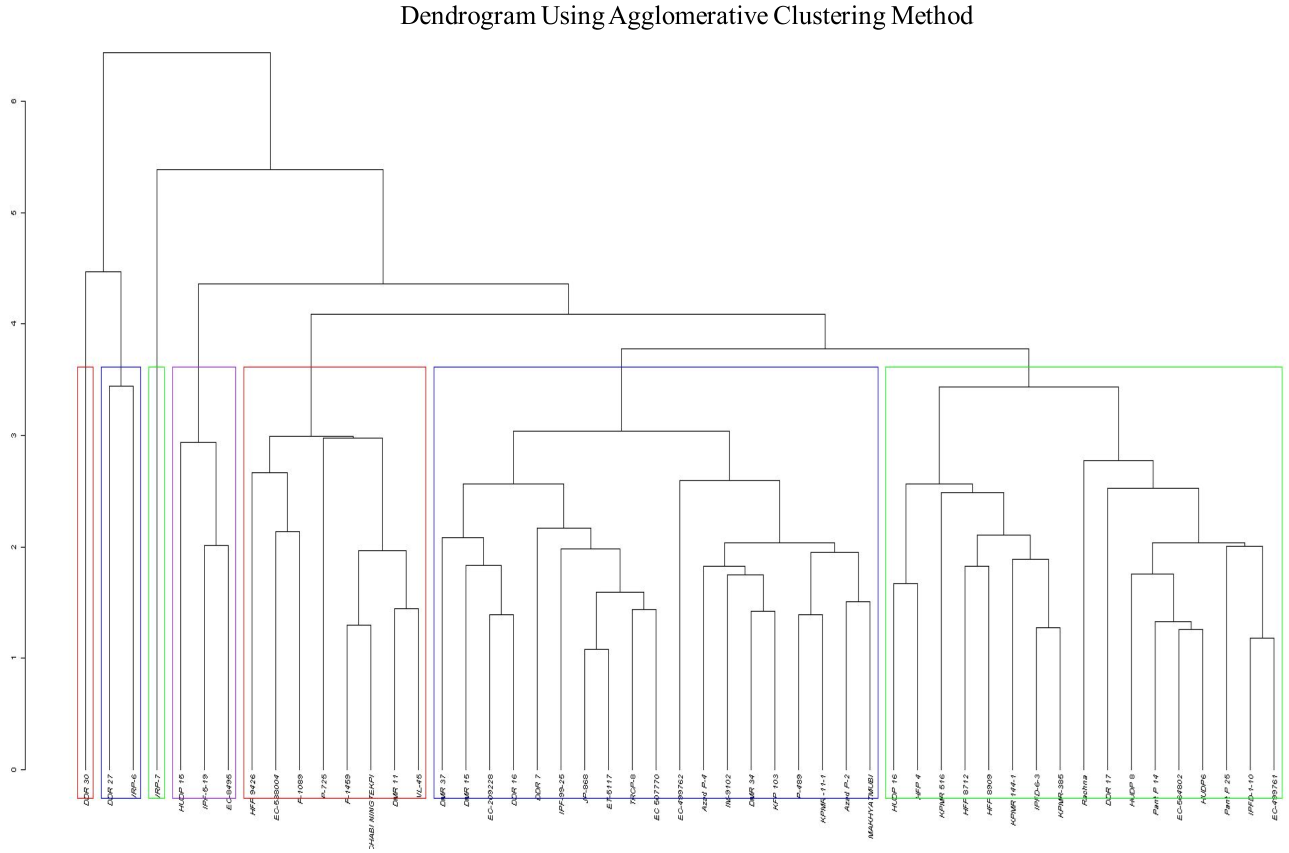

Fig 1: Clustering Pattern of 51 diverse field pea genotypes using Agglomerative Average Linkage method.

