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SHORT COMMUNICATION

Genetic Diversity in Edible Podded Pea (*Pisum sativum* var. *saccharatum*)

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Thirty-six genotypes of snap pea were evaluated during winter 2016-17. D^2 analysis dispersed genotypes in seven polygenotypic clusters with maximum in cluster VI. Genotypes from clusters I and VII followed by II and VII would be paying preposition in hybridization programme with higher inter-cluster divergence. Cluster III showed the highest means for most of economic traits. Genotypes 'DPEPP-15-1', 'DPEPP-10-1', 'DPEPP-2', 'DPEPP-12-2', 'Arka Apoorva' and 'DPEPP-4-2' showed promise either directly as varieties or as potential parents in future breeding program.

Key Words: Cluster analysis, Edible podded pea *(Pisum sativum* var. *saccharatum)*, Genetic diversity, Genotypes, Hybridization, Selection

Edible podded pea is one of the popular, cool-season oriental vegetables that share the cultivation pattern with the garden pea. These are grown for their tender fresh pods that lack the parchment layer inside the pod. Edible-podded peas consist of snow pea (*Pisum sativum* var. *macrocarpon*) and sugar snaps/snap peas (*Pisum sativum* var. *saccharatum*) which can be eaten as whole pods. The combinations of two or three recessive genes contribute to make the whole pod suitable for consumption in the fresh stage (Myers *et al*., 2001). They are an excellent source of dietary fibre, folic acid, and vitamin C, rich in iron and manganese and a decent source of riboflavin, vitamin B_6, pantothenic acid, magnesium, phosphorus, potassium, vitamin A and vitamin K.

Since it is a recently introduced crop, and therefore, the most important task in edible pod pea breeding involves the development of high yielding varieties with stable productivity carrying resistance to diseases and unfavourable environmental conditions. Knowledge about levels and patterns of genetic diversity can be an invaluable source and introgression of desirable genes from variable germplasm into the existing genetic base, indicating thereby that the success in crop improvement through selection ultimately depend upon the genetic variability (Sharma *et al*., 2020). Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts on a smaller number of hybrid combinations (Fuzzato *et al*., 2002), providing better scope to isolate superior recombinants. Therefore, the breeder needs to identify the appropriate genotypes based on genetic divergence for the hybridization purpose. Keeping these points in view, the present investigation was undertaken to gather information on the genetic divergence in edible pod pea.

The experimental material comprised of 36 genotypes of which 29 are advanced breeding lines (F_7) and seven varieties from different institutes (Table 1). They were laid out in Randomized Complete Block Design with three replications in first week of November 2016 with inter and intra-row spacing of 45 cm and 10 cm, respectively. Observations were recorded on randomly selected ten plants of each genotype over the three replications for yield and related horticultural traits besides, quality parameters such as moisture content in seeds (%), total soluble solids for fresh seed (Brix), total soluble solids for whole pod (Brix), ascorbic acid (mg/100g), protein content (%) and total sugars (%) were also estimated by following standard procedures.

The analysis of variance revealed that mean squares due to genotypes were significant for all the traits. Thus, it highlighted the presence of sufficient genetic variability among the genotypes. The multivariate analysis (D^2) illustrated different clustering patterns by arranging 36 genotypes into seven clusters following Tocher's procedure (Fig. 1), and all of them were

