***Pak. J. Bot.*, 41(6): 2987-2993, 2009.**

GENETIC DIVERSITY FOR DETERMINING YIELD POTENTIAL AND SELECTION CRITERIA IN *PISUM SATIVUM* L., GENETIC RESOURCES

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Abstract

Two hundred and sixty three genotypes of *Pisum sativum* were analyzed for numerical taxonomy to investigate inter and intra-cluster distances and superior accessions were identified with broad genetic base. High variance for grain yield per plant, biomass per plant and pods per plant indicated the scope of improvement through simple selection for high mean values for these traits. Based on average mean variance, five clusters with varying degrees on inter cluster distances were observed. Thirty-seven accessions of cluster-IV were early in maturity and high yielding, whereas 66 members of cluster-V were late in maturity and low yielding. Among selected genotypes, some exhibited better performance for more than two characters, hence these are suggested to evaluate under wide range of climatic conditions.

Introduction

Pea (*Pisum sativum* L.) of family *Papilionaceae,* is the second most important food legume world wide after *Phaseolus vulgaris* (Tar'an *et al*., 2005). Increasing demand of protein rich raw materials for feed and food has led to a greater interest in this crop as a protein source (Santalla *et al*. 2001). It is a cheap source of protein that is known as poor man meat in the developing world and used in rotation with cereals and oil seed crops. It provides balance diet in combination with wheat, rice and other cereals. It Pakistan it is cultivated under a wide range of agro-ecological regions, but the average yield per hectare is very low as compared with its potential and yield obtained in many other countries. It is cultivated during winter in plains of Pakistan and during summer in highlands (Nazir *et al.,* 1994) with area, production and yield of 903,000 ha, 524,000 t and 580 kg^{-1}, respectively (Anon., 2006).

The prime and long term objective of plant breeding is to increase productivity to meet the increasing food requirements of people. New varieties with improved agronomic traits have been the major contributing factor to increase food production. The estimate of genetic diversity and its relationship with germplasm collections and evaluation are useful for facilitating efficient germplasm collection, management and utilization (Nisar *et al*., 2008). Genetic diversity is a vital source of various disease resistant and high yielding genes hence crop improvement mainly depends on the extent of heritable diversity existing in crop species. Frequent use of few parents in breeding program led to the low genetic diversity among pea varieties (Baranger *et al*., 2004). Diverse genetic background provides desirable allelic variation among parental lines to produce new and valuable combinations (Tar'an *et al*., 2005). In order to develop high yielding and resistant varieties it is necessary to utilize the various existing genetic resources with minimum genetic erosion. It is practical to curb human activities for the prevention of genetic erosion. The only practical, though not ideal, solution to the problem of genetic erosion is collection and conservation of germplasm of cultivated plant species.

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The present study was conducted to investigate the extent of genetic diversity in pea germplasm sampled from a broad based collection during previous four years' evaluation under Agricultural Linkage Program (ALP) project. These accessions were sampled from various diverse groups based on agronomic performance or geographic origin. Selection from this material is expected to enhance mean average of pea cultivars without losing genetic diversity that will ultimately enhance the selection scope for the best cultivars.

Materials and Methods

Two hundred and sixty three genotypes of *Pisum sativum* were selected from a diverse collection from more than 50 countries preserved in genebank at Plant Genetic Resources Programme, NARC, Islamabad. The experiment was planted in an augmented design during winter season from October 2007 to April 2008 at National Agricultural Research Centre (NARC), Islamabad, Pakistan (33.40^o N and 73.07^o E, 540 masl). Two rows of 4 meter length for each genotype were planted with 10 cm intra-row spacing, whereas inter-row distance was kept 50 cm. Two varieties (Meteor and Green feast) were used as check after every twenty genotypes and recommended cultural practices were followed during evaluation without application of any chemical pesticide. Days to maturity were recorded at 90% maturity that was represented by a single value for each genotype. Pods plant^{-1}, grain yield plant^{-1} and biomass plant^{-1} were recorded on fifteen plants sampled randomly within each genotype. Harvest index was determined as economic yield expressed in percentage over total biomass.

Single plant data were analyzed for variation within and between genotypes for partitioning phenotypic, genetic and environmental components of variation for calculation of correlation and path coefficient using the computer software following the methods of Dewey & Lu, (1959). The averaged data were analyzed for numerical taxonomic to investigate inter and intra-cluster distances with the help of computer software "STATISTICA" for Windows XP. The mean performance of individual clusters was investigated to identify the best genotypes from various clusters for future utilization in pea improvement program.

