Short Communication

Comparative investigation of genetic diversity in garden pea (*Pisum sativum* var. *hortense* L.) for yield and yield attributing characters

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Pisum sativum var. *hortense* L., the garden pea or green pea, belongs to the legume family, viz., fabaceae It is a cool season vegetable crop cultivated worldwide mainly for its immature seeds and pods for vegetable purpose as well as for various processed products. Being one of the world's oldest crops, it was domesticated over 9000 years ago and has been produced in association with cereals since that time (McPhee 2003). It is being recognized as a pivotal source of numerous nutrients like protein, carbohydrates, fibre, etc. along with vitamin A, B$_1$, B$_2$, and C. It is also rich in several non-nutritive biologically active components like phenols, tannins, alkaloids, flavonoids, protease inhibitors, phytic acid, etc. (Rungruangmaitree and Jiraungkoorskul 2017). Being a leguminous crop, it augments the soil nutrient status through the fixation of atmospheric nitrogen as well as acts an effective cover and thus checks soil erosion. With the exploitation of diversity in plant genetic resources, a wide window of opportunity for plant breeders can be opened to develop new and improved cultivars with desirable characteristics vis-à-vis both farmer as well as breeder-preferred traits. As well defined at the Rio de Janeiro Earth Summit, genetic diversity is the key pillar of biodiversity and diversity within species, between species, and of ecosystems (Govindaraj et al. 2015). For initiating any crop improvement program, variation in the existing germplasm is of high requisite. Maximization of genetic diversity among the parental lines is one of the major approaches in order to develop high yielding varieties. This is usually measured by the estimation of morphological and physiological differences. For various applications in plant breeding,

knowhow about the patterns and levels of genetic diversity can be considered as an essential aid. In order to accomplish the higher level of productivity, genetic diversity is important as it makes available the genetic building blocks for further development.

Keeping these points in concern, an experiment was designed and conducted at Vegetable Research Farm, Institute of Agricultural Sciences, BHU, Varanasi (UP) during the second fortnight of October 2012-13. The experimental material (seeds) of twenty-four genotypes of garden pea comprised of five commercial cultivars as checks, viz., Arkel, Kashi Mukti, Kashi Nandini, Kashi Shakti, and Kashi Udai; and nineteen germplasm accessions, viz., VRPMR-9, VRPMR-10, VRP-200, VRP-266, VRP-38, VRP-152, VRP-229, VRP-342, VRP-360, VRP-401, VRP-392, VRP-305, VRP-231, VRP-324, PC-531, AP-1, AP-2, VRP- 372, and VRP-4 were collected from ICAR-Indian Institute of Vegetable Research, Varanasi. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications of each genotype. The unit plot size was 4 m^2 (2 m × 2 m); and the pure and disease free seeds were sown in lines at a spacing of 30 cm × 10 cm. To attain a healthy crop stand, good agricultural practices were followed during the experiment. The observations were recorded from five randomly selected plants per replication for each genotype on various yield and yield contributing traits, viz., days to first flowering, days to 50% flowering, days to first pod initiation, number of pods per plant, average pod weight (g), number of seeds per pod, weight of seeds per pod (g), pod length (cm), pod width (cm), shelling (%), plant height (cm), number of primary branches per plant, TSS (^{0}Brix) and average pod yield per plant (g). Genetic divergence was estimated by using D^2 statistics (Mahalanobis, 1936) and grouping of the genotypes into various clusters was performed following Tocher's method as described by Rao (1952).

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Selection of genetically diverse parents based on the information about the genetic diversity and variability present in the germplasm is of high requisite for a successful breeding programme. Distribution of twenty-four genotypes of garden pea grouped into four clusters was presented in Table 1. Cluster I has accommodated highest number of genotypes (17) followed by cluster II (5) while cluster III and cluster IV consisted of 1 genotype each. Average intra- and inter-cluster distances for four clusters as presented in the Table 2 revealed that less divergence was there among the genotypes within a cluster while greater divergence was detected among the genotypes belonging to various clusters. The average intra-cluster distance was found to be highest in cluster II (10.25) followed by cluster I (9.08), whereas minimum distance (0.00) was recorded in both cluster III and cluster IV. This information reflected that cluster II which consisted of five genotypes, viz., VRP-4, Arkel, VRPMR-9, VRPMR-10, and VRP-342 was the most divergent.