Table 5: Clustering Pattern of Fieldpea genotypes evaluated

Cluster Number	Number of Genotypes	Genotypes
I	19	TRCP-8 JP-868 IM-9102 IPF-99-25 ET-5117 EC-209228 EC-499762 EC 507770 DDR 16 DDR 7 DMR 15 DMR 34 DMR 37 P-489 KFP 103 KPMR -11-1 Azad P-4 Azad P-2 MAKHYATMUBI
II	3	IPF-5-19 EC-8495 HUDP 15
III	17	IPFD-1-10 IPFD-6-3 EC-499761 EC-564802 DDR 17 HFP 8712 HUDP6 HUDP 16 HUDP 8 HFP 8909 HFP 4 Pant P 14 Pant P 25 KPMR 144-1 KPMR 516 KPMR-385 Rachna
IV	8	EC-538004 DMR 11 HFP 9426 P-1459 P-725 P-1089 VL-45 MAKUCHABI NINGTEKPI
V	2	DDR 27 VRP-6
VI	1	DDR 30
VII	1	VRP-7

being more closely related than with members of different cluster. The number of genotypes among clusters varied from 1 to 19. The maximum numbers of genotypes were included in cluster I and there was only one genotype in Cluster VI and VII. The two local genotypes *Makhyatmubi* and *Makuchabi Ningtekpi* were included in separate clusters I and IV respectively, indicating wide divergence within local landraces. Cluster II included most promising varieties for the region HUDP-15, IPF-5-19 along with germplasm line EC-8495 which were relatively late maturing but produced highest number of pods per plant, highest seeds per pod and highest seed yield per plant (Table 6). A special trial coordinated by IIPR, Kanpur in North East Hill region (Anonymous 2015), also reiterated HUDP -15 and IPF 5-19 as promising varieties in Manipur. Cluster IV included low performing genotypes with lowest pod length (5.08 cm), lowest 100 seed weight (14.28 g) and low mean value of seed yield/plant (1.34g). Among early maturing genotypes, DDR 30 (Cluster VI) was found promising with larger pod length, highest 100 seed weight and high seed yield per plant.

Table 6: Descriptive statistics within seven clusters for different traits

Characters	Descriptive statistics	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
DFF	Min	77.00(TRCP8)	87.50(EC 8495)	79.75(DDR 17)	77.25(P 725)	61.75(DDR 27)	65.25	83.50
	Max	88.25(DMR 34/KPMR- 11- 1)	90.50(IPF 5 19)	97.50(KPMR 144 1)	89.25(P 1089)	62.50(VRP 6)	-	-
	Mean	83.96	89.33	88.29	82.69	62.12		
	SD	3.46	1.61	5.91	3.96	0.53		
FBN	Min	70.75(TRCP 8)	79.75(EC 8495)	71.75(DDR 17)	69.00(P 725)	54(DDR 27)	57.50	76.25
	Max	81.75(P-489)	83.50(HUDP 15)	92.50(KPMR 516)	79.50(HFP 9426)	56(VRP 6)	-	-
	Mean	76.33	82.00	80.57	73.56	55		
	SD	2.95	1.98	6.39	3.58	1.41		
PH	Min	46.20(DMR 15)	46.02(HUDP 15)	30.35(HFP 8909)	46.40(HFP 9426)	34.25(VRP 6)	37.10	37.25
	Max	93.65(IPF 99 25)	88.25(EC 8495)	51.40(IPFD 6 3)	78.70(DMR 11)	35.10(DDR 27)	-	-
	Mean	72.11	71.62	41.14	63.19	34.67		
	SD	14.36	22.50	7.00	9.37	0.60		
PL	Min	4.73(EC 499762)	5.75 (IPF 5 19)	5.31(HFP 8909)	4.38(P 725)	5.51(DDR 27)	7.05	7.27
	Max	6.12(DMR 15)	6.16(EC 8495)	6.64(PANT P 14)	5.72(DMR 11)	6.42(VRP 6)	-	-
	Mean	5.58	5.90	5.91	5.08	5.96		
	SD	0.31	0.22	0.39	0.53	0.64		
PP	Min	2.65(Makhaymubi/Azad P 2)	4.70(IPF 5 19)	1.65(HUDP 8)	1.45(HFP 9426)	2.05(VRP 6)	3.10	1.65
	Max	5.70(DDR 16/DDR7)	5.55(EC 8495)	4.25(DDR17/KPMR 144-1)	3.3(DMR 11)	3.10(DDR 27)		
	Mean	4.18	5.02	2.76	2.58	2.58		
	SD	1.00	0.46	0.77	0.68	0.74		
SP	Min	2.93(KPMR 11-1)	5.15(HUDP 15)	3.79(HUDP 16)	3.05(HFP 9426)	4.45	4.70	5.65
	Max	4.55(ET 5117)	6.20(IPF 5 19)	5.50(KPMR 516)	4.85(DMR 11)	4.48	-	-
	Mean	3.92	5.72	4.63	3.97	4.64		
	SD	0.44	0.53	0.46	0.56	0.27		
DTM	Min	112 (DDR 7/DDR 34)	118	110.75(RACHNA)	109.00(MAKUCHABI)	105.50(DDR 27)	105.00	107.75
	Max	120.50(EC 209228/EC 499762/P 489)	118	127.25(KPMR 516)	115.50(HFP 9426)	107.75(VRP 6)	-	-
	Mean	116.78	118	120.18	112.16	106.62		
	SD	2.99	-	4.69	2.52	1.59		
100SW	Min	16.70(Azad P 2)	15.03(HUDP 15)	15.29(Rachna)	11.07(EC 538004)	16.66(VRP 6)	27.32	15.52
	Max	21.01(KPMR 11-1)	20.07(EC 8495)	20.56(EC 499761)	16.61(P 725)	21.11(DDR 27)		
	Mean	18.74	17.22	18.12	14.28	18.88		
	SD	1.19	2.58	1.45	1.84	3.15		
SYP	Min	1.62(Makhyatmubi)	3.18(HUDP 15)	1.19(HUDP 16)	0.64(EC 538004)	1.43(VRP 6)	3.25	1.08
	Max	3.68(DMR 37)	3.55(IPF 5 19)	2.78(IPFD 1 10)	1.92(VL 45)	3.01(DDR 27)	-	-
	Mean	2.50	3.31	2.07	1.34			
	SD	0.61	0.20	0.46	0.42	2.22		
						1.12		