Results

Results regarding the basic statistics for five quantitative traits in pea germplasm showed high variance for grain yield^{-1}, biomass plant^{-1} and pods plant^{-1} (Table 1). High magnitude of range coupled with variance (expressed as in percentage) indicated the scope of improvement through simple selection for these traits. Low genetic variance for days to maturity restricted the scope selection from this material. In general, genotypic correlation coefficients were higher as compared to phenotypic except for grain yield with pods plant^{-1} that indicated high environmental effects (Table 2). Biomass plant^{-1} exhibited significant genotypic correlation with pods plants^{-1} that indicated more reliability for this character in determining yield potential in pea. Grain yield had significant genotypic (0.76), phenotypic (0.78) and environmental correlation (0.79) with pods plant^{-1} and biomass plant^{-1} (g). Harvest index (%) had also significant association with pods plant^{-1} and grain yield plant^{-1}, whereas negatively correlated with biomass plant^{-1} that indicated the degree of influence of grain yield for determination of economic yield.

Table 1. Basic statistics for quantitative traits in *Pisum sativum* germplasm.

Variables	Mean ± SE	σ	σ^2 (%)	Range
Days to maturity	164 ± 0.20	3.30	2.00	159-172
Biomass plant^{-1} (g)	21.58 ± 0.74	11.97	55.46	3.60-120.00
Pods plant^{-1} (g)	13.7 ± 0.46	7.54	54.95	2.0-42.0
Grain yield plant^{-1} (g)	5.12 ± 0.19	3.01	58.78	0.52-15.98
Harvest index (%)	26.60 ± 0.70	11.43	42.96	2.60-67.50

Table 2. Genotypic (*rG*), phenotypic (*rP*) and environmental (*rE*) correlation among yield and yield components in *Pisum sativum* germplasm.

Variables		Pods plant^{-1}	Biomass plant^{-1}	Grain yield plant^{-1}
Biomass plant^{-1}	*rG*	0.62**		
	rP	0.52**		
	rE	0.46**		
Grain yield plant^{-1}	*rG*	0.76**	0.59**	
	rP	0.78**	0.53**	
	rE	0.79**	0.51**	
Harvest index	*rG*	0.32**	-0.19**	0.56**
	rP	0.20**	-0.17**	0.40**
	rE	0.13*	-0.17**	0.30**

Genotypic correlations were partitioned into direct and indirect effects through yield contributing characters towards grain yield (Table 3). Direct effects of all the three yield components *i.e*., pod plant^{-1}, biomass plant^{-1}, and harvest index were positive towards grain yield^{-1}. The highest direct effect (0.61) was found for harvest index followed by biomass plant^{-1} (0.58) and pods plant^{-1} (0.20). Positive direct effect contributed by all the three traits indicated their originality as yield components. Negative indirect effect of biomass (-0.11) through harvest index indicated the selection for genotypes accessions with optimum harvest index rather than very high keeping in consideration of biomass.

Genetic diversity: All the genotypes were categorized into five clusters using mean variances for linkage. Cluster-I consisted of 73 genotypes, cluster-II of 59, cluster-III of 28, cluster-IV of 37 and cluster-V has 66 genotypes (Table 4). High genetic distance (1.92) was observed between cluster-IV and cluster-V, whereas the lowest distance (0.76) was recorded between cluster-I and cluster-V (Table 5). These results indicate the scope of selection from various clusters for crop improvement with maximum diversity among improved cultivars. Mean values along with standard deviation of five clusters presented in the Table 6 revealed that the genotypes of cluster-IV were early maturing (161 days) and high yielding (9.49g), whereas the members of cluster-V were late in maturity (167 days) and low yielding (2.33 g). The genotypes grouped in cluster-I and III had medium yield potential with intermediate maturity and the genotypes in cluster-II were early in maturity (160 days) with low yield potential. On the basis of performance, the best genotypes were identified and are presented in Table 7. Twenty two genotypes matured within 160 days, 22 produced pods > 25 plant^{-1}, whereas 18 produced >10 g of grains plant^{-1}. Some of the genotypes were better for more than one character hence could be tested under wider range of climatic conditions to reduce varietal development span.

Table 3. Direct (highlighted) and indirect effects of three traits on grain yield in *Pisum sativum*.