Table 1: Clustering pattern of 24 genotypes of garden pea on the basis of genetic divergence

Cluster	Number of genotypes	Name of genotypes
I	17	VRP-266, VRP-152, VRP-229,VRP-360,VRP-305,VRP-401, VRP-231, VRP-200, VRP-324, PC-531, AP-1, VRP-38, VRP-392, VRP-372, Kashi Udai, Kashi Shakti, Kashi Mukti
II	5	VRP-4, Arkel, VRPMR-9, VRPMR-10, VRP-342
III	1	Kashi Nandini
IV	1	AP-2

Table 2: Average intra- (bold face) and inter-cluster distance among twenty-four garden pea genotypes

Cluster	I	II	III	IV
I	**9.08**	17.63	13.69	17.19
II		**10.25**	22.68	23.55
III			**0.00**	13.62
IV				**0.00**

Based on the inter-cluster distance, the maximum diversity was observed in between cluster II and IV (23.55) followed by cluster II and cluster III (22.68) revealing that genotypes belonging to above clusters are more divergent, hence, can be utilized for getting the superior recombinants in segregating generations in the hybridization programmes. From the cluster means of various economic traits (Table 3), cluster I had highest mean value for traits like number of pods per plant (12.8) and average pod yield per plant (69.4 g) whereas cluster II was observed to be superior for five traits, viz., average pod weight (6.3 g), number of seeds per pod

Table 3: Cluster means of 15 quantitative traits in garden pea

Traits	Cluster				
	I	II	III	IV	Overall mean
Days to first flowering	56.88	33.93	60.67	51.00	50.60
Days to 50% flowering	61.10	36.73	65.33	57.33	55.10
Days to first pod initiation	65.18	38.20	69.33	62.00	58.70
Number of pods per plant	12.84	8.72	10.20	10.47	10.60
Average pod weight (g)	5.44	6.32	3.69	5.18	5.20
Number of seeds per pod	6.99	7.14	6.07	5.47	6.40
Weight of seeds per pod (g)	2.89	2.91	2.01	1.87	2.40
Shelling (%)	52.90	47.35	54.29	36.36	47.70
TSS (^{0}Brix)	22.20	20.60	23.33	25.33	22.90
Plant height (cm)	60.51	50.25	101.33	130.33	85.60
Pod length (cm)	8.27	8.38	6.45	8.03	7.80
Pod width (cm)	1.36	1.47	1.33	1.37	1.40
No. of primary branches/plant	2.61	2.05	3.90	1.53	2.50
Average pod yield per plant (g)	69.42	53.31	37.45	53.83	53.50

(7.1), weight of seeds per pod (2.9 g), pod length (8.4 cm), and pod width (1.5 cm). Cluster III recorded highest values for the traits like days to first flowering (60.7), days to 50% flowering (65.3), days to first pod initiation (69.3), shelling percentage (54.3), and number of primary branches per plant (3.9). Cluster IV showed maximum TSS (^{0}Brix) and plant height (cm) with mean values of 25.33 and 130.33, respectively. The genotypes of cluster I and II can be used as prospective donors for their respective traits. Crosses can also be attempted among genotypes of these clusters for combining desirable traits. Genotypes of any cluster with high mean values can be directly or indirectly utilized for hybridization and/or for further selection. Similar studies on clustering pattern were carried out by Gupta et al. (2017), Kumar and Kumar (2016) and Katiyar and Dixit (2009).

The contribution of different traits towards the genetic divergence aids in the selection of suitable parents. Amongst the 14 characters studied, the important trait with highest contribution towards genetic divergence is days to first flowering (31.16%) followed by plant height (28.99%), average pod weight (25.72%) and weight of seeds per pod (7.61%) while remaining characters have negligible effect. These results are in accordance with the studies conducted by Singh and Singh (2006) and Gupta and Singh (2006). In conclusion, the maximum inter-cluster distance was observed between cluster II and IV. If crossing attempt was made between the genotypes of these clusters, it

may yield maximum heterosis or desirable segregants. Among the studied traits; days to first flowering, plant height, and average pod weight had the maximum contribution towards genetic diversity while other had negligible contribution towards genetic divergence. Therefore, it is clear that the estimation of genetic diversity can be essential for the selection of most efficient genotypes for developing suitable breeding strategies.

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