

EVALUATION OF GENETIC DIVERSITY OF PEA GERMPLASM THROUGH PHENOTYPIC TRAIT ANALYSIS

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Abstract

Genetic diversity of 246 accessions of *Pisum sativum* L. collected from various localities of the world was evaluated at vegetative stages to ascertain the extent of genetic diversity and assess geographical heterogeneity among the germplasm. It was concluded that, high degree of allelic variation was present in seed coat color and seed shape. Descriptive statistical analysis revealed that considerable extent of genetic diversity was available for biological yield, number of locules per fresh pod, grain yield and harvest index. It was also observed that 100 seeds weight was positively correlated with all the observed parameters, but negatively correlated with number of seed per dry pod. Biomass proved high significance of correlation with number of locules per fresh pod, number of pod per plant and 100 seed weight. Harvest index correlated with all the traits except number of locules per fresh pod and biomass. Accessions with best performance were assorted for the desired parameters and communicated for its utilization in breeding programs.

Introduction

Pea [*Pisum sativum* L., family Papilionaceae, (Ali, 1977)] is a multipurpose crop cultivated as an integral part of cropping systems of 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. Pea is among the four important cultivated legumes next to soybean, groundnut and beans (Husle, 1994). It represents about 40% of the total trade in pulses. The major exporting countries, including the European Economic Commission (EEC) are Australia, Canada and USA (Oram & Agcaoili, 1994). In Pakistan it is cultivated under a wide range of agro-ecological regions, but the average/hectare yield 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). During 2005-06, the crop was grown over an area of 135600 ha with 81900 tones production of dry peas (Anon., 2006). Powdery mildew disease adversely affect the main yield of peas (Nisar *et al.*, 2006) causing 86% loss to the peas germplasm. Little attention has been given to varietals improvement of peas outside the temperate regions of developed countries including Pakistan. Keeping in view the importance of pea crop and the importance of its genetic diversity, the available germplasm was evaluated for economically important traits, phenotypic elaboration and their further utilization in the breeding programs.

Materials and Methods

The experiments were conducted during winter season 2004-2005 under field condition in institute of Agri-Biotechnology and Genetic Resources, National Agricultural Research Institute, Islamabad, Pakistan. Germplasm consisting of 246 accessions, collected/acquired from different parts of the world were characterized. Approved cultural practices were used for irrigation, pesticides and weeding etc. Data was recorded both on qualitative and quantitative traits for ten plants randomly sampled. The averages were analyzed for simple statistics.

Qualitative traits of the germplasm included cotyledon color, flower color, seed coat color, seed surface and seed shape. Whereas quantitative traits comprised of fresh pod length, fresh pod width, fresh pod thickness, fresh pod weight, number of locules per fresh pod, dry pod length, number of seeds per dry pod, 100 seeds weight, biomass, grain yield and harvest index. The mean value of each character for each accession was calculated and subjected to statistical analysis i.e., Standard deviation, variance, standard error and correlation coefficient, using statistical software, MINITAB, Microsoft Excel and STATISTICA.

Results and Discussion

Analysis of the basic data collected on the 12 continuously varying traits is given in Table 1, whereas the frequency distribution of the qualitative traits is provided in Fig. 1. Among these traits huge amount of variance had been recorded for biomass (Table 1). Considerable differences in variances were also recorded in the minimum and maximum values i.e., 9g to 452.6g, 0.16 to 50.60% and 2 to 503 for biomass, harvest index and number of locules/fresh, also exhibited sufficient amount of variation (Table 1)

The correlation coefficients among the quantitative traits (Table 2) revealed that the grain yield per plant was positively correlated with all the other traits except the 100 seeds weight which was negatively correlated with number of seeds per pod. After keen observation of all the traits and using different statistical analysis, the best performance and genetically diverse gene pools were selected (Table 3) for developing improved genotypes.