Variables	**Pods plant^{-1}**	**Biomass plant^{-1}**	**Harvest index**	***r* with grain yield plant^{-1}**
Pods plant^{-1}	**0.20**	0.36	0.19	0.76
Biomass plant^{-1}	0.13	**0.58**	-0.11	0.59
Harvest index	0.07	-0.11	**0.61**	0.56

Table 4. The accessions of five clusters in *Pisum sativum* germplasm.

Cluster	***f***	**Accessions**
Cluster-I	73	10623, 002928, 009035, 009052, 012072, 018338, 018345, 018348, 018351, 018353, 019363, 019638, 019643, 019643-A, 019661, 019662, 019664, 019664-A, 019666, 019683, 019699, 019725, 019766, 019769, 019770, 019771, 019772, 019774, 019782, 020040, 020165, 020320, 10399, 10601, 10607, 10610, 10616, 10618, 10621, 10623, 10624, 10626, 10632, 10633, 10643, 10645, 10672, 10693, 109F, 110F, 11288, 11293, 112F, 11302, 11309, 11337, 11343, 11373, 11F, 27F, GEL001, GEL003, GEL004, GEL005, GEL009, GEL012, GEL013, GEL014, GEL016, GEL017, GEL018, GEL019, GEL025
Cluster-II	59	692, 2930, 2933, 2961, 3049, 9047, 10804, 16568, 002984, 009032, 009034, 009050, 009051, 009055, 010695, 018311, 018321, 018341, 018346, 018350, 018354, 018359, 018360, 018364, 018369, 018370-A, 019352, 019579, 019586, 019589, 019633, 019656, 019657, 019679, 019775, 019776, 019780, 019781, 10600, 10604, 10609, 10611, 10614, 10615, 10619, 10620, 10622, 10634, 10679, 10680, 10691, 11273, 11331, 11348, 11374, 11760-3, 15F, 3049-A, 41F
Cluster-III	28	10627, 10687, 19648, 018347, 018368, 018370, 019645, 019649, 019652, 019653, 019654, 019659, 019661-A, 019669-A, 019673, 019700, 019716, 10603, 10640, 11275, 11316, 11318, 11320, 11328, 11329, 11336, GEL024, GEL027
Cluster-IV	37	10603, 10607, 10608, 10629, 009055-A, 013250, 018314, 018315, 018327, 018355, 018356, 018377, 01876, 019598, 019641, 019669, 019698, 019707, 019729, 019777, 019783, 0511001, 10240, 10599, 10602, 10605, 10613, 10628, 10630, 10639, 10641, 10644, 10646, 10677, 11270, 11314, 11319
Cluster-V	66	002945, 009027, 009028, 009030, 009033, 009040, 009053, 009056, 0093036, 010617, 013210, 016602, 016607, 016660, 018347-A, 018357, 019599, 019667, 019671, 019688, 019700-A, 019778, 10608, 10617, 10625, 10627, 10629, 10631, 10636, 10637, 10642, 10692, 107F, 11274, 11295, 11298, 11300, 11305, 11310, 11313, 11321, 11323, 11332, 11338, 11339, 11372, 20F, 22F, 26F, 37F, 53F, 59F, GEL002, GEL006, GEL007, GEL008, GEL011, GEL015, GEL020, GEL021, GEL022, GEL023, GEL026, GEL028, GEL030, PSO10128

***f*- Frequency of genotypes**

Table 5. Inter-cluster distances in *Pisum sativum* germplasm.

Clusters	**Cluster-I**	**Cluster-II**	**Cluster-III**	**Cluster-IV**
Cluster-II	0.83			
Cluster-III	1.34	1.58		
Cluster-IV	1.28	1.18	1.16	
Cluster-V	0.76	1.15	1.64	1.92

Table 6. Individual cluster performance for five quantitative traits in *Pisum sativum* germplasm.

Characters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Days to maturity	166 ± 1.33	160 ± 1.12	165 ± 2.77	161 ± 2.43	167 ± 1.53
Biomass plant^{-1}	17.78 ± 6.01	15.77 ± 6.13	44.87 ± 16.53	26.13 ± 6.14	18.53 ± 8.23
Pods plant^{-1}	12.4 ± 4.55	11.9 ± 4.71	22.6 ± 7.74	23.2 ± 5.98	7.6 ± 3.58
Grain yield plant^{-1}	4.88 ± 1.65	4.24 ± 1.36	8.36 ± 2.74	9.49 ± 2.47	2.33 ± 1.17
Harvest index	29.74 ± 7.44	29.89 ± 9.23	21.49 ± 6.82	40.34 ± 9.07	14.65 ± 6.31

Table 7. Selected accessions for yield traits in *Pisum sativum*.