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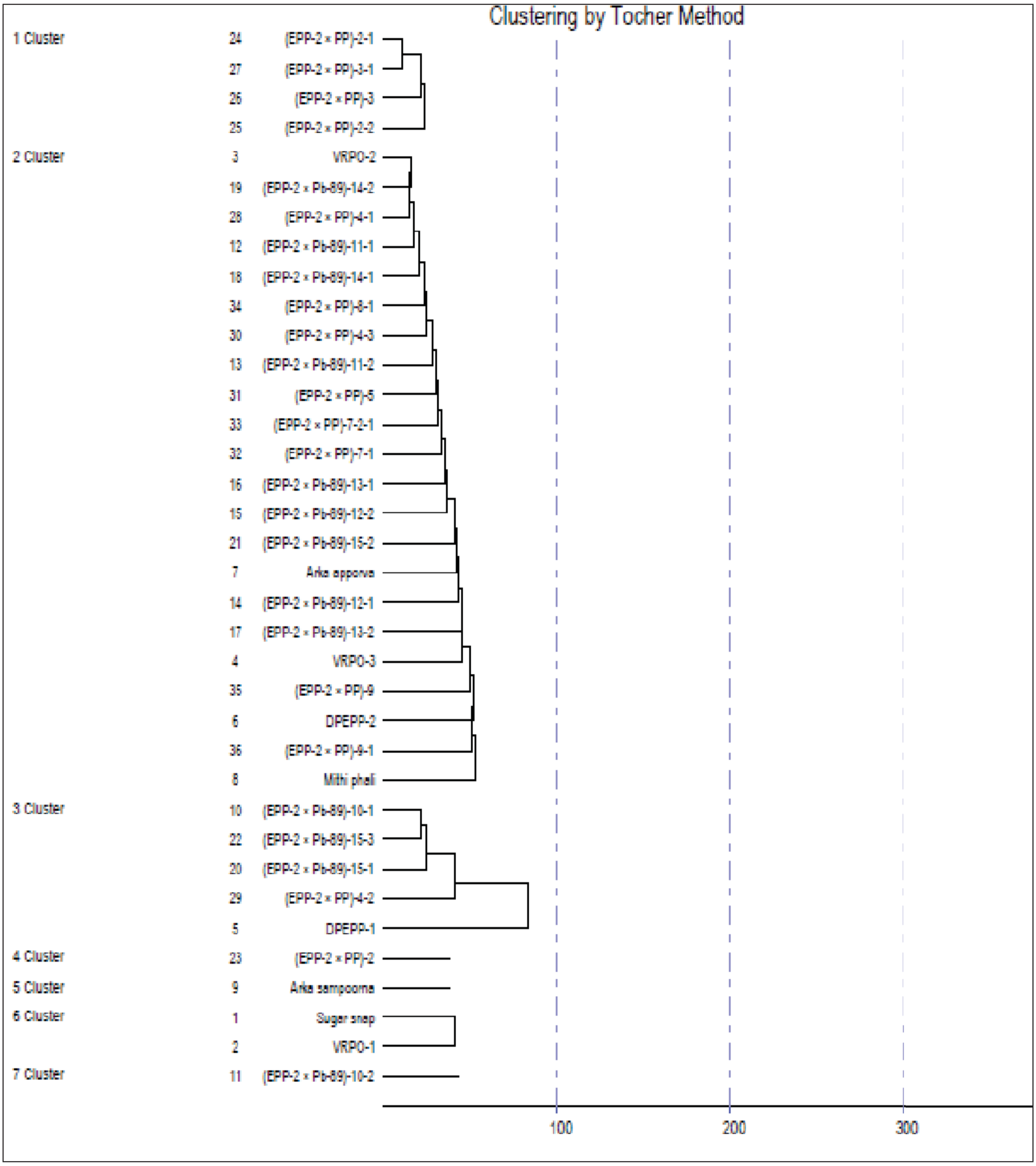

Fig. 1. Dendrogram showing grouping of 36 edible-podded pea genotypes based on D^2 statistics using Tocher's method

polygenotypic. Cluster VI was the largest, with nine genotypes constituting ¼th of the total genotypes. Similarly, clusters I, II and III contained six genotypes each while cluster VII contained five genotypes and clusters IV and V each contained only two genotypes suggesting the diverse origin of these genotypes. This suggests that genetic diversity is not always related to geographical diversity (Sekhon *et al.*, 2019).

The intra-cluster distance varied from 9.844 to 11.321, respectively highest in cluster VII, followed by

Table 1. Plant characteristic and source of genetic material

Genotype	Plant Characteristics	Source
DPEPP-2, DPEPP-10-1, DPEPP-10-2, DPEPP-11-1, DPEPP-11-2, DPEPP-12-1, DPEPP-12-2, DPEPP-13-1, DPEPP-13-2, DPEPP-14-1, DPEPP-14-2, DPEPP-P-2, DPEPP-P-2-1, DPEPP-P-2-2, DPEPP-P-3, DPEPP-P-3-1, DPEPP-P-4-1, DPEPP-P-4-2, DPEPP-P-4-3, DPEPP-P-5	Afilla type	Department of Vegetable Science & Floriculture, CSKHPKV, Palampur
DPEPP-15-1, DPEPP-15-2, DPEPP-15-3, DPEPP-P-7-1, DPEPP-P-7-2-1, DPEPP-P-8-1, DPEPP-P-9, DPEPP-P-9-1, DPDPEPP-1	Non-afilla plant, normal plant like garden pea	Department of Vegetable Science & Floriculture, CSKHPKV, Palampur
Arka Sampoorna, Arka Apoorva,	Non-afilla	Indian Institute of Horticultural Research, Hessarghata, Karnatka
Mithi Phali	Non-afilla	Punjab Agricultural University, Ludhiana, Punjab
Sugar Snap, VRPO-1, VRPO-2, VRPO-3	Non-afilla	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh

cluster V, I, IV, VI, III and II. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within-cluster would be low. Consequently, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance. The inter-cluster distance ranged from 148.266 to 801.751. The highest inter-cluster level genetic divergence was recorded between clusters I and VII followed by II and VII, IV and VII, V and VII and VI and VII. This specifies that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity, and selection of parents from these diverse clusters would be helpful in hybridization programme (Sharma *et al*., 2013).