The results show that immense genetic diversity is present among the germplasm. As the phenotypic characterization is the first step toward the classification of crop germplasm (Smith *et al.*, 1991; Ghafoor *et al.*, 2003). It can very wisely be used for improvement of peas. During present study highest level of allelic variation among qualitative traits was observed in seed color and seed shape (Fig. 1). Considerable degree of allelic variation was observed for flower color, cotyledon color and seed surface as well. All these parameters are of much importance for description of the genotypes. As the quantitative traits are economically more important and are generally used for the improvement of the crop (Amurrio *et al.*, 1995), analysis revealed that high degree of variation in biomass, grain yield, number of pods per plant, 100 seeds weight and harvest index is available for crop improvement of the crop. Further higher variance for these traits indicates the importance of the germplasm for the further improvement through simple selection from these genotypes. The lower level of variance in the fresh pod length, fresh pod width, fresh pod thickness, fresh pod weight, dry pod length and number of seeds per pod might be due to the narrow genetic base of the germplasm.

Table 1. Basic data for 12 quantitative traits of 246 accessions of *Pisum sativum*.

Analysis	Mean ± SE	Stander variation	Variance	Min	Max
Fresh pod length	5.6 ± 0.1	1.1	1.3	3.46	9.06
Fresh pod width	11.0 ± 0.1	2.0	3.9	5.6	15.9
Fresh pod thickness	8.5 ± 0.1	1.9	3.7	3.08	12.88
Fresh pod weight	2.4 ± 0.1	1.3	1.6	0.44	7.14
Number of locules /FP	4.3 ± 0.2	2.8	7.6	1	9.4
Dry pod length	5.1 ± 0.1	1.0	0.9	2.94	8.02
Number of seeds /DP	4.6 ± 0.1	1.2	1.3	2.2	7.8
Number of pods per plant	57.2 ± 4.8	75.2	566.8	2	503
100 seeds weight	12.6 ± 0.3	5.2	26.9	3.03	31.6
Biomass	111.4 ± 8.6	134.3	1803.0	9	452.66
Grain Yield	20.9 ± 1.7	26.2	687.2	0.24	213.4
Harvest Index	22.9 ± 1.0	15.4	238.6	0.16	50.60

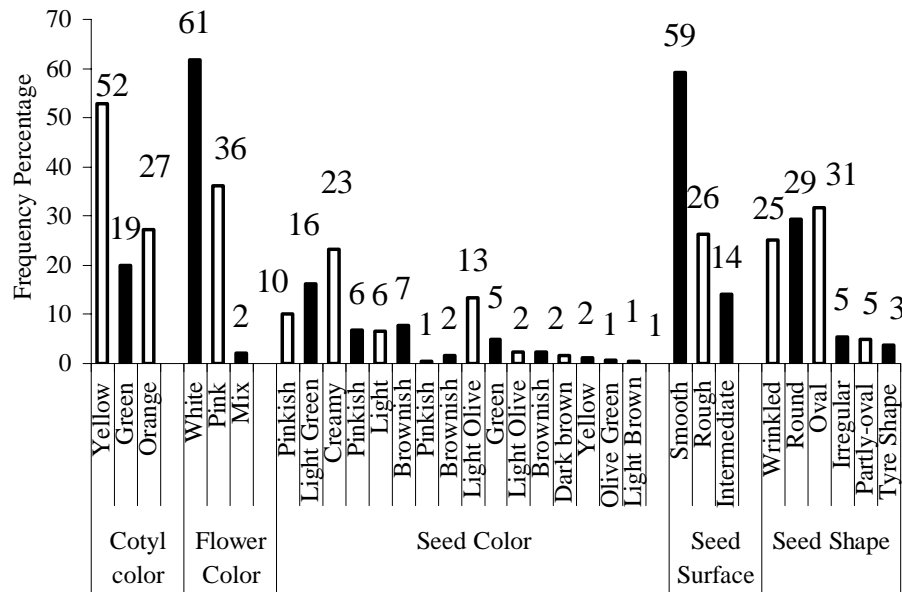


Fig. 1. Frequency Distribution of some qualitative traits among the genotypes

Genetic diversity in these traits can be improved by broadening gene pool through international sources, wide hybridization, mutation or other genetic modification. It is concluded that sufficient genetic diversity is available at phenotypic level which provide an opportunity for selecting designed traits. List of the better genotypes with respect to the traits evaluated is given in Table 3, seeds of all these germplasm are available on request from the first author.