Trait of interest	Selection criterion	Accessions
Days to maturity	< 160 days	019707, 2930, 013250, 10644, 10629, 019352, 10641, 10646, 10639, 009055-A, 10677, 10630, 10613, 9047, 2961, 3049-A, 10620, 692, 11760-3, 3049, 10634, 019579
Pods plant^{-1}	> 25	10627, 018370, 10603, 10607, 018355, 019777, 009055-A, 009035, 019673, 10687, 11314, GEL024, 018314, 019698, 019783, 10644, 019659, 10630, 10608, 018356, 11329, 019700
Grain yield plant^{-1}	> 10 g	11314, 10607, GEL027, 019698, 019777, 018355, 11329, 10627, 018356, 019645, 018314, 019700, 10603, 11318, 10599, 019783, 019669-A, 11336
Biomass plant^{-1}	> 40 g	10640, 10627, 019659, 019661-A, 10603, 019653, 019673, 11329, 019669-A, GEL027, 11275, 10687, 11314, 019700, 11320, 019716, 11328, 10607, 018368
Harvest index	> 40 %	11270, 01876, 10644, 019777, 10604, 010695, 019683, 018359, 019638, 018356, 10680, 10672, 019641, 10240, 018315, 10619, 019669, GEL012, 018311, 10691, 11331, 10613, 3049, 11319, 10599, 10622, 11337, GEL001, 019729, 10602

Discussion

The primary objective of the study was to investigate the amount genetic diversity in a broad based pea germplasm. High variability for grain yield and biomass indicated the scope of improvement through simple selection that has been suggested in various legumes (Coulibaly *et al*., 2002). Heritable variation provides an estimate of diversity within and between genotypes (Sultana & Ghafoor 2008 and Qureshi *et al*., 2009). As the genotypes had broader genetic base and favourable alleles of economic importance were expected for selection of better germplasm for enhancing the capacity of breeding programmes. The best genotypes identified in the present study could serve preliminary base material for the researchers working on pea improvement program and the material is available for research purposes on request. Based on results, the traits of economic importance (grain yield and harvest index) showed high genetic variability, suggested to accelerate the breeding process in pea. Singh *et al*., (2007) presented information on basis of study of 40 advance lines and 5 varieties and observed high genotypic coefficient of variation for grain yield plant^{-1} and number of pods plant^{-1} in peas and also observed that biological yield plant^{-1}, harvest index and pods plant^{-1} were highly correlated with grain yield plant^{-1}. Sharma *et al*., (2007) observed grain yield plant^{-1} positively correlated with number of pods plant^{-1} and phenotypic and genotypic coefficients of variation of moderate magnitude for pods plant^{-1} and grain yield plant^{-1}. Arshad *et al*., (2006) reported similar results between number of pods plant^{-1} and grain yield in soybean.

The productivity of most of the grain crops depends upon harvest index. The germplasm, under study showed harvest index range from 14.6 to 40.3 that suggest good scope of selection for yield improvement in pea based on harvest index keeping grain yield in consideration (Ghafoor & Arshad, 2008). The present study revealed that the material under study had broad genetic base for pods plant^{-1}, grain yield and biomass. Eighteen genotypes identified for higher grain yield could be evaluated for dry pea production that will ultimately enhance grain legume productivity in the country as substitute of conventional pulses which are under serious threat due to many reasons. At present most of the pea crop is consumed as green pods in Pakistan, but due to high grain production in the identified genotypes this crop is suggested to evaluate for dry pea consumption as already utilized in most of the Mediterranean and European countries including USA (Javaid *et al*., 2002). As these accessions have significant variation for grain yield and pods per plant and due to this variation the selected accessions can potentially be utilized in the development of hybrids and other new high yielding varieties.

Acknowledgements

Authors acknowledge USDA, Nordic Gene bank and Centre for Genetic Resources, Netherlands for providing seed material for research purposes. This work is a part of ALP funded project under Agricultural Linkage Program and financial support is highly acknowledged.

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(Received for publication 24 December 2008)