COPHENETIC CORRELATION **COEFFICIENT = 0.791**

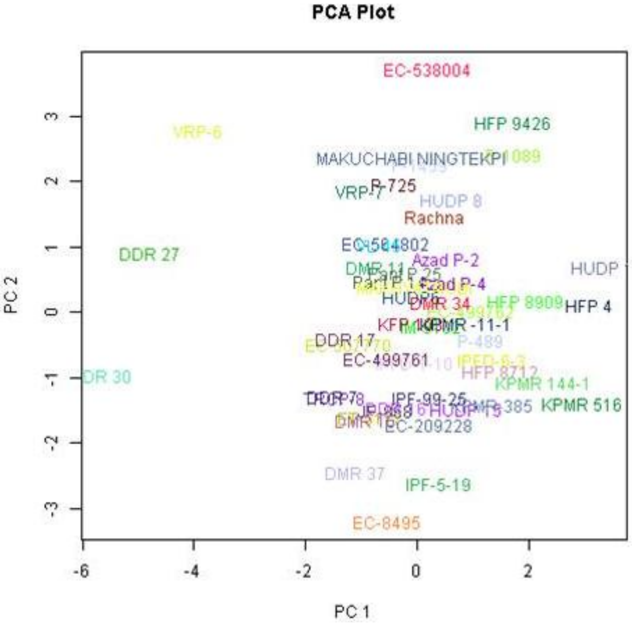

Fig 2: Scatter plot of PC1 vs PC2

As the irrigation facility during *rabi* is poor in the state, short duration genotypes with higher yield potential is very much needed which can make best use of residual moisture.

The genetic variability present in different cluster groups for yield related traits can be effectively exploited by hybridization and selection. Results of the diversity analysis revealed that members of Cluster II (HUDP-15, IPF-5-19, EC-8495) and Cluster VI (DDR-30) with higher seed yield per plant may be included as one of the parents for hybridization with local land races, *Makhyatmubi* (Cluster I), *Makuchabi Ningtekpi* (Cluster IV) for future field pea improvement in the region. The hybridization programme thus would include diverse and unique parents combination which may help to broaden the genetic base of the varieties to be developed.

Also, the genotypes showing higher seed yield per plant (HUDP-15, IPF-5-19, EC-8495) may be recommended for general cultivation on further evaluation under yield trials to replace the older varieties like 'Rachna' in the region. As the region experiences huge water shortage during winter accompanied by late planting in rice-pea cropping pattern, early maturing genotypes DDR-30, DDR-27 may be promoted to reap better yield.