The cluster means of different traits revealed substantial distinctions among the clusters for each trait (Table 2). Cluster III seemed to be the most important with the highest cluster means for most economic traits, namely, pod yield/plant, average pod weight,

Table 2. Cluster means for different characters in edible podded pea

Clusters/ Characters	C1	C2	C3	C4	C5	C6	C7	Mean
First flowering node	13.38	13.09	12.85	12.47	**11.53**	13.10	11.87	12.61
Days to Flowering	104.75	101.08	98.40	100.33	95.00	93.67	**91.67**	97.84
Days to First Picking	136.50	134.09	131.60	134.00	130.00	**128.00**	132.00	132.31
Number of branches/ plant	1.55	1.72	**1.96**	1.73	1.73	1.57	1.27	1.65
Internodal Length (cm)	8.03	5.98	6.25	8.64	**5.41**	9.92	5.57	7.11
Nodes/ plant	20.97	19.92	19.79	**21.93**	20.47	21.90	16.53	20.22
Plant Height (cm)	95.95	78.43	78.59	106.60	75.13	127.43	**67.40**	89.93
Pod Length (cm)	8.96	9.34	**10.00**	9.26	7.58	7.21	9.74	8.87
Pod Breadth (cm)	1.94	1.89	1.93	**2.02**	1.74	1.51	1.72	1.82
Seeds per Pod	5.76	6.16	**6.35**	5.50	4.60	5.70	6.30	5.77
Pods per Plant	19.70	16.24	18.33	15.72	**22.43**	19.14	8.58	17.16
Average Pod Weight (g)	4.51	4.49	**5.51**	4.71	2.85	3.33	5.13	4.36
Harvest Duration (days)	16.67	17.76	19.27	**21.00**	20.33	17.83	17.67	18.65
Moisture Content (%)	79.05	77.43	78.80	79.10	73.32	**80.20**	79.85	78.25
Total soluble solids (^{o}Brix) Seed	14.11	15.03	15.32	14.13	**15.47**	14.87	15.00	14.85
Total soluble solids (^{o}Brix) Pod	9.58	10.43	10.33	10.13	11.07	**11.67**	9.93	10.45
Ascorbic Acid (mg/100g)	24.18	24.72	24.61	23.87	22.94	23.87	**27.90**	24.58
Protein Content (%)	25.46	23.60	23.08	23.10	21.93	24.09	**28.23**	24.22
Total Sugars (%)	**8.83**	6.57	7.20	6.40	7.13	6.50	6.40	7.00
Pod Yield/ Plant (g)	88.67	72.81	**101.13**	74.00	62.67	64.67	44.00	72.56
Straw Yield/ plant (g)	14.04	26.10	26.96	21.50	**35.61**	20.38	19.17	23.39
100 Seed Weight (g)	25.33	23.29	23.07	20.00	22.67	22.33	**26.67**	23.34
Dry Pods/plant (g)	19.61	**23.49**	20.44	22.61	22.03	19.89	21.71	21.40
Harvest Index (%)	52.56	44.30	43.44	49.09	38.15	46.02	**55.87**	47.06
Seed Yield/ plant (g)	23.31	**26.49**	23.72	19.84	19.48	24.55	23.37	22.97

Where, C1 to C7 represents different clusters; bold values indicate highest mean pod length, seeds/pod and branches/plant. On the other hand, cluster VII with five genotypes recorded maximum cluster means for the quality traits, *i.e.* ascorbic acid and protein content and 100 seed weight and harvest index. Different clusters of genotypes based on means revealed divergence for other characters and thereby can be utilized as indicators for selecting diverse parents for a specific trait in hybridization programmes (Sekhon *et al*., 2019). Apart from selecting genotypes from the clusters that have higher inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence regarding a character of interest (Gemechu *et al*., 2005). Straw yield per plant contributed a maximum (22.06%) towards total genetic divergence followed by average pod weight (16.19), total sugars (12.86) and pod yield per plant (12.06).

The selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters. Therefore, it could be suggested that crossing should be made between genotypes belonging to distance clusters. Accordingly, genotypes viz.,'DEPP-15-1', and 'DEPP-15-3' from the cluster II along with other top performing genotypes namely, 'DEPP-10-1', 'DPEPP-2'and 'DEPP-14-2'offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants.

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