Table 2. Correlation coefficient among 12 traits in the pea germplasm

Traits	FPL	FPWD	FPT	FPWt	NoI/FP	DPL	No.S/DP	NoP/PI	100SW	Biomass	GY
FPW	0.67***										
FPT	0.549***	0.77***									
FPWt	0.79***	0.70***	0.81***								
NoI/FP	0.42***	0.11	-0.16**	0.10							
DPL	0.68***	0.51***	0.43***	0.49***	0.32***						
No.S/DP	0.16**	-0.05	-0.09	0.13*	0.33***	0.13*					
NoP/PI	0.15**	0.04	0.02	0.07	0.37***	0.15**	0.18**				
100.S.W	0.52***	0.53***	0.52***	0.53***	0.21**	0.5***	-0.15*	0.23**			
B.mass.	0.17	0.028	-0.01	0.06	0.36***	0.07	0.07	0.47***	0.23***		
GY	0.30***	0.21**	0.27***	0.34***	0.28***	0.27***	0.19**	0.67***	0.45***	0.53***	
HI	0.14**	0.24***	0.43***	0.33***	-0.31***	0.20**	-0.04	0.08	0.40***	-0.22***	0.40***

FPL-Fresh Pod Length, FPWD- Fresh Pod Width, FPT- Fresh Pod Thickness, FPWt Fresh Pod Weight, NoI/FP- Number of Locules /FP, DPL- Dry Pod Length
 No.S/DP- Number of Seeds /DP, NoP/PI- Number of Pods per Plant,

Table 3. Best accessions for different genetic parameters.

Genetic parameter	Range		Accessions of best performance
Fresh pod length	8.14 - 9.06	cm	19679, 19710, 19637, 19654, 9051, 19638, 19684, 9050, 19704, 19639, 19644
Fresh pod width	14 - 15.9	mm	19669, 19644, 19637, 9051, 19711, 19715, 19662, 19756, 19792, 19701, 9046, 19686
Fresh pod thickness	11.0 - 12.8	mm	19768, 19711, 19644, 19637, 19783, 18306, 18387, 19641, 18343, 19775, 18368, 19686
Fresh pod weight	5.1 - 7.1	mg	19654, 18301, 19638, 19679, 19641, 19686, 19704, 19637, 19644, 19710, 19639
Number of locules per fresh pod	8 - 9.4	Number	19654, 19660, 18389, 19677, 19661, 19684, 19710, 19662, 19704, 19644, 19665, 19685, 19679, 18301
Dry pod length	6.8 - 8.02	cm	19638, 19681, 19722, 19662, 19733, 19710, 19665, 19690, 19707, 19791, 19711, 19684, 9051, 19654
Number of seeds per dry pod	7 - 8	Number	18377, 19671, 19724, 18394, 19676, 19675, 19677, 19709, 9051, 19722, 18379, 18410, 18301
100 seeds weight	20.5 - 31.6	g	19737, 19654, 19711, 19779, 19697, 18343, 19710, 19653, 19680, 19644, 19681, 19686, 19667
Biomass	> 350.5	g	19655, 19722, 19779, 19708, 19688, 19721, 19720, 19660, 18301, 18362
Grain yield	> 90.0	g	19668, 19653, 18301, 19654, 19656, 19779, 19662, 19660, 19673
Harvest index	48.6 - 50.6	% g	19737, 19775, 19772, 19771, 18343, 19780, 19784, 18372, 19756, 19751, 19652, 18337

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