ACKNOWLEDGEMENT

The work was carried out as part of institute project (IXX11470). We are grateful to Director, ICAR-RC-NEH region, Barapani, for providing necessary support for carrying out the work. We would like to acknowledge ICAR-Indian Institute of Pulses Research, Kanpur for sharing Field pea germplasm seeds. Authors would like to thank Dr. Diwakar Sastry, Professor (GPB), RARI,Jaipur for critical review of the manuscript and also anonymous reviewer/s for improvement of the article.

REFERENCES

AICRP MULLaRP-http://www.aicrpmullarp.res.in.

Ana Paula Rodino, Josefina Herna´ndez-Nistal, Maria Hermida , Marta Santalla and Antonio M. De Ron.(2009).Sources of variation for sustainable field pea breeding. *Euphytica*. **166**: 95-107

Anonymous. (2015). Annual Report(2014-15) on Promotion of Pulses in NEH region. ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh 208024 (India).39 pp.

Chaudhary, D. K. and Sharma, R. R.(2003). Genetic variability, correlation and path analysis for green pod yield and its components in garden pea. *Indian J. Hort.* **60:** 251-256.

Economic Survey Manipur. (2013-14). Directorate of Economics and Statistics, Government of Manipur, Imphal.

Espósito, M.A., Martin, E.A., Cravero, V.P. and Liberatti, D. (2009). Relationships among agronomic traits and seed yield in pea. *BAG* 20: 01-08

Gatti, I., Espósito, M.A., Almirón, P., Cravero, V.P and E.L. (2011).Diversity of pea (*Pisum sativum*) accessions based on morphological data for sustainable field pea breeding in Argentina.Genetics and Mol Resch **10:** 3403-3410.

Ghobary, H. M. M. (2010). Study of relationship between yield and some yield components in garden pea (*Pisum sativum* L.) by using correlation and path analysis. *J. Agric. Res.* **36:** 351-360

Gomez and Gomez. (2010). Statistical Procedures for Agricultural Research, Second Edition, John Wiley Publication, U. K.

Javaid, A., Ghafoor, A. and Rashid, A. (2002). Evaluation of local and Exotic pea *Pisum sativum* germplasm for vegetable and dry grain traits. *Pak. J. Bot*. **34:**419-427.

Jeffers, J.N.R. (1967). Two case studies in the application of principal component analysis. *Appl. Stat.* **16:** 225–236.

Joshi, P.K., Narsinghani, V.G. and Yadav, R.K. (1992). Genetic variability and correlation studies of yield and its component in powdery mildew resistant field pea (*Pisum sativum* L. var. *arvense). Adv. Plant Sci.***5:**614–618.

Kumar, B. L., Ram, J.D. Singh and B. Singh. (2003). Correlation and path coefficient analyses in pea (*Pisum sativum* L.). *Prog. Agric.* **3:**141–142

Lezzoni, A.F. and Pritts, M.P. (1991). Application of principal component analysis to horticultural research. *Hort scie* **26:**334-338.

Mohammadi, S.A. and Prasanna, B.M. (2003). Analysis of genetic diversity in crop plants-salient statistical tools and considerations. *Crop Sci.,* **43:** 1235-1248.

Necat, T., Yesim, T., Bunyamin, Y. and Yusuf, D.(2008). Relationships between yield and some yield components in pea (*Pisum sativum ssp arvense* L.) genotypes by using correlation and path analysis. *Afr. J. Biotechnol.* **7:** 4285-4287.

Santalla. M., Amurrio, J.M. and De Ron A. M. (2001). Food and feed potential breeding of green, dry and vegetable pea germplasm. *Can. J. Plant Sci.* **81:** 601-610.

Sardana, S.R, Mahajan, K., Gautam, N. K. and Ram, B.(2007).Genetic Variability in pea (*Pisum sativum* L.) germplasm for utilization. *J. Plant Breed.Genet.* **39:**31-41.

Singh, A. K and Srivastava, C.P. (2015). Effect of plant types on grain yield and lodging resistance in Pea (*Pisum sativum* L.). *Indian J.Genet.* **75:**69